

Table S4. Gene Ontology (GO) enrichment analysis results for FBXO32-associated genes in neuroblastoma. The table lists GO terms, their IDs, descriptions, set sizes, enrichment scores, NES values, p-values, adjusted p-values, q-values, and ranked list statistics.

Category	GO ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalue	rank
CC	GO:0062023	collagen-containing extracellular matrix	419	0.622359334752938	3.4038177534				
BP	GO:0006261	DNA-templated DNA replication	153	-0.678254245220459	-3.34174712567727				
CC	GO:0098687	chromosomal region	320	-0.610966238100794	-3.32816319160539	1e-10		1.572	
BP	GO:0007059	chromosome segregation	313	-0.6050581038997	-3.28739688219756	1e-10		1.5	
CC	GO:0000775	chromosome, centromeric region	196	-0.636180903459182	-3.28352664120749				
MF	GO:0005201	extracellular matrix structural constituent	169	0.663807250727674	3.27706144				
CC	GO:0000228	nuclear chromosome	193	-0.638526548556083	-3.27521971900732	1e-10		1.57	
BP	GO:0006260	DNA replication	269	-0.606106630248585	-3.2514951331265	1e-10		1.572	14700
BP	GO:0030198	extracellular matrix organization	296	0.616250388110422	3.24528853002795	1e-10		1.5	
BP	GO:0045229	external encapsulating structure organization	299	0.614664545358549	3.24159				
BP	GO:0043062	extracellular structure organization	297	0.614681542847434	3.2375966084512				
BP	GO:0098813	nuclear chromosome segregation	256	-0.606386922160187	-3.23407149205547				
CC	GO:0000793	condensed chromosome	232	-0.613151639853428	-3.19780065195442	1e-10		1	
BP	GO:0000819	sister chromatid segregation	186	-0.625412319003262	-3.18264193380175	1e-10		1.5	
CC	GO:0000779	condensed chromosome, centromeric region	144	-0.647731103086135	-3.1759				
CC	GO:0000776	kinetochore	136	-0.653537392075658	-3.15248565991341	1e-10		1.572	1470019
BP	GO:0000725	recombinational repair	152	-0.636918480625387	-3.13808776759982	1e-10		1.5	
BP	GO:0000070	mitotic sister chromatid segregation	161	-0.630172061727385	-3.12963265724				
BP	GO:0000724	double-strand break repair via homologous recombination	151	-0.63455968071					
BP	GO:0044786	cell cycle DNA replication	42	-0.795322747005784	-3.08673240525602	1e-10		1	
BP	GO:0006302	double-strand break repair	245	-0.582825419856659	-3.0829465559551	1e-10		1.5	
MF	GO:0140097	catalytic activity, acting on DNA	209	-0.593158257556677	-3.07662559499412				
BP	GO:0006281	DNA repair	476	-0.541134386310469	-3.07518665502321	1e-10		1.572	1470019
CC	GO:0005788	endoplasmic reticulum lumen	302	0.575942608408233	3.04802437760188	1e-10		1	
BP	GO:0001525	angiogenesis	493	0.543056425889894	3.02576175281783	1e-10		1.572	1470019
CC	GO:0005681	spliceosomal complex	186	-0.589935223260674	-3.00210360865361	1e-10		1.57	
BP	GO:0006397	mRNA processing	448	-0.528628003336172	-2.98669970945775	1e-10		1.572	14
MF	GO:0003697	single-stranded DNA binding	110	-0.643899474023831	-2.98432958365754	1e-10		1	
CC	GO:0044815	DNA packaging complex	95	-0.658417160627749	-2.98023132273986	1e-10		1.5	
BP	GO:0034508	centromere complex assembly	27	-0.857947117795112	-2.970026939409	1e-10		1	
BP	GO:0033260	nuclear DNA replication	37	-0.783546107817597	-2.96795901100464	1e-10		1.5	
BP	GO:0032392	DNA geometric change	90	-0.659847848671167	-2.9652827323786	1e-10		1.572	
CC	GO:0043202	lysosomal lumen	94	0.658454518514221	2.95922460182099	1e-10		1.572	14700
BP	GO:0000375	RNA splicing, via transesterification reactions	285	-0.551185837629448	-2.95708				
BP	GO:0033044	regulation of chromosome organization	199	-0.571106027474003	-2.954767103				
MF	GO:0005518	collagen binding	66	0.696978279755082	2.95468439034708	1e-10		1.572	14700
BP	GO:0006310	DNA recombination	286	-0.548314100848004	-2.95051691690399	1e-10		1.572	
BP	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleoph							
BP	GO:0000398	mRNA splicing, via spliceosome	281	-0.548744640688874	-2.94992327302477	1e-10		1	
CC	GO:0034708	methyltransferase complex	90	-0.656139369182598	-2.94861723863943	1e-10		1	
MF	GO:0008094	ATP-dependent activity, acting on DNA	98	-0.644036074883475	-2.9481474961				
BP	GO:0071103	DNA conformation change	97	-0.645332301935039	-2.93959692514304	1e-10		1	
BP	GO:0030199	collagen fibril organization	60	0.701140502051849	2.92209966088922	1e-10		1	
BP	GO:0043542	endothelial cell migration	205	0.575709380671545	2.90433902869018	1e-10		1	
BP	GO:0060326	cell chemotaxis	292	0.552380731138604	2.90413841284953	1e-10		1.572	14700
BP	GO:0008380	RNA splicing	393	-0.521298636842423	-2.9031698660085	1e-10		1.572	1470019
MF	GO:0050840	extracellular matrix binding	52	0.711911003794127	2.89763094001728	1e-10		1	
BP	GO:0030335	positive regulation of cell migration	494	0.518998802688569	2.891429451704	1e-10		1	

BP,"GO:0071824","protein-DNA complex subunit organization",158,-0.583141222817997,-2.8877771

BP,"GO:0006270","DNA replication initiation",38,-0.761594096240409,-2.8798325311026,1e-10,1.5

BP,"GO:0002685","regulation of leukocyte migration",208,0.569975297806895,2.87498719095247,1e-10,1.5

BP,"GO:0031589","cell-substrate adhesion",350,0.536827751507158,2.87122686055958,1e-10,1.57

BP,"GO:0010594","regulation of endothelial cell migration",158,0.586128439095999,2.86958583664

BP,"GO:0051304","chromosome separation",92,-0.633893556786981,-2.86553428036644,1e-10,1.5

BP,"GO:0042060","wound healing",409,0.524673933946681,2.86448410013393,1e-10,1.572147001

BP,"GO:0032835","glomerulus development",65,0.677245391495689,2.86112019096435,1e-10,1.57

CC,"GO:0005604","basement membrane",93,0.638002738269951,2.86098606750537,1e-10,1.57214

BP,"GO:0085029","extracellular matrix assembly",45,0.724080178265197,2.85173621632665,1e-10

CC,"GO:0032432","actin filament bundle",70,0.666165315116303,2.85061241946885,1e-10,1.57214

BP,"GO:0051983","regulation of chromosome segregation",85,-0.640603848530124,-2.85016536541

BP,"GO:0065004","protein-DNA complex assembly",125,-0.598209149930554,-2.84788204825986,1

BP,"GO:0090329","regulation of DNA-templated DNA replication",51,-0.700725798354313,-2.84587

BP,"GO:0032508","DNA duplex unwinding",84,-0.641499161257482,-2.84255113468504,1e-10,1.57

CC,"GO:0001725","stress fiber",64,0.674019744494303,2.84026480389238,1e-10,1.5721470019342

CC,"GO:0097517","contractile actin filament bundle",64,0.674019744494303,2.84026480389238,1e-10,1.5721470019342

MF,"GO:0003678","DNA helicase activity",67,-0.662638603553307,-2.83089475784096,1e-10,1.572

CC,"GO:0000781","chromosome, telomeric region",136,-0.586218432858879,-2.82775741001608,1

BP,"GO:0003158","endothelium development",121,0.605864032471868,2.82775101285936,1e-10,1

BP,"GO:0140014","mitotic nuclear division",278,-0.52595113214848,-2.8232557914256,1e-10,1.572

CC,"GO:0005657","replication fork",55,-0.683867723890169,-2.82243038498013,1e-10,1.57214700

BP,"GO:0061448","connective tissue development",243,0.548307751382286,2.8207300587405,1e-10,1.57214700

BP,"GO:0050900","leukocyte migration",365,0.524596768781912,2.81823300661783,1e-10,1.57214

BP,"GO:0010965","regulation of mitotic sister chromatid separation",63,-0.667539135176098,-2.814

CC,"GO:0071013","catalytic step 2 spliceosome",85,-0.632369796828526,-2.81353054182317,1e-10

BP,"GO:0007091","metaphase/anaphase transition of mitotic cell cycle",61,-0.668989522923678,-2.

MF,"GO:0005178","integrin binding",147,0.582963710515793,2.81163515849438,1e-10,1.57214700

BP,"GO:0051306","mitotic sister chromatid separation",66,-0.661591584680148,-2.80992486973951

CC,"GO:0070603","SWI/SNF superfamily-type complex",84,-0.633529146049476,-2.8072351481004

CC,"GO:1904949","ATPase complex",85,-0.630796094060983,-2.8065288462608,1e-10,1.57214700

BP,"GO:0000280","nuclear division",414,-0.500302031924503,-2.80241288820852,1e-10,1.5721470

BP,"GO:0030595","leukocyte chemotaxis",222,0.551159276972962,2.80180949180619,1e-10,1.572

MF,"GO:0019838","growth factor binding",131,0.592241703494975,2.7996224019082,1e-10,1.5721

BP,"GO:0006338","chromatin remodeling",191,-0.547993031981991,-2.79874139443776,1e-10,1.57

CC,"GO:0031248","protein acetyltransferase complex",92,-0.618415842242912,-2.79556682110946

CC,"GO:1902493","acetyltransferase complex",92,-0.618415842242912,-2.79556682110946,1e-10,1

BP,"GO:0030071","regulation of mitotic metaphase/anaphase transition",59,-0.672113678672259,-2.

CC,"GO:0000123","histone acetyltransferase complex",82,-0.634291979831441,-2.79133890063953

BP,"GO:1901342","regulation of vasculature development",266,0.534746153144973,2.78296970242

BP,"GO:0022613","ribonucleoprotein complex biogenesis",387,-0.499198889631821,-2.7771832403

CC,"GO:0035097","histone methyltransferase complex",62,-0.659872584746521,-2.7771168441770

BP,"GO:0033045","regulation of sister chromatid segregation",70,-0.646849144930893,-2.77405400

BP,"GO:0045765","regulation of angiogenesis",262,0.533012130454727,2.7724433776307,1e-10,1.5

BP,"GO:0090130","tissue migration",291,0.527084581294338,2.77164030180329,1e-10,1.57214700

BP,"GO:0034502","protein localization to chromosome",82,-0.628605112787101,-2.7663126135219

BP,"GO:0071674","mononuclear cell migration",188,0.552810317079945,2.76603295704042,1e-10,

BP,"GO:0072006","nephron development",144,0.576534728664412,2.76570037505257,1e-10,1.572

BP,"GO:0097529","myeloid leukocyte migration",214,0.544688517017121,2.76452165898839,1e-10,

BP,"GO:0051216","cartilage development",183,0.554766226009549,2.76390955979416,1e-10,1.572

BP,"GO:0006325","chromatin organization",490,-0.484167692023634,-2.75825175679605,1e-10,1.5

BP,"GO:0043534","blood vessel endothelial cell migration",111,0.597758098269651,2.75618766216

MF,"GO:0003684","damaged DNA binding",66,-0.648862727981788,-2.75586261769722,1e-10,1.57

BP,"GO:0010632","regulation of epithelial cell migration",217,0.542274076220805,2.754849386510

BP,"GO:0043535","regulation of blood vessel endothelial cell migration",86,0.620262438150744,2.7

BP,"GO:0001503","ossification",386,0.506637430060968,2.74901166948668,1e-10,1.572147001934

BP,"GO:0090132","epithelium migration",286,0.52617080959481,2.74511293895521,1e-10,1.57214

BP,"GO:0010631","epithelial cell migration",283,0.526097067206565,2.74509259502667,1e-10,1.57

BP,"GO:0061437","renal system vasculature development",28,0.782876872342728,2.743584169859

BP,"GO:0061440","kidney vasculature development",28,0.782876872342728,2.74358416985983,1e

BP,"GO:0051383","kinetochore organization",21,-0.847850362730066,-2.74239153662092,1e-10,1.!

CC,"GO:0005925","focal adhesion",411,0.501328764929626,2.74134135292358,1e-10,1.572147001

CC,"GO:0005684","U2-type spliceosomal complex",88,-0.610787863467494,-2.74102889362291,1e-

BP,"GO:0042116","macrophage activation",97,0.606289012497379,2.74035410735383,1e-10,1.5721

CC,"GO:0005775","vacuolar lumen",166,0.556727722425949,2.73909011454886,1e-10,1.57214700

MF,"GO:0140375","immune receptor activity",141,0.57228897798931,2.73695622762802,1e-10,1.5

BP,"GO:0032637","interleukin-8 production",83,0.618619779588927,2.7366696257845,1e-10,1.572

BP,"GO:0007596","blood coagulation",218,0.538503565389158,2.73570194253907,1e-10,1.5721470

CC,"GO:0030055","cell-substrate junction",419,0.500015571201311,2.73469326029891,1e-10,1.572

BP,"GO:1902099","regulation of metaphase/anaphase transition of cell cycle",62,-0.6495227844570

BP,"GO:0002062","chondrocyte differentiation",102,0.597747403335608,2.73167990706396,1e-10,

BP,"GO:0044784","metaphase/anaphase transition of cell cycle",64,-0.645474051622828,-2.730215

BP,"GO:1903053","regulation of extracellular matrix organization",46,0.691672840163268,2.727496

BP,"GO:1905818","regulation of chromosome separation",70,-0.635659791451481,-2.72606774158

BP,"GO:0007599","hemostasis",224,0.535513667178771,2.72569845922004,1e-10,1.572147001934

BP,"GO:0032677","regulation of interleukin-8 production",82,0.619698486457508,2.7245143680298

BP,"GO:0032963","collagen metabolic process",91,0.606396502931777,2.7191225176142,1e-10,1.5

BP,"GO:0001570","vasculogenesis",79,0.621487300869052,2.71486998796527,1e-10,1.5721470019

BP,"GO:0007160","cell-matrix adhesion",227,0.53211357935435,2.71416032979033,1e-10,1.57214

BP,"GO:0070374","positive regulation of ERK1 and ERK2 cascade",200,0.539270390161498,2.71230

BP,"GO:0006275","regulation of DNA replication",127,-0.566078538874935,-2.70724807504295,1e-

BP,"GO:0050817","coagulation",222,0.532423721814822,2.70656759265022,1e-10,1.57214700193

BP,"GO:0001667","ameboidal-type cell migration",402,0.494770108366297,2.70127534437796,1e-1

BP,"GO:0045446","endothelial cell differentiation",105,0.589955958484886,2.70056550474625,1e-

CC,"GO:0042641","actomyosin",71,0.630794207141427,2.69859502337903,1e-10,1.572147001934

MF,"GO:0042393","histone binding",238,-0.512857044473502,-2.69829511014369,1e-10,1.5721470

MF,"GO:0017116","single-stranded DNA helicase activity",23,-0.818344455753867,-2.696935931248

BP,"GO:0035150","regulation of tube size",138,0.566649771590523,2.69484806260126,1e-10,1.572

CC,"GO:0097525","spliceosomal snRNP complex",56,-0.653159990917088,-2.69196254815951,1e-1

BP,"GO:0050921","positive regulation of chemotaxis",138,0.564791451695029,2.68601034657076,1

CC,"GO:0005581","collagen trimer",85,0.606136520774361,2.68505861427534,1e-10,1.5721470019

BP,"GO:0048285","organelle fission",456,-0.474086309821811,-2.68497349774254,1e-10,1.5721470

BP,"GO:0061138","morphogenesis of a branching epithelium",182,0.539601805700325,2.684086658

BP,"GO:0035296","regulation of tube diameter",137,0.564312484477937,2.67869423570986,1e-10,

BP,"GO:0097746","blood vessel diameter maintenance",137,0.564312484477937,2.6786942357098

BP,"GO:0007051","spindle organization",178,-0.529130928663706,-2.67688893698307,1e-10,1.572

BP,"GO:0050818","regulation of coagulation",70,0.624163706583307,2.67088179674659,1e-10,1.57

BP,"GO:0072009","nephron epithelium development",111,0.57873101734587,2.66845617706758,1

BP,"GO:0071347","cellular response to interleukin-1",105,0.582326011675317,2.665638878681,1e-

BP,"GO:0048002","antigen processing and presentation of peptide antigen",58,0.645690560312346,

BP,"GO:0010634","positive regulation of epithelial cell migration",140,0.556148037108621,2.663909

BP,"GO:0030336","negative regulation of cell migration",255,0.516209920613018,2.6631686583387

BP,"GO:0010595","positive regulation of endothelial cell migration",98,0.588642186866621,2.66196

BP,"GO:0002274","myeloid leukocyte activation",218,0.523774387944655,2.66087488114754,1e-10

CC,"GO:0071011","precatalytic spliceosome",51,-0.65471534372814,-2.65901320882207,1e-10,1.57

MF,"GO:0031491","nucleosome binding",49,-0.660932896011007,-2.65717314341818,1e-10,1.5721

BP,"GO:0043410","positive regulation of MAPK cascade",464,0.480275605954134,2.6566139162059

BP,"GO:0048660","regulation of smooth muscle cell proliferation",132,0.560781346335085,2.65517

BP,"GO:0050673","epithelial cell proliferation",383,0.490007800078196,2.65467918680566,1e-10,1

BP,"GO:0002687","positive regulation of leukocyte migration",137,0.559137576896156,2.65412984

BP,"GO:2001251","negative regulation of chromosome organization",83,-0.602915304107781,-2.65

BP,"GO:0010569","regulation of double-strand break repair via homologous recombination",62,-0.6

BP,"GO:0002237","response to molecule of bacterial origin",326,0.498118442333485,2.6507087275

BP,"GO:0032611","interleukin-1 beta production",92,0.591763857482154,2.64916289106304,1e-10

BP,"GO:0032651","regulation of interleukin-1 beta production",92,0.591763857482154,2.64916289

CC,"GO:0000792","heterochromatin",62,-0.629467801430565,-2.64915632900771,1e-10,1.5721470

BP,"GO:0070555","response to interleukin-1",131,0.560213685914763,2.64822077825163,1e-10,1.5

BP,"GO:0001818","negative regulation of cytokine production",263,0.50946305098841,2.647493821

BP,"GO:0022618","ribonucleoprotein complex assembly",157,-0.53271526590369,-2.645055821359

BP,"GO:0045785","positive regulation of cell adhesion",427,0.482600253514735,2.64430422094422

CC,"GO:0009897","external side of plasma membrane",365,0.492177712205557,2.64407170650338

BP,"GO:0048754","branching morphogenesis of an epithelial tube",151,0.543616046646689,2.64290

BP,"GO:0030193","regulation of blood coagulation",66,0.622576988492242,2.6392766648822,1e-10

CC,"GO:0071005","U2-type precatalytic spliceosome",49,-0.656201983540234,-2.63815327977231,

BP,"GO:0045766","positive regulation of angiogenesis",155,0.54051005441914,2.6374218469493,1e

BP,"GO:1904018","positive regulation of vasculature development",155,0.54051005441914,2.63742

BP,"GO:0033002","muscle cell proliferation",183,0.529303080822906,2.63704922276531,1e-10,1.5

CC,"GO:0000922","spindle pole",160,-0.531220843095194,-2.63646413867923,1e-10,1.5721470019

CC,"GO:0005814","centriole",129,-0.549875433094086,-2.63411543766369,1e-10,1.572147001934

CC,"GO:0120114","Sm-like protein family complex",76,-0.606603100943878,-2.63225294560756,1e

BP,"GO:0071826","ribonucleoprotein complex subunit organization",165,-0.528816204963591,-2.63

BP,"GO:0022612","gland morphogenesis",122,0.562357127110109,2.62546991205093,1e-10,1.572

BP,"GO:0032496","response to lipopolysaccharide",310,0.493906505875918,2.6246296231897,1e-1

BP,"GO:0001763","morphogenesis of a branching structure",196,0.522174452678657,2.6204671590

MF,"GO:0008083","growth factor activity",154,0.537649765554506,2.62046505221289,1e-10,1.572

BP,"GO:0033627","cell adhesion mediated by integrin",82,0.596000255621078,2.62032471480057,1

BP,"GO:0048659","smooth muscle cell proliferation",134,0.551622765173377,2.62008982338803,1e

BP,"GO:0001704","formation of primary germ layer",117,0.563703545989144,2.62003775437168,1e

CC,"GO:0030532","small nuclear ribonucleoprotein complex",65,-0.617853732393073,-2.617819295

BP,"GO:0050920","regulation of chemotaxis",213,0.515776784481514,2.61589499074735,1e-10,1.5

CC,"GO:0072686","mitotic spindle",151,-0.532951206698377,-2.61520105438788,1e-10,1.57214700

BP,"GO:0030168","platelet activation",129,0.555098299378977,2.61497939026345,1e-10,1.572147

BP,"GO:0019221","cytokine-mediated signaling pathway",457,0.473039656975594,2.614413256658

BP,"GO:0032635","interleukin-6 production",140,0.545362368978785,2.61224675011869,1e-10,1.5

BP,"GO:0032675","regulation of interleukin-6 production",140,0.545362368978785,2.612246750118

BP,"GO:0110148","biomineralization",162,0.531855181441634,2.61084329408726,1e-10,1.5721470

BP,"GO:0002548","monocyte chemotaxis",65,0.617030559481814,2.60673400564097,1e-10,1.5721

BP,"GO:0060191","regulation of lipase activity",86,0.58732037756173,2.60561685594796,1e-10,1.5

BP,"GO:0034728","nucleosome organization",84,-0.587686197884828,-2.60410016025843,1e-10,1.5

MF,"GO:0019955","cytokine binding",138,0.54754427766507,2.6039869948459,1e-10,1.572147001

BP,"GO:0003018","vascular process in circulatory system",258,0.501956647949367,2.603767645555

BP,"GO:0072073","kidney epithelium development",140,0.542979468144595,2.60083282551728,1e-1

BP,"GO:0034341","response to interferon-gamma",136,0.546575244559807,2.6007706086823,1e-1

BP,"GO:0071219","cellular response to molecule of bacterial origin",205,0.515396125263776,2.6000

BP,"GO:0031214","biomineral tissue development",160,0.530572441982516,2.59974312800414,1e-

BP,"GO:1900046","regulation of hemostasis",68,0.611307637870022,2.59856059163096,1e-10,1.57

BP,"GO:0048771","tissue remodeling",161,0.528924386030958,2.59823608453842,1e-10,1.5721470

BP,"GO:0061041","regulation of wound healing",121,0.556216861602351,2.59603262360443,1e-10

BP,"GO:0031497","chromatin assembly",128,-0.541883788850124,-2.59453287662575,1e-10,1.5721

BP,"GO:0070371","ERK1 and ERK2 cascade",305,0.491457793345883,2.59423166161097,1e-10,1.57

BP,"GO:2000146","negative regulation of cell motility",270,0.498047144263441,2.58850198059866,

MF,"GO:0004386","helicase activity",149,-0.527439969673785,-2.58686623454185,1e-10,1.5721470

CC,"GO:0005819","spindle",380,-0.464822171499657,-2.58424343866702,1e-10,1.57214700193424

BP,"GO:0110149","regulation of biomineralization",95,0.573293474038628,2.58409446302811,1e-1

BP,"GO:0002688","regulation of leukocyte chemotaxis",119,0.554859548666136,2.58120586062277

BP,"GO:0000075","cell cycle checkpoint signaling",161,-0.519599427529073,-2.58049417904112,1e-

BP,"GO:0006282","regulation of DNA repair",132,-0.537430548467276,-2.58030956228746,1e-10,1.

BP,"GO:0046718","viral entry into host cell",141,0.539116620558148,2.57831034460698,1e-10,1.57

BP,"GO:0014068","positive regulation of phosphatidylinositol 3-kinase signaling",77,0.59317979484

BP,"GO:0019882","antigen processing and presentation",101,0.5653371273893,2.5751610209104,1

BP,"GO:0030278","regulation of ossification",110,0.560006699047149,2.57508375514947,1e-10,1.5

BP,"GO:0050878","regulation of body fluid levels",375,0.476464998359215,2.57478685205791,1e-1

BP,"GO:0002683","negative regulation of immune system process",394,0.472768069357335,2.5747

BP,"GO:0061982","meiosis I cell cycle process",120,-0.545450046247532,-2.57357696858,1e-10,1.5

BP,"GO:0071222","cellular response to lipopolysaccharide",197,0.51136404184534,2.571225903841

BP,"GO:0097530","granulocyte migration",147,0.532497846901259,2.5682381958998,1e-10,1.5721

BP,"GO:0045667","regulation of osteoblast differentiation",117,0.552089585510679,2.56605722657

BP,"GO:0034446","substrate adhesion-dependent cell spreading",106,0.559275931814644,2.565580

BP,"GO:0034470","ncRNA processing",382,-0.461175866455787,-2.56425304804402,1e-10,1.57214

BP,"GO:0070167","regulation of biomineral tissue development",93,0.571645560825402,2.5634215

BP,"GO:0032602","chemokine production",91,0.571313157879619,2.56180644955752,1e-10,1.5721

BP,"GO:0070372","regulation of ERK1 and ERK2 cascade",282,0.491932290352679,2.561487086861

BP,"GO:0006399","tRNA metabolic process",157,-0.515632215982871,-2.56023448521323,1e-10,1.!

CC,"GO:0031091","platelet alpha granule",88,0.575907376626423,2.5578540845035,1e-10,1.57214

BP,"GO:2000779","regulation of double-strand break repair",94,-0.56466568738359,-2.5576537887

BP,"GO:0001935","endothelial cell proliferation",143,0.532383907533268,2.55597862817053,1e-10

BP,"GO:0010810","regulation of cell-substrate adhesion",205,0.506649697691317,2.555946698597

BP,"GO:0032612","interleukin-1 production",108,0.55819140619152,2.55357440861073,1e-10,1.57

BP,"GO:0032652","regulation of interleukin-1 production",108,0.55819140619152,2.553574408610

BP,"GO:0051271","negative regulation of cellular component movement",278,0.490820998863863,!

BP,"GO:0042254","ribosome biogenesis",281,-0.47493355133641,-2.5531320624267,1e-10,1.57214

BP,"GO:0014812","muscle cell migration",78,0.585487104164276,2.55182123813405,1e-10,1.57214

BP,"GO:0072080","nephron tubule development",91,0.56853833922517,2.54936397693584,1e-10,1

BP,"GO:0007127","meiosis I",114,-0.54486194160983,-2.54761304557027,1e-10,1.57214700193424

BP,"GO:0044409","entry into host",148,0.527068763005038,2.54629560013415,1e-10,1.572147001

BP,"GO:0007229","integrin-mediated signaling pathway",100,0.560722296418156,2.5454949506290

BP,"GO:0071621","granulocyte chemotaxis",122,0.545017272933395,2.54451554475366,1e-10,1.57

BP,"GO:0006364","rRNA processing",208,-0.490093001182794,-2.54430207011209,1e-10,1.5721470

BP,"GO:1990868","response to chemokine",95,0.564369623956045,2.54387061149035,1e-10,1.572

BP,"GO:1990869","cellular response to chemokine",95,0.564369623956045,2.54387061149035,1e-1

BP,"GO:0002040","sprouting angiogenesis",119,0.546008280719049,2.54002977425301,1e-10,1.57147001

BP,"GO:0001649","osteoblast differentiation",215,0.500714405687578,2.53726639162056,1e-10,1.57147001

BP,"GO:0016072","rRNA metabolic process",240,-0.482166634116044,-2.53694052470271,1e-10,1.57147001

BP,"GO:0032642","regulation of chemokine production",90,0.566066967594757,2.53482139810378,1e-10,1.57147001

BP,"GO:0045132","meiotic chromosome segregation",82,-0.575575829530507,-2.53294579518934,1e-10,1.57147001

BP,"GO:0050886","endocrine process",83,0.572541474252101,2.5328269702737,1e-10,1.57214700

BP,"GO:0007044","cell-substrate junction assembly",92,0.565652568104608,2.5322698804775,1e-10,1.57147001

BP,"GO:1903034","regulation of response to wounding",150,0.521649617371663,2.5300389145936,1e-10,1.57147001

BP,"GO:0007052","mitotic spindle organization",117,-0.538174376354856,-2.52885911863499,1e-10,1.57147001

BP,"GO:1903046","meiotic cell cycle process",187,-0.496689486937165,-2.52609325838521,1e-10,1.57147001

BP,"GO:0090287","regulation of cellular response to growth factor stimulus",278,0.48471827381398,1e-10,1.57147001

BP,"GO:0050678","regulation of epithelial cell proliferation",323,0.474036888717421,2.5189464837,1e-10,1.57147001

BP,"GO:0150115","cell-substrate junction organization",98,0.556834510526393,2.51811989415223,1e-10,1.57147001

CC,"GO:0071162","CMG complex",11,-0.947256913470116,-2.51673131136358,1e-10,1.57214700

MF,"GO:0004896","cytokine receptor activity",96,0.55727083277157,2.51527812199437,1e-10,1.57147001

BP,"GO:0008015","blood circulation",486,0.452173261501805,2.51524157540863,1e-10,1.57214700

BP,"GO:0140013","meiotic nuclear division",168,-0.50319567497133,-2.51364150159016,1e-10,1.57147001

BP,"GO:0002064","epithelial cell development",198,0.498940565421192,2.51311800975596,1e-10,1.57147001

BP,"GO:1902850","microtubule cytoskeleton organization involved in mitosis",144,-0.512478696831,1e-10,1.57147001

BP,"GO:1903510","mucopolysaccharide metabolic process",86,0.565603098259777,2.50926925559,1e-10,1.57147001

BP,"GO:0071216","cellular response to biotic stimulus",230,0.489706198780845,2.50570003827173,1e-10,1.57147001

BP,"GO:0002698","negative regulation of immune effector process",112,0.543826563006097,2.50471827381398,1e-10,1.57147001

BP,"GO:0050866","negative regulation of cell activation",202,0.496219968701434,2.504446884373,1e-10,1.57147001

BP,"GO:0007093","mitotic cell cycle checkpoint signaling",122,-0.52789414239968,-2.50090740970,1e-10,1.57147001

BP,"GO:0010811","positive regulation of cell-substrate adhesion",119,0.537399578907292,2.499982,1e-10,1.57147001

CC,"GO:0030666","endocytic vesicle membrane",187,0.498970837327181,2.4996559278224,1e-10,1.57147001

BP,"GO:0034660","ncRNA metabolic process",493,-0.437493996775826,-2.49882975527733,1e-10,1.57147001

BP,"GO:0061326","renal tubule development",94,0.555860312330904,2.49814598453543,1e-10,1.57147001

MF,"GO:0005125","cytokine activity",230,0.488155749979275,2.49776679251927,1e-10,1.57214700

BP,"GO:0050729","positive regulation of inflammatory response",130,0.530139731780765,2.497264,1e-10,1.57147001

CC,"GO:0045335","phagocytic vesicle",134,0.525636386452643,2.4966600979823,1e-10,1.57214700

BP,"GO:0007200","phospholipase C-activating G protein-coupled receptor signaling pathway",102,0.537399578907292,2.499982,1e-10,1.57147001

BP,"GO:0051225","spindle assembly",114,-0.533377455806462,-2.49391499176992,1e-10,1.57214700

BP,"GO:0040013","negative regulation of locomotion",305,0.471924009468562,2.49111973360468,1e-10,1.57147001

BP,"GO:0001655","urogenital system development",349,0.465670317463301,2.4908564430891,1e-10,1.57147001

BP,"GO:0051321","meiotic cell cycle",244,-0.471463298534811,-2.48875894253221,1e-10,1.57214700

BP,"GO:0010389","regulation of G2/M transition of mitotic cell cycle",89,-0.553363916986494,-2.48875894253221,1e-10,1.57214700

BP,"GO:0001819","positive regulation of cytokine production",450,0.449698205771711,2.48556304,1e-10,1.57147001

BP,"GO:0006475","internal protein amino acid acetylation",168,-0.49743256127352,-2.4848526973,1e-10,1.57147001

BP,"GO:0030282","bone mineralization",114,0.537294245499579,2.48458457677962,1e-10,1.57214700

BP,"GO:0001656","metanephros development",89,0.557308531692725,2.48305977920598,1e-10,1.57147001

BP,"GO:0002367","cytokine production involved in immune response",99,0.547135068030479,2.48119418225743,1e-10,1.57147001

BP,"GO:0072001","renal system development",309,0.467729033241158,2.48119418225743,1e-10,1.57147001

MF,"GO:0140101","catalytic activity, acting on a tRNA",99,-0.541409869739685,-2.48002191977891,1e-10,1.57147001

BP,"GO:0018393","internal peptidyl-lysine acetylation",166,-0.496559046820925,-2.4777336579354,1e-10,1.57147001

BP,"GO:0051052","regulation of DNA metabolic process",430,-0.440144461580593,-2.47674002022,1e-10,1.57147001

BP,"GO:0001822","kidney development",300,0.469213327331965,2.47652882534597,1e-10,1.57214700

BP,"GO:0048705","skeletal system morphogenesis",222,0.486925450968536,2.47527785038549,1e-10,1.57147001

BP,"GO:1902749","regulation of cell cycle G2/M phase transition",98,-0.54045597186283,-2.473997,1e-10,1.57147001

BP,"GO:0071675","regulation of mononuclear cell migration",112,0.537067176976888,2.473631599,1e-10,1.57147001

BP,"GO:0071346","cellular response to interferon-gamma",115,0.534505615868284,2.47223712272

BP,"GO:0044839","cell cycle G2/M phase transition",144,-0.50408708097468,-2.47159849402901,1e-10,1.572147001

BP,"GO:0032103","positive regulation of response to external stimulus",411,0.451085491418682,2.47223712272

MF,"GO:0030546","signaling receptor activator activity",467,0.445162328718165,2.4662165744557

MF,"GO:0003729","mRNA binding",299,-0.457150411669963,-2.46225869011379,1e-10,1.572147001

CC,"GO:0030667","secretory granule membrane",298,0.467301513622291,2.46048082399994,1e-10,1.572147001

BP,"GO:0060840","artery development",96,0.544862097180829,2.45927048743403,1e-10,1.572147001

MF,"GO:0005539","glycosaminoglycan binding",219,0.48338450708606,2.45824172037752,1e-10,1.572147001

CC,"GO:0030139","endocytic vesicle",334,0.460584057704125,2.45776344788249,1e-10,1.572147001

CC,"GO:0070820","tertiary granule",160,0.501340971489014,2.45651232948588,1e-10,1.572147001

BP,"GO:0016573","histone acetylation",161,-0.494010252067352,-2.45341028551289,1e-10,1.572147001

BP,"GO:0001936","regulation of endothelial cell proliferation",127,0.524353435389458,2.452924381

BP,"GO:0008033","tRNA processing",114,-0.524510149903181,-2.45245409594828,1e-10,1.572147001

MF,"GO:0048018","receptor ligand activity",460,0.442769047750418,2.45138707469861,1e-10,1.572147001

BP,"GO:2000027","regulation of animal organ morphogenesis",128,0.521619217300638,2.44656923

BP,"GO:0071706","tumor necrosis factor superfamily cytokine production",160,0.498480365870517

BP,"GO:1903555","regulation of tumor necrosis factor superfamily cytokine production",160,0.498480365870517

BP,"GO:0031123","RNA 3'-end processing",103,-0.5345919519359,-2.44216954164225,1e-10,1.572147001

BP,"GO:0032640","tumor necrosis factor production",155,0.500464880221916,2.44202119449308,1e-10,1.572147001

BP,"GO:0032680","regulation of tumor necrosis factor production",155,0.500464880221916,2.44202119449308,1e-10,1.572147001

BP,"GO:0003012","muscle system process",409,0.446952254211601,2.44015862590623,1e-10,1.572147001

BP,"GO:1990266","neutrophil migration",122,0.522197881264387,2.43797892709547,1e-10,1.572147001

MF,"GO:0016887","ATP hydrolysis activity",296,-0.452673584293395,-2.43754647065448,1e-10,1.572147001

BP,"GO:0000723","telomere maintenance",127,-0.509581474244339,-2.43705311274895,1e-10,1.572147001

BP,"GO:0016571","histone methylation",146,-0.496821796809983,-2.43623985202377,1e-10,1.572147001

BP,"GO:0034968","histone lysine methylation",115,-0.518484789963726,-2.43386487340465,1e-10,1.572147001

BP,"GO:0006022","aminoglycan metabolic process",129,0.516385734276341,2.43261068187273,1e-10,1.572147001

BP,"GO:0018394","peptidyl-lysine acetylation",177,-0.48145994650303,-2.43191450590889,1e-10,1.572147001

MF,"GO:0030246","carbohydrate binding",258,0.468759177557854,2.43156452866752,1e-10,1.572147001

BP,"GO:0050727","regulation of inflammatory response",335,0.454939235848876,2.4304556992184

BP,"GO:0032200","telomere organization",131,-0.507190515344314,-2.42863164836806,1e-10,1.572147001

BP,"GO:0071560","cellular response to transforming growth factor beta stimulus",236,0.473764140

BP,"GO:0006403","RNA localization",189,-0.476390149060156,-2.42398705170953,1e-10,1.572147001

BP,"GO:0002224","toll-like receptor signaling pathway",115,0.523793377954766,2.42269004323916

BP,"GO:0030203","glycosaminoglycan metabolic process",118,0.520348810362346,2.422536360958

BP,"GO:0072676","lymphocyte migration",112,0.525325117741865,2.41954985652885,1e-10,1.572147001

BP,"GO:0071356","cellular response to tumor necrosis factor",212,0.477145315247388,2.41826841

BP,"GO:0008217","regulation of blood pressure",178,0.485675143501339,2.41741634170332,1e-10,1.572147001

BP,"GO:0006936","muscle contraction",329,0.452822561281358,2.4171617708269,1e-10,1.572147001

BP,"GO:0006909","phagocytosis",225,0.474743664820395,2.41570458711515,1e-10,1.572147001

BP,"GO:0000086","G2/M transition of mitotic cell cycle",131,-0.504451862335756,-2.415517879144

BP,"GO:0042476","odontogenesis",126,0.515681036604341,2.41510922732105,1e-10,1.572147001

BP,"GO:0090257","regulation of muscle system process",219,0.474689842076094,2.4140251847648

BP,"GO:0018022","peptidyl-lysine methylation",122,-0.5087055114041,-2.41000094648298,1e-10,1.572147001

BP,"GO:0071559","response to transforming growth factor beta",242,0.467948132225109,2.407423

BP,"GO:0031570","DNA integrity checkpoint signaling",115,-0.512404637337322,-2.4053234963212

CC,"GO:0032993","protein-DNA complex",123,-0.50630280808713,-2.40144558417894,1e-10,1.572147001

BP,"GO:0016570","histone modification",466,-0.423271819159549,-2.39994787135931,1e-10,1.572147001

BP,"GO:0050679","positive regulation of epithelial cell proliferation",188,0.479285863590083,2.398

BP,"GO:0030856","regulation of epithelial cell differentiation",139,0.501847826523337,2.39445234

BP,"GO:0007179","transforming growth factor beta receptor signaling pathway",186,0.47849111806

BP,"GO:0006937","regulation of muscle contraction",155,0.490277496739812,2.39231179956272,1

BP,"GO:0045834","positive regulation of lipid metabolic process",144,0.497556888739154,2.386835

BP,"GO:0050731","positive regulation of peptidyl-tyrosine phosphorylation",185,0.47671403844040

BP,"GO:0052126","movement in host environment",172,0.479934417118276,2.38350981818454,1e

BP,"GO:0050777","negative regulation of immune response",170,0.481183366210216,2.382057356

BP,"GO:0044772","mitotic cell cycle phase transition",401,-0.426214707560812,-2.38077793029398

BP,"GO:0050730","regulation of peptidyl-tyrosine phosphorylation",249,0.461709459012376,2.3801

CC,"GO:0042581","specific granule",158,0.485509047987121,2.37697029308961,1e-10,1.57214700

BP,"GO:0048706","embryonic skeletal system development",126,0.506893129182312,2.373952475

BP,"GO:0007517","muscle organ development",315,0.446476935527136,2.3731020432366,1e-10,1.

BP,"GO:0002009","morphogenesis of an epithelium",500,0.426563022667377,2.37197016105297,1e

BP,"GO:0022409","positive regulation of cell-cell adhesion",280,0.455956029539719,2.37103112514

BP,"GO:0007204","positive regulation of cytosolic calcium ion concentration",310,0.4458368378828

BP,"GO:0007162","negative regulation of cell adhesion",276,0.4554929876784,2.36877930804659,1

BP,"GO:0006479","protein methylation",175,-0.469330057491681,-2.3682530472954,1e-10,1.57214

BP,"GO:0008213","protein alkylation",175,-0.469330057491681,-2.3682530472954,1e-10,1.5721470

BP,"GO:0043414","macromolecule methylation",289,-0.440054180666275,-2.36619276395013,1e-1

BP,"GO:0031960","response to corticosteroid",153,0.485325330347601,2.36461202326015,1e-10,1

CC,"GO:0098798","mitochondrial protein-containing complex",237,-0.450074842942296,-2.3636843

BP,"GO:0051480","regulation of cytosolic calcium ion concentration",340,0.442602071604203,2.363

BP,"GO:0090101","negative regulation of transmembrane receptor protein serine/threonine kinase

BP,"GO:0070663","regulation of leukocyte proliferation",244,0.457144371086358,2.3529050602824

BP,"GO:0072503","cellular divalent inorganic cation homeostasis",473,0.424870010873143,2.35241

BP,"GO:0090068","positive regulation of cell cycle process",227,-0.45235394540381,-2.35240752870

BP,"GO:0051384","response to glucocorticoid",136,0.494350423077073,2.35226908559308,1e-10,1

BP,"GO:0007178","transmembrane receptor protein serine/threonine kinase signaling pathway",344

BP,"GO:0044770","cell cycle phase transition",491,-0.411820922571502,-2.34747106753406,1e-10,1

BP,"GO:0007098","centrosome cycle",126,-0.491418987594801,-2.3474215342802,1e-10,1.5721470

BP,"GO:0072507","divalent inorganic cation homeostasis",492,0.420770293280442,2.34583475322,

BP,"GO:0006473","protein acetylation",206,-0.452022038971869,-2.34337866179596,1e-10,1.57214

BP,"GO:0050684","regulation of mRNA processing",137,-0.483253423244906,-2.34255658775125,1e

BP,"GO:0034612","response to tumor necrosis factor",231,0.457709718181381,2.34212124470919,

BP,"GO:0002250","adaptive immune response",423,0.427839047392639,2.3419686480465,1e-10,1.

BP,"GO:0045598","regulation of fat cell differentiation",127,0.500483838328504,2.34126245798584

BP,"GO:0022407","regulation of cell-cell adhesion",431,0.426756090211717,2.34080977735225,1e-

BP,"GO:0048017","inositol lipid-mediated signaling",172,0.470638554233453,2.33734355116099,1e

BP,"GO:0014065","phosphatidylinositol 3-kinase signaling",137,0.492298662038572,2.33685701543

BP,"GO:0043405","regulation of MAP kinase activity",180,0.469416037457648,2.33384062688574,1

CC,"GO:0005766","primary lysosome",146,0.484023731637848,2.33121597682723,1e-10,1.5721470

CC,"GO:0042582","azurophil granule",146,0.484023731637848,2.33121597682723,1e-10,1.5721470

MF,"GO:0005126","cytokine receptor binding",260,0.449180760734894,2.3293034861005,1e-10,1.5

BP,"GO:0002460","adaptive immune response based on somatic recombination of immune receptor

BP,"GO:0018205","peptidyl-lysine modification",363,-0.420348890454814,-2.32640142999643,1e-1

BP,"GO:0002695","negative regulation of leukocyte activation",180,0.467478419518297,2.32420718

MF,"GO:0008201","heparin binding",157,0.476303188933867,2.32248070518191,1e-10,1.57214700

BP,"GO:0043491","protein kinase B signaling",184,0.465009241055792,2.3221068427582,1e-10,1.5

BP,"GO:0022408","negative regulation of cell-cell adhesion",182,0.466595801209944,2.3209402778

BP,"GO:0007369","gastrulation",180,0.466462373071859,2.319155611054,1e-10,1.5721470019342

BP,"GO:0031023","microtubule organizing center organization",139,-0.476012768529476,-2.318177

BP,"GO:0032102","negative regulation of response to external stimulus",372,0.429476734066441,2. BP,"GO:1901990","regulation of mitotic cell cycle phase transition",284,-0.431208253112267,-2.314 BP,"GO:0002573","myeloid leukocyte differentiation",205,0.458042563521655,2.3107333990033,1e-10,1.57214700193424 CC,"GO:0043292","contractile fiber",235,0.449745810384645,2.30566928365319,1e-10,1.57214700193424 BP,"GO:0070661","leukocyte proliferation",320,0.433390631601057,2.30537315122729,1e-10,1.57214700193424 BP,"GO:0055074","calcium ion homeostasis",448,0.41737691652833,2.30528722402209,1e-10,1.57214700193424 BP,"GO:0050657","nucleic acid transport",152,-0.467588769977408,-2.30380283186693,1e-10,1.57214700193424 BP,"GO:0050658","RNA transport",152,-0.467588769977408,-2.30380283186693,1e-10,1.57214700193424 BP,"GO:0060348","bone development",218,0.453358203306384,2.30314708604577,1e-10,1.57214700193424 BP,"GO:0090092","regulation of transmembrane receptor protein serine/threonine kinase signaling",286,0.441008988840891,2.30081080019423,1e-10,1.57214700193424 BP,"GO:0060485","mesenchyme development",286,0.441008988840891,2.30081080019423,1e-10,1.57214700193424 BP,"GO:0007159","leukocyte cell-cell adhesion",358,0.427484114883658,2.29758290976285,1e-10,1.57214700193424 CC,"GO:0030016","myofibril",225,0.450874688117036,2.2942487346524,1e-10,1.57214700193424 BP,"GO:0006874","cellular calcium ion homeostasis",436,0.417864396191193,2.29422717573561,1e-10,1.57214700193424 BP,"GO:0051236","establishment of RNA localization",155,-0.462871471259464,-2.29346884339761,1e-10,1.57214700193424 BP,"GO:0060537","muscle tissue development",375,0.424143357023952,2.29204399654482,1e-10,1.57214700193424 BP,"GO:0002221","pattern recognition receptor signaling pathway",162,0.466723543023158,2.29114700193424 BP,"GO:0048762","mesenchymal cell differentiation",229,0.447441507315246,2.2832498744347,1e-10,1.57214700193424 BP,"GO:1903311","regulation of mRNA metabolic process",279,-0.425198083605799,-2.28145126103,1e-10,1.57214700193424 BP,"GO:0048015","phosphatidylinositol-mediated signaling",168,0.462259488119324,2.2804838405,1e-10,1.57214700193424 MF,"GO:0004866","endopeptidase inhibitor activity",173,0.457341661885536,2.27198633844102,1e-10,1.57214700193424 CC,"GO:0031983","vesicle lumen",319,0.425582920279092,2.26293582546091,1e-10,1.57214700193424 BP,"GO:0045444","fat cell differentiation",218,0.445016897449777,2.26077164398395,1e-10,1.57214700193424 BP,"GO:0032259","methylation",328,-0.412967306277,-2.25970917075241,1e-10,1.57214700193424 BP,"GO:0051701","biological process involved in interaction with host",186,0.451274477732171,2.25970917075241,1e-10,1.57214700193424 BP,"GO:0043543","protein acylation",247,-0.42582241923944,-2.25550491229041,1e-10,1.57214700193424 CC,"GO:0060205","cytoplasmic vesicle lumen",317,0.42485198280341,2.2548139504486,1e-10,1.57214700193424 BP,"GO:0050867","positive regulation of cell activation",339,0.421908669721483,2.2547082993686,1e-10,1.57214700193424 CC,"GO:0034774","secretory granule lumen",314,0.424967752383065,2.25407601827223,1e-10,1.57214700193424 MF,"GO:0030414","peptidase inhibitor activity",179,0.452137113084347,2.25350963495298,1e-10,1.57214700193424 CC,"GO:0098857","membrane microdomain",316,0.422349210300704,2.24547047887929,1e-10,1.57214700193424 BP,"GO:1901987","regulation of cell cycle phase transition",370,-0.405176776722954,-2.244112693,1e-10,1.57214700193424 BP,"GO:0042445","hormone metabolic process",227,0.439534165359666,2.24193901733201,1e-10,1.57214700193424 MF,"GO:0140098","catalytic activity, acting on RNA",339,-0.408964521058406,-2.24065671086421,1e-10,1.57214700193424 BP,"GO:0042742","defense response to bacterium",257,0.432439718069255,2.24055663542007,1e-10,1.57214700193424 BP,"GO:0032944","regulation of mononuclear cell proliferation",225,0.439573916519545,2.2367454,1e-10,1.57214700193424 BP,"GO:0031348","negative regulation of defense response",220,0.439717170585266,2.236098938,1e-10,1.57214700193424 BP,"GO:0010959","regulation of metal ion transport",372,0.413988283033126,2.23353957925388,1e-10,1.57214700193424 CC,"GO:0045121","membrane raft",315,0.420002976080915,2.23238837528371,1e-10,1.57214700193424 BP,"GO:1903039","positive regulation of leukocyte cell-cell adhesion",236,0.435600033921633,2.2314700193424 CC,"GO:0030017","sarcomere",206,0.441292095743929,2.22755773579211,1e-10,1.57214700193424 BP,"GO:0002696","positive regulation of leukocyte activation",327,0.417039497238044,2.22171740,1e-10,1.57214700193424 BP,"GO:0006959","humoral immune response",224,0.436268764836953,2.22055415763075,1e-10,1.57214700193424 BP,"GO:0018108","peptidyl-tyrosine phosphorylation",360,0.412831861258113,2.21834748229453,1e-10,1.57214700193424 BP,"GO:0050670","regulation of lymphocyte proliferation",222,0.435656419364554,2.21465253682,1e-10,1.57214700193424 BP,"GO:1903037","regulation of leukocyte cell-cell adhesion",322,0.414297495673897,2.205057856,1e-10,1.57214700193424 BP,"GO:0042063","gliogenesis",278,0.42364989753944,2.2040073643016,1e-10,1.57214700193424 BP,"GO:0018212","peptidyl-tyrosine modification",363,0.410032927239749,2.20084109538212,1e-10,1.57214700193424 BP,"GO:0019932","second-messenger-mediated signaling",291,0.418203330802346,2.19909526314,1e-10,1.57214700193424 BP,"GO:1902105","regulation of leukocyte differentiation",273,0.422969862169574,2.19872337141,1e-10,1.57214700193424

BP,"GO:0002697","regulation of immune effector process",333,0.411628491615366,2.19471870867

BP,"GO:0044706","multi-multicellular organism process",207,0.434944354079684,2.193110572890

CC,"GO:0043235","receptor complex",402,0.401380835636336,2.19140189893515,1e-10,1.5721470

BP,"GO:0052547","regulation of peptidase activity",423,0.400236957724349,2.1908762477206,1e-1

BP,"GO:0051054","positive regulation of DNA metabolic process",246,-0.413168472787975,-2.1900

BP,"GO:0031349","positive regulation of defense response",264,0.420462200420324,2.1854201465

BP,"GO:1903706","regulation of hemopoiesis",343,0.406591352283182,2.17283434383288,1e-10,1.

BP,"GO:0043122","regulation of I-kappaB kinase/NF-kappaB signaling",246,0.422174721237662,2.17

BP,"GO:0010948","negative regulation of cell cycle process",266,-0.406412515020264,-2.169975612

MF,"GO:0061134","peptidase regulator activity",219,0.426354604340745,2.16821735223482,1e-10

BP,"GO:0043588","skin development",288,0.414546443756949,2.16816809670031,1e-10,1.5721470

BP,"GO:0002443","leukocyte mediated immunity",368,0.402013757330887,2.16533414454256,1e-1

BP,"GO:0044403","biological process involved in symbiotic interaction",276,0.415283864637784,2.1

BP,"GO:0060562","epithelial tube morphogenesis",325,0.4057561176079,2.15739050772462,1e-10,

BP,"GO:0140694","non-membrane-bounded organelle assembly",359,-0.389384153790586,-2.15220

BP,"GO:2001020","regulation of response to DNA damage stimulus",221,-0.414103891793923,-2.14

BP,"GO:1903522","regulation of blood circulation",244,0.417425644378498,2.1484742524901,1e-10

BP,"GO:0006869","lipid transport",368,0.397867681683053,2.14300247304525,1e-10,1.572147001

BP,"GO:0052548","regulation of endopeptidase activity",396,0.393439771483384,2.1429275375069

BP,"GO:0010876","lipid localization",419,0.391542698767208,2.14143166954862,1e-10,1.57214700

BP,"GO:0007249","I-kappaB kinase/NF-kappaB signaling",278,0.410815012748935,2.137234822250

BP,"GO:0051251","positive regulation of lymphocyte activation",285,0.408820385997917,2.1349062

BP,"GO:0010466","negative regulation of peptidase activity",244,0.413308890873743,2.1272854754

BP,"GO:0032943","mononuclear cell proliferation",292,0.404478734230911,2.1265445426372,1e-10

BP,"GO:0048545","response to steroid hormone",317,0.398297605376759,2.11388208925779,1e-10

CC,"GO:0000151","ubiquitin ligase complex",290,-0.392239733067967,-2.10914195626344,1e-10,1.

BP,"GO:0046651","lymphocyte proliferation",288,0.403241531654632,2.10904094671415,1e-10,1.5

CC,"GO:0015629","actin cytoskeleton",478,0.379901663967941,2.10744155509195,1e-10,1.572147

BP,"GO:0043270","positive regulation of ion transport",261,0.404026096657959,2.0955697161996,

BP,"GO:0032970","regulation of actin filament-based process",367,0.388374867588866,2.09376580

BP,"GO:0008544","epidermis development",344,0.391843276972362,2.09337821718267,1e-10,1.57

BP,"GO:0048568","embryonic organ development",445,0.379522778558879,2.09327722740782,1e-

CC,"GO:0005911","cell-cell junction",474,0.377288994602764,2.09262584232709,1e-10,1.57214700

BP,"GO:0051249","regulation of lymphocyte activation",437,0.380826862390737,2.0923833455430

BP,"GO:0006816","calcium ion transport",394,0.383080742391885,2.08628269726931,1e-10,1.5721

BP,"GO:0019058","viral life cycle",302,0.392965784695592,2.07966778951459,1e-10,1.5721470019

BP,"GO:0043068","positive regulation of programmed cell death",488,0.373034464174369,2.075200

BP,"GO:0019216","regulation of lipid metabolic process",310,0.390172484497552,2.0733848385934

BP,"GO:0006401","RNA catabolic process",261,-0.387695402725287,-2.06968276685334,1e-10,1.57

BP,"GO:0045787","positive regulation of cell cycle",304,-0.382370274456502,-2.0688251851026,1e-

BP,"GO:0043065","positive regulation of apoptotic process",476,0.372783979913366,2.0669256559

BP,"GO:0007346","regulation of mitotic cell cycle",436,-0.365075107059998,-2.06438599855922,1e

MF,"GO:0003779","actin binding",425,0.375939192351725,2.06171564850514,1e-10,1.5721470019

BP,"GO:0060249","anatomical structure homeostasis",302,0.388912401898165,2.05821632994563,

BP,"GO:0051051","negative regulation of transport",401,0.376396176950546,2.05379764630765,1e

BP,"GO:0034329","cell junction assembly",404,0.376217857178421,2.05272145429555,1e-10,1.572

BP,"GO:0036293","response to decreased oxygen levels",277,0.394477728024535,2.051633727602

BP,"GO:0002449","lymphocyte mediated immunity",277,0.394330037957082,2.0508656083856,1e-

BP,"GO:0042692","muscle cell differentiation",338,0.383694730342157,2.05075117552838,1e-10,1.

BP,"GO:0070482","response to oxygen levels",299,0.388634585743146,2.04956570068181,1e-10,1.

BP,"GO:0030099","myeloid cell differentiation",365,0.379905155960899,2.04092231143421,1e-10,1.572147001

BP,"GO:0042110","T cell activation",490,0.366136741227877,2.0397811718631,1e-10,1.572147001

BP,"GO:0010817","regulation of hormone levels",485,0.362900266696999,2.02015211191937,1e-10,1.572147001

BP,"GO:0007015","actin filament organization",417,0.367046207425935,2.00929158395037,1e-10,1.572147001

BP,"GO:1903131","mononuclear cell differentiation",423,0.366611866156703,2.00681424889408,1e-10,1.572147001

CC,"GO:0045177","apical part of cell",408,0.36707245351638,2.00403963832648,1e-10,1.572147001

CC,"GO:0005743","mitochondrial inner membrane",428,-0.356343954642932,-2.00326663617098,1e-10,1.572147001

BP,"GO:0051090","regulation of DNA-binding transcription factor activity",419,0.364871013339655,2.00929158395037,1e-10,1.572147001

BP,"GO:0002764","immune response-regulating signaling pathway",384,0.366691028425914,1.9881332448622,1e-10,1.572147001

BP,"GO:0048608","reproductive structure development",426,0.361507238871016,1.981332448622,1e-10,1.572147001

MF,"GO:0015631","tubulin binding",354,-0.356726872679738,-1.97176225591546,1e-10,1.572147001

BP,"GO:0061458","reproductive system development",429,0.358909036481274,1.96832257126603,1e-10,1.572147001

BP,"GO:1901652","response to peptide",464,0.354604707870127,1.96147334988686,1e-10,1.572147001

BP,"GO:0033674","positive regulation of kinase activity",459,0.354137971122038,1.9592519080671,1e-10,1.572147001

BP,"GO:0048732","gland development",426,0.357213631268315,1.95780023916674,1e-10,1.572147001

BP,"GO:0050778","positive regulation of immune response",483,0.347101279598127,1.9294149091332448622,1e-10,1.572147001

BP,"GO:1902532","negative regulation of intracellular signal transduction",470,0.348071101541973,1.9294149091332448622,1e-10,1.572147001

BP,"GO:0090066","regulation of anatomical structure size",466,0.346378476828554,1.920072339832448622,1e-10,1.572147001

CC,"GO:0019866","organelle inner membrane",483,-0.33449226165516,-1.90460451096356,1e-10,1.572147001

BP,"GO:0035825","homologous recombination",54,-0.625693912071463,-2.55295717160959,1.01010101010101,1.572147001

BP,"GO:0001666","response to hypoxia",265,0.405493704814049,2.10839253722511,1.0537777327,1e-10,1.572147001

BP,"GO:0050863","regulation of T cell activation",327,0.377950125988495,2.01347444909188,1.1010101010101,1.572147001

BP,"GO:0002718","regulation of cytokine production involved in immune response",97,0.5460313782448622,1.572147001

CC,"GO:0005796","Golgi lumen",97,0.546024471451226,2.46796556133126,1.13536503093956e-10,1.572147001

BP,"GO:1905952","regulation of lipid localization",142,0.482569006351218,2.31814836914025,1.1610101010101,1.572147001

MF,"GO:0001653","peptide receptor activity",150,0.464300709969888,2.25189250634555,1.328236,1e-10,1.572147001

BP,"GO:0071459","protein localization to chromosome, centromeric region",23,-0.80913342958725,1.01010101010101,1.572147001

BP,"GO:0001837","epithelial to mesenchymal transition",149,0.473105139063325,2.288651928429,1e-10,1.572147001

BP,"GO:0043123","positive regulation of I-kappaB kinase/NF-kappaB signaling",186,0.442705792390,1.92787260174973,1.491789757991,1e-10,1.572147001

CC,"GO:0031252","cell leading edge",403,0.352923520981029,1.92787260174973,1.491789757991,1e-10,1.572147001

BP,"GO:0097191","extrinsic apoptotic signaling pathway",215,0.41932528841508,2.1248439217385,1e-10,1.572147001

BP,"GO:0034109","homotypic cell-cell adhesion",91,0.550029959277051,2.46637116210565,1.5646,1e-10,1.572147001

BP,"GO:0003007","heart morphogenesis",241,0.413176299040987,2.12630024715511,1.568009315,1e-10,1.572147001

BP,"GO:0031060","regulation of histone methylation",75,-0.568479117375832,-2.46431814175198,1e-10,1.572147001

BP,"GO:0045165","cell fate commitment",257,0.400909684965859,2.0771932302263,1.807447866,1e-10,1.572147001

BP,"GO:0051568","histone H3-K4 methylation",67,-0.594206931265879,-2.53854405368645,1.8582,1e-10,1.572147001

CC,"GO:0005774","vacuolar membrane",421,0.352434968024655,1.93188520099906,1.905019719,1e-10,1.572147001

BP,"GO:0071496","cellular response to external stimulus",294,0.384996570487461,2.024915247900,1e-10,1.572147001

BP,"GO:0051924","regulation of calcium ion transport",232,0.413839201139008,2.11817095051027,1e-10,1.572147001

BP,"GO:0072012","glomerulus vasculature development",26,0.788842961618162,2.7307704583439,1e-10,1.572147001

MF,"GO:0030020","extracellular matrix structural constituent conferring tensile strength",41,0.6979,1e-10,1.572147001

BP,"GO:0000245","spliceosomal complex assembly",56,-0.627572164926509,-2.58650374753893,2.024915247900,1e-10,1.572147001

BP,"GO:0033047","regulation of mitotic sister chromatid segregation",45,-0.667352188397757,-2.63,1e-10,1.572147001

BP,"GO:1901343","negative regulation of vasculature development",92,0.542864106602756,2.4302,1e-10,1.572147001

MF,"GO:0061135","endopeptidase regulator activity",186,0.438701584162589,2.19520877103435,2.024915247900,1e-10,1.572147001

BP,"GO:0051250","negative regulation of lymphocyte activation",152,0.463763945744652,2.254098,1e-10,1.572147001

BP,"GO:0003015","heart process",240,0.402324926697609,2.06639177303306,3.00239639679686e-10,1.572147001

MF,"GO:0008528","G protein-coupled peptide receptor activity",144,0.464191383948856,2.226777,1e-10,1.572147001

BP,"GO:0031099","regeneration",174,0.443097414331848,2.20244313054181,3.14175728508289e-10,1.572147001

BP,"GO:0003002","regionalization",349,0.364297439612322,1.94861598566614,3.16067484441559,1e-10,1.572147001

BP,"GO:0045005","DNA-templated DNA replication maintenance of fidelity",45,-0.665603633425489
CC,"GO:0061695","transferase complex, transferring phosphorus-containing groups",246,-0.3879680
BP,"GO:1901988","negative regulation of cell cycle phase transition",224,-0.403914521740867,-2.10
BP,"GO:0007088","regulation of mitotic nuclear division",111,-0.499676714527959,-2.31509328010
BP,"GO:0048662","negative regulation of smooth muscle cell proliferation",51,0.650090391684289,
BP,"GO:0007131","reciprocal meiotic recombination",52,-0.62804537684001,-2.54376277816593,3.
BP,"GO:0140527","reciprocal homologous recombination",52,-0.62804537684001,-2.543762778165
CC,"GO:0016324","apical plasma membrane",346,0.363700011581243,1.94222033955452,3.804943
BP,"GO:0032757","positive regulation of interleukin-8 production",62,0.61270322535848,2.5688314
BP,"GO:0051346","negative regulation of hydrolase activity",345,0.365938064859688,1.9568547872
BP,"GO:0044703","multi-organism reproductive process",199,0.426248931715941,2.140770021161
BP,"GO:0010951","negative regulation of endopeptidase activity",235,0.409646314456327,2.100094
BP,"GO:0006402","mRNA catabolic process",217,-0.40296586490127,-2.08807987351459,4.4140690
BP,"GO:0070098","chemokine-mediated signaling pathway",88,0.544662779399235,2.41908329621
BP,"GO:0019722","calcium-mediated signaling",196,0.430850103975181,2.16216734111186,4.8262
BP,"GO:0006405","RNA export from nucleus",82,-0.548911471215837,-2.41560352539727,4.885801
BP,"GO:0050728","negative regulation of inflammatory response",140,0.469664239854077,2.24965
BP,"GO:0032755","positive regulation of interleukin-6 production",90,0.545472224817508,2.442599
BP,"GO:0051091","positive regulation of DNA-binding transcription factor activity",259,0.395512236
BP,"GO:0007492","endoderm development",77,0.562251000008541,2.44306801266122,5.7751894
CC,"GO:0005765","lysosomal membrane",379,0.3495094209688,1.89229192291569,5.85615161285
CC,"GO:0098852","lytic vacuole membrane",379,0.3495094209688,1.89229192291569,5.856151612
BP,"GO:2000181","negative regulation of blood vessel morphogenesis",91,0.538315440047678,2.41
BP,"GO:0035265","organ growth",155,0.462660903558912,2.2575564779954,5.98278281429804e-
BP,"GO:0070665","positive regulation of leukocyte proliferation",153,0.464563366174027,2.263455
BP,"GO:0051303","establishment of chromosome localization",76,-0.56287039588668,-2.442482168
BP,"GO:0048562","embryonic organ morphogenesis",292,0.382901454296125,2.01310212154794,6
BP,"GO:0060538","skeletal muscle organ development",159,0.449781328059244,2.2009206934146
BP,"GO:0035924","cellular response to vascular endothelial growth factor stimulus",58,0.619851725
BP,"GO:0016032","viral process",398,0.345887135410172,1.88347750213836,6.38972945434837e-
BP,"GO:0014066","regulation of phosphatidylinositol 3-kinase signaling",104,0.514304362916222,2.
MF,"GO:0003712","transcription coregulator activity",475,-0.32034268614065,-1.82194927099475,
BP,"GO:0032956","regulation of actin cytoskeleton organization",327,0.370200514704075,1.972189
BP,"GO:0050819","negative regulation of coagulation",51,0.645456355901876,2.60610610737459,6
BP,"GO:0001885","endothelial cell development",63,0.599034728310063,2.50869955907915,6.8184
CC,"GO:0031461","cullin-RING ubiquitin ligase complex",167,-0.428987580980922,-2.137297160690
BP,"GO:0072028","nephron morphogenesis",77,0.560555682681836,2.43570159529226,7.0419891
BP,"GO:0002761","regulation of myeloid leukocyte differentiation",113,0.503385518786106,2.3206
BP,"GO:0030593","neutrophil chemotaxis",101,0.527184447256306,2.40137216119857,7.36297297
BP,"GO:0051310","metaphase plate congression",64,-0.600081590293374,-2.53821520821002,7.38
BP,"GO:0022616","DNA strand elongation",36,-0.69826700869266,-2.63695581146144,7.49593006
BP,"GO:0051896","regulation of protein kinase B signaling",155,0.460966792574437,2.24929005392
BP,"GO:0060541","respiratory system development",198,0.42605681004734,2.1460091977193,8.27
BP,"GO:0045860","positive regulation of protein kinase activity",382,0.346218098178846,1.8760592
BP,"GO:0072210","metanephric nephron development",40,0.675506401246922,2.61136370112997
BP,"GO:0050870","positive regulation of T cell activation",215,0.408709282359932,2.071049513047
CC,"GO:0030670","phagocytic vesicle membrane",73,0.567208336000358,2.44594460807107,8.510
MF,"GO:0140030","modification-dependent protein binding",155,-0.446316634620307,-2.21144174
BP,"GO:0140053","mitochondrial gene expression",97,-0.5172090190484,-2.35597387189828,9.287
BP,"GO:0002819","regulation of adaptive immune response",177,0.434377124138783,2.160386679

BP,"GO:0007519","skeletal muscle tissue development",149,0.458760429550915,2.2192592197526
BP,"GO:0048661","positive regulation of smooth muscle cell proliferation",78,0.563335051286301,2
BP,"GO:0043967","histone H4 acetylation",72,-0.563298302100433,-2.43174732002747,1.01725750
BP,"GO:0016525","negative regulation of angiogenesis",90,0.540142416097343,2.41873246934839,
CC,"GO:0005912","adherens junction",162,0.443424569196072,2.17674303704447,1.025417631621
BP,"GO:0030111","regulation of Wnt signaling pathway",311,0.371141763634398,1.9675624499428
CC,"GO:0031261","DNA replication preinitiation complex",12,-0.920049268386747,-2.552251719641
BP,"GO:0060070","canonical Wnt signaling pathway",291,0.379417924084139,1.99514470151214,1
BP,"GO:0003014","renal system process",108,0.516922553822477,2.36478059323951,1.089977039
BP,"GO:0006268","DNA unwinding involved in DNA replication",21,-0.819407348514984,-2.6503919
BP,"GO:0090305","nucleic acid phosphodiester bond hydrolysis",226,-0.393592245404624,-2.04914
BP,"GO:0061333","renal tubule morphogenesis",76,0.555587735006216,2.41754138704589,1.1477
BP,"GO:0045216","cell-cell junction organization",192,0.423484311187517,2.12836348335179,1.15
BP,"GO:0044344","cellular response to fibroblast growth factor stimulus",103,0.517179412288546,2
BP,"GO:0071774","response to fibroblast growth factor",109,0.501110321858354,2.2992738754472
MF,"GO:0001968","fibronectin binding",30,0.743168696834205,2.66802333894822,1.20602126410
BP,"GO:0016055","Wnt signaling pathway",424,0.33650860656368,1.84254446773074,1.217368358
BP,"GO:0006939","smooth muscle contraction",107,0.504913535474228,2.31599533335422,1.2560
BP,"GO:0010001","glial cell differentiation",211,0.405024599574533,2.048510673714,1.264461920
CC,"GO:1902562","H4 histone acetyltransferase complex",39,-0.677427549656529,-2.553711517281
BP,"GO:0015931","nucleobase-containing compound transport",210,-0.399150688342198,-2.075521
BP,"GO:0030323","respiratory tube development",178,0.433564202789027,2.15803753398566,1.45
BP,"GO:0032760","positive regulation of tumor necrosis factor production",98,0.514944530858952,
BP,"GO:0007062","sister chromatid cohesion",47,-0.646231399733424,-2.58814584923038,1.54102
BP,"GO:0001823","mesonephros development",99,0.524330796180934,2.37788202287008,1.54015
BP,"GO:0198738","cell-cell signaling by wnt",426,0.335984125514114,1.84144652865633,1.5816181
BP,"GO:0061005","cell differentiation involved in kidney development",58,0.611406611370397,2.52
BP,"GO:0043903","regulation of biological process involved in symbiotic interaction",55,0.62230266
BP,"GO:0060193","positive regulation of lipase activity",65,0.59488658634354,2.51318361836678,1
BP,"GO:0045841","negative regulation of mitotic metaphase/anaphase transition",40,-0.676002643
BP,"GO:0000018","regulation of DNA recombination",109,-0.490544971724909,-2.27038708912002
BP,"GO:0008608","attachment of spindle microtubules to kinetochore",33,-0.719027552035526,-2.6
BP,"GO:0060349","bone morphogenesis",97,0.524473490869035,2.37055769653647,1.7302410583
BP,"GO:0009615","response to virus",363,0.350738136931129,1.88257784727723,1.810196463334
BP,"GO:0045637","regulation of myeloid cell differentiation",187,0.43011059591836,2.1546920586
BP,"GO:0001657","ureteric bud development",94,0.522445598572857,2.34797366399499,1.852732
BP,"GO:1905314","semi-lunar valve development",41,0.677671937907331,2.62986922675265,1.870
BP,"GO:1902107","positive regulation of leukocyte differentiation",153,0.455318055786553,2.21840
BP,"GO:1903708","positive regulation of hemopoiesis",153,0.455318055786553,2.21840996502119
BP,"GO:0150063","visual system development",376,0.345720952665853,1.86886555964821,1.9256
BP,"GO:0014706","striated muscle tissue development",224,0.405374635384628,2.0633068524578
BP,"GO:0033046","negative regulation of sister chromatid segregation",42,-0.670653781580879,-2.6
BP,"GO:0033048","negative regulation of mitotic sister chromatid segregation",42,-0.670653781580
BP,"GO:2000816","negative regulation of mitotic sister chromatid separation",42,-0.6706537815808
BP,"GO:1903844","regulation of cellular response to transforming growth factor beta stimulus",123,
BP,"GO:0045839","negative regulation of mitotic nuclear division",48,-0.625812209375923,-2.50427
BP,"GO:0032946","positive regulation of mononuclear cell proliferation",140,0.458558159144306,2.
CC,"GO:0016607","nuclear speck",390,-0.334500058647168,-1.86274472433421,2.21803147185373
BP,"GO:0072163","mesonephric epithelium development",95,0.518016663493678,2.334936733991
BP,"GO:0072164","mesonephric tubule development",95,0.518016663493678,2.33493673399136,2

BP,"GO:0010608","post-transcriptional regulation of gene expression",479,-0.313960177666034,-1.7

BP,"GO:1904062","regulation of cation transmembrane transport",320,0.364861599383573,1.94084

BP,"GO:0051897","positive regulation of protein kinase B signaling",105,0.502104337290909,2.2984

BP,"GO:0052372","modulation by symbiont of entry into host",49,0.636411959699782,2.555700742

MF,"GO:0004867","serine-type endopeptidase inhibitor activity",94,0.519056346505937,2.3327416

BP,"GO:0002526","acute inflammatory response",110,0.496518399877242,2.28314494778757,2.47

BP,"GO:0030324","lung development",174,0.429453842591223,2.13462691251782,2.58031363736

CC,"GO:1990391","DNA repair complex",37,-0.682013324825869,-2.5833675553314,2.64893330229

BP,"GO:1903557","positive regulation of tumor necrosis factor superfamily cytokine production",102

BP,"GO:0048738","cardiac muscle tissue development",211,0.39993685045485,2.02277814194236,

CC,"GO:0005874","microtubule",417,-0.327765440604627,-1.84067738140062,2.872534956164926

BP,"GO:0002366","leukocyte activation involved in immune response",273,0.375802505401902,1.95

BP,"GO:0051145","smooth muscle cell differentiation",57,0.605202669381013,2.49859792105771,2

BP,"GO:0003073","regulation of systemic arterial blood pressure",94,0.517191749393384,2.3243618

BP,"GO:0009612","response to mechanical stimulus",195,0.422616794639966,2.12282810587303,2

BP,"GO:0060284","regulation of cell development",476,0.325871582885002,1.80681673970074,2.9

BP,"GO:0051985","negative regulation of chromosome segregation",44,-0.65474320067602,-2.5611

BP,"GO:1905819","negative regulation of chromosome separation",44,-0.65474320067602,-2.56114

BP,"GO:0051235","maintenance of location",314,0.364792108283111,1.93489773829882,3.0602218

CC,"GO:0043596","nuclear replication fork",27,-0.752520740357753,-2.6050636746358,3.13080638

BP,"GO:0042310","vasoconstriction",81,0.539237511770168,2.36908935619943,3.15848924552939

BP,"GO:0051028","mRNA transport",120,-0.472496796767978,-2.22936432447941,3.201603802425

BP,"GO:0014909","smooth muscle cell migration",65,0.589459534639869,2.49025626086569,3.266

BP,"GO:0003179","heart valve morphogenesis",54,0.612735909966938,2.51519816271489,3.29927

BP,"GO:0043406","positive regulation of MAP kinase activity",115,0.486370568520951,2.249599142

CC,"GO:0034399","nuclear periphery",126,-0.46619802162352,-2.22694544334586,3.376333615478

BP,"GO:0014910","regulation of smooth muscle cell migration",58,0.604172430477116,2.493430869

BP,"GO:0048880","sensory system development",382,0.339614072917839,1.84027386878455,3.510

CC,"GO:0030684","preribosome",71,-0.548655729173283,-2.36833534216358,3.53785401747837e

BP,"GO:0045861","negative regulation of proteolysis",327,0.360274286953194,1.91930898170182,3

BP,"GO:0002263","cell activation involved in immune response",276,0.37790141756294,1.96526638

MF,"GO:0008017","microtubule binding",257,-0.375108154497262,-1.9950565013301,3.630641478

CC,"GO:0031093","platelet alpha granule lumen",65,0.587434366836187,2.48170064931637,3.6860

BP,"GO:0000077","DNA damage checkpoint signaling",107,-0.487812694504399,-2.2501856476558,

BP,"GO:0001894","tissue homeostasis",259,0.383837788260811,1.98912879782433,3.88392061934

MF,"GO:0000217","DNA secondary structure binding",35,-0.697083731373352,-2.62274906814101,

BP,"GO:0002699","positive regulation of immune effector process",230,0.394347987552748,2.0177

BP,"GO:1901992","positive regulation of mitotic cell cycle phase transition",89,-0.514473151423444

BP,"GO:0051784","negative regulation of nuclear division",55,-0.602264330414179,-2.48564025844

BP,"GO:1900047","negative regulation of hemostasis",49,0.62944910163459,2.52773932378347,4.3

BP,"GO:0034501","protein localization to kinetochore",17,-0.84928904037764,-2.60574605778238,

BP,"GO:1903083","protein localization to condensed chromosome",17,-0.84928904037764,-2.60574

BP,"GO:0048704","embryonic skeletal system morphogenesis",93,0.526133798725179,2.359333867

MF,"GO:0003688","DNA replication origin binding",16,-0.855243261148209,-2.61530646062436,4.4

BP,"GO:0048041","focal adhesion assembly",83,0.533670669835808,2.36086908388577,4.61908118

BP,"GO:0006271","DNA strand elongation involved in DNA replication",15,-0.867407124659072,-2.5

BP,"GO:0007565","female pregnancy",179,0.423345564933532,2.11000884882979,4.651658587978

BP,"GO:0045669","positive regulation of osteoblast differentiation",62,0.590788926172203,2.47695

CC,"GO:0046540","U4/U6 x U5 tri-snRNP complex",30,-0.712547703764819,-2.55127793807984,4.7

CC,"GO:0097526","spliceosomal tri-snRNP complex",30,-0.712547703764819,-2.55127793807984,4.

BP,"GO:0050000","chromosome localization",78,-0.542332359475861,-2.37852359183077,4.79751!
BP,"GO:0031297","replication fork processing",37,-0.676413127936395,-2.56215482176577,4.9547!
BP,"GO:0060047","heart contraction",231,0.393704236433977,2.01460231158696,5.209561429708
BP,"GO:0000956","nuclear-transcribed mRNA catabolic process",113,-0.478133677185494,-2.23572
BP,"GO:0070192","chromosome organization involved in meiotic cell cycle",62,-0.572542517462537
BP,"GO:0051146","striated muscle cell differentiation",250,0.379408499927759,1.9544253382146,5
BP,"GO:0051053","negative regulation of DNA metabolic process",124,-0.462433580293079,-2.1982
BP,"GO:0000768","syncytium formation by plasma membrane fusion",53,0.609413661147381,2.492
BP,"GO:0140253","cell-cell fusion",53,0.609413661147381,2.49232512835075,5.65351647573722e-
BP,"GO:0046634","regulation of alpha-beta T cell activation",102,0.501623667347529,2.2923985706
BP,"GO:0070527","platelet aggregation",69,0.573242349439934,2.44998206835473,5.87176517502
BP,"GO:0051783","regulation of nuclear division",138,-0.450225071694357,-2.18848664033391,5.9
BP,"GO:0061045","negative regulation of wound healing",70,0.564721714414279,2.416521389097,1
BP,"GO:0007266","Rho protein signal transduction",130,0.470041561222537,2.21416752410578,6.1
BP,"GO:0001654","eye development",372,0.342146555507055,1.84594082719303,6.212876803298
BP,"GO:0030509","BMP signaling pathway",152,0.442641740940016,2.15143564798792,6.3732482
BP,"GO:0009100","glycoprotein metabolic process",354,0.350050067361434,1.87674458884677,6.4
BP,"GO:0042098","T cell proliferation",197,0.41131695590824,2.06817203631299,6.623759940048
BP,"GO:2001057","reactive nitrogen species metabolic process",72,0.55753736071597,2.399159487
BP,"GO:0007389","pattern specification process",449,0.331418993003458,1.8317222239489,6.7571
BP,"GO:0001510","RNA methylation",72,-0.547139672689042,-2.36199084531426,6.781994789320
CC,"GO:0005876","spindle microtubule",81,-0.530620005330057,-2.33040371284354,6.7756695469
BP,"GO:1902100","negative regulation of metaphase/anaphase transition of cell cycle",42,-0.659109
BP,"GO:0043087","regulation of GTPase activity",353,0.346984165736766,1.85993734617353,7.252
BP,"GO:1901653","cellular response to peptide",340,0.348728554286583,1.86224596847369,7.721!
BP,"GO:0031532","actin cytoskeleton reorganization",108,0.500034691194555,2.28752319847411,7
BP,"GO:0060317","cardiac epithelial to mesenchymal transition",32,0.706080797389548,2.5589122
BP,"GO:0030195","negative regulation of blood coagulation",48,0.631018740752349,2.5270711453!
BP,"GO:0046209","nitric oxide metabolic process",71,0.559391399330865,2.39312731357542,8.009
BP,"GO:0002831","regulation of response to biotic stimulus",327,0.355924502539992,1.8961361364
BP,"GO:0006809","nitric oxide biosynthetic process",66,0.567084688155231,2.40402940058031,8.1
BP,"GO:0071772","response to BMP",163,0.429197418713383,2.10293452165063,8.476829881797
BP,"GO:0071773","cellular response to BMP stimulus",163,0.429197418713383,2.10293452165063,
BP,"GO:2001236","regulation of extrinsic apoptotic signaling pathway",149,0.439378552982187,2.1!
BP,"GO:0030500","regulation of bone mineralization",74,0.556644524543435,2.41241321533239,9.
BP,"GO:0097553","calcium ion transmembrane import into cytosol",143,0.445700463778952,2.1398
BP,"GO:0062013","positive regulation of small molecule metabolic process",134,0.46160577427793!
BP,"GO:0017015","regulation of transforming growth factor beta receptor signaling pathway",120,0.
BP,"GO:0045786","negative regulation of cell cycle",344,-0.336652457084463,-1.84986454730472,9
BP,"GO:0032722","positive regulation of chemokine production",68,0.569281580948641,2.4199152
BP,"GO:0046631","alpha-beta T cell activation",155,0.44246678345254,2.15901915549231,1.02420
BP,"GO:0071260","cellular response to mechanical stimulus",70,0.560194011912914,2.3971467313!
BP,"GO:0043030","regulation of macrophage activation",55,0.602710039958866,2.46101150436485
BP,"GO:0002822","regulation of adaptive immune response based on somatic recombination of imm
BP,"GO:0009451","RNA modification",151,-0.431458826179253,-2.11717613726603,1.16768507989
BP,"GO:0006334","nucleosome assembly",52,-0.595422366983181,-2.41163029021884,1.17263720
BP,"GO:0031098","stress-activated protein kinase signaling cascade",241,0.386886800500164,1.991
BP,"GO:0072088","nephron epithelium morphogenesis",74,0.554112248526494,2.40143871390682
BP,"GO:0045600","positive regulation of fat cell differentiation",63,0.575563456763652,2.41040414
CC,"GO:0035579","specific granule membrane",89,0.514186005490488,2.29092955994429,1.23376

CC,"GO:0000313","organellar ribosome",80,-0.520148820341054,-2.28777530793844,1.250061520.
CC,"GO:0005761","mitochondrial ribosome",80,-0.520148820341054,-2.28777530793844,1.250061.
BP,"GO:2001252","positive regulation of chromosome organization",83,-0.523334903639822,-2.301
BP,"GO:0072078","nephron tubule morphogenesis",72,0.550611405032016,2.36935615349397,1.29
BP,"GO:2000781","positive regulation of double-strand break repair",55,-0.591058406542412,-2.439
BP,"GO:0045739","positive regulation of DNA repair",81,-0.525125875988555,-2.30627431838485,1
BP,"GO:0050680","negative regulation of epithelial cell proliferation",121,0.466670031965382,2.178
MF,"GO:0008757","S-adenosylmethionine-dependent methyltransferase activity",131,-0.445661621
MF,"GO:0035064","methylated histone binding",74,-0.53777536658614,-2.32701214455886,1.3474
MF,"GO:0140034","methylation-dependent protein binding",74,-0.53777536658614,-2.3270121445
BP,"GO:0036230","granulocyte activation",43,0.646322645946978,2.53738082916922,1.355074173
BP,"GO:0061035","regulation of cartilage development",62,0.581914370967674,2.43974547457388
BP,"GO:0030098","lymphocyte differentiation",374,0.340723171802712,1.84128119811359,1.3789
BP,"GO:0042246","tissue regeneration",63,0.573929369845859,2.40356074369302,1.38090010122
BP,"GO:0003170","heart valve development",64,0.581662710173371,2.4510797153006,1.38957935
BP,"GO:0090288","negative regulation of cellular response to growth factor stimulus",96,0.5032371
BP,"GO:0002478","antigen processing and presentation of exogenous peptide antigen",36,0.680379
BP,"GO:0002690","positive regulation of leukocyte chemotaxis",92,0.507583421988223,2.27231039
BP,"GO:0043484","regulation of RNA splicing",151,-0.42984224184756,-2.10924352918556,1.44750
BP,"GO:0001952","regulation of cell-matrix adhesion",117,0.480209356744787,2.23196510581843,
BP,"GO:0002456","T cell mediated immunity",104,0.488844891125795,2.23445873613845,1.51455.
BP,"GO:0010038","response to metal ion",342,0.346519035283287,1.85296349804805,1.56078731
BP,"GO:0006949","syncytium formation",56,0.603235220936307,2.48477739177165,1.5629962062
BP,"GO:0006400","tRNA modification",82,-0.517367961895296,-2.27678949742783,1.60244440901
BP,"GO:0001959","regulation of cytokine-mediated signaling pathway",144,0.434555692867555,2.0
BP,"GO:0031663","lipopolysaccharide-mediated signaling pathway",60,0.581897578895581,2.42513
BP,"GO:1901222","regulation of NIK/NF-kappaB signaling",92,0.506039728341459,2.265399707629.
BP,"GO:1901989","positive regulation of cell cycle phase transition",112,-0.471705876429112,-2.20
BP,"GO:0031056","regulation of histone modification",167,-0.406321619735693,-2.0243710603523,
BP,"GO:0060393","regulation of pathway-restricted SMAD protein phosphorylation",60,0.58117193
BP,"GO:0048024","regulation of mRNA splicing, via spliceosome",102,-0.488289565893196,-2.23682
BP,"GO:0010543","regulation of platelet activation",47,0.627726337358146,2.48870769045173,1.75
BP,"GO:0030316","osteoclast differentiation",94,0.503621847865786,2.26337601203172,1.777747
BP,"GO:0072593","reactive oxygen species metabolic process",207,0.395235461088533,1.99288727
BP,"GO:0008202","steroid metabolic process",310,0.353795867643728,1.88007872691014,1.79137
BP,"GO:0031577","spindle checkpoint signaling",39,-0.650294347899923,-2.45142697060314,1.800
BP,"GO:0030850","prostate gland development",49,0.613855870321388,2.46512008439958,1.8236
BP,"GO:0010517","regulation of phospholipase activity",64,0.579497582560539,2.44195604228524
BP,"GO:0051607","defense response to virus",271,0.3666657687236,1.9088325689503,1.87223976
BP,"GO:0007264","small GTPase mediated signal transduction",487,0.311512263461589,1.7342664
BP,"GO:0051047","positive regulation of secretion",294,0.359506599217724,1.89084903679848,1.9
BP,"GO:0050671","positive regulation of lymphocyte proliferation",138,0.454812791686192,2.1629
CC,"GO:0098636","protein complex involved in cell adhesion",43,0.642470926522196,2.522259466
BP,"GO:0008016","regulation of heart contraction",196,0.406241500599855,2.03867214397116,1.9
BP,"GO:0050764","regulation of phagocytosis",93,0.513060413978068,2.30070908498,2.038138098
BP,"GO:0007094","mitotic spindle assembly checkpoint signaling",38,-0.665304693578037,-2.51573
BP,"GO:0071173","spindle assembly checkpoint signaling",38,-0.665304693578037,-2.51573129193
BP,"GO:0071174","mitotic spindle checkpoint signaling",38,-0.665304693578037,-2.5157312919301
BP,"GO:0048708","astrocyte differentiation",76,0.530677487347792,2.30914886705059,2.1387283
BP,"GO:0019884","antigen processing and presentation of exogenous antigen",45,0.6394417442012

CC,"GO:0070821","tertiary granule membrane",71,0.547748155977761,2.34331645892116,2.15899

MF,"GO:0048306","calcium-dependent protein binding",79,0.533079892227871,2.32867606236437

CC,"GO:0045178","basal part of cell",265,0.375084811798377,1.9502793967784,2.17048138811636

BP,"GO:0042129","regulation of T cell proliferation",167,0.420457819832909,2.0731862911848,2.21

BP,"GO:0032964","collagen biosynthetic process",40,0.640825726191208,2.47729560672849,2.226

BP,"GO:0060759","regulation of response to cytokine stimulus",154,0.436522421599949,2.1275778

BP,"GO:0051403","stress-activated MAPK cascade",234,0.380180801170491,1.9493691980571,2.30

BP,"GO:0051056","regulation of small GTPase mediated signal transduction",290,0.36264177496226

BP,"GO:0046596","regulation of viral entry into host cell",42,0.638705004025267,2.4798023982051

BP,"GO:0048247","lymphocyte chemotaxis",60,0.578006463340388,2.40892158643807,2.37195982

MF,"GO:0005543","phospholipid binding",445,0.32380692235564,1.78597358297669,2.4361851611

BP,"GO:0045926","negative regulation of growth",231,0.383441035833875,1.96208505182739,2.45

BP,"GO:0140546","defense response to symbiont",272,0.366071906123967,1.90820639710123,2.45

MF,"GO:0016741","transferase activity, transferring one-carbon groups",191,-0.394832029798868,-

BP,"GO:0003205","cardiac chamber development",162,0.422579823343634,2.07441750403325,2.45

BP,"GO:0060993","kidney morphogenesis",93,0.510891107043522,2.29098129457473,2.513281460

CC,"GO:0031674","I band",138,0.452857390758196,2.15367926240208,2.63305132110399e-08,2.6

BP,"GO:0061311","cell surface receptor signaling pathway involved in heart development",30,0.7089

MF,"GO:0070851","growth factor receptor binding",137,0.447757156535657,2.12542615519043,2.6

BP,"GO:0006956","complement activation",56,0.597935763858625,2.46294847549111,2.78959693

BP,"GO:1901888","regulation of cell junction assembly",194,0.404174180954168,2.02615640473171

BP,"GO:1905517","macrophage migration",52,0.600381566699787,2.44368213753364,2.961997698

BP,"GO:0048565","digestive tract development",126,0.452265736589089,2.1181138651711,3.02671

MF,"GO:0001664","G protein-coupled receptor binding",270,0.365827384975517,1.9013158121141

BP,"GO:0045428","regulation of nitric oxide biosynthetic process",54,0.591221581980908,2.426884

CC,"GO:0051233","spindle midzone",36,-0.654921722235652,-2.47326541280396,3.1855292403821

BP,"GO:0034765","regulation of ion transmembrane transport",442,0.321542367408285,1.7708993

MF,"GO:1901681","sulfur compound binding",248,0.371999694665783,1.91861670917213,3.53274

BP,"GO:0032368","regulation of lipid transport",107,0.477653617739493,2.19095641515218,3.5834

BP,"GO:0002700","regulation of production of molecular mediator of immune response",156,0.4232

CC,"GO:0042383","sarcolemma",128,0.451178195291499,2.11617719720047,3.68050092845856e-1

BP,"GO:0043434","response to peptide hormone",386,0.328539465639951,1.78265317827477,3.67

BP,"GO:0031124","mRNA 3'-end processing",60,-0.549624102674763,-2.2951976687628,3.8487433

CC,"GO:0030133","transport vesicle",383,0.322680234672833,1.74816095344368,4.0878943615321

BP,"GO:0060675","ureteric bud morphogenesis",63,0.561836292688174,2.35291610507752,4.1017

CC,"GO:0072562","blood microparticle",112,0.471299385904461,2.17071737679144,4.2896354104

BP,"GO:0003206","cardiac chamber morphogenesis",121,0.45637339414332,2.13003290897741,4.3

CC,"GO:0030018","Z disc",126,0.448997269617039,2.10280652558892,4.35556802907266e-08,4.23

BP,"GO:0032692","negative regulation of interleukin-1 production",36,0.669355482953348,2.49188

BP,"GO:0001706","endoderm formation",54,0.587404538532373,2.41121630388323,4.4310981105

BP,"GO:0003176","aortic valve development",37,0.655124233004045,2.46551977228457,4.4477731

BP,"GO:0060425","lung morphogenesis",50,0.599300989732691,2.42286291072021,4.45686030881

BP,"GO:0007099","centriole replication",40,-0.64087436063604,-2.45232904830241,4.76054837271

BP,"GO:0046635","positive regulation of alpha-beta T cell activation",67,0.557124977512707,2.3685

BP,"GO:0043010","camera-type eye development",325,0.348588762633741,1.85343376222915,4.7

BP,"GO:0010518","positive regulation of phospholipase activity",53,0.589352098878761,2.41027911

BP,"GO:0019229","regulation of vasoconstriction",63,0.560108710430919,2.34568115751568,4.936

BP,"GO:0010596","negative regulation of endothelial cell migration",51,0.598734194063036,2.4174

BP,"GO:0007009","plasma membrane organization",144,0.424581619966705,2.03676463394083,5.1

MF,"GO:0008168","methyltransferase activity",180,-0.396253197413189,-2.01282346138311,5.168

BP,"GO:0002504","antigen processing and presentation of peptide or polysaccharide antigen via MH
BP,"GO:0072171","mesonephric tubule morphogenesis",64,0.567496342044316,2.39138378335706
BP,"GO:0060402","calcium ion transport into cytosol",160,0.421420649067701,2.06491206425852,
BP,"GO:0014902","myotube differentiation",105,0.475832329644799,2.17815644879992,5.272137:
BP,"GO:0032731","positive regulation of interleukin-1 beta production",58,0.579092630030711,2.38
MF,"GO:0002020","protease binding",130,0.454376034183451,2.14037383418668,5.401252088377
BP,"GO:0006023","aminoglycan biosynthetic process",80,0.517805463087815,2.26563429398717,5
BP,"GO:0015850","organic hydroxy compound transport",238,0.375316232147652,1.922165772194
BP,"GO:0060828","regulation of canonical Wnt signaling pathway",240,0.371367147859089,1.90738
BP,"GO:0070588","calcium ion transmembrane transport",290,0.357663015496649,1.87591829847:
BP,"GO:0071897","DNA biosynthetic process",178,-0.398775226223379,-2.01741560281903,5.9116
BP,"GO:0042475","odontogenesis of dentin-containing tooth",88,0.500229837624316,2.221737357:
BP,"GO:0014074","response to purine-containing compound",132,0.447818832278973,2.12031864(
BP,"GO:0045601","regulation of endothelial cell differentiation",36,0.665720541608986,2.47835665
BP,"GO:0006024","glycosaminoglycan biosynthetic process",76,0.518481091141486,2.25607841436
CC,"GO:0016363","nuclear matrix",108,-0.461564336139405,-2.13865391940704,6.1024989889043
BP,"GO:0030178","negative regulation of Wnt signaling pathway",160,0.420151167873042,2.05869:
BP,"GO:1904705","regulation of vascular associated smooth muscle cell proliferation",52,0.5911663
BP,"GO:0060389","pathway-restricted SMAD protein phosphorylation",64,0.565517156765739,2.38
BP,"GO:0048844","artery morphogenesis",69,0.550852587258333,2.35429040162208,6.404434497
BP,"GO:0017148","negative regulation of translation",159,-0.401597248457851,-1.99303842712082
MF,"GO:0005044","scavenger receptor activity",46,0.618742197872271,2.43990702502575,6.74745
BP,"GO:0034724","DNA replication-independent chromatin organization",18,-0.791626916221418,7:
BP,"GO:0007143","female meiotic nuclear division",27,-0.718940130245497,-2.48881488189959,6.8
BP,"GO:1902969","mitotic DNA replication",13,-0.87128879664975,-2.46968811533688,6.91103013
BP,"GO:0061013","regulation of mRNA catabolic process",160,-0.400770642591543,-1.98903608689
BP,"GO:0035904","aorta development",58,0.57540768306438,2.37471822115619,7.149702923503!
BP,"GO:0046849","bone remodeling",88,0.497521697423476,2.20970933440439,7.3399223925563
BP,"GO:0051382","kinetochore assembly",16,-0.824866967313376,-2.52241672839846,7.49712312
BP,"GO:0010633","negative regulation of epithelial cell migration",66,0.547343010595064,2.320338
BP,"GO:0046890","regulation of lipid biosynthetic process",160,0.418047962717132,2.04838629422
CC,"GO:0030496","midbody",190,-0.380836110489634,-1.93907251379967,8.1753818946015e-08,
BP,"GO:0051298","centrosome duplication",71,-0.51727264973932,-2.23286668264302,8.2550866(
BP,"GO:1905168","positive regulation of double-strand break repair via homologous recombination"
MF,"GO:0042277","peptide binding",296,0.35328767602224,1.86047824863969,8.36211151099018
BP,"GO:1902106","negative regulation of leukocyte differentiation",98,0.47938681995914,2.167885
BP,"GO:0002042","cell migration involved in sprouting angiogenesis",53,0.583358601545745,2.3857
BP,"GO:0003180","aortic valve morphogenesis",32,0.681460979719345,2.46968739093702,8.43604
BP,"GO:0035850","epithelial cell differentiation involved in kidney development",48,0.60632305246
BP,"GO:0001658","branching involved in ureteric bud morphogenesis",57,0.573544833427878,2.36:
BP,"GO:0110110","positive regulation of animal organ morphogenesis",34,0.674761102941858,2.45
BP,"GO:0071887","leukocyte apoptotic process",107,0.467988978890617,2.14662554085401,8.672:
BP,"GO:0002253","activation of immune response",294,0.348387831366191,1.83236913259588,8.8
BP,"GO:0045814","negative regulation of gene expression, epigenetic",71,-0.515970117992316,-2.2
BP,"GO:0032609","interferon-gamma production",113,0.463625407507905,2.13737355902699,9.66
BP,"GO:0032649","regulation of interferon-gamma production",113,0.463625407507905,2.1373735
BP,"GO:0043547","positive regulation of GTPase activity",264,0.363121337693006,1.887381758050
BP,"GO:0006406","mRNA export from nucleus",60,-0.539317316121263,-2.25215713914464,1.0149
BP,"GO:0051092","positive regulation of NF-kappaB transcription factor activity",153,0.4237414734:
BP,"GO:0120254","olefinic compound metabolic process",154,0.425333647326618,2.073044628225

CC,"GO:0097431","mitotic spindle pole",36,-0.641387735771843,-2.42215527325319,1.0436529025
BP,"GO:0003044","regulation of systemic arterial blood pressure mediated by a chemical signal",48,
BP,"GO:1903038","negative regulation of leukocyte cell-cell adhesion",128,0.441684653444647,2.07
BP,"GO:0051988","regulation of attachment of spindle microtubules to kinetochore",13,-0.8662807
BP,"GO:1903707","negative regulation of hemopoiesis",100,0.473500695311081,2.1495375460063
BP,"GO:0010717","regulation of epithelial to mesenchymal transition",91,0.492576411039837,2.208
BP,"GO:0150076","neuroinflammatory response",65,0.552882387238627,2.33573086095644,1.110
BP,"GO:0001933","negative regulation of protein phosphorylation",305,0.34634575917039,1.82823
BP,"GO:0022617","extracellular matrix disassembly",57,0.570143793824848,2.35385627001898,1.1
BP,"GO:0002703","regulation of leukocyte mediated immunity",224,0.376006412826365,1.9138262
MF,"GO:0038024","cargo receptor activity",78,0.520455660977933,2.26838439266109,1.16969772
BP,"GO:0051591","response to cAMP",88,0.49318385699408,2.19044310634311,1.1942415627197
MF,"GO:0043021","ribonucleoprotein complex binding",138,-0.424507266581919,-2.063475670386
BP,"GO:0045621","positive regulation of lymphocyte differentiation",104,0.468254575178006,2.140
BP,"GO:0007080","mitotic metaphase plate congression",51,-0.579235953288546,-2.352466710263
BP,"GO:0061028","establishment of endothelial barrier",47,0.607902630769153,2.41011387001571
MF,"GO:0042562","hormone binding",84,0.507523788512278,2.24709426495823,1.230918316735
BP,"GO:1990874","vascular associated smooth muscle cell proliferation",53,0.577216616740583,2.3
BP,"GO:0032543","mitochondrial translation",68,-0.527287933367778,-2.26739618648971,1.25227
BP,"GO:0030728","ovulation",23,0.739302237240907,2.48875212039833,1.29659972889358e-07,1
BP,"GO:0002269","leukocyte activation involved in inflammatory response",46,0.612146436544858,
MF,"GO:0008236","serine-type peptidase activity",181,0.397579883484884,1.97846698982165,1.31
BP,"GO:0034103","regulation of tissue remodeling",73,0.520564362574034,2.24480409574077,1.34
BP,"GO:0055123","digestive system development",138,0.437495071999305,2.08061982247986,1.30
BP,"GO:0006513","protein monoubiquitination",73,-0.511074182423094,-2.20595817499961,1.378
BP,"GO:0043487","regulation of RNA stability",156,-0.402845130074278,-2.00591008152003,1.529
BP,"GO:0003094","glomerular filtration",20,0.765044931142832,2.4955968083853,1.53174085099
BP,"GO:0031507","heterochromatin assembly",64,-0.548710755425302,-2.32092769859513,1.5397
BP,"GO:0043536","positive regulation of blood vessel endothelial cell migration",49,0.59160504834
MF,"GO:0004879","nuclear receptor activity",52,0.579843598334809,2.36008818792155,1.5584971
MF,"GO:0098531","ligand-activated transcription factor activity",52,0.579843598334809,2.3600881
BP,"GO:0001774","microglial cell activation",43,0.616092001552606,2.41869914901964,1.5644913
MF,"GO:0004857","enzyme inhibitor activity",365,0.327204395111729,1.75780386210814,1.56283
BP,"GO:0070302","regulation of stress-activated protein kinase signaling cascade",192,0.392563292
BP,"GO:0098534","centriole assembly",44,-0.611700539920969,-2.39277746554439,1.5927581446
BP,"GO:0071711","basement membrane organization",32,0.673603743456685,2.44121192733307,1
CC,"GO:0000118","histone deacetylase complex",70,-0.51839524662884,-2.22317122811781,1.672
CC,"GO:0005902","microvillus",89,0.489863198940307,2.1825605341217,1.71280963277336e-07,1
CC,"GO:0009925","basal plasma membrane",247,0.360438282644689,1.857562378347,1.73041486
BP,"GO:0110053","regulation of actin filament organization",247,0.360363159006053,1.857175219
BP,"GO:0006284","base-excision repair",42,-0.623040783343662,-2.41808772977166,1.760205193
BP,"GO:0032409","regulation of transporter activity",261,0.35569935894574,1.84491252135463,1.7
MF,"GO:0017171","serine hydrolase activity",185,0.394271162403223,1.97374265227724,1.765268
BP,"GO:1902751","positive regulation of cell cycle G2/M phase transition",31,-0.680886275304767,-
BP,"GO:1901991","negative regulation of mitotic cell cycle phase transition",158,-0.4062469809260
BP,"GO:0072132","mesenchyme morphogenesis",53,0.571569030530469,2.33755156505042,1.793
BP,"GO:1903313","positive regulation of mRNA metabolic process",115,-0.443667846025751,-2.082
MF,"GO:0004175","endopeptidase activity",406,0.319365866978385,1.74096496754779,1.8157811
BP,"GO:0045936","negative regulation of phosphate metabolic process",395,0.319704783839906,1.
BP,"GO:0046632","alpha-beta T cell differentiation",110,0.454646744857132,2.09060614632864,1.8

BP,"GO:0051928","positive regulation of calcium ion transport",115,0.45142592308385,2.08797043

BP,"GO:0010971","positive regulation of G2/M transition of mitotic cell cycle",28,-0.7056509735557

BP,"GO:1905330","regulation of morphogenesis of an epithelium",64,0.551974924953106,2.325977

BP,"GO:0051569","regulation of histone H3-K4 methylation",38,-0.63920544860363,-2.4170416420

BP,"GO:0080164","regulation of nitric oxide metabolic process",56,0.575585094952978,2.37088416

BP,"GO:0006337","nucleosome disassembly",17,-0.805004003565989,-2.46987292790025,2.044513

BP,"GO:0010712","regulation of collagen metabolic process",35,0.654738789557573,2.4179317987

BP,"GO:0043500","muscle adaptation",98,0.470947394089918,2.12972073342922,2.134222182699

BP,"GO:2000379","positive regulation of reactive oxygen species metabolic process",64,0.55058975

MF,"GO:0051015","actin filament binding",209,0.380833598649708,1.92403475229243,2.16043244

MF,"GO:0017056","structural constituent of nuclear pore",26,-0.703096623097042,-2.40728143195

BP,"GO:2001233","regulation of apoptotic signaling pathway",347,0.330129493866322,1.76164237

BP,"GO:0019724","B cell mediated immunity",137,0.429069633936851,2.03671970186532,2.20518

BP,"GO:0034394","protein localization to cell surface",65,0.543384788146277,2.29560689279064,2

BP,"GO:0032330","regulation of chondrocyte differentiation",45,0.61218274070986,2.41103643642

BP,"GO:1905521","regulation of macrophage migration",39,0.634923131538156,2.43669473595236

BP,"GO:0061900","glial cell activation",49,0.586515372054058,2.35532621477184,2.360213649784

BP,"GO:0045445","myoblast differentiation",79,0.507988992531362,2.21907039469933,2.3644589

BP,"GO:0031062","positive regulation of histone methylation",48,-0.578032717381963,-2.31308013

BP,"GO:0034405","response to fluid shear stress",32,0.669612664332375,2.42674783021984,2.452

BP,"GO:0008360","regulation of cell shape",145,0.419184608921277,2.01724464048118,2.4668075

BP,"GO:0042326","negative regulation of phosphorylation",342,0.332820108946541,1.7797103492

MF,"GO:0033218","amide binding",370,0.322171687824924,1.73602328542429,2.47470080645707

BP,"GO:0030857","negative regulation of epithelial cell differentiation",44,0.612970376313963,2.40

CC,"GO:0044665","MLL1/2 complex",32,-0.662154175119424,-2.43970741109877,2.514613932050

BP,"GO:0009595","detection of biotic stimulus",37,0.635100637909831,2.39016220324667,2.56067

BP,"GO:0050766","positive regulation of phagocytosis",68,0.535945283869443,2.27820856089111,

BP,"GO:0010863","positive regulation of phospholipase C activity",39,0.633997154330272,2.433141

BP,"GO:0002286","T cell activation involved in immune response",115,0.44791455192852,2.071729

MF,"GO:0000400","four-way junction DNA binding",17,-0.801153460990786,-2.45805888620344,2.

BP,"GO:0030216","keratinocyte differentiation",159,0.40665903720118,1.98990983908132,2.64216

BP,"GO:0072202","cell differentiation involved in metanephros development",24,0.7364053080579

BP,"GO:0040029","regulation of gene expression, epigenetic",121,-0.436636009009106,-2.0611911

BP,"GO:0070304","positive regulation of stress-activated protein kinase signaling cascade",129,0.43

BP,"GO:0060324","face development",48,0.592157329948226,2.37144098170658,2.78463443347e

BP,"GO:1903054","negative regulation of extracellular matrix organization",11,0.882213299622507,

BP,"GO:0006303","double-strand break repair via nonhomologous end joining",55,-0.557429625329

CC,"GO:0005759","mitochondrial matrix",444,-0.296156924178384,-1.67378908943048,2.91455279

BP,"GO:0010563","negative regulation of phosphorus metabolic process",396,0.318049821318501,1

BP,"GO:0051283","negative regulation of sequestering of calcium ion",116,0.444341784145774,2.06

BP,"GO:1901654","response to ketone",184,0.388445548450713,1.93977234527289,2.9345597516

BP,"GO:0060688","regulation of morphogenesis of a branching structure",51,0.579086667760568,2.

CC,"GO:0101003","ficolin-1-rich granule membrane",57,0.557633328035822,2.30220642544064,2.9

BP,"GO:0060740","prostate gland epithelium morphogenesis",26,0.711895639120574,2.464398714

CC,"GO:0090734","site of DNA damage",83,-0.494229406304344,-2.17344431728761,3.1533829637

BP,"GO:0002495","antigen processing and presentation of peptide antigen via MHC class II",30,0.676

BP,"GO:0036297","interstrand cross-link repair",27,-0.704006451400799,-2.43711772300334,3.263

MF,"GO:0004536","deoxyribonuclease activity",55,-0.556949470780677,-2.29861865725724,3.2899

BP,"GO:0061037","negative regulation of cartilage development",25,0.722021482909425,2.4796744

BP,"GO:0030512","negative regulation of transforming growth factor beta receptor signaling pathwa

BP,"GO:0042303","molting cycle",113,0.450855368017712,2.07850201248949,3.43597824773572e
BP,"GO:0042633","hair cycle",113,0.450855368017712,2.07850201248949,3.43597824773572e-07,
BP,"GO:1901224","positive regulation of NIK/NF-kappaB signaling",64,0.547255644096273,2.30609:
BP,"GO:0098739","import across plasma membrane",178,0.394074207684349,1.96147865964918,3
BP,"GO:0030879","mammary gland development",131,0.430101728687023,2.03316049448357,3.60
CC,"GO:0030027","lamellipodium",194,0.384112666172401,1.92558648072589,3.60163406095615
CC,"GO:0000940","outer kinetochore",12,-0.86914674974469,-2.41104619380919,3.606692594865
BP,"GO:0090090","negative regulation of canonical Wnt signaling pathway",129,0.43027928514129:
BP,"GO:0009954","proximal/distal pattern formation",34,0.656947789222045,2.39462230476639,3
BP,"GO:0006509","membrane protein ectodomain proteolysis",43,0.605372785286274,2.37661686:
BP,"GO:0006352","DNA-templated transcription, initiation",111,-0.439631395866386,-2.036892376
BP,"GO:0032412","regulation of ion transmembrane transporter activity",235,0.363240774642227,1
BP,"GO:0045862","positive regulation of proteolysis",347,0.327540955917787,1.74782937190766,3
CC,"GO:0098800","inner mitochondrial membrane protein complex",114,-0.435731103447203,-2.03
BP,"GO:0031341","regulation of cell killing",97,0.476484545972107,2.15365338267767,3.83417216
BP,"GO:0046683","response to organophosphorus",123,0.434102699433982,2.03391784354095,3.8
BP,"GO:0010952","positive regulation of peptidase activity",179,0.389214773185603,1.9398965845
CC,"GO:0000794","condensed nuclear chromosome",69,-0.523411134047708,-2.24269144682138,3
BP,"GO:1903035","negative regulation of response to wounding",85,0.494346417202129,2.1898517
BP,"GO:0043537","negative regulation of blood vessel endothelial cell migration",35,0.64625388888
BP,"GO:0003151","outflow tract morphogenesis",77,0.498719154250972,2.16701226504444,4.048:
MF,"GO:0001618","virus receptor activity",73,0.506277572765961,2.18319587477542,4.071206897
MF,"GO:0043236","laminin binding",26,0.708557673205409,2.45284353942028,4.15694855173233
BP,"GO:0042119","neutrophil activation",38,0.638998544933442,2.42818538796985,4.1556832651
BP,"GO:0001938","positive regulation of endothelial cell proliferation",91,0.479107184448147,2.14:
BP,"GO:0060350","endochondral bone morphogenesis",56,0.565647309294447,2.32994957368331,
BP,"GO:0097696","receptor signaling pathway via STAT",169,0.399758787090892,1.9735158185624
BP,"GO:0006417","regulation of translation",363,-0.312967373638191,-1.73210340768672,4.42706
BP,"GO:0002275","myeloid cell activation involved in immune response",89,0.479198176115755,2.1
CC,"GO:0042611","MHC protein complex",22,0.745347779935835,2.48242291097679,4.510270231
BP,"GO:0043409","negative regulation of MAPK cascade",159,0.402654567408638,1.970314716112
MF,"GO:0003713","transcription coactivator activity",261,-0.337481226238106,-1.80161815995655
BP,"GO:0090307","mitotic spindle assembly",65,-0.525432795967259,-2.22623582232329,4.666364
BP,"GO:0071900","regulation of protein serine/threonine kinase activity",355,0.318893644149468,1
CC,"GO:0000428","DNA-directed RNA polymerase complex",96,-0.458109018934836,-2.075945500:
BP,"GO:0000727","double-strand break repair via break-induced replication",12,-0.86629558074423
CC,"GO:0071565","nBAF complex",15,-0.812882304350821,-2.40886895355613,4.96136974194293
MF,"GO:0008009","chemokine activity",48,0.584027365362986,2.33888252093578,5.02484866639
BP,"GO:0010742","macrophage derived foam cell differentiation",36,0.637214310069496,2.372233:
BP,"GO:0010833","telomere maintenance via telomere lengthening",77,-0.493955726493153,-2.160
BP,"GO:0003231","cardiac ventricle development",122,0.431282709151214,2.01352436357158,5.3:
BP,"GO:0045930","negative regulation of mitotic cell cycle",205,-0.363354205535978,-1.881917788
BP,"GO:0090049","regulation of cell migration involved in sprouting angiogenesis",37,0.6257785490
BP,"GO:0000380","alternative mRNA splicing, via spliceosome",77,-0.492436464133701,-2.1534215
BP,"GO:0071248","cellular response to metal ion",186,0.384736782693284,1.92517554163839,5.66
BP,"GO:0034110","regulation of homotypic cell-cell adhesion",35,0.640319242238659,2.364680819
BP,"GO:0007076","mitotic chromosome condensation",17,-0.789901960428493,-2.4235375962297:
BP,"GO:1903531","negative regulation of secretion by cell",130,0.432902751164665,2.03922225564
BP,"GO:0030510","regulation of BMP signaling pathway",97,0.47141675791381,2.13074758439585,
BP,"GO:0051209","release of sequestered calcium ion into cytosol",115,0.438741677109776,2.0293

BP,"GO:0016064","immunoglobulin mediated immune response",134,0.426509471411252,2.025828

BP,"GO:0034754","cellular hormone metabolic process",136,0.418917736803381,1.9933375105771

BP,"GO:0006336","DNA replication-independent chromatin assembly",17,-0.788857718077129,-2.4

BP,"GO:0006941","striated muscle contraction",164,0.398853367509203,1.95968972805001,6.3881

MF,"GO:0016893","endonuclease activity, active with either ribo- or deoxyribonucleic acids and proc

BP,"GO:0062197","cellular response to chemical stress",310,0.330343710162236,1.7554534658104

BP,"GO:0006940","regulation of smooth muscle contraction",60,0.539930901317014,2.2502364348

CC,"GO:0001726","ruffle",172,0.390418388180232,1.93894421453428,6.78318301373233e-07,5.22

BP,"GO:0002704","negative regulation of leukocyte mediated immunity",67,0.52971728272007,2.25

BP,"GO:0022898","regulation of transmembrane transporter activity",244,0.35470601094728,1.825

BP,"GO:0050868","negative regulation of T cell activation",117,0.445748376113059,2.07179391131

BP,"GO:0032886","regulation of microtubule-based process",235,-0.348802809135392,-1.82050927

BP,"GO:1900262","regulation of DNA-directed DNA polymerase activity",13,-0.842701014832162,-2

BP,"GO:1900264","positive regulation of DNA-directed DNA polymerase activity",13,-0.84270101483

BP,"GO:0062012","regulation of small molecule metabolic process",306,0.331794593509624,1.7537

CC,"GO:0098644","complex of collagen trimers",22,0.736508784060362,2.45298413559976,7.46084

BP,"GO:0007435","salivary gland morphogenesis",34,0.646224447509893,2.35553494703899,7.559

MF,"GO:0050431","transforming growth factor beta binding",24,0.721991630227808,2.4467082211

BP,"GO:0035272","exocrine system development",47,0.587074242816384,2.32753685166736,7.675

BP,"GO:0048008","platelet-derived growth factor receptor signaling pathway",52,0.5589928524874

BP,"GO:0051282","regulation of sequestering of calcium ion",117,0.44422636788375,2.0647197691

BP,"GO:0007043","cell-cell junction assembly",141,0.418142798450048,1.9997563823028,7.720827

BP,"GO:1903036","positive regulation of response to wounding",63,0.529981982045689,2.2195133

MF,"GO:0031406","carboxylic acid binding",167,0.389831120866061,1.92217268304796,7.7559759

BP,"GO:0051168","nuclear export",151,-0.399274128120987,-1.95924525121257,7.7895407942873

BP,"GO:1900274","regulation of phospholipase C activity",41,0.607533323875283,2.3576794364839

CC,"GO:0030880","RNA polymerase complex",98,-0.444552460249407,-2.03498883635456,7.85757

BP,"GO:0048333","mesodermal cell differentiation",30,0.667966037820983,2.39804096448473,7.90

BP,"GO:0048525","negative regulation of viral process",86,0.477381261617549,2.11787758352323,

BP,"GO:0003279","cardiac septum development",102,0.455767013971343,2.08283563829894,7.92

CC,"GO:0055029","nuclear DNA-directed RNA polymerase complex",95,-0.456977793726453,-2.068

BP,"GO:0048863","stem cell differentiation",205,0.373543317156535,1.88445155029196,7.9852676

BP,"GO:0007431","salivary gland development",36,0.628505942472164,2.33981346351899,8.01656

MF,"GO:0031492","nucleosomal DNA binding",24,-0.701670438925241,-2.3507789359852,8.03498

BP,"GO:0001909","leukocyte mediated cytotoxicity",124,0.424498287533848,1.98799232645593,8.

BP,"GO:0060512","prostate gland morphogenesis",28,0.686078029324691,2.40435359255294,8.20

BP,"GO:0001937","negative regulation of endothelial cell proliferation",38,0.629427897489928,2.39

BP,"GO:1901214","regulation of neuron death",300,0.329521029268201,1.73922665875816,8.3720

MF,"GO:0001228","DNA-binding transcription activator activity, RNA polymerase II-specific",453,0.3

BP,"GO:0055001","muscle cell development",168,0.388256289925045,1.91540080389398,8.428350

BP,"GO:0009913","epidermal cell differentiation",221,0.363449382412348,1.84804830665412,8.56

BP,"GO:0000387","spliceosomal snRNP assembly",37,-0.614839458296052,-2.32892269180384,8.60

BP,"GO:1903532","positive regulation of secretion by cell",269,0.340817521738312,1.76830288576

BP,"GO:0042311","vasodilation",46,0.586098528028994,2.31118213823587,8.657367670534e-07,6

BP,"GO:0032526","response to retinoic acid",107,0.447018611871472,2.05043625547577,8.714754

CC,"GO:0071339","MLL1 complex",31,-0.66012404484512,-2.39323585702188,8.77355215651425e

BP,"GO:0007520","myoblast fusion",40,0.591519649490827,2.28668882831332,8.80809370043753

BP,"GO:0035767","endothelial cell chemotaxis",27,0.692917249804846,2.41672715614107,8.93116

BP,"GO:0007498","mesoderm development",126,0.420941312042556,1.97141095893083,8.958694

BP,"GO:0002440","production of molecular mediator of immune response",203,0.371883929174777

BP,"GO:0002720","positive regulation of cytokine production involved in immune response",67,0.52

BP,"GO:0060986","endocrine hormone secretion",47,0.585570987948614,2.32157699029548,9.089

BP,"GO:0030217","T cell differentiation",258,0.348384954212739,1.8071550116597,9.39220890583

BP,"GO:0060412","ventricular septum morphogenesis",39,0.617166095144635,2.36854715247815,1

BP,"GO:0051208","sequestering of calcium ion",121,0.430966772669755,2.01145250850027,9.6043

CC,"GO:0010369","chromocenter",15,-0.802331728312981,-2.37760372004857,9.63083365608668

MF,"GO:0004252","serine-type endopeptidase activity",164,0.395141262059026,1.94145100797701

BP,"GO:0038061","NIK/NF-kappaB signaling",119,0.432863267992948,2.01367932998125,9.728910

BP,"GO:0097205","renal filtration",21,0.735465351896411,2.42336812282257,9.9404528177894e-C

MF,"GO:0005520","insulin-like growth factor binding",23,0.711629456420946,2.39559577854818,1

BP,"GO:0032872","regulation of stress-activated MAPK cascade",189,0.384411640525147,1.931672

BP,"GO:0016485","protein processing",234,0.354845724563066,1.81946411653568,1.00044009487

BP,"GO:0035051","cardiocyte differentiation",134,0.42235590785457,2.00609997607651,1.0078210

BP,"GO:0010888","negative regulation of lipid storage",21,0.734525834636587,2.4202724009474,1

BP,"GO:0045582","positive regulation of T cell differentiation",91,0.470076020088208,2.107852345

BP,"GO:0006979","response to oxidative stress",401,0.311288500986222,1.69853901234533,1.0490

CC,"GO:0101002","ficolin-1-rich granule",181,0.380154773819033,1.89175484542005,1.053646361

CC,"GO:0030894","replisome",15,-0.800698980071143,-2.37276528707041,1.06535516386847e-06

BP,"GO:1904064","positive regulation of cation transmembrane transport",139,0.407723668865398

BP,"GO:0098801","regulation of renal system process",33,0.64923969861987,2.37151750643278,1

BP,"GO:0001974","blood vessel remodeling",41,0.602734083378533,2.33905482745388,1.1005208

BP,"GO:0046578","regulation of Ras protein signal transduction",180,0.379998832166588,1.889276

BP,"GO:0046638","positive regulation of alpha-beta T cell differentiation",49,0.565133314265481,2

BP,"GO:0044774","mitotic DNA integrity checkpoint signaling",78,-0.486656767658517,-2.13434544

MF,"GO:0008173","RNA methyltransferase activity",58,-0.53015517593535,-2.20613816522951,1.1

BP,"GO:0003198","epithelial to mesenchymal transition involved in endocardial cushion formation",

BP,"GO:0046889","positive regulation of lipid biosynthetic process",79,0.486691185594587,2.12603

CC,"GO:0045334","clathrin-coated endocytic vesicle",87,0.476703057133049,2.12005744536212,1

BP,"GO:0032729","positive regulation of interferon-gamma production",76,0.485880734372025,2.1

BP,"GO:0072659","protein localization to plasma membrane",269,0.338684546210035,1.757236122

BP,"GO:0098657","import into cell",225,0.351841250929617,1.79032304544508,1.29391620292621

CC,"GO:0031253","cell projection membrane",330,0.325885800521332,1.73785046539793,1.31289

BP,"GO:0001707","mesoderm formation",68,0.514923766625713,2.18884981105415,1.3521754091

MF,"GO:0016779","nucleotidyltransferase activity",109,-0.428529074778305,-1.98335919185574,1

BP,"GO:1904407","positive regulation of nitric oxide metabolic process",40,0.583236699284714,2.2

BP,"GO:0006376","mRNA splice site selection",30,-0.640737619351914,-2.29416184167492,1.42321

BP,"GO:0035023","regulation of Rho protein signal transduction",82,0.48451490902957,2.13017759

BP,"GO:0002931","response to ischemia",50,0.557510802507698,2.25391292332798,1.4947923168

BP,"GO:0030261","chromosome condensation",33,-0.644664839443755,-2.38672079588419,1.5035

MF,"GO:0140272","exogenous protein binding",74,0.504086932851349,2.18463655864466,1.51210

BP,"GO:0032732","positive regulation of interleukin-1 production",68,0.513585814157015,2.183162

MF,"GO:0001216","DNA-binding transcription activator activity",457,0.296928313181245,1.6410744

BP,"GO:0032874","positive regulation of stress-activated MAPK cascade",127,0.419836541647093,1

BP,"GO:0019218","regulation of steroid metabolic process",96,0.458045705739579,2.067419062271

BP,"GO:0072678","T cell migration",62,0.525183238239407,2.201893427526,1.60305715359647e-C

MF,"GO:0048029","monosaccharide binding",71,0.500658945912507,2.14186453292328,1.6041926

BP,"GO:0090100","positive regulation of transmembrane receptor protein serine/threonine kinase s

BP,"GO:0045619","regulation of lymphocyte differentiation",175,0.379599859196208,1.8847229221

CC,"GO:0070461","SAGA-type complex",32,-0.636144423208028,-2.34387446632027,1.7096745431

BP,"GO:0070664","negative regulation of leukocyte proliferation",86,0.470069064916277,2.0854371

MF,"GO:0004518","nuclease activity",187,-0.366189168906647,-1.86238689401893,1.73328727081

BP,"GO:0060048","cardiac muscle contraction",127,0.418792018834332,1.95910827945126,1.7423

MF,"GO:0042379","chemokine receptor binding",63,0.51988235889267,2.17721708423555,1.76480

CC,"GO:0016581","NuRD complex",14,-0.809840540982991,-2.34906390121072,1.77147000855447

CC,"GO:0090545","CHD-type complex",14,-0.809840540982991,-2.34906390121072,1.77147000855

BP,"GO:0032986","protein-DNA complex disassembly",19,-0.745450860471302,-2.35286221685546

BP,"GO:0001910","regulation of leukocyte mediated cytotoxicity",82,0.48217230693163,2.11987830

BP,"GO:0060401","cytosolic calcium ion transport",176,0.385122291330903,1.91037228257037,1.8

BP,"GO:0007265","Ras protein signal transduction",335,0.322562457990835,1.72324939816396,1.8

BP,"GO:0033108","mitochondrial respiratory chain complex assembly",82,-0.471385948849974,-2.0

BP,"GO:0051048","negative regulation of secretion",153,0.398402618436905,1.94110540445004,1.

BP,"GO:0060411","cardiac septum morphogenesis",67,0.518402890228099,2.20396679169776,1.85

BP,"GO:0007568","aging",157,0.391759024889653,1.91023868310365,1.86958605133168e-06,1.30

BP,"GO:1905954","positive regulation of lipid localization",90,0.464020464932917,2.077861933311

BP,"GO:0032691","negative regulation of interleukin-1 beta production",30,0.656333308896433,2.3

BP,"GO:0090303","positive regulation of wound healing",52,0.546199427139728,2.22314917323210

BP,"GO:0070997","neuron death",339,0.323156675361779,1.7269710016046,1.95391774817309e-

BP,"GO:0042770","signal transduction in response to DNA damage",163,-0.375788600021268,-1.876

BP,"GO:0019915","lipid storage",80,0.47754445558532,2.08947408361747,1.97026058564653e-06,

BP,"GO:0046637","regulation of alpha-beta T cell differentiation",66,0.508524670694276,2.1557772

CC,"GO:0071007","U2-type catalytic step 2 spliceosome",30,-0.637441730633882,-2.282360908027

BP,"GO:0010812","negative regulation of cell-substrate adhesion",58,0.534377532337321,2.205386

BP,"GO:0009991","response to extracellular stimulus",462,0.297480442657553,1.64744430614179,

BP,"GO:0051960","regulation of nervous system development",423,0.297807394380909,1.63018211

BP,"GO:2000116","regulation of cysteine-type endopeptidase activity",219,0.361228204908431,1.83

BP,"GO:0007272","ensheathment of neurons",136,0.407804019825386,1.94045507808999,2.09329

BP,"GO:0008366","axon ensheathment",136,0.407804019825386,1.94045507808999,2.0932920468

BP,"GO:0048251","elastic fiber assembly",11,0.85569691005775,2.40322813304259,2.09924713410

BP,"GO:0000076","DNA replication checkpoint signaling",17,-0.768751203147561,-2.358643903053

BP,"GO:0045661","regulation of myoblast differentiation",52,0.544614949582532,2.2167000087031

MF,"GO:0033293","monocarboxylic acid binding",79,0.479426198371696,2.09429829955261,2.1494

BP,"GO:0031109","microtubule polymerization or depolymerization",119,-0.412307068107392,-1.94

BP,"GO:0016042","lipid catabolic process",315,0.319552620540905,1.69847738233533,2.16738429

BP,"GO:0003156","regulation of animal organ formation",29,0.667222184523711,2.3674670156615

CC,"GO:0008305","integrin complex",31,0.659186282246617,2.38161190453738,2.17604885852180

BP,"GO:0051043","regulation of membrane protein ectodomain proteolysis",23,0.70122979235909,

BP,"GO:0045670","regulation of osteoclast differentiation",63,0.517714960323597,2.168140228458

BP,"GO:0022604","regulation of cell morphogenesis",293,0.32903237349831,1.7290175757354,2.20

BP,"GO:0032331","negative regulation of chondrocyte differentiation",19,0.745437186838033,2.393

BP,"GO:0048645","animal organ formation",64,0.520995170422863,2.19543159920366,2.22527589

BP,"GO:0006898","receptor-mediated endocytosis",237,0.347388165491964,1.77885944782343,2.2

BP,"GO:0048332","mesoderm morphogenesis",70,0.50400998079658,2.15672758426961,2.2547770

BP,"GO:0006367","transcription initiation from RNA polymerase II promoter",75,-0.47432665495483

BP,"GO:0042092","type 2 immune response",37,0.607997694702263,2.28816194283964,2.3278102

CC,"GO:0005635","nuclear envelope",450,-0.279281992190239,-1.57826680583686,2.37798331086

BP,"GO:0050686","negative regulation of mRNA processing",29,-0.647040516751868,-2.2922932700

BP,"GO:0007259","receptor signaling pathway via JAK-STAT",162,0.383269151391998,1.8814439130

BP,"GO:0060325","face morphogenesis",30,0.652209970324302,2.34147567050738,2.50385323077

BP,"GO:0002686","negative regulation of leukocyte migration",45,0.58325230010832,2.2970960363

BP,"GO:0045931","positive regulation of mitotic cell cycle",117,-0.419734804148881,-1.9723164712

BP,"GO:0032613","interleukin-10 production",56,0.543596366322683,2.23911985641574,2.634077
BP,"GO:0032653","regulation of interleukin-10 production",56,0.543596366322683,2.23911985641
MF,"GO:0048407","platelet-derived growth factor binding",11,0.852188065448276,2.39337352917
BP,"GO:0062207","regulation of pattern recognition receptor signaling pathway",94,0.45330017179
BP,"GO:0009636","response to toxic substance",221,0.354837223315916,1.80425765297586,2.653
BP,"GO:1903900","regulation of viral life cycle",131,0.411295237755226,1.94425916753675,2.6664
MF,"GO:0030021","extracellular matrix structural constituent conferring compression resistance",22
MF,"GO:0043394","proteoglycan binding",35,0.616861098289363,2.27805055807876,2.688773041
BP,"GO:0002474","antigen processing and presentation of peptide antigen via MHC class I",28,0.666
MF,"GO:0004520","endodeoxyribonuclease activity",36,-0.601973358151727,-2.2733096728931,2.7
BP,"GO:0032733","positive regulation of interleukin-10 production",39,0.600125127287038,2.30314
BP,"GO:0045933","positive regulation of muscle contraction",42,0.58053606488372,2.25395873974
CC,"GO:0030135","coated vesicle",278,0.331031192031131,1.72216537590978,2.82862322702962
BP,"GO:0045987","positive regulation of smooth muscle contraction",30,0.650023362848966,2.333
BP,"GO:0034142","toll-like receptor 4 signaling pathway",38,0.611977473023282,2.3255056987909
BP,"GO:0006942","regulation of striated muscle contraction",87,0.466681880426197,2.0754899311
BP,"GO:0010743","regulation of macrophage derived foam cell differentiation",31,0.6552092623294
BP,"GO:0002063","chondrocyte development",28,0.663176290746444,2.32409467873739,3.10670
BP,"GO:0002483","antigen processing and presentation of endogenous peptide antigen",18,0.74476
BP,"GO:0019886","antigen processing and presentation of exogenous peptide antigen via MHC class
BP,"GO:0035987","endodermal cell differentiation",45,0.580523857353071,2.28635026637764,3.15
BP,"GO:0006298","mismatch repair",27,-0.671652700614886,-2.3251160513012,3.1968705459577
MF,"GO:0005161","platelet-derived growth factor receptor binding",13,0.817536852760055,2.3910
BP,"GO:0090501","RNA phosphodiester bond hydrolysis",139,-0.388402868278779,-1.89151813587
BP,"GO:0071677","positive regulation of mononuclear cell migration",65,0.509762220037068,2.153
CC,"GO:0098858","actin-based cell projection",205,0.362454444817351,1.82851040046861,3.41735
BP,"GO:0003071","renal system process involved in regulation of systemic arterial blood pressure",2
BP,"GO:0044060","regulation of endocrine process",35,0.612728616732654,2.26278942077797,3.4
BP,"GO:0050792","regulation of viral process",150,0.38729677317901,1.87841776358728,3.474779
CC,"GO:0000786","nucleosome",34,-0.616275605722234,-2.31471753070159,3.48854719029655e-
BP,"GO:2000106","regulation of leukocyte apoptotic process",83,0.468734653122733,2.073603092
MF,"GO:0042162","telomeric DNA binding",36,-0.596421481483145,-2.25234340459819,3.5558936
BP,"GO:0043488","regulation of mRNA stability",145,-0.390745248792045,-1.91647925288567,3.58
BP,"GO:0042273","ribosomal large subunit biogenesis",68,-0.48934131791233,-2.10422156076987,
MF,"GO:0003823","antigen binding",57,0.523400802163764,2.16087638460662,3.75528391683099
BP,"GO:0002821","positive regulation of adaptive immune response",104,0.433507410483241,1.98
BP,"GO:0043583","ear development",213,0.34846901372077,1.76735047960559,3.8638277948303
BP,"GO:0030574","collagen catabolic process",40,0.569054843767112,2.19984467981738,3.896978
BP,"GO:0097084","vascular associated smooth muscle cell development",11,0.845869786423203,2.3
BP,"GO:0043966","histone H3 acetylation",70,-0.478732762167767,-2.05307612237958,3.9586095
BP,"GO:0034655","nucleobase-containing compound catabolic process",380,-0.299158730350415,-1
BP,"GO:0070828","heterochromatin organization",72,-0.481794466869237,-2.07989692005932,3.9
BP,"GO:0050830","defense response to Gram-positive bacterium",87,0.462152626809205,2.055346
BP,"GO:1900024","regulation of substrate adhesion-dependent cell spreading",55,0.5339144040813
BP,"GO:0045429","positive regulation of nitric oxide biosynthetic process",38,0.608080138355315,2
BP,"GO:1902903","regulation of supramolecular fiber organization",346,0.312060621791768,1.6664
BP,"GO:0014002","astrocyte development",40,0.568185927598059,2.19648563519692,4.23583815
BP,"GO:2000377","regulation of reactive oxygen species metabolic process",131,0.40570883667224
BP,"GO:0042088","T-helper 1 type immune response",45,0.575391923316405,2.2661385238228,4.2
BP,"GO:0002709","regulation of T cell mediated immunity",84,0.470467101440766,2.083023396002

BP,"GO:0034249","negative regulation of cellular amide metabolic process",181,-0.36054714119279

BP,"GO:0044773","mitotic DNA damage checkpoint signaling",74,-0.473706987107338,-2.04978134

BP,"GO:0034767","positive regulation of ion transmembrane transport",153,0.389452389085066,1.8

BP,"GO:0014911","positive regulation of smooth muscle cell migration",32,0.632072545203142,2.29

BP,"GO:0045923","positive regulation of fatty acid metabolic process",36,0.605884851654157,2.255

CC,"GO:0044391","ribosomal subunit",173,-0.370086398859402,-1.86128002613373,4.5930100467

BP,"GO:0048715","negative regulation of oligodendrocyte differentiation",12,0.834329483737236,2

BP,"GO:0038066","p38MAPK cascade",52,0.535562561106586,2.17985484015094,4.649868547898

BP,"GO:0051017","actin filament bundle assembly",149,0.387794732126382,1.87596178573084,4.6

BP,"GO:0061572","actin filament bundle organization",149,0.387794732126382,1.87596178573084

BP,"GO:2000113","negative regulation of cellular macromolecule biosynthetic process",179,-0.35748

BP,"GO:0015711","organic anion transport",352,0.310092219223704,1.66109600927106,4.6839818

BP,"GO:0006304","DNA modification",111,-0.413372539368965,-1.9152303084188,4.71478157692

BP,"GO:0090077","foam cell differentiation",37,0.597412379404813,2.24832475952854,4.7500383

BP,"GO:0042274","ribosomal small subunit biogenesis",68,-0.484581758184371,-2.08375492974417

BP,"GO:0006301","postreplication repair",32,-0.622056927529897,-2.29196908098677,4.77065818

BP,"GO:0032204","regulation of telomere maintenance",77,-0.470449560292149,-2.0572729802890

BP,"GO:0034121","regulation of toll-like receptor signaling pathway",68,0.498453147876485,2.1188

BP,"GO:0007188","adenylate cyclase-modulating G protein-coupled receptor signaling pathway",220

BP,"GO:0051893","regulation of focal adhesion assembly",63,0.504967168926525,2.1147537098712

BP,"GO:0090109","regulation of cell-substrate junction assembly",63,0.504967168926525,2.114753

BP,"GO:0048730","epidermis morphogenesis",34,0.619566658936655,2.25836537563543,5.048107

BP,"GO:0000910","cytokinesis",155,-0.37323157012744,-1.84931461671316,5.07177403314122e-0

CC,"GO:0016514","SWI/SNF complex",24,-0.672983000716849,-2.25466853753238,5.08917537869

BP,"GO:0046942","carboxylic acid transport",272,0.329277113567493,1.71640785325859,5.117785

CC,"GO:0030669","clathrin-coated endocytic vesicle membrane",68,0.497906591050537,2.1165128

CC,"GO:0000315","organellar large ribosomal subunit",53,-0.527945261700563,-2.1492549870645,5

CC,"GO:0005762","mitochondrial large ribosomal subunit",53,-0.527945261700563,-2.14925498706

BP,"GO:1901976","regulation of cell cycle checkpoint",33,-0.622314044549836,-2.30397220512207,

BP,"GO:0045088","regulation of innate immune response",217,0.348804859203411,1.77199112870

BP,"GO:0033628","regulation of cell adhesion mediated by integrin",47,0.559636651859893,2.2187

BP,"GO:0150116","regulation of cell-substrate junction organization",68,0.495910835101834,2.1080

BP,"GO:0010862","positive regulation of pathway-restricted SMAD protein phosphorylation",48,0.54

BP,"GO:0060438","trachea development",18,0.737228154075751,2.32611100884276,5.597312487

BP,"GO:0001912","positive regulation of leukocyte mediated cytotoxicity",55,0.529792449869023,2

BP,"GO:1904035","regulation of epithelial cell apoptotic process",79,0.469392563908104,2.0504679

BP,"GO:0002825","regulation of T-helper 1 type immune response",29,0.655444996649599,2.32567

MF,"GO:0003953","NAD+ nucleosidase activity",28,0.654470273829749,2.29358452951852,5.76112

BP,"GO:0140353","lipid export from cell",42,0.571222647631889,2.21779895660661,5.7718739063

BP,"GO:0034764","positive regulation of transmembrane transport",200,0.358005355398536,1.800

MF,"GO:0004714","transmembrane receptor protein tyrosine kinase activity",60,0.51293907954302

BP,"GO:0090330","regulation of platelet aggregation",28,0.652959365526993,2.28828956648155,6.

CC,"GO:0005769","early endosome",367,0.301999256409307,1.62810668228821,6.2853947048395

BP,"GO:0009952","anterior/posterior pattern specification",211,0.345908029482202,1.7495142054

BP,"GO:0035633","maintenance of blood-brain barrier",35,0.602284755743545,2.22422053805751,

BP,"GO:2000401","regulation of lymphocyte migration",61,0.504347078632175,2.10407432674306,

BP,"GO:0030048","actin filament-based movement",127,0.40675493247366,1.90279881200893,6.4

BP,"GO:0046633","alpha-beta T cell proliferation",39,0.588419443447989,2.25822385287528,6.514

BP,"GO:0006029","proteoglycan metabolic process",78,0.470501078963101,2.05065942071741,6.5

CC,"GO:0005643","nuclear pore",91,-0.440942361519056,-1.98221690765403,6.63205419788757e-

BP,"GO:0042102","positive regulation of T cell proliferation",100,0.430236057628121,1.9531303093
BP,"GO:0042552","myelination",134,0.398776076340301,1.89410083374902,6.76517957355951e-0
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BP,"GO:0007189","adenylate cyclase-activating G protein-coupled receptor signaling pathway",132,0
BP,"GO:0002763","positive regulation of myeloid leukocyte differentiation",54,0.525037781963605,
MF,"GO:0045182","translation regulator activity",135,-0.387505520290522,-1.86830891949806,6.9
MF,"GO:0019199","transmembrane receptor protein kinase activity",78,0.4686114117236,2.042423
BP,"GO:0050779","RNA destabilization",86,-0.446498630042431,-1.99247779066477,7.2954268321
BP,"GO:0003281","ventricular septum development",69,0.495916291682594,2.11949801548052,7.4
MF,"GO:0003735","structural constituent of ribosome",158,-0.372263648544698,-1.8434889714130
BP,"GO:0022602","ovulation cycle process",49,0.538805259856305,2.16373212649496,7.60639270
MF,"GO:0008276","protein methyltransferase activity",73,-0.463926338308272,-2.00245313456577
BP,"GO:0003177","pulmonary valve development",21,0.704838924548315,2.32245363710283,7.64
BP,"GO:0043968","histone H2A acetylation",22,-0.678068992101477,-2.21512440058618,7.696372
BP,"GO:0051057","positive regulation of small GTPase mediated signal transduction",66,0.48914359
BP,"GO:0034113","heterotypic cell-cell adhesion",60,0.510166884286728,2.12619079229988,7.827
BP,"GO:2001026","regulation of endothelial cell chemotaxis",21,0.703711573653247,2.3187390008
BP,"GO:0031667","response to nutrient levels",432,0.289612809502613,1.58910016970014,8.0203
BP,"GO:0035710","CD4-positive, alpha-beta T cell activation",99,0.442438579564931,2.0064942823
BP,"GO:2000516","positive regulation of CD4-positive, alpha-beta T cell activation",37,0.5890071025
BP,"GO:0042698","ovulation cycle",70,0.485967664565998,2.07952204751197,8.19102918603816e
BP,"GO:0009914","hormone transport",281,0.323245115761521,1.68231556440758,8.2347899131
BP,"GO:0043367","CD4-positive, alpha-beta T cell differentiation",81,0.455250638105653,2.000100
BP,"GO:0030204","chondroitin sulfate metabolic process",29,0.649503292281773,2.3045960651598
BP,"GO:0032465","regulation of cytokinesis",87,-0.440751875713736,-1.96613031315358,8.394265
BP,"GO:0072243","metanephric nephron epithelium development",21,0.703044089229247,2.31653
CC,"GO:0005721","pericentric heterochromatin",21,-0.700267495840264,-2.26503135267806,8.496
BP,"GO:0002702","positive regulation of production of molecular mediator of immune response",11
BP,"GO:0003197","endocardial cushion development",47,0.55326838136843,2.19350884876095,8.5
MF,"GO:0098631","cell adhesion mediator activity",64,0.505461403580369,2.12997355944296,8.60
CC,"GO:0016323","basolateral plasma membrane",222,0.341324391294558,1.73511715990036,8.60
MF,"GO:0017069","snRNA binding",44,-0.559272451208665,-2.18769549970442,8.6673464027516
CC,"GO:0031304","intrinsic component of mitochondrial inner membrane",51,-0.526456525442483,
BP,"GO:0022404","molting cycle process",92,0.437215455840026,1.95729250167249,8.749908353
BP,"GO:0022405","hair cycle process",92,0.437215455840026,1.95729250167249,8.749908353380
BP,"GO:0045143","homologous chromosome segregation",54,-0.50658737799999,-2.066978525378
BP,"GO:1902893","regulation of miRNA transcription",57,0.512373840035008,2.11535123072937,9
BP,"GO:0060760","positive regulation of response to cytokine stimulus",61,0.499409392595541,2.0
BP,"GO:0110150","negative regulation of biomineralization",27,0.657819559404405,2.29431493226
BP,"GO:0046330","positive regulation of JNK cascade",95,0.436679913460459,1.96831500372658,9
BP,"GO:1904356","regulation of telomere maintenance via telomere lengthening",59,-0.500927894
BP,"GO:0043502","regulation of muscle adaptation",75,0.476429924918933,2.07346483544051,9.3
MF,"GO:0001540","amyloid-beta binding",81,0.452646341577457,1.98865918365639,9.430127467
BP,"GO:0060395","SMAD protein signal transduction",81,0.452583034241344,1.98838104882177,9
BP,"GO:1903556","negative regulation of tumor necrosis factor superfamily cytokine production",59
BP,"GO:0002444","myeloid leukocyte mediated immunity",101,0.439545003949365,2.00216668297
BP,"GO:0010544","negative regulation of platelet activation",19,0.719794849603546,2.3113293748
BP,"GO:0002705","positive regulation of leukocyte mediated immunity",128,0.399404436331742,1.0
BP,"GO:0044728","DNA methylation or demethylation",91,-0.434939856022272,-1.9552331816109
BP,"GO:0098754","detoxification",126,0.400295926072325,1.87472161296101,9.89473004212444e

BP,"GO:0032370","positive regulation of lipid transport",68,0.487875601408695,2.07387284715793

BP,"GO:0050810","regulation of steroid biosynthetic process",66,0.485114257150129,2.056533990

BP,"GO:2001022","positive regulation of response to DNA damage stimulus",114,-0.401082973283,-

MF,"GO:0008194","UDP-glycosyltransferase activity",136,0.389773452948887,1.85466017819831,1

BP,"GO:0110151","positive regulation of biomineralization",49,0.533713092313938,2.14328301932

BP,"GO:0010950","positive regulation of endopeptidase activity",161,0.374451843931538,1.839420

BP,"GO:0002707","negative regulation of lymphocyte mediated immunity",55,0.521023903966506,2

BP,"GO:0043628","ncRNA 3'-end processing",41,-0.555261856007967,-2.13445615910154,1.030149

BP,"GO:0003184","pulmonary valve morphogenesis",17,0.743635624567363,2.31229935457898,1.0

BP,"GO:0048245","eosinophil chemotaxis",19,0.718079446788624,2.30582105406377,1.033110400

BP,"GO:1903076","regulation of protein localization to plasma membrane",99,0.43907612831718,1.

BP,"GO:0018023","peptidyl-lysine trimethylation",46,-0.541755525716693,-2.16369475394458,1.04

BP,"GO:0070507","regulation of microtubule cytoskeleton organization",147,-0.371818666005607,-

BP,"GO:0070168","negative regulation of biomineral tissue development",26,0.658827531116911,2.

BP,"GO:0008154","actin polymerization or depolymerization",185,0.357163256764388,1.787978480

BP,"GO:0000082","G1/S transition of mitotic cell cycle",198,-0.346206687067215,-1.7838612125123

CC,"GO:0031305","integral component of mitochondrial inner membrane",50,-0.523161216435074,

BP,"GO:0045685","regulation of glial cell differentiation",72,0.474822745011911,2.04322718787028

BP,"GO:0009101","glycoprotein biosynthetic process",289,0.315629372890487,1.6534250039377,1.

BP,"GO:0072698","protein localization to microtubule cytoskeleton",53,-0.514125163865505,-2.092

BP,"GO:0006289","nucleotide-excision repair",57,-0.502913817183593,-2.08089485927023,1.12231

BP,"GO:0032720","negative regulation of tumor necrosis factor production",57,0.508950648512309

CC,"GO:0005849","mRNA cleavage factor complex",19,-0.717293334019477,-2.26398877982338,1.1

CC,"GO:0015030","Cajal body",57,-0.502480809621684,-2.07910321390513,1.15090918862308e-05

BP,"GO:0046660","female sex differentiation",124,0.39308560092301,1.84088176848759,1.151122

BP,"GO:0001906","cell killing",171,0.372513056523628,1.84830160011585,1.17635590687577e-05,

BP,"GO:0044843","cell cycle G1/S phase transition",224,-0.32989700426408,-1.71526403500862,1.1

BP,"GO:0034134","toll-like receptor 2 signaling pathway",16,0.748999896807442,2.2937597142896

BP,"GO:0098781","ncRNA transcription",51,-0.522039555133626,-2.12017342487134,1.1815931320

BP,"GO:0045453","bone resorption",63,0.490695717611348,2.0549862507745,1.18381234035784e

BP,"GO:0045638","negative regulation of myeloid cell differentiation",76,0.458693763668888,1.995

CC,"GO:0035578","azurophil granule lumen",86,0.448227269583299,1.98853738698862,1.1841626

BP,"GO:0010714","positive regulation of collagen metabolic process",23,0.67797599075525,2.28230

BP,"GO:0032967","positive regulation of collagen biosynthetic process",23,0.67797599075525,2.282

BP,"GO:0098581","detection of external biotic stimulus",25,0.673705184338447,2.31373938626389

BP,"GO:0001759","organ induction",24,0.674714480371632,2.28649391068137,1.21581870346491

BP,"GO:1900026","positive regulation of substrate adhesion-dependent cell spreading",41,0.570392

BP,"GO:0006958","complement activation, classical pathway",36,0.589934392212346,2.1962185879

BP,"GO:0031032","actomyosin structure organization",190,0.358713429868633,1.80606192949649,

BP,"GO:0071902","positive regulation of protein serine/threonine kinase activity",202,0.3594456227

CC,"GO:0005840","ribosome",202,-0.341727079617599,-1.7626567807499,1.27667840252571e-05,

BP,"GO:0072109","glomerular mesangium development",15,0.765010345460429,2.3102363732387

BP,"GO:0072677","eosinophil migration",23,0.677181066663647,2.2796303469099,1.29232297193

BP,"GO:1905523","positive regulation of macrophage migration",25,0.672180989768213,2.3085047

BP,"GO:0000302","response to reactive oxygen species",185,0.354362777728663,1.7739591313736

BP,"GO:0098789","pre-mRNA cleavage required for polyadenylation",13,-0.803406693134457,-2.27

BP,"GO:0071375","cellular response to peptide hormone stimulus",279,0.321702597462872,1.67638

BP,"GO:0045824","negative regulation of innate immune response",69,0.487240237211777,2.08241

BP,"GO:1905953","negative regulation of lipid localization",39,0.577903402637985,2.217865611047

BP,"GO:0071385","cellular response to glucocorticoid stimulus",50,0.526687126859173,2.12929851

BP,"GO:0009266","response to temperature stimulus",170,0.367093880457826,1.81726705399701, MF,"GO:0016796","exonuclease activity, active with either ribo- or deoxyribonucleic acids and produ BP,"GO:0061614","miRNA transcription",58,0.505707664668212,2.08706494753492,1.36379255716 BP,"GO:0048745","smooth muscle tissue development",22,0.684555342334163,2.27995026132389, BP,"GO:0048025","negative regulation of mRNA splicing, via spliceosome",20,-0.692372693962315,- BP,"GO:0048644","muscle organ morphogenesis",77,0.461552704745472,2.00551826338024,1.380 BP,"GO:0051571","positive regulation of histone H3-K4 methylation",27,-0.644720551004861,-2.231 BP,"GO:0050918","positive chemotaxis",58,0.504679921996083,2.08282343439215,1.39079747660 BP,"GO:0010718","positive regulation of epithelial to mesenchymal transition",49,0.5297612568869 BP,"GO:0030514","negative regulation of BMP signaling pathway",53,0.511517282191309,2.091957 BP,"GO:1990778","protein localization to cell periphery",323,0.303960125554927,1.6151892557185 MF,"GO:0048019","receptor antagonist activity",31,0.629856403943389,2.27564430598917,1.4275 BP,"GO:0033135","regulation of peptidyl-serine phosphorylation",137,0.390827491089407,1.855190 BP,"GO:0010883","regulation of lipid storage",51,0.522492772645941,2.1096261480748,1.4504401 CC,"GO:0005847","mRNA cleavage and polyadenylation specificity factor complex",15,-0.748905070 BP,"GO:0072170","metanephric tubule development",20,0.696728268379333,2.27274604680004,1. BP,"GO:0046700","heterocycle catabolic process",418,-0.277398000295299,-1.55749376280049,1.4 BP,"GO:0060602","branch elongation of an epithelium",18,0.721392783262762,2.27614705918408, BP,"GO:0046579","positive regulation of Ras protein signal transduction",58,0.503870511373416,2.(BP,"GO:0002455","humoral immune response mediated by circulating immunoglobulin",49,0.52900 BP,"GO:1902905","positive regulation of supramolecular fiber organization",168,0.36367193459879 BP,"GO:0032965","regulation of collagen biosynthetic process",31,0.628839560346573,2.27197049: BP,"GO:0006821","chloride transport",109,0.406705307919703,1.86610981397791,1.48544137293 CC,"GO:0005770","late endosome",265,0.328868771261768,1.70997590054493,1.50185342665639 BP,"GO:0050890","cognition",294,0.311998152173819,1.64097517765868,1.51064422516449e-05, BP,"GO:0000184","nuclear-transcribed mRNA catabolic process, nonsense-mediated decay",39,-0.56 BP,"GO:0000460","maturation of 5.8S rRNA",34,-0.595969138675899,-2.23844689006236,1.514594 BP,"GO:0045778","positive regulation of ossification",48,0.535489635970098,2.14450113811757,1. BP,"GO:0070199","establishment of protein localization to chromosome",22,-0.668905594904761,-: CC,"GO:0071564","npBAF complex",12,-0.815026432748059,-2.26091437275503,1.5254761161406 BP,"GO:1903312","negative regulation of mRNA metabolic process",85,-0.442130856454701,-1.967: CC,"GO:1990023","mitotic spindle midzone",14,-0.773871414515311,-2.24473005736444,1.549981 BP,"GO:0006953","acute-phase response",48,0.534858346601044,2.14197298317398,1.567656355 BP,"GO:0002711","positive regulation of T cell mediated immunity",55,0.51424093928936,2.099770 CC,"GO:0005884","actin filament",110,0.405482479960641,1.86453367240247,1.58461173901435e BP,"GO:0001913","T cell mediated cytotoxicity",45,0.554001640535347,2.18189447749307,1.58599 BP,"GO:1902275","regulation of chromatin organization",37,-0.566162361900699,-2.144540910776 BP,"GO:0001942","hair follicle development",89,0.434200720496918,1.93455919630995,1.6057802 BP,"GO:0050864","regulation of B cell activation",119,0.403180308599684,1.87559424352882,1.61: BP,"GO:0001954","positive regulation of cell-matrix adhesion",54,0.512608322428427,2.104187937 BP,"GO:0051592","response to calcium ion",142,0.381119142640328,1.83080700859764,1.6277978 CC,"GO:0030134","COPII-coated ER to Golgi transport vesicle",89,0.433827047246326,1.932894314 BP,"GO:0035909","aorta morphogenesis",32,0.609733743402076,2.20974022390704,1.6454857288 MF,"GO:0016798","hydrolase activity, acting on glycosyl bonds",135,0.381237728960285,1.8130303 BP,"GO:0035050","embryonic heart tube development",84,0.448076816733327,1.98388896822684 CC,"GO:0015934","large ribosomal subunit",109,-0.402130910156196,-1.86118068511506,1.690710 MF,"GO:0019865","immunoglobulin binding",21,0.687783706121031,2.26625646539667,1.7067521 BP,"GO:0010469","regulation of signaling receptor activity",165,0.372096090585414,1.8319263061: BP,"GO:0008347","glial cell migration",47,0.543334412540009,2.15412425845676,1.728281115102 BP,"GO:0060323","head morphogenesis",34,0.597307458248157,2.17722897586449,1.7458253968

BP,"GO:0001990","regulation of systemic arterial blood pressure by hormone",38,0.5873619781624
BP,"GO:2001257","regulation of cation channel activity",156,0.369485378455428,1.7975180736476
BP,"GO:0071622","regulation of granulocyte chemotaxis",49,0.523799439266376,2.1034718088738
BP,"GO:0002294","CD4-positive, alpha-beta T cell differentiation involved in immune response",66,0.5873619781624
BP,"GO:2001044","regulation of integrin-mediated signaling pathway",15,0.756300166143463,2.283741111111111
BP,"GO:0002832","negative regulation of response to biotic stimulus",104,0.418280751209192,1.911111111111111
BP,"GO:0032945","negative regulation of mononuclear cell proliferation",80,0.450681408429275,1.111111111111111
BP,"GO:2000249","regulation of actin cytoskeleton reorganization",39,0.573254135558587,2.200022222222222
BP,"GO:0045911","positive regulation of DNA recombination",62,-0.480362547291446,-2.021637137137137
BP,"GO:0097028","dendritic cell differentiation",46,0.543645853369143,2.1437770711661,1.933937500000000
BP,"GO:0060343","trabecula formation",24,0.667509652436722,2.26207796040919,1.940958634121212
BP,"GO:0061036","positive regulation of cartilage development",30,0.621957860545465,2.232868686868687
BP,"GO:0071604","transforming growth factor beta production",42,0.549107996694668,2.131937777777778
BP,"GO:0098773","skin epidermis development",93,0.440112005612124,1.97358763633607,2.004111111111111
BP,"GO:0006354","DNA-templated transcription, elongation",74,-0.454890261333425,-1.968359334444444
BP,"GO:0051402","neuron apoptotic process",231,0.329109601246803,1.68406865377599,2.013636363636364
BP,"GO:0045071","negative regulation of viral genome replication",53,0.506351484944636,2.070833333333333
MF,"GO:0003777","microtubule motor activity",66,-0.461496030717696,-1.96007507354659,2.035666666666667
BP,"GO:0002828","regulation of type 2 immune response",32,0.606732274129001,2.198862578614286
MF,"GO:0016757","glycosyltransferase activity",256,0.324974837798339,1.67700733761529,2.069444444444444
BP,"GO:0016049","cell growth",457,0.280526697659243,1.55042543768114,2.06864366276004e-05
BP,"GO:0044270","cellular nitrogen compound catabolic process",424,-0.275664635864336,-1.550722222222222
CC,"GO:0035577","azurophil granule membrane",54,0.506449458592231,2.07890663341057,2.076666666666667
BP,"GO:0010565","regulation of cellular ketone metabolic process",119,0.39961872014509,1.859022222222222
BP,"GO:0015718","monocarboxylic acid transport",115,0.403903288356092,1.86816503666521,2.100000000000000
BP,"GO:1901215","negative regulation of neuron death",199,0.345017225536342,1.732796209574333
BP,"GO:0072224","metanephric glomerulus development",16,0.739698810551207,2.265275789198198
CC,"GO:0043601","nuclear replisome",13,-0.794087600147693,-2.25085954985544,2.121299545371371
BP,"GO:0002292","T cell differentiation involved in immune response",75,0.464645572915096,2.022222222222222
CC,"GO:0000152","nuclear ubiquitin ligase complex",44,-0.544619085121172,-2.13037620393748,2.000000000000000
BP,"GO:0070293","renal absorption",20,0.690968051582617,2.2539560671945,2.1429454591078e-05
BP,"GO:0070169","positive regulation of biomineral tissue development",48,0.528981528481952,2.100000000000000
BP,"GO:0043981","histone H4-K5 acetylation",16,-0.731884014466681,-2.23807784102574,2.237583333333333
BP,"GO:0043982","histone H4-K8 acetylation",16,-0.731884014466681,-2.23807784102574,2.237583333333333
BP,"GO:0007548","sex differentiation",274,0.316932290250555,1.65183973341182,2.241972639961111
MF,"GO:0004527","exonuclease activity",74,-0.452647829156311,-1.95865608784113,2.269175977222222
CC,"GO:0044545","NSL complex",11,-0.799437306233946,-2.12399494948062,2.30383993431124e-05
BP,"GO:0031638","zymogen activation",62,0.488991931347616,2.05015705253094,2.326735310666667
BP,"GO:1901136","carbohydrate derivative catabolic process",159,0.369635131789706,1.808740291111111
BP,"GO:0045910","negative regulation of DNA recombination",29,-0.616095336337576,-2.182662686868687
BP,"GO:0071384","cellular response to corticosteroid stimulus",56,0.510224390612799,2.101657833333333
BP,"GO:0002824","positive regulation of adaptive immune response based on somatic recombination",226,0.329320662386436,1.676611111111111
CC,"GO:0005583","fibrillar collagen trimer",12,0.809258098718177,2.28774470887726,2.369379564646465
CC,"GO:0098643","banded collagen fibril",12,0.809258098718177,2.28774470887726,2.369379564646465
BP,"GO:0046328","regulation of JNK cascade",138,0.383807721725011,1.82529588320291,2.383822222222222
BP,"GO:0015849","organic acid transport",309,0.302237370780185,1.6032992453858,2.415056849444444
BP,"GO:1904888","cranial skeletal system development",70,0.469606150925915,2.009508894732333
BP,"GO:0003416","endochondral bone growth",28,0.628969079304782,2.20421584833389,2.438744444444444
CC,"GO:0000930","gamma-tubulin complex",16,-0.730572614647277,-2.23406762244121,2.451957777777778

BP,"GO:0045123","cellular extravasation",69,0.47761972340492,2.04130026153487,2.47220800503
BP,"GO:0071241","cellular response to inorganic substance",210,0.330470170559955,1.6666951917
BP,"GO:1904752","regulation of vascular associated smooth muscle cell migration",20,0.6889449387
BP,"GO:0019883","antigen processing and presentation of endogenous antigen",25,0.661249902213
BP,"GO:0048246","macrophage chemotaxis",37,0.570177899401163,2.14582946847666,2.4959079
BP,"GO:0007219","Notch signaling pathway",170,0.360723727215477,1.78573215180307,2.504423
BP,"GO:1904019","epithelial cell apoptotic process",103,0.422499655461083,1.94106877168483,2.1
BP,"GO:0014013","regulation of gliogenesis",92,0.424358231188724,1.89973426793173,2.5372376
BP,"GO:0061014","positive regulation of mRNA catabolic process",86,-0.429386807737403,-1.91611
BP,"GO:0021782","glial cell development",108,0.412832159346129,1.8885952479105,2.546687830
BP,"GO:0051482","positive regulation of cytosolic calcium ion concentration involved in phospholipa
CC,"GO:1902554","serine/threonine protein kinase complex",95,-0.415786986752155,-1.882000463
BP,"GO:0070646","protein modification by small protein removal",155,-0.35789295563639,-1.77331
BP,"GO:0046879","hormone secretion",272,0.316881528926395,1.65179395224008,2.59386557523
BP,"GO:0032354","response to follicle-stimulating hormone",18,0.710093312208819,2.2404948342
BP,"GO:0061157","mRNA destabilization",82,-0.437229682446018,-1.92412368425369,2.63718360
CC,"GO:0031256","leading edge membrane",169,0.361914595664947,1.78668787923609,2.646315
BP,"GO:0060441","epithelial tube branching involved in lung morphogenesis",29,0.63062191078829
BP,"GO:0002719","negative regulation of cytokine production involved in immune response",27,0.63
BP,"GO:0140448","signaling receptor ligand precursor processing",35,0.575023608179168,2.123545
BP,"GO:0048701","embryonic cranial skeleton morphogenesis",46,0.539259212511619,2.12647908
BP,"GO:0032620","interleukin-17 production",35,0.57468143215568,2.12228224614942,2.7324097
BP,"GO:0032660","regulation of interleukin-17 production",35,0.57468143215568,2.122282246149
MF,"GO:0034212","peptide N-acetyltransferase activity",41,-0.541998087899984,-2.083469527794
BP,"GO:1900744","regulation of p38MAPK cascade",42,0.545137309734298,2.11652139800167,2.7
BP,"GO:0048010","vascular endothelial growth factor receptor signaling pathway",51,0.5133554751
BP,"GO:0008406","gonad development",221,0.33530796124165,1.70495628818332,2.75987818497
BP,"GO:0001523","retinoid metabolic process",83,0.440577174100206,1.94903915127835,2.78491
BP,"GO:0006312","mitotic recombination",25,-0.654193228707477,-2.21804020206465,2.81203779
BP,"GO:0061314","Notch signaling involved in heart development",11,0.810479595801111,2.276231
BP,"GO:1901201","regulation of extracellular matrix assembly",15,0.747809144437718,2.258290879
BP,"GO:0048144","fibroblast proliferation",78,0.450916655295326,1.96530152317092,2.955057604
BP,"GO:0034104","negative regulation of tissue remodeling",22,0.671772761113552,2.23737715204
BP,"GO:0000959","mitochondrial RNA metabolic process",45,-0.52922598503163,-2.088241001593
BP,"GO:0031069","hair follicle morphogenesis",30,0.612345638690275,2.19836016033556,3.07147
MF,"GO:0140142","nucleocytoplasmic carrier activity",28,-0.63172082597347,-2.21516430940495,3
BP,"GO:0031343","positive regulation of cell killing",62,0.485607859075374,2.03596892550788,3.09
BP,"GO:2001056","positive regulation of cysteine-type endopeptidase activity",136,0.378285663733
BP,"GO:0010212","response to ionizing radiation",132,-0.37045184104792,-1.77861200958721,3.12
BP,"GO:0050672","negative regulation of lymphocyte proliferation",79,0.446524472327379,1.95057
BP,"GO:0045604","regulation of epidermal cell differentiation",54,0.499960456555868,2.052270156
BP,"GO:0140718","facultative heterochromatin assembly",29,-0.60964383369577,-2.159806721408
BP,"GO:0002689","negative regulation of leukocyte chemotaxis",20,0.682233752745306,2.2254645
BP,"GO:0034308","primary alcohol metabolic process",104,0.409225521615702,1.87052694714511
CC,"GO:1902911","protein kinase complex",111,-0.391269851449224,-1.81282452726549,3.234506
BP,"GO:0046545","development of primary female sexual characteristics",109,0.395410616625353,
BP,"GO:0002011","morphogenesis of an epithelial sheet",53,0.49852611135715,2.0388272099695,3
BP,"GO:0071539","protein localization to centrosome",32,-0.589456940720351,-2.17185441221401
CC,"GO:0005685","U1 snRNP",18,-0.698210774133232,-2.17955982201681,3.29662350113176e-05
BP,"GO:0009303","rRNA transcription",28,-0.630803294646207,-2.21194693463218,3.30659107370

CC,"GO:0098791","Golgi apparatus subcompartment",356,0.296728102605679,1.59201782460543,1.59201782460543
BP,"GO:0043271","negative regulation of ion transport",132,0.384232068131964,1.8192500127202,1.8192500127202
CC,"GO:0005614","interstitial matrix",11,0.806064062632443,2.26383408609265,3.4256332924372
CC,"GO:0033116","endoplasmic reticulum-Golgi intermediate compartment membrane",73,0.44736,0.44736,0.44736
MF,"GO:0042605","peptide antigen binding",23,0.65910894230369,2.21879320134843,3.45271339
BP,"GO:0003081","regulation of systemic arterial blood pressure by renin-angiotensin",24,0.656001,0.656001,0.656001
BP,"GO:1905508","protein localization to microtubule organizing center",34,-0.582780191893009,-2.1905508,1.8192500127202
CC,"GO:0030662","coated vesicle membrane",167,0.353832069230504,1.74466916943476,3.51983
BP,"GO:0060021","roof of mouth development",91,0.42436644901758,1.90288756888412,3.52729
BP,"GO:0030100","regulation of endocytosis",200,0.340392073042906,1.71202820660329,3.52679
BP,"GO:0007144","female meiosis I",10,-0.833340240674702,-2.15618178155136,3.5509613397215
BP,"GO:0002043","blood vessel endothelial cell proliferation involved in sprouting angiogenesis",23,0.65910894230369,2.21879320134843,3.45271339
BP,"GO:0001569","branching involved in blood vessel morphogenesis",33,0.589500150548389,2.15618178155136,3.5509613397215
BP,"GO:0001890","placenta development",145,0.368193002061067,1.77185742096234,3.58714058
BP,"GO:0008585","female gonad development",105,0.405119816797555,1.85446487453457,3.6128
BP,"GO:0019885","antigen processing and presentation of endogenous peptide antigen via MHC class II",20,0.680009400783264,2.21820865832242,3.6225
BP,"GO:0032495","response to muramyl dipeptide",18,0.703092919821367,2.21840711317685,3.6225
MF,"GO:0004497","monooxygenase activity",99,0.423369523885515,1.92001459233578,3.6495859
BP,"GO:0035886","vascular associated smooth muscle cell differentiation",27,0.633533766407572,2.21840711317685,3.6225
CC,"GO:0042470","melanosome",108,0.405714809708462,1.85603530218169,3.68641591842701e-05
CC,"GO:0048770","pigment granule",108,0.405714809708462,1.85603530218169,3.68641591842701e-05
MF,"GO:0099604","ligand-gated calcium channel activity",26,0.636132039801133,2.2021247148248
BP,"GO:0043297","apical junction assembly",70,0.461826867915639,1.97622027963867,3.7323746
BP,"GO:0070252","actin-mediated cell contraction",97,0.422733326856882,1.91070427583019,3.7323746
BP,"GO:0043032","positive regulation of macrophage activation",25,0.654788033881379,2.2487712
BP,"GO:0043281","regulation of cysteine-type endopeptidase activity involved in apoptotic process",25,0.654788033881379,2.2487712
BP,"GO:0046640","regulation of alpha-beta T cell proliferation",36,0.574130208834948,2.13738248
BP,"GO:1905332","positive regulation of morphogenesis of an epithelium",36,0.574061851298682,2.13738248
MF,"GO:0004529","exodeoxyribonuclease activity",22,-0.652312137664596,-2.13098158118272,3.8
MF,"GO:0016895","exodeoxyribonuclease activity, producing 5'-phosphomonoesters",22,-0.652312137664596,-2.13098158118272,3.8
BP,"GO:2001238","positive regulation of extrinsic apoptotic signaling pathway",49,0.5147548928456
CC,"GO:0031225","anchored component of membrane",162,0.35594626174384,1.7473175837271,3.8
MF,"GO:0016888","endodeoxyribonuclease activity, producing 5'-phosphomonoesters",15,-0.72997
BP,"GO:0046605","regulation of centrosome cycle",50,-0.502461412778411,-2.02814851246136,3.8
BP,"GO:0099024","plasma membrane invagination",63,0.470597183199541,1.97081553072412,3.8
BP,"GO:0051307","meiotic chromosome separation",22,-0.651784701069925,-2.12925854461236,3.8
BP,"GO:0033119","negative regulation of RNA splicing",25,-0.648444465445731,-2.19854903727241
BP,"GO:0009410","response to xenobiotic stimulus",395,0.284151130278573,1.54686051143514,3.8
CC,"GO:0032592","integral component of mitochondrial membrane",81,-0.428953605199873,-1.885
BP,"GO:2000278","regulation of DNA biosynthetic process",116,-0.380822783423372,-1.786749913
BP,"GO:0042481","regulation of odontogenesis",17,0.722066679785981,2.24523175392987,3.9974
BP,"GO:0023061","signal release",440,0.279470146184706,1.53607353924088,4.01023982531599e-05
CC,"GO:0031901","early endosome membrane",163,0.354007053879672,1.7345250042348,4.04927
BP,"GO:1904738","vascular associated smooth muscle cell migration",21,0.672818956760521,2.216
BP,"GO:0048736","appendage development",172,0.351899945610657,1.74764914843542,4.062646
BP,"GO:0060173","limb development",172,0.351899945610657,1.74764914843542,4.06264675752
BP,"GO:0014745","negative regulation of muscle adaptation",10,0.822904214238009,2.2330118411
BP,"GO:0045686","negative regulation of glial cell differentiation",25,0.652727481212223,2.241694
BP,"GO:0030488","tRNA methylation",39,-0.547598722287495,-2.06429331766231,4.11910387026

BP,"GO:0021675","nerve development",81,0.429998257117098,1.88915695196407,4.22973771409

BP,"GO:2000514","regulation of CD4-positive, alpha-beta T cell activation",63,0.469455679797932,1

CC,"GO:0000800","lateral element",12,-0.79586393545585,-2.20775687527393,4.28134864700088

BP,"GO:1905475","regulation of protein localization to membrane",166,0.357130923753897,1.7570

BP,"GO:0055078","sodium ion homeostasis",56,0.499590522376511,2.05785602706977,4.2983902

CC,"GO:0035267","NuA4 histone acetyltransferase complex",25,-0.646151471823428,-2.190774649

CC,"GO:0043189","H4/H2A histone acetyltransferase complex",25,-0.646151471823428,-2.1907746

BP,"GO:0016125","sterol metabolic process",145,0.365718089652765,1.75994738494228,4.331127

BP,"GO:0045639","positive regulation of myeloid cell differentiation",95,0.415233066195586,1.8716

BP,"GO:0010232","vascular transport",87,0.43052099793731,1.91467042932552,4.3676625988737

BP,"GO:0150104","transport across blood-brain barrier",87,0.43052099793731,1.91467042932552,4

CC,"GO:0070822","Sin3-type complex",13,-0.780509039498076,-2.2123708076741,4.376489728045

BP,"GO:0048016","inositol phosphate-mediated signaling",54,0.495452548501731,2.033765802580

BP,"GO:0043524","negative regulation of neuron apoptotic process",139,0.36851595822814,1.7582

BP,"GO:0002577","regulation of antigen processing and presentation",20,0.675092326742922,2.202

BP,"GO:0060055","angiogenesis involved in wound healing",25,0.650033938632436,2.23244404405

BP,"GO:0031668","cellular response to extracellular stimulus",230,0.324559630564794,1.660687730

BP,"GO:0045740","positive regulation of DNA replication",39,-0.545982680824205,-2.05820129542

CC,"GO:0016528","sarcoplasm",75,0.454794916797727,1.97930738183088,4.52797130611731e-05

BP,"GO:1903670","regulation of sprouting angiogenesis",35,0.56592869334901,2.08995862973311,

BP,"GO:0045682","regulation of epidermis development",60,0.475899726654156,1.9833776907820

BP,"GO:0043114","regulation of vascular permeability",47,0.527234435494989,2.09029367767108,

BP,"GO:2001235","positive regulation of apoptotic signaling pathway",122,0.382870201901018,1.78

BP,"GO:0002706","regulation of lymphocyte mediated immunity",165,0.359793767997886,1.77135

BP,"GO:0098659","inorganic cation import across plasma membrane",109,0.390987615806093,1.79

BP,"GO:0099587","inorganic ion import across plasma membrane",109,0.390987615806093,1.7939

BP,"GO:0032350","regulation of hormone metabolic process",36,0.570132153070857,2.122498448

BP,"GO:0001558","regulation of cell growth",391,0.281773998685503,1.53206487872137,4.937557

BP,"GO:0042531","positive regulation of tyrosine phosphorylation of STAT protein",64,0.482323911

MF,"GO:0003887","DNA-directed DNA polymerase activity",23,-0.642351307086328,-2.1169329227

BP,"GO:0033209","tumor necrosis factor-mediated signaling pathway",99,0.418020661179062,1.89

BP,"GO:0003382","epithelial cell morphogenesis",33,0.581699280809388,2.12480849654039,5.058

MF,"GO:0016410","N-acyltransferase activity",78,-0.438076744683749,-1.92128655806145,5.06904

BP,"GO:0032233","positive regulation of actin filament bundle assembly",59,0.483384703228752,2.1

BP,"GO:0086003","cardiac muscle cell contraction",70,0.45766848741809,1.95842600121827,5.108

BP,"GO:0014031","mesenchymal cell development",87,0.427583676579229,1.90160718183541,5.10

BP,"GO:0051315","attachment of mitotic spindle microtubules to kinetochore",15,-0.725248149247

BP,"GO:0070897","transcription preinitiation complex assembly",40,-0.533862879354286,-2.042845

BP,"GO:0002287","alpha-beta T cell activation involved in immune response",67,0.47280142393414

BP,"GO:0002293","alpha-beta T cell differentiation involved in immune response",67,0.4728014239

BP,"GO:0035107","appendage morphogenesis",138,0.374579866871508,1.78141045692959,5.2147

BP,"GO:0035108","limb morphogenesis",138,0.374579866871508,1.78141045692959,5.214714907

BP,"GO:0014033","neural crest cell differentiation",94,0.416883126018102,1.87355507162514,5.24

BP,"GO:0070198","protein localization to chromosome, telomeric region",29,-0.600103031913628,-

CC,"GO:0035861","site of double-strand break",63,-0.464039407659913,-1.95625478611418,5.2892

BP,"GO:0015698","inorganic anion transport",179,0.346376461699651,1.72638491991139,5.28959

MF,"GO:0017046","peptide hormone binding",50,0.508780038947334,2.05690347120919,5.335987

MF,"GO:0045296","cadherin binding",309,0.295543026564708,1.56778729991949,5.343720011731

BP,"GO:0030888","regulation of B cell proliferation",63,0.464588738420636,1.94565274456961,5.3

MF,"GO:0005319","lipid transporter activity",154,0.368590258021514,1.79648156032459,5.398150

BP,"GO:0032715","negative regulation of interleukin-6 production",46,0.523557818579981,2.06456

BP,"GO:0045292","mRNA cis splicing, via spliceosome",24,-0.630733074923663,-2.11312026915487

BP,"GO:0071692","protein localization to extracellular region",339,0.299443921714395,1.60024845

CC,"GO:0042575","DNA polymerase complex",19,-0.691811285187973,-2.18355993724909,5.58503

MF,"GO:0005507","copper ion binding",57,0.488992830420676,2.01882201007284,5.58573096517

BP,"GO:0002532","production of molecular mediator involved in inflammatory response",74,0.4522

BP,"GO:0060135","maternal process involved in female pregnancy",58,0.481014331536148,1.98515

BP,"GO:0071383","cellular response to steroid hormone stimulus",191,0.341308930154108,1.71862

BP,"GO:1903055","positive regulation of extracellular matrix organization",25,0.646412243437125,2

BP,"GO:0002823","negative regulation of adaptive immune response based on somatic recombination",

BP,"GO:0001961","positive regulation of cytokine-mediated signaling pathway",54,0.490918981190

BP,"GO:0006911","phagocytosis, engulfment",54,0.490668942910243,2.01412974763579,5.683216

BP,"GO:0001914","regulation of T cell mediated cytotoxicity",37,0.557636372385991,2.0986302026

BP,"GO:0043433","negative regulation of DNA-binding transcription factor activity",163,0.34905328

BP,"GO:2001212","regulation of vasculogenesis",16,0.722418946093338,2.21235741480282,5.8741

MF,"GO:0034061","DNA polymerase activity",29,-0.596901800820945,-2.11466507192969,5.88740

BP,"GO:0072577","endothelial cell apoptotic process",54,0.490309876744206,2.01265582951476,5.

BP,"GO:0033619","membrane protein proteolysis",57,0.486845596335324,2.0099570878028,5.911

CC,"GO:0034709","methylosome",12,-0.789868871984003,-2.19112634082197,5.94025802365109

MF,"GO:0035091","phosphatidylinositol binding",258,0.315452025632149,1.63632413560326,6.08

BP,"GO:0090596","sensory organ morphogenesis",262,0.312576021235815,1.6258529038393,6.11

BP,"GO:0055117","regulation of cardiac muscle contraction",70,0.454295805909517,1.9439938361

BP,"GO:0002701","negative regulation of production of molecular mediator of immune response",3

BP,"GO:0060445","branching involved in salivary gland morphogenesis",22,0.65830379693051,2.19

BP,"GO:0031400","negative regulation of protein modification process",473,0.271667974482803,1.5

BP,"GO:0006814","sodium ion transport",243,0.318253321403191,1.63723147760151,6.225620441

BP,"GO:0043407","negative regulation of MAP kinase activity",57,0.486284263312308,2.007639607

BP,"GO:0006346","DNA methylation-dependent heterochromatin assembly",22,-0.64237699313370

BP,"GO:0072234","metanephric nephron tubule development",18,0.693261563385288,2.18738710

BP,"GO:0001542","ovulation from ovarian follicle",10,0.813583930185125,2.20772055655424,6.334

BP,"GO:0001916","positive regulation of T cell mediated cytotoxicity",27,0.622960237899767,2.172

BP,"GO:0046599","regulation of centriole replication",22,-0.641112014878088,-2.09439287772783,

BP,"GO:0006997","nucleus organization",128,-0.367246924256493,-1.75837372962397,6.43267135

CC,"GO:0043256","laminin complex",12,0.79198333453168,2.2389095468599,6.51309426307785

BP,"GO:0010721","negative regulation of cell development",170,0.351323365992256,1.7391964625

BP,"GO:1902895","positive regulation of miRNA transcription",43,0.530930804362179,2.084367077

BP,"GO:0060439","trachea morphogenesis",10,0.813158094000822,2.20656501836951,6.55462157

BP,"GO:0006790","sulfur compound metabolic process",318,0.299576007143882,1.5916575540273

BP,"GO:0032467","positive regulation of cytokinesis",39,-0.537598086428682,-2.02659373047284,6

CC,"GO:0042827","platelet dense granule",20,0.666657265917661,2.17465364109493,6.592846437

MF,"GO:0070182","DNA polymerase binding",19,-0.688166379437422,-2.17205554242011,6.75753

BP,"GO:0000381","regulation of alternative mRNA splicing, via spliceosome",60,-0.44797727510982

MF,"GO:0030374","nuclear receptor coactivator activity",55,-0.484086021627309,-1.997899664883

BP,"GO:0090051","negative regulation of cell migration involved in sprouting angiogenesis",15,0.72

BP,"GO:0007202","activation of phospholipase C activity",29,0.614177262653031,2.1792506976342

BP,"GO:0043486","histone exchange",21,-0.660543971654579,-2.13654469828683,6.89862582588

CC,"GO:0071556","integral component of lumenal side of endoplasmic reticulum membrane",26,0.6

CC,"GO:0098553","lumenal side of endoplasmic reticulum membrane",26,0.622360986703185,2.15

MF,"GO:0070577","lysine-acetylated histone binding",23,-0.63737288687724,-2.10052604149383,7

MF,"GO:0140033","acetylation-dependent protein binding",23,-0.63737288687724,-2.10052604149

BP,"GO:0097006","regulation of plasma lipoprotein particle levels",70,0.451166363559002,1.930601e-05

BP,"GO:0014743","regulation of muscle hypertrophy",54,0.488598916871471,2.00563257029593,7.1e-05

BP,"GO:0016578","histone deubiquitination",38,-0.553580251168639,-2.09326519698776,7.147461e-05

BP,"GO:0034143","regulation of toll-like receptor 4 signaling pathway",22,0.655577275799958,2.1811e-05

BP,"GO:0042093","T-helper cell differentiation",64,0.475399678879919,2.00329587780464,7.29844e-05

BP,"GO:0048145","regulation of fibroblast proliferation",76,0.436228361359672,1.89817026428493,7.3e-05

BP,"GO:0042509","regulation of tyrosine phosphorylation of STAT protein",76,0.436168214121315,1.89817026428493,7.3e-05

BP,"GO:0006805","xenobiotic metabolic process",106,0.396125913371739,1.81715859327431,7.3511e-05

CC,"GO:0035770","ribonucleoprotein granule",252,-0.297533268255134,-1.58329172181172,7.4950e-05

BP,"GO:0048546","digestive tract morphogenesis",47,0.519127265238397,2.05815168240241,7.5311e-05

BP,"GO:0019233","sensory perception of pain",92,0.411762859367125,1.84334827678504,7.53797e-05

BP,"GO:0008543","fibroblast growth factor receptor signaling pathway",77,0.43920024990739,1.90817026428493,7.53797e-05

BP,"GO:0061383","trabecula morphogenesis",45,0.52402549332521,2.06383563927173,7.6114414e-05

MF,"GO:0020037","heme binding",131,0.371344585011514,1.75540596498092,7.68530844251523,7.68530844251523e-05

BP,"GO:2001028","positive regulation of endothelial cell chemotaxis",15,0.727158382941667,2.1950e-05

BP,"GO:0006690","icosanoid metabolic process",111,0.390653707275884,1.80125527581959,7.7761e-05

BP,"GO:0003401","axis elongation",27,0.61928864036864,2.15992844035863,7.79375137668215e-05

CC,"GO:0098573","intrinsic component of mitochondrial membrane",83,-0.426466995243553,-1.8711e-05

MF,"GO:1902936","phosphatidylinositol bisphosphate binding",100,0.400012435578121,1.8159249e-05

BP,"GO:0002285","lymphocyte activation involved in immune response",192,0.337037098378234,1.8159249e-05

BP,"GO:0048566","embryonic digestive tract development",33,0.571738042210086,2.088422471811e-05

CC,"GO:0044853","plasma membrane raft",106,0.395070813111287,1.81231850470568,7.8824411e-05

BP,"GO:0060415","muscle tissue morphogenesis",70,0.450361787951842,1.92715963569131,8.0331e-05

BP,"GO:0050922","negative regulation of chemotaxis",61,0.467340196701748,1.94968614153973,8.0331e-05

CC,"GO:0005938","cell cortex",289,0.299271285329985,1.56773313457381,8.22054972085597e-05

BP,"GO:0030501","positive regulation of bone mineralization",39,0.546842085307163,2.098659136e-05

BP,"GO:0016574","histone ubiquitination",48,-0.492384850546747,-1.97034801683786,8.31683668e-05

BP,"GO:0010639","negative regulation of organelle organization",328,-0.284028349829303,-1.55411e-05

BP,"GO:0003203","endocardial cushion morphogenesis",37,0.54974997897728,2.06895024591945,8.31683668e-05

BP,"GO:0010092","specification of animal organ identity",37,0.549512359450668,2.0680559794404,8.31683668e-05

BP,"GO:0090279","regulation of calcium ion import",40,0.52391543606169,2.02534535522939,8.3411e-05

BP,"GO:0014855","striated muscle cell proliferation",59,0.477852362113928,1.98878330223341,8.411e-05

BP,"GO:0016101","diterpenoid metabolic process",86,0.421275149757775,1.86896568404097,8.4311e-05

BP,"GO:0070265","necrotic cell death",53,0.483783946357888,1.9785360307321,8.5140962619560,8.5140962619560e-05

BP,"GO:0030522","intracellular receptor signaling pathway",249,0.317147630953711,1.6349184113e-05

BP,"GO:0038065","collagen-activated signaling pathway",17,0.706642739356421,2.1972717499681e-05

BP,"GO:0098787","mRNA cleavage involved in mRNA processing",14,-0.740589422370628,-2.14819e-05

BP,"GO:0033631","cell-cell adhesion mediated by integrin",16,0.713650741984142,2.185505403957e-05

BP,"GO:0007260","tyrosine phosphorylation of STAT protein",79,0.430526875768905,1.8806892633e-05

BP,"GO:0036336","dendritic cell migration",33,0.569515390549361,2.0803036563257,8.674350961e-05

BP,"GO:0050767","regulation of neurogenesis",347,0.287388127821206,1.53356519808636,8.6925e-05

BP,"GO:1904754","positive regulation of vascular associated smooth muscle cell migration",11,0.7881e-05

BP,"GO:0031058","positive regulation of histone modification",101,-0.39827653434757,-1.8242627e-05

MF,"GO:0001786","phosphatidylserine binding",57,0.480863294866613,1.98525897133852,8.9479e-05

MF,"GO:0090079","translation regulator activity, nucleic acid binding",101,-0.3981880463945,-1.8242627e-05

BP,"GO:0055076","transition metal ion homeostasis",131,0.369238886695567,1.74545198818024,8.9479e-05

CC,"GO:0005901","caveola",75,0.443726467965845,1.93113652136345,8.99545334973231e-05

BP,"GO:0046850","regulation of bone remodeling",49,0.499595512569306,2.00627377150552,9.011e-05

BP,"GO:0008207","C21-steroid hormone metabolic process",37,0.548037658362174,2.06250603256e-05

BP,"GO:0007019","microtubule depolymerization",44,-0.517560550363554,-2.02453184384088,9.011e-05

BP,"GO:0010972","negative regulation of G2/M transition of mitotic cell cycle",54,-0.468229201206

BP,"GO:0016073","snRNA metabolic process",54,-0.468130898391563,-1.91006834371162,9.13105

BP,"GO:0006378","mRNA polyadenylation",42,-0.525493089872849,-2.03949472758742,9.1924080

BP,"GO:0043631","RNA polyadenylation",42,-0.525493089872849,-2.03949472758742,9.192408011

BP,"GO:0002396","MHC protein complex assembly",18,0.685811887207465,2.16388179427098,9.2

BP,"GO:0002501","peptide antigen assembly with MHC protein complex",18,0.685811887207465,2.

BP,"GO:0030279","negative regulation of ossification",32,0.580365227256439,2.10330558395849,9

BP,"GO:0014009","glial cell proliferation",39,0.544997986037288,2.09158189033768,9.3086090260

BP,"GO:0050654","chondroitin sulfate proteoglycan metabolic process",34,0.568640357445026,2.07

BP,"GO:0034248","regulation of cellular amide metabolic process",417,-0.267077567352829,-1.4998

BP,"GO:0046883","regulation of hormone secretion",225,0.318601262024899,1.62118336097312,9

BP,"GO:0006287","base-excision repair, gap-filling",13,-0.762235986001013,-2.16057541764253,9.3

BP,"GO:0150077","regulation of neuroinflammatory response",33,0.567641396325279,2.073458403

BP,"GO:0045622","regulation of T-helper cell differentiation",37,0.547533248709948,2.0606077178

MF,"GO:0043177","organic acid binding",136,0.364396104919144,1.73390706773644,9.485969446

BP,"GO:0030326","embryonic limb morphogenesis",116,0.383963523708467,1.78219860767296,9.5

BP,"GO:0035113","embryonic appendage morphogenesis",116,0.383963523708467,1.78219860767

BP,"GO:0045920","negative regulation of exocytosis",31,0.59719539150703,2.15764146198646,9.5

BP,"GO:1902930","regulation of alcohol biosynthetic process",47,0.514528686029445,2.039919980

CC,"GO:0032040","small-subunit processome",34,-0.565080734227539,-2.12243072682606,9.62969

BP,"GO:0045124","regulation of bone resorption",41,0.532211572395608,2.06537523257492,9.763

BP,"GO:0046885","regulation of hormone biosynthetic process",22,0.65140489341201,2.169540817

BP,"GO:1902622","regulation of neutrophil migration",42,0.525161216788504,2.03896327197861,9

BP,"GO:0002281","macrophage activation involved in immune response",17,0.702978635137733,2.1

CC,"GO:0097346","INO80-type complex",26,-0.599069113461108,-2.05110920166272,9.891217468

BP,"GO:0051044","positive regulation of membrane protein ectodomain proteolysis",15,0.72070621

MF,"GO:0016891","endoribonuclease activity, producing 5'-phosphomonoesters",27,-0.6116632126

BP,"GO:0010324","membrane invagination",70,0.44747188643247,1.91479335216494,9.948909511

BP,"GO:0045580","regulation of T cell differentiation",146,0.361348158804012,1.74037045280932,9

MF,"GO:0031490","chromatin DNA binding",88,-0.406040735562197,-1.8221864819734,0.0001002

BP,"GO:0045662","negative regulation of myoblast differentiation",25,0.634911393390841,2.18050

BP,"GO:0034472","snRNA 3'-end processing",23,-0.630831749180744,-2.07896906855793,0.000101

BP,"GO:0030225","macrophage differentiation",47,0.513512235911197,2.03589012376282,0.00010

BP,"GO:0060143","positive regulation of syncytium formation by plasma membrane fusion",22,0.650

BP,"GO:0045777","positive regulation of blood pressure",35,0.553170981222445,2.0428447603217

BP,"GO:2001237","negative regulation of extrinsic apoptotic signaling pathway",94,0.407333182020

BP,"GO:0031145","anaphase-promoting complex-dependent catabolic process",16,-0.703051279527

BP,"GO:0090189","regulation of branching involved in ureteric bud morphogenesis",21,0.654304208

BP,"GO:0006913","nucleocytoplasmic transport",300,-0.282909587911918,-1.52383016108557,0.000

BP,"GO:0051169","nuclear transport",300,-0.282909587911918,-1.52383016108557,0.00010349347

BP,"GO:0072010","glomerular epithelium development",26,0.614679778030693,2.12786252886686

BP,"GO:0006986","response to unfolded protein",131,0.367171954543126,1.73568126530974,0.000

BP,"GO:0046916","cellular transition metal ion homeostasis",109,0.379909885650894,1.743162806

BP,"GO:0014912","negative regulation of smooth muscle cell migration",23,0.639260939380111,2.1

BP,"GO:0031623","receptor internalization",110,0.382766247019615,1.76007741763952,0.0001052

BP,"GO:0002429","immune response-activating cell surface receptor signaling pathway",216,0.3215

BP,"GO:0002757","immune response-activating signal transduction",216,0.32155936698069,1.6331

BP,"GO:0050714","positive regulation of protein secretion",126,0.371401338265948,1.7393984564

BP,"GO:0042790","nucleolar large rRNA transcription by RNA polymerase I",14,-0.736552734004029

CC,"GO:0070469","respirasome",84,-0.414566433648724,-1.83698803917457,0.0001072131791704

BP,"GO:0010887","negative regulation of cholesterol storage",10,0.804260086659656,2.182419613

BP,"GO:1904375","regulation of protein localization to cell periphery",120,0.386566385247082,1.80

CC,"GO:0048188","Set1C/COMPASS complex",15,-0.711583848061051,-2.10868440642853,0.00011

BP,"GO:0002768","immune response-regulating cell surface receptor signaling pathway",243,0.3126

BP,"GO:0090504","epiboly",32,0.575486168499017,2.08562335379205,0.00011554915066916,0.0

BP,"GO:0001659","temperature homeostasis",176,0.347953258386463,1.72599788538443,0.00011

BP,"GO:0030301","cholesterol transport",73,0.430180145161585,1.85504468071948,0.0001127055

BP,"GO:0060142","regulation of syncytium formation by plasma membrane fusion",27,0.612611510

BP,"GO:0030490","maturation of SSU-rRNA",46,-0.499686270845846,-1.99567611500963,0.000114

BP,"GO:0046697","decidualization",23,0.636154360412095,2.14151998144209,0.000114928723366

BP,"GO:0032231","regulation of actin filament bundle assembly",97,0.407423088955901,1.8415038

BP,"GO:0006066","alcohol metabolic process",344,0.290095716882456,1.54980342986096,0.00011

BP,"GO:0000729","DNA double-strand break processing",18,-0.672054561708588,-2.097909650164

CC,"GO:0005903","brush border",101,0.405470640891979,1.84695492116435,0.000117895475737

BP,"GO:0010744","positive regulation of macrophage derived foam cell differentiation",18,0.679571

BP,"GO:0034138","toll-like receptor 3 signaling pathway",18,0.679365512332491,2.1435421158676

MF,"GO:0019956","chemokine binding",33,0.563706671039818,2.0590857917433,0.000118924200

BP,"GO:0140747","regulation of ncRNA transcription",17,-0.696236967572908,-2.13615936069158,

BP,"GO:0007063","regulation of sister chromatid cohesion",17,-0.695833966763927,-2.1349228938

MF,"GO:0019787","ubiquitin-like protein transferase activity",437,-0.258680114354874,-1.4620989

BP,"GO:0010463","mesenchymal cell proliferation",41,0.527202563654751,2.04593656733404,0.00

BP,"GO:0031952","regulation of protein autophosphorylation",41,0.526298251514495,2.042427166

BP,"GO:0010171","body morphogenesis",45,0.51572428847206,2.03114195806147,0.00011996381

BP,"GO:0008625","extrinsic apoptotic signaling pathway via death domain receptors",81,0.4108752

BP,"GO:0043038","amino acid activation",26,-0.594987239522919,-2.03713357012619,0.00012155

MF,"GO:0015278","calcium-release channel activity",17,0.698748212894019,2.1727240980797,0.00

BP,"GO:0045723","positive regulation of fatty acid biosynthetic process",21,0.650447533063307,2.1

BP,"GO:0098868","bone growth",31,0.590538193874882,2.13358929106211,0.0001227891658636

BP,"GO:0061097","regulation of protein tyrosine kinase activity",86,0.414860916346885,1.8405092

CC,"GO:0016010","dystrophin-associated glycoprotein complex",17,0.698149955004902,2.1708638

BP,"GO:0045628","regulation of T-helper 2 cell differentiation",11,0.781783086967398,2.19564087

MF,"GO:0050135","NAD(P)+ nucleosidase activity",16,0.706574885852281,2.16383609023839,0.00

MF,"GO:0061809","NAD+ nucleotidase, cyclic ADP-ribose generating",16,0.706574885852281,2.163

BP,"GO:1904707","positive regulation of vascular associated smooth muscle cell proliferation",31,0.!

CC,"GO:1902555","endoribonuclease complex",31,-0.577096099607924,-2.09222355906336,0.0001

BP,"GO:2000105","positive regulation of DNA-templated DNA replication",14,-0.732290237911384,-

BP,"GO:0030177","positive regulation of Wnt signaling pathway",137,0.366859377162339,1.741418

BP,"GO:2000811","negative regulation of anoikis",17,0.697479017300766,2.16877759517672,0.000

BP,"GO:0035456","response to interferon-beta",27,0.610283790574621,2.12852171027606,0.0001

CC,"GO:0016592","mediator complex",39,-0.527460458178728,-1.98837772046116,0.00012737928

BP,"GO:0035914","skeletal muscle cell differentiation",64,0.466325158377503,1.96505658080222,C

BP,"GO:0000288","nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay",5

BP,"GO:0070200","establishment of protein localization to telomere",17,-0.692478706152703,-2.12

BP,"GO:0048638","regulation of developmental growth",306,0.291136984407112,1.5388608286491

BP,"GO:0007584","response to nutrient",148,0.353625307414916,1.70838157669018,0.000130782

MF,"GO:0046906","tetrapyrrole binding",139,0.355102964728344,1.69429273638675,0.000131277

BP,"GO:0003096","renal sodium ion transport",11,0.780595714229878,2.19230612956533,0.00013

BP,"GO:0002691","regulation of cellular extravasation",36,0.547131633099121,2.03687169035662,

MF,"GO:0048020","CCR chemokine receptor binding",40,0.516408537568814,1.99632528643926,0.

BP,"GO:0070278","extracellular matrix constituent secretion",13,0.746309865890224,2.182732695

BP,"GO:2000241","regulation of reproductive process",167,0.341316929557128,1.68295973086749

BP,"GO:0042113","B cell activation",251,0.30885686898482,1.59395727269668,0.00013388447270

BP,"GO:0072273","metanephric nephron morphogenesis",25,0.630219154704733,2.164393141267:

BP,"GO:0006641","triglyceride metabolic process",95,0.402497238303389,1.81423813802879,0.000

BP,"GO:0051231","spindle elongation",10,-0.805197285380291,-2.08336479213574,0.00013885459

BP,"GO:0043370","regulation of CD4-positive, alpha-beta T cell differentiation",49,0.4912502548341

BP,"GO:0044070","regulation of anion transport",87,0.41711979028703,1.85507079045036,0.00014

CC,"GO:0000307","cyclin-dependent protein kinase holoenzyme complex",46,-0.496336920285933,-

BP,"GO:0032682","negative regulation of chemokine production",21,0.647433149394669,2.1333008

BP,"GO:0019439","aromatic compound catabolic process",438,-0.268346641083091,-1.5165119123

BP,"GO:0071320","cellular response to cAMP",53,0.473257066879131,1.93548414673162,0.000142

BP,"GO:0002708","positive regulation of lymphocyte mediated immunity",107,0.389102160363974,

BP,"GO:0031061","negative regulation of histone methylation",21,-0.646937338089443,-2.0925337:

BP,"GO:1904706","negative regulation of vascular associated smooth muscle cell proliferation",22,0.

CC,"GO:0044291","cell-cell contact zone",67,0.455574098382643,1.93685298234197,0.0001453944

BP,"GO:1904892","regulation of receptor signaling pathway via STAT",105,0.390106226491727,1.78

BP,"GO:0016486","peptide hormone processing",33,0.559402897264522,2.04336513437509,0.0001

BP,"GO:0045671","negative regulation of osteoclast differentiation",30,0.58251334030259,2.091260

BP,"GO:0038084","vascular endothelial growth factor signaling pathway",39,0.53854527663309,2.00

BP,"GO:0098742","cell-cell adhesion via plasma-membrane adhesion molecules",269,0.3002338850

CC,"GO:0030136","clathrin-coated vesicle",185,0.329687174080808,1.65043173187125,0.00014927

BP,"GO:0046636","negative regulation of alpha-beta T cell activation",41,0.521050422750036,2.022

BP,"GO:0001945","lymph vessel development",29,0.598529393769961,2.12372824303767,0.00015:

BP,"GO:0010611","regulation of cardiac muscle hypertrophy",52,0.48058017907594,1.95606471683

BP,"GO:2000047","regulation of cell-cell adhesion mediated by cadherin",19,0.670035545788323,2.

CC,"GO:0005686","U2 snRNP",20,-0.647413733014527,-2.07723025022982,0.000153279345696823

BP,"GO:0032717","negative regulation of interleukin-8 production",18,0.674425946387586,2.12795

BP,"GO:0007254","JNK cascade",170,0.341754712931717,1.69182765886604,0.0001537932429373

MF,"GO:1990782","protein tyrosine kinase binding",108,0.387125604877372,1.7709947279153,0.00

BP,"GO:0014014","negative regulation of gliogenesis",37,0.535950027119386,2.01701497555676,0.

BP,"GO:0002820","negative regulation of adaptive immune response",59,0.466653459982336,1.942

BP,"GO:0061082","myeloid leukocyte cytokine production",29,0.596835698031478,2.117718597542

BP,"GO:0045932","negative regulation of muscle contraction",21,0.644890776123221,2.124923690:

BP,"GO:0010745","negative regulation of macrophage derived foam cell differentiation",13,0.74134

BP,"GO:0000731","DNA synthesis involved in DNA repair",33,-0.557822687737031,-2.065208039555

MF,"GO:0015267","channel activity",461,0.266579173753104,1.47688728225177,0.0001574081796

BP,"GO:0045940","positive regulation of steroid metabolic process",31,0.585773199756213,2.11637

BP,"GO:0010257","NADH dehydrogenase complex assembly",49,-0.468014132703118,-1.881574652

BP,"GO:0032981","mitochondrial respiratory chain complex I assembly",49,-0.468014132703118,-1.

BP,"GO:0061298","retina vasculature development in camera-type eye",19,0.667023005407534,2.14

CC,"GO:0042613","MHC class II protein complex",15,0.711464323613035,2.14853402758012,0.0001

BP,"GO:0035592","establishment of protein localization to extracellular region",332,0.28551998167:

BP,"GO:0002762","negative regulation of myeloid leukocyte differentiation",48,0.492133310066508

BP,"GO:1903672","positive regulation of sprouting angiogenesis",20,0.649334725779124,2.1181470

BP,"GO:0051604","protein maturation",299,0.295634885358584,1.55910756063388,0.0001651743:

MF,"GO:0034713","type I transforming growth factor beta receptor binding",10,0.794427324729624

MF,"GO:0008307","structural constituent of muscle",42,0.517305377753283,2.00846260522842,0.00

MF,"GO:0004842","ubiquitin-protein transferase activity",412,-0.264683600311335,-1.48475718104

BP,"GO:0009060","aerobic respiration",150,-0.335637371740503,-1.64604389160763,0.000172312:

MF,"GO:0046873","metal ion transmembrane transporter activity",420,0.270149138509489,1.48036

BP,"GO:0006968","cellular defense response",51,0.477917785842632,1.92964938546019,0.000172

MF,"GO:0003707","nuclear steroid receptor activity",24,0.623643070456648,2.11342149089841,0.0

BP,"GO:0035115","embryonic forelimb morphogenesis",30,0.575554483238027,2.06627754997856

BP,"GO:0046785","microtubule polymerization",81,-0.405889385150193,-1.78260548161849,0.000

MF,"GO:0016298","lipase activity",121,0.377583570389278,1.76229692865438,0.00017429762063

BP,"GO:0042554","superoxide anion generation",40,0.513425112507411,1.98479200134232,0.0001

BP,"GO:0045907","positive regulation of vasoconstriction",32,0.566369418529698,2.052583277961

BP,"GO:0048872","homeostasis of number of cells",271,0.298355659835046,1.55321562360816,0.0

BP,"GO:0003093","regulation of glomerular filtration",10,0.793031822446658,2.15195088233709,0.

BP,"GO:1901861","regulation of muscle tissue development",43,0.513771527853827,2.0170019316

BP,"GO:0035637","multicellular organismal signaling",159,0.346059607589136,1.69337787938933,(

BP,"GO:0030041","actin filament polymerization",156,0.342144917628601,1.66450882526134,0.00

BP,"GO:0006639","acylglycerol metabolic process",122,0.364264593989287,1.70063770056402,0.00

BP,"GO:0043039","tRNA aminoacylation",25,-0.617800961573826,-2.09465232826138,0.000181075

BP,"GO:0043403","skeletal muscle tissue regeneration",33,0.555465784044041,2.02898380041318,

BP,"GO:0007129","homologous chromosome pairing at meiosis",46,-0.487563959537939,-1.947261

BP,"GO:0007004","telomere maintenance via telomerase",65,-0.444793451217528,-1.88457043838

BP,"GO:0032623","interleukin-2 production",62,0.456640008718629,1.91451775443872,0.0001825

BP,"GO:0032663","regulation of interleukin-2 production",62,0.456640008718629,1.914517754438

BP,"GO:0045913","positive regulation of carbohydrate metabolic process",72,0.435685228627578,1

MF,"GO:0005216","ion channel activity",415,0.269510556554404,1.47377135501842,0.0001830859

BP,"GO:0038127","ERBB signaling pathway",114,0.379766380214765,1.75613585845071,0.0001839

BP,"GO:0051651","maintenance of location in cell",209,0.323157574836547,1.63264587645787,0.0

BP,"GO:0007566","embryo implantation",51,0.476860775979502,1.92538158356363,0.0001859974

CC,"GO:0005680","anaphase-promoting complex",21,-0.639753761188682,-2.06929828343285,0.00

BP,"GO:0062125","regulation of mitochondrial gene expression",26,-0.584666841438497,-2.001798

BP,"GO:0048839","inner ear development",186,0.329362932426625,1.64809160536006,0.0001892

BP,"GO:0006278","RNA-templated DNA biosynthetic process",66,-0.431290182035062,-1.83178419

CC,"GO:1905354","exoribonuclease complex",20,-0.640286344111063,-2.05436198673703,0.00019

BP,"GO:0006801","superoxide metabolic process",64,0.461490457906058,1.94468354321901,0.000

BP,"GO:1902750","negative regulation of cell cycle G2/M phase transition",55,-0.462694767933105,

BP,"GO:0030449","regulation of complement activation",18,0.669188279557786,2.11143079040355

BP,"GO:0060443","mammary gland morphogenesis",44,0.517145460922626,2.02985586521434,0.0

BP,"GO:0010878","cholesterol storage",19,0.662233954925113,2.12649589514255,0.00019574155

MF,"GO:0004713","protein tyrosine kinase activity",135,0.351600620682517,1.6720868403801,0.00

BP,"GO:2000042","negative regulation of double-strand break repair via homologous recombination

BP,"GO:0034698","response to gonadotropin",30,0.573318588067706,2.05825054275494,0.000201

BP,"GO:0048146","positive regulation of fibroblast proliferation",46,0.500200586673353,1.9724578

BP,"GO:0030858","positive regulation of epithelial cell differentiation",53,0.467651716032448,1.912

BP,"GO:0071300","cellular response to retinoic acid",66,0.4431973754213,1.87883669410799,0.000

BP,"GO:0006413","translational initiation",118,-0.364068427119261,-1.71066489945548,0.0002019

CC,"GO:0070847","core mediator complex",26,-0.58235386084694,-1.99387906297813,0.00020561

MF,"GO:0016758","hexosyltransferase activity",188,0.331204526671579,1.65720972997339,0.0002

BP,"GO:0061337","cardiac conduction",93,0.407726722889901,1.82836280091962,0.000206399356

CC,"GO:0098576","luminal side of membrane",31,0.580039464185858,2.09565782876789,0.00020

BP,"GO:0001893","maternal placenta development",33,0.552790529370928,2.01921173424881,0.0

CC,"GO:0005689","U12-type spliceosomal complex",28,-0.597233660314813,-2.09423313956126,0.

MF,"GO:0004222","metalloendopeptidase activity",105,0.385268442568931,1.76359379222309,0.0

MF,"GO:0005496","steroid binding",100,0.387639123517911,1.75975422751029,0.0002099553505

MF,"GO:1901981","phosphatidylinositol phosphate binding",164,0.337633426398834,1.6588972576

BP,"GO:0016045","detection of bacterium",17,0.686214388153132,2.13375077041587,0.00021027

BP,"GO:0043620","regulation of DNA-templated transcription in response to stress",51,0.474961937

BP,"GO:1901655","cellular response to ketone",88,0.409382933681314,1.81824691181552,0.00021

BP,"GO:0060572","morphogenesis of an epithelial bud",15,0.704889894937122,2.12868006828338,

BP,"GO:0060394","negative regulation of pathway-restricted SMAD protein phosphorylation",11,0.7

BP,"GO:0035567","non-canonical Wnt signaling pathway",72,0.433482423231275,1.8653341313458

BP,"GO:0002468","dendritic cell antigen processing and presentation",14,0.715098006887115,2.133

BP,"GO:1901836","regulation of transcription of nucleolar large rRNA by RNA polymerase I",11,-0.74

BP,"GO:0032210","regulation of telomere maintenance via telomerase",51,-0.466544928611005,-1.1

BP,"GO:0034599","cellular response to oxidative stress",262,0.300715956060622,1.5641632024713

BP,"GO:0043277","apoptotic cell clearance",49,0.480118841001593,1.9280594274223,0.000218588

BP,"GO:0044319","wound healing, spreading of cells",31,0.579337206578972,2.09312060200566,0.

BP,"GO:0090505","epiboly involved in wound healing",31,0.579337206578972,2.09312060200566,0

BP,"GO:0003229","ventricular cardiac muscle tissue development",56,0.472260944023076,1.945283

BP,"GO:0000712","resolution of meiotic recombination intermediates",14,-0.717587894159909,-2.0

MF,"GO:0005506","iron ion binding",145,0.346271492393203,1.6663644067924,0.00022220952995

CC,"GO:0005746","mitochondrial respirasome",77,-0.416739132219071,-1.82239761476448,0.0002

BP,"GO:0042730","fibrinolysis",24,0.617199745181182,2.09158614508105,0.000223343748506926

BP,"GO:0002028","regulation of sodium ion transport",86,0.408198183335797,1.81095039045414,0

BP,"GO:0050856","regulation of T cell receptor signaling pathway",43,0.508603606818289,1.996713

BP,"GO:0043523","regulation of neuron apoptotic process",198,0.325456777503922,1.63929603168

CC,"GO:0016529","sarcoplasmic reticulum",68,0.436358928100969,1.85488458531349,0.00022913

MF,"GO:0035173","histone kinase activity",14,-0.715264104194204,-2.07473076731252,0.00023014

BP,"GO:0070509","calcium ion import",80,0.416874195614304,1.82401411570644,0.000230838760

BP,"GO:0007064","mitotic sister chromatid cohesion",23,-0.612197202714596,-2.01755705852509,0

MF,"GO:0061733","peptide-lysine-N-acetyltransferase activity",34,-0.546972772104943,-2.0544176

MF,"GO:0022803","passive transmembrane transporter activity",462,0.266424383012394,1.475456

BP,"GO:0032689","negative regulation of interferon-gamma production",39,0.52942187667168,2.03

BP,"GO:0019985","translesion synthesis",22,-0.609099099785896,-1.98981267987092,0.000238780

MF,"GO:0051539","4 iron, 4 sulfur cluster binding",40,-0.50862459775106,-1.94627052096162,0.00

BP,"GO:0043627","response to estrogen",68,0.4343215300382,1.84622396668647,0.000242231092

BP,"GO:0055067","monovalent inorganic cation homeostasis",155,0.349607828287472,1.70591336

MF,"GO:0008509","anion transmembrane transporter activity",309,0.28432401639535,1.508273049

BP,"GO:0050869","negative regulation of B cell activation",34,0.548592542979348,1.999659579039

CC,"GO:0098802","plasma membrane signaling receptor complex",179,0.329273413019118,1.64114

MF,"GO:0023023","MHC protein complex binding",33,0.549679588858907,2.00784821180646,0.00

BP,"GO:0097242","amyloid-beta clearance",37,0.525275857696754,1.9768433952085,0.000251911

BP,"GO:0051767","nitric-oxide synthase biosynthetic process",19,0.658545107477922,2.114650656

BP,"GO:0051769","regulation of nitric-oxide synthase biosynthetic process",19,0.658545107477922,

BP,"GO:0032332","positive regulation of chondrocyte differentiation",19,0.658441737544053,2.114

BP,"GO:0051004","regulation of lipoprotein lipase activity",18,0.663036707407233,2.092021277050

BP,"GO:0071605","monocyte chemotactic protein-1 production",18,0.662709300286794,2.0909882

BP,"GO:0071637","regulation of monocyte chemotactic protein-1 production",18,0.66270930028679

BP,"GO:0010885","regulation of cholesterol storage",17,0.682146387111643,2.12110151603388,0.0

BP,"GO:0014032","neural crest cell development",82,0.412199974562762,1.81224382137458,0.000

BP,"GO:0010720","positive regulation of cell development",287,0.298029446792398,1.55589389713

MF,"GO:0015026","coreceptor activity",43,0.506696905280606,1.98922785967777,0.00025532431

BP,"GO:0010934","macrophage cytokine production",17,0.679602702291251,2.11319204992692,0.0

BP,"GO:0010935","regulation of macrophage cytokine production",17,0.679602702291251,2.113192

MF,"GO:0061980","regulatory RNA binding",40,-0.506618528388436,-1.93859422358878,0.0002591

BP,"GO:0061299","retina vasculature morphogenesis in camera-type eye",11,0.767209593860331,2
BP,"GO:0046620","regulation of organ growth",85,0.413711456541702,1.83265563472823,0.00026
BP,"GO:0035455","response to interferon-alpha",19,0.657934757943105,2.11269076680889,0.0002
BP,"GO:0044771","meiotic cell cycle phase transition",12,-0.753986987211054,-2.09158862554669,
BP,"GO:0019730","antimicrobial humoral response",101,0.392321150382801,1.78705781948196,0.0
BP,"GO:2000736","regulation of stem cell differentiation",60,0.448550244490063,1.8693949550489
BP,"GO:0070373","negative regulation of ERK1 and ERK2 cascade",67,0.444656695102114,1.890438
BP,"GO:0015918","sterol transport",88,0.406085921949413,1.80360345478168,0.00026687788337
BP,"GO:0010875","positive regulation of cholesterol efflux",26,0.59490733993383,2.059415458319
MF,"GO:0017147","Wnt-protein binding",30,0.567518835235607,2.03742905769766,0.0002676787
BP,"GO:0031110","regulation of microtubule polymerization or depolymerization",84,-0.399680865
BP,"GO:0044818","mitotic G2/M transition checkpoint",42,-0.50544880687982,-1.9617007267496
BP,"GO:0030194","positive regulation of blood coagulation",23,0.619430024535652,2.08521996735
BP,"GO:1900048","positive regulation of hemostasis",23,0.619430024535652,2.08521996735031,0.0
BP,"GO:0009306","protein secretion",331,0.286331091195126,1.52909655863599,0.000272576888
BP,"GO:0032905","transforming growth factor beta1 production",15,0.698634490802653,2.1097895
BP,"GO:0060260","regulation of transcription initiation from RNA polymerase II promoter",48,-0.470
BP,"GO:0030206","chondroitin sulfate biosynthetic process",18,0.661210426319847,2.08625897331
BP,"GO:0120193","tight junction organization",74,0.423521143535149,1.83547660775949,0.00027
BP,"GO:1905207","regulation of cardiocyte differentiation",27,0.591283677719197,2.062253929064
BP,"GO:0097305","response to alcohol",228,0.309434259160767,1.57874614513039,0.0002791088
BP,"GO:0010043","response to zinc ion",52,0.468338192006911,1.90623719582711,0.00028043223
BP,"GO:0008334","histone mRNA metabolic process",18,-0.647529550998688,-2.02135149615439,0.0
MF,"GO:0015085","calcium ion transmembrane transporter activity",129,0.359925498718818,1.695
BP,"GO:0043552","positive regulation of phosphatidylinositol 3-kinase activity",33,0.5461160518054
CC,"GO:0005682","U5 snRNP",17,-0.674745259321889,-2.07021957884158,0.000288091330668092
CC,"GO:0016580","Sin3 complex",10,-0.788030395383523,-2.03894723775608,0.000288306159112
BP,"GO:0033138","positive regulation of peptidyl-serine phosphorylation",105,0.381147431898014,
CC,"GO:0030864","cortical actin cytoskeleton",77,0.417922416437214,1.81593787713375,0.000289
BP,"GO:0051147","regulation of muscle cell differentiation",122,0.359423345586969,1.6780354227
CC,"GO:0080008","Cul4-RING E3 ubiquitin ligase complex",34,-0.543937572080082,-2.04301747791
MF,"GO:0005262","calcium channel activity",113,0.368197678203508,1.69743928857887,0.000291
MF,"GO:0043178","alcohol binding",89,0.397019637498894,1.76890077464664,0.00029235520535
BP,"GO:0014829","vascular associated smooth muscle contraction",25,0.614550213990402,2.11058
BP,"GO:0035270","endocrine system development",131,0.354657979295598,1.67652567860729,0.0
MF,"GO:0030983","mismatched DNA binding",14,-0.710216702906418,-2.06009002316594,0.00029
BP,"GO:0035520","monoubiquitinated protein deubiquitination",33,-0.544634967944412,-2.016383
BP,"GO:0030308","negative regulation of cell growth",177,0.330885396608927,1.64566770091293,0.0
BP,"GO:0030038","contractile actin filament bundle assembly",100,0.383256506635775,1.73985858
BP,"GO:0043149","stress fiber assembly",100,0.383256506635775,1.73985858716339,0.000295171
CC,"GO:0031258","lamellipodium membrane",22,0.630549097624076,2.10007941067793,0.000295
CC,"GO:0005747","mitochondrial respiratory chain complex I",41,-0.492064170196364,-1.89152088
CC,"GO:0030964","NADH dehydrogenase complex",41,-0.492064170196364,-1.89152088763999,0.0
CC,"GO:0045271","respiratory chain complex I",41,-0.492064170196364,-1.89152088763999,0.0002
BP,"GO:0010758","regulation of macrophage chemotaxis",27,0.590157027841319,2.058324447794
CC,"GO:0012507","ER to Golgi transport vesicle membrane",58,0.448068070901008,1.84918527090
BP,"GO:0043984","histone H4-K16 acetylation",19,-0.660039476876171,-2.08327876339579,0.0003
BP,"GO:0006383","transcription by RNA polymerase III",52,-0.46025732142152,-1.86417333171241
BP,"GO:0003272","endocardial cushion formation",28,0.578185645675865,2.0262458130479,0.000
BP,"GO:1903306","negative regulation of regulated secretory pathway",23,0.617973339078759,2.08

BP,"GO:0051014","actin filament severing",16,0.689586702625366,2.11181096917901,0.000307774

BP,"GO:0070431","nucleotide-binding oligomerization domain containing 2 signaling pathway",14,0.

MF,"GO:0008186","ATP-dependent activity, acting on RNA",76,-0.415891727236885,-1.8046927593

BP,"GO:0050848","regulation of calcium-mediated signaling",72,0.424464017184479,1.8265266971

BP,"GO:0035929","steroid hormone secretion",21,0.628229977301129,2.07002613633325,0.000310

CC,"GO:0016591","RNA polymerase II, holoenzyme",74,-0.412631698556059,-1.78550196500326,0.

BP,"GO:0061647","histone H3-K9 modification",49,-0.453713055280655,-1.82407949821564,0.0003

BP,"GO:0015936","coenzyme A metabolic process",18,-0.645777011856606,-2.01588070704299,0.0

BP,"GO:0018149","peptide cross-linking",35,0.529657444699112,1.95600993616457,0.0003184909

MF,"GO:0016538","cyclin-dependent protein serine/threonine kinase regulator activity",46,-0.47961

BP,"GO:0090075","relaxation of muscle",32,0.553186410378626,2.00480664808198,0.0003198840

BP,"GO:0030212","hyaluronan metabolic process",28,0.576361100494524,2.0198517127065,0.0003

CC,"GO:0000795","synaptonemal complex",39,-0.5091320511531,-1.91928477592624,0.000320595

CC,"GO:0099086","synaptonemal structure",39,-0.5091320511531,-1.91928477592624,0.00032059

MF,"GO:0038187","pattern recognition receptor activity",26,0.589436211571796,2.0404758259319

BP,"GO:0060571","morphogenesis of an epithelial fold",23,0.616895270071413,2.07668708968568,

BP,"GO:0042255","ribosome assembly",57,-0.449067132913194,-1.85809468027631,0.0003258948

BP,"GO:0002399","MHC class II protein complex assembly",14,0.704508562109156,2.10198883863

BP,"GO:0002503","peptide antigen assembly with MHC class II protein complex",14,0.70450856210

BP,"GO:0060071","Wnt signaling pathway, planar cell polarity pathway",53,0.460125610740323,1.8

CC,"GO:0098803","respiratory chain complex",76,-0.412934167376307,-1.79185892180075,0.0003

BP,"GO:2000001","regulation of DNA damage checkpoint",15,-0.687166992542026,-2.03632829178

MF,"GO:0098632","cell-cell adhesion mediator activity",54,0.462297163052098,1.89766742282116,

MF,"GO:0003730","mRNA 3'-UTR binding",93,-0.385002817845113,-1.74471961389097,0.00033458

BP,"GO:0031529","ruffle organization",53,0.459884654364452,1.88079485789248,0.000335173088

BP,"GO:0002347","response to tumor cell",37,0.519519190688627,1.95517853285726,0.00033666

BP,"GO:2000112","regulation of cellular macromolecule biosynthetic process",446,-0.254889574835

BP,"GO:0044242","cellular lipid catabolic process",213,0.307121882884532,1.55764784138968,0.00

CC,"GO:0005802","trans-Golgi network",237,0.302088949575338,1.54689720438268,0.000342068

CC,"GO:0005742","mitochondrial outer membrane translocase complex",18,-0.643342509031636,-2

BP,"GO:0071277","cellular response to calcium ion",82,0.407039965964592,1.78955776053678,0.00

BP,"GO:0070988","demethylation",71,-0.410172073553068,-1.77055476961482,0.00034465112503

BP,"GO:0060761","negative regulation of response to cytokine stimulus",71,0.422559843191509,1.8

BP,"GO:0032784","regulation of DNA-templated transcription, elongation",55,-0.451207736388943,

BP,"GO:0007611","learning or memory",256,0.299295254638317,1.54448984894442,0.0003502887

BP,"GO:0008535","respiratory chain complex IV assembly",24,-0.599674824425922,-2.00906703132

BP,"GO:0000466","maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, I

BP,"GO:0032206","positive regulation of telomere maintenance",51,-0.457394807979493,-1.85762

CC,"GO:0005677","chromatin silencing complex",13,-0.728159254502351,-2.06398413916474,0.000

BP,"GO:0070498","interleukin-1-mediated signaling pathway",27,0.586241032651238,2.044666407

BP,"GO:0032205","negative regulation of telomere maintenance",33,-0.538199902941958,-1.99255

BP,"GO:0006999","nuclear pore organization",14,-0.703553629446586,-2.04076277966118,0.00035

MF,"GO:0004553","hydrolase activity, hydrolyzing O-glycosyl compounds",85,0.40747179411155,1.8

MF,"GO:0034062","5'-3' RNA polymerase activity",38,-0.5180276516647,-1.95882936939649,0.000

MF,"GO:0097747","RNA polymerase activity",38,-0.5180276516647,-1.95882936939649,0.0003603

BP,"GO:0071214","cellular response to abiotic stimulus",309,0.280792740733114,1.4895404501604

BP,"GO:0104004","cellular response to environmental stimulus",309,0.280792740733114,1.489540

BP,"GO:0043312","neutrophil degranulation",11,0.758004127502028,2.12885756950126,0.000362

CC,"GO:0016459","myosin complex",55,0.462486370494179,1.88844419859971,0.00036627166981

BP,"GO:0036303","lymph vessel morphogenesis",22,0.627725571220614,2.09067549639471,0.0003

BP,"GO:2000403","positive regulation of lymphocyte migration",36,0.526819067939838,1.96125169

BP,"GO:0002507","tolerance induction",29,0.575326072752334,2.04139720183847,0.00036919599

BP,"GO:0061640","cytoskeleton-dependent cytokinesis",85,-0.398769921882587,-1.7742013612983

CC,"GO:0071004","U2-type prespliceosome",16,-0.671960288116077,-2.05483300790187,0.000373

CC,"GO:0071010","prespliceosome",16,-0.671960288116077,-2.05483300790187,0.0003738829026

BP,"GO:0001958","endochondral ossification",27,0.584214319544307,2.03759772389394,0.000373

BP,"GO:0036075","replacement ossification",27,0.584214319544307,2.03759772389394,0.0003737

BP,"GO:0010824","regulation of centrosome duplication",45,-0.476920880573615,-1.881853434068

MF,"GO:0003899","DNA-directed 5'-3' RNA polymerase activity",36,-0.51413605099528,-1.9415983

MF,"GO:0030547","signaling receptor inhibitor activity",41,0.49900695161943,1.93651670165372,0

BP,"GO:0007100","mitotic centrosome separation",14,-0.702862082612293,-2.03875684439093,0.0

BP,"GO:0032494","response to peptidoglycan",12,0.751844559990937,2.12543861685395,0.000382

BP,"GO:0034368","protein-lipid complex remodeling",30,0.558775222990816,2.00603892832974,0.

BP,"GO:0034369","plasma lipoprotein particle remodeling",30,0.558775222990816,2.006038928329

BP,"GO:0045599","negative regulation of fat cell differentiation",49,0.470115669700409,1.8878887

BP,"GO:0035065","regulation of histone acetylation",59,-0.443568066025254,-1.84341636902772,0

MF,"GO:0008080","N-acetyltransferase activity",59,-0.442880975581798,-1.84056090248835,0.000

CC,"GO:0036064","ciliary basal body",139,-0.332317081759197,-1.61838090896395,0.00038145492

MF,"GO:0015293","symporter activity",143,0.343638748799068,1.64981188445632,0.00038325144

BP,"GO:0043161","proteasome-mediated ubiquitin-dependent protein catabolic process",399,-0.261

BP,"GO:0043618","regulation of transcription from RNA polymerase II promoter in response to stres

BP,"GO:0048864","stem cell development",87,0.402192645160536,1.78868479881491,0.00038900

BP,"GO:0050708","regulation of protein secretion",239,0.307666809576409,1.57915884197894,0.0

BP,"GO:0032615","interleukin-12 production",62,0.443113825164248,1.85780761500672,0.000392

BP,"GO:0032655","regulation of interleukin-12 production",62,0.443113825164248,1.857807615006

BP,"GO:0043551","regulation of phosphatidylinositol 3-kinase activity",54,0.458188849121428,1.880

BP,"GO:0090382","phagosome maturation",26,0.585085461965576,2.02541465523718,0.00039773

BP,"GO:0042542","response to hydrogen peroxide",117,0.368260448631762,1.71163776726651,0.0

BP,"GO:0034135","regulation of toll-like receptor 2 signaling pathway",11,0.754370735498311,2.118

BP,"GO:2000756","regulation of peptidyl-lysine acetylation",68,-0.416253501518572,-1.7899359007

MF,"GO:0008327","methyl-CpG binding",25,-0.597633479590011,-2.02627454039754,0.000404628

BP,"GO:0006700","C21-steroid hormone biosynthetic process",20,0.629843582567609,2.054566431

BP,"GO:0050829","defense response to Gram-negative bacterium",75,0.418773442172541,1.822538

BP,"GO:0071280","cellular response to copper ion",26,0.583863990838218,2.02118623788087,0.00

BP,"GO:0046597","negative regulation of viral entry into host cell",22,0.62516530581127,2.0821483

BP,"GO:1904996","positive regulation of leukocyte adhesion to vascular endothelial cell",22,0.62511

BP,"GO:0050854","regulation of antigen receptor-mediated signaling pathway",62,0.4414539871979

BP,"GO:0051255","spindle midzone assembly",12,-0.743477502445822,-2.06243491445066,0.00041

BP,"GO:0002283","neutrophil activation involved in immune response",18,0.652083452429841,2.05

BP,"GO:0045603","positive regulation of endothelial cell differentiation",11,0.753500581804625,2.1

BP,"GO:0010464","regulation of mesenchymal cell proliferation",29,0.571852946680579,2.0290737

BP,"GO:0034340","response to type I interferon",60,0.437308971568306,1.82254540107721,0.0004

BP,"GO:0007422","peripheral nervous system development",73,0.408905077048333,1.76330125091

BP,"GO:0010522","regulation of calcium ion transport into cytosol",96,0.387933733603827,1.75096

CC,"GO:0030665","clathrin-coated vesicle membrane",106,0.373941261871086,1.7153903707158,0

BP,"GO:0002715","regulation of natural killer cell mediated immunity",49,0.468483088451394,1.88

MF,"GO:0035259","nuclear glucocorticoid receptor binding",13,0.716350948750683,2.09511184135

MF,"GO:0005109","frizzled binding",38,0.527960962992896,2.00624415489299,0.00042868950884

BP,"GO:0043280","positive regulation of cysteine-type endopeptidase activity involved in apoptotic

BP,"GO:0042572","retinol metabolic process",51,0.462227968441848,1.86629989857715,0.0004313

BP,"GO:0098656","anion transmembrane transport",243,0.297506908558219,1.53050303873607,0.
BP,"GO:0033344","cholesterol efflux",53,0.455265547403078,1.86190405008109,0.0004403241111
BP,"GO:2000351","regulation of endothelial cell apoptotic process",48,0.474466815735311,1.90012
BP,"GO:0007173","epidermal growth factor receptor signaling pathway",102,0.382253714781599,1.
BP,"GO:0060419","heart growth",76,0.410866854792762,1.78781417126813,0.0004476264957514
BP,"GO:0045916","negative regulation of complement activation",12,0.746022928441851,2.108981
BP,"GO:0042773","ATP synthesis coupled electron transport",74,-0.404996597775514,-1.752464058
BP,"GO:0042775","mitochondrial ATP synthesis coupled electron transport",74,-0.404996597775514
MF,"GO:0004620","phospholipase activity",98,0.375308845807635,1.69722359734154,0.00045263
BP,"GO:0043299","leukocyte degranulation",74,0.415803294642034,1.80202861744833,0.0004544
CC,"GO:1904090","peptidase inhibitor complex",11,0.751748716193351,2.11128922226982,0.0004
BP,"GO:0032355","response to estradiol",121,0.362022062900706,1.6896665815806,0.000462199
MF,"GO:0005160","transforming growth factor beta receptor binding",24,0.600160814737461,2.03
BP,"GO:0001708","cell fate specification",93,0.396173329406504,1.77655409257765,0.0004632111
BP,"GO:0097237","cellular response to toxic substance",108,0.372315320341545,1.7032416898795
BP,"GO:0003161","cardiac conduction system development",37,0.512595472474455,1.9291215450
MF,"GO:0008170","N-methyltransferase activity",78,-0.405005068520043,-1.77624309789841,0.00
BP,"GO:0018126","protein hydroxylation",26,0.579552858553075,2.00626221211263,0.000465185
MF,"GO:0044548","S100 protein binding",14,0.695343942790798,2.07464505808435,0.000466108
BP,"GO:0002076","osteoblast development",18,0.648539377197907,2.04627912896158,0.0004664
MF,"GO:0042805","actinin binding",36,0.521028265679524,1.93969359480621,0.00046656689495
MF,"GO:0051536","iron-sulfur cluster binding",63,-0.426348466798753,-1.79736077358922,0.0004
MF,"GO:0051540","metal cluster binding",63,-0.426348466798753,-1.79736077358922,0.00046782
BP,"GO:0050873","brown fat cell differentiation",48,0.473591197129492,1.89661347862831,0.0004
BP,"GO:0097501","stress response to metal ion",18,0.648012931428004,2.04461808102932,0.0004
BP,"GO:0002534","cytokine production involved in inflammatory response",53,0.453974004946722,
BP,"GO:1900015","regulation of cytokine production involved in inflammatory response",53,0.45397
BP,"GO:0031128","developmental induction",34,0.533272819482014,1.94381807657728,0.0004716
BP,"GO:0010927","cellular component assembly involved in morphogenesis",108,0.3721933248583
BP,"GO:0031057","negative regulation of histone modification",46,-0.471005135937071,-1.8811277
BP,"GO:1904357","negative regulation of telomere maintenance via telomere lengthening",25,-0.59
MF,"GO:0000049","tRNA binding",58,-0.432865560103266,-1.80128625712732,0.00048237944007
MF,"GO:0003743","translation initiation factor activity",50,-0.45490294948876,-1.83618227560649
BP,"GO:0044380","protein localization to cytoskeleton",57,-0.441185482896541,-1.8254829594568
BP,"GO:0045651","positive regulation of macrophage differentiation",15,0.680860039697354,2.056
BP,"GO:1903901","negative regulation of viral life cycle",25,0.602688631748231,2.069843690306,0.
BP,"GO:0070486","leukocyte aggregation",13,0.713770515197543,2.08756484654179,0.000490341
MF,"GO:0030515","snoRNA binding",30,-0.537254681786029,-1.9236410552285,0.0004913101952
BP,"GO:1903078","positive regulation of protein localization to plasma membrane",58,0.439668525
BP,"GO:0043117","positive regulation of vascular permeability",17,0.662816468064616,2.06099605
BP,"GO:0002566","somatic diversification of immune receptors via somatic mutation",13,-0.720534
BP,"GO:0031445","regulation of heterochromatin assembly",25,-0.594313672366729,-2.015018743
BP,"GO:0120261","regulation of heterochromatin organization",25,-0.594313672366729,-2.0150187
BP,"GO:0051150","regulation of smooth muscle cell differentiation",29,0.567025151245981,2.01194
BP,"GO:0015937","coenzyme A biosynthetic process",11,-0.726092123601275,-1.9291268888263,0.
MF,"GO:0016209","antioxidant activity",77,0.409825150291548,1.78075399678462,0.00049581692
BP,"GO:0031639","plasminogen activation",24,0.598689579510903,2.02885830638477,0.00049920
BP,"GO:0031953","negative regulation of protein autophosphorylation",12,0.742375537110562,2.0
BP,"GO:0006379","mRNA cleavage",19,-0.644380206801286,-2.03385350030141,0.0005033088551
BP,"GO:0003330","regulation of extracellular matrix constituent secretion",10,0.758348241997474,;

BP,"GO:0033314","mitotic DNA replication checkpoint signaling",10,-0.774367015142764,-2.003594
BP,"GO:0048713","regulation of oligodendrocyte differentiation",40,0.497328411801553,1.9225655
CC,"GO:0036379","myofilament",24,0.598310180717689,2.02757258767613,0.0005083621569390
BP,"GO:0046641","positive regulation of alpha-beta T cell proliferation",23,0.60316825722682,2.03
BP,"GO:0006638","neutral lipid metabolic process",123,0.361165588050913,1.69218282901147,0.0
MF,"GO:0035198","miRNA binding",28,-0.579089246361408,-2.03060874006055,0.0005123772400
BP,"GO:0001960","negative regulation of cytokine-mediated signaling pathway",68,0.423015087279
BP,"GO:0097254","renal tubular secretion",27,0.574559176437373,2.0039229285998,0.0005144226
BP,"GO:0016556","mRNA modification",27,-0.577393250113098,-1.99881026685651,0.0005144226
BP,"GO:0061756","leukocyte adhesion to vascular endothelial cell",46,0.480153607099259,1.89340
BP,"GO:0070542","response to fatty acid",61,0.435579080996401,1.81718265143213,0.000517957
BP,"GO:0051926","negative regulation of calcium ion transport",55,0.455724015716759,1.86083186
BP,"GO:0006305","DNA alkylation",67,-0.425440890544337,-1.81754938567545,0.00051923737396
BP,"GO:0006306","DNA methylation",67,-0.425440890544337,-1.81754938567545,0.000519237373
BP,"GO:0015914","phospholipid transport",95,0.386182195442421,1.74069881858722,0.00051894
BP,"GO:0055092","sterol homeostasis",81,0.387072801124763,1.70056799314403,0.000518743161
BP,"GO:1901983","regulation of protein acetylation",80,-0.386037930395611,-1.69791415562118,0
BP,"GO:0006925","inflammatory cell apoptotic process",21,0.616864538946339,2.03257686569136
CC,"GO:0043209","myelin sheath",42,0.498253364291861,1.93449226152589,0.000523232457154
MF,"GO:0003724","RNA helicase activity",74,-0.40258037646741,-1.74200880778105,0.000523374
BP,"GO:0014896","muscle hypertrophy",80,0.403004522142382,1.76332798915033,0.00052466038
CC,"GO:0090665","glycoprotein complex",20,0.62394201505865,2.03531536255241,0.0005259709
BP,"GO:0031664","regulation of lipopolysaccharide-mediated signaling pathway",24,0.59620681170
BP,"GO:0090190","positive regulation of branching involved in ureteric bud morphogenesis",18,0.64
BP,"GO:1903169","regulation of calcium ion transmembrane transport",141,0.346472365700926,1.6
BP,"GO:0030832","regulation of actin filament length",147,0.334060809836166,1.61117596355944,
BP,"GO:0043372","positive regulation of CD4-positive, alpha-beta T cell differentiation",31,0.561043
BP,"GO:0032570","response to progesterone",37,0.508923461781357,1.91530215856585,0.000534
BP,"GO:0051496","positive regulation of stress fiber assembly",49,0.462167642439151,1.85597107
BP,"GO:0090183","regulation of kidney development",32,0.54150757539401,1.96248130244852,0.0
BP,"GO:0003338","metanephros morphogenesis",32,0.54150461036848,1.96247055687924,0.0005
BP,"GO:0071168","protein localization to chromatin",25,-0.592492534163568,-2.00884418017354,0
BP,"GO:0000469","cleavage involved in rRNA processing",27,-0.575964006103746,-1.993862533922
BP,"GO:0016180","snRNA processing",27,-0.575774003887437,-1.99320478743709,0.00054173644
BP,"GO:0010453","regulation of cell fate commitment",25,0.600929033169757,2.06380061296346,
BP,"GO:0048710","regulation of astrocyte differentiation",28,0.565145790927934,1.980547772490
CC,"GO:0005793","endoplasmic reticulum-Golgi intermediate compartment",125,0.3580251610680
BP,"GO:0002755","MyD88-dependent toll-like receptor signaling pathway",24,0.595256800010093,
BP,"GO:0080182","histone H3-K4 trimethylation",20,-0.614749779522152,-1.97242778956756,0.00
MF,"GO:0008028","monocarboxylic acid transmembrane transporter activity",58,0.4374857564782
BP,"GO:0000281","mitotic cytokinesis",70,-0.402473893254024,-1.72603507723045,0.0005629716
BP,"GO:0016331","morphogenesis of embryonic epithelium",149,0.33297062388274,1.6107494878
BP,"GO:0045668","negative regulation of osteoblast differentiation",44,0.497134320908959,1.9513
BP,"GO:0009187","cyclic nucleotide metabolic process",37,0.506669965713968,1.90682126466664,
CC,"GO:0030175","filopodium",98,0.370895883015777,1.67726727425404,0.000575680950564717
MF,"GO:0008408","3'-5' exonuclease activity",50,-0.450552232748867,-1.81862092769051,0.00057
BP,"GO:0051223","regulation of protein transport",470,0.251911664487704,1.39431548833744,0.0
BP,"GO:0048641","regulation of skeletal muscle tissue development",25,0.600134870442053,2.061
BP,"GO:0001991","regulation of systemic arterial blood pressure by circulatory renin-angiotensin",1
BP,"GO:0090218","positive regulation of lipid kinase activity",37,0.505914947129916,1.9039797986

BP,"GO:0071634","regulation of transforming growth factor beta production",38,0.52074759657267
BP,"GO:1903019","negative regulation of glycoprotein metabolic process",17,0.659112705257464,2
BP,"GO:0055017","cardiac muscle tissue growth",67,0.433178071598629,1.84163727226709,0.0005
MF,"GO:0032356","oxidized DNA binding",10,-0.766220034809969,-1.98251518296932,0.00059800
BP,"GO:0010874","regulation of cholesterol efflux",36,0.514216206482418,1.91433353574141,0.00
BP,"GO:0070613","regulation of protein processing",62,0.433463962290702,1.81734941281996,0.0
BP,"GO:0046851","negative regulation of bone remodeling",18,0.64066699407167,2.021440092423
MF,"GO:0042054","histone methyltransferase activity",51,-0.446177266073549,-1.8120718497447,
CC,"GO:0000178","exosome (RNase complex)",19,-0.639049135696451,-2.01702707156806,0.0006
BP,"GO:0001946","lymphangiogenesis",17,0.658710583591086,2.0482290075575,0.0006053847735
BP,"GO:0003159","morphogenesis of an endothelium",17,0.658658572658054,2.04806728205255,0.
BP,"GO:0061154","endothelial tube morphogenesis",17,0.658658572658054,2.04806728205255,0.0
MF,"GO:0004812","aminoacyl-tRNA ligase activity",22,-0.591574361485056,-1.93256264207791,0.0
BP,"GO:0006418","tRNA aminoacylation for protein translation",22,-0.591574361485056,-1.932562
MF,"GO:0016875","ligase activity, forming carbon-oxygen bonds",22,-0.591574361485056,-1.93256
BP,"GO:0090025","regulation of monocyte chemotaxis",26,0.570571652973761,1.97517159957044,
BP,"GO:0030947","regulation of vascular endothelial growth factor receptor signaling pathway",26,C
BP,"GO:0010612","regulation of cardiac muscle adaptation",10,0.752697768697321,2.04250142508
BP,"GO:1903242","regulation of cardiac muscle hypertrophy in response to stress",10,0.7526977686
BP,"GO:0007190","activation of adenylate cyclase activity",29,0.561082867821536,1.990858837477
BP,"GO:0000212","meiotic spindle organization",14,-0.687625372259047,-1.99456048170875,0.000
CC,"GO:0001891","phagocytic cup",26,0.569408909815287,1.97114648326429,0.000627770453733
BP,"GO:0072111","cell proliferation involved in kidney development",20,0.618889132256333,2.0188
MF,"GO:0072341","modified amino acid binding",87,0.39568489340597,1.75974265683913,0.00063
BP,"GO:0032740","positive regulation of interleukin-17 production",23,0.598101202794508,2.01341
BP,"GO:0043616","keratinocyte proliferation",45,0.475062711093378,1.87099934360464,0.000635
BP,"GO:0060346","bone trabecula formation",10,0.749035280307956,2.03256299020553,0.000639
BP,"GO:0035313","wound healing, spreading of epidermal cells",19,0.635488351197385,2.04061323
BP,"GO:0006692","prostanoid metabolic process",45,0.474449258269846,1.86858330504097,0.000
BP,"GO:0006693","prostaglandin metabolic process",45,0.474449258269846,1.86858330504097,0.0
BP,"GO:0032490","detection of molecule of bacterial origin",12,0.738240328521459,2.08697992411
BP,"GO:0035136","forelimb morphogenesis",37,0.502817633719505,1.89232325005619,0.0006482
BP,"GO:0034112","positive regulation of homotypic cell-cell adhesion",15,0.670627400886902,2.025
BP,"GO:0050820","positive regulation of coagulation",24,0.5905757129715,2.00136177715035,0.00
MF,"GO:0036002","pre-mRNA binding",35,-0.514491371029316,-1.93575277000836,0.0006610222
BP,"GO:0055088","lipid homeostasis",147,0.33225056886586,1.60244516768716,0.0006608977959
MF,"GO:0005546","phosphatidylinositol-4,5-bisphosphate binding",75,0.411357788804413,1.79026
BP,"GO:0033028","myeloid cell apoptotic process",31,0.557575734267137,2.01449733129455,0.000
MF,"GO:0004402","histone acetyltransferase activity",32,-0.532715972445593,-1.96279228436761,
CC,"GO:0016605","PML body",102,-0.367453240457895,-1.68327768835006,0.00066741911396903
BP,"GO:0051961","negative regulation of nervous system development",138,0.339570485577631,1.
BP,"GO:0001780","neutrophil homeostasis",16,0.669902072012854,2.05152816689545,0.00067525
BP,"GO:0055069","zinc ion homeostasis",39,0.504584304769106,1.93648310827241,0.0006752796
BP,"GO:0002335","mature B cell differentiation",33,0.524869824585188,1.91722407032117,0.0006
MF,"GO:0002039","p53 binding",64,-0.430446512971056,-1.82069555743238,0.0006788524178485
BP,"GO:0033630","positive regulation of cell adhesion mediated by integrin",21,0.611288995130531
BP,"GO:0002053","positive regulation of mesenchymal cell proliferation",23,0.597185924599921,2.0
BP,"GO:0040036","regulation of fibroblast growth factor receptor signaling pathway",31,0.55702996
BP,"GO:1901889","negative regulation of cell junction assembly",30,0.546185897501124,1.9608424
BP,"GO:0010955","negative regulation of protein processing",27,0.566587317219318,1.9761190188

BP,"GO:1903318","negative regulation of protein maturation",27,0.566587317219318,1.976119018;

BP,"GO:0003230","cardiac atrium development",35,0.514761714930837,1.90100042818018,0.0006

BP,"GO:0008064","regulation of actin polymerization or depolymerization",146,0.336545103067265

BP,"GO:0070129","regulation of mitochondrial translation",23,-0.586201209262392,-1.9318846643;

BP,"GO:1990748","cellular detoxification",101,0.377596753695155,1.71998687973747,0.000694709

BP,"GO:0046394","carboxylic acid biosynthetic process",291,0.285387694406319,1.500692798702,0

BP,"GO:0034123","positive regulation of toll-like receptor signaling pathway",27,0.56572514684547

BP,"GO:0032211","negative regulation of telomere maintenance via telomerase",18,-0.6220606692;

BP,"GO:0000002","mitochondrial genome maintenance",30,-0.529793742147586,-1.8969271515890

BP,"GO:0051098","regulation of binding",350,0.277240048878085,1.48282027694501,0.000702071

BP,"GO:0002716","negative regulation of natural killer cell mediated immunity",20,0.614059161320

MF,"GO:0039706","co-receptor binding",13,0.70504489036737,2.06204500890246,0.000706266054

BP,"GO:0007263","nitric oxide mediated signal transduction",25,0.595989604522316,2.0468368862

BP,"GO:1904874","positive regulation of telomerase RNA localization to Cajal body",15,-0.67028371

BP,"GO:0046486","glycerolipid metabolic process",370,0.262075176597043,1.41219302098139,0.00

BP,"GO:0097709","connective tissue replacement",10,0.746712656897419,2.02626037868835,0.00

MF,"GO:0008175","tRNA methyltransferase activity",31,-0.537502352450832,-1.94867905988905,0

BP,"GO:0072079","nephron tubule formation",19,0.632213925032289,2.03009873842116,0.000726

BP,"GO:0072087","renal vesicle development",19,0.632153917512406,2.02990604859642,0.000726

BP,"GO:0043589","skin morphogenesis",11,0.741690812288921,2.08304155964715,0.00072894348

CC,"GO:0034358","plasma lipoprotein particle",35,0.513301549649655,1.89560807916853,0.00073

CC,"GO:1990777","lipoprotein particle",35,0.513301549649655,1.89560807916853,0.00073495938;

BP,"GO:0071498","cellular response to fluid shear stress",19,0.631966451807515,2.0293040784785

BP,"GO:0048026","positive regulation of mRNA splicing, via spliceosome",22,-0.585309985865011,-

BP,"GO:0010939","regulation of necrotic cell death",34,0.522681051219416,1.90521031360944,0.0

BP,"GO:0031054","pre-miRNA processing",12,-0.731409960840928,-2.02895909432747,0.00074372

CC,"GO:0045120","pronucleus",12,-0.730946877825864,-2.0276744844026,0.000743720562809851

BP,"GO:0042832","defense response to protozoan",23,0.594855741423199,2.0024942617828,0.000

BP,"GO:1901731","positive regulation of platelet aggregation",10,0.745150631413966,2.022021706

BP,"GO:0071229","cellular response to acid chemical",75,0.407520084109061,1.773563162053,0.00

BP,"GO:0060390","regulation of SMAD protein signal transduction",30,0.543869425425003,1.95252

BP,"GO:2000353","positive regulation of endothelial cell apoptotic process",18,0.632564280722015,

MF,"GO:0004519","endonuclease activity",113,-0.346139320837045,-1.61852429968074,0.0007602

BP,"GO:0016053","organic acid biosynthetic process",293,0.283626590416575,1.49041674702773,0

BP,"GO:0034453","microtubule anchoring",22,-0.584545043755549,-1.9095991775876,0.000763294

BP,"GO:0042044","fluid transport",31,0.550483322417526,1.98887274997689,0.000764883343052

BP,"GO:0051493","regulation of cytoskeleton organization",495,0.252084122287044,1.4040231604

BP,"GO:0008037","cell recognition",154,0.334627011537206,1.63094721775861,0.00077017549758

CC,"GO:0031965","nuclear membrane",279,-0.278737663949001,-1.49560033179186,0.0007703179

BP,"GO:0017004","cytochrome complex assembly",34,-0.521182396858239,-1.95754954357966,0.0

MF,"GO:0000993","RNA polymerase II complex binding",34,-0.521179270240887,-1.9575378000741

BP,"GO:0010761","fibroblast migration",45,0.470440250230864,1.85279412345655,0.00077803072

BP,"GO:0097152","mesenchymal cell apoptotic process",15,0.665307057141415,2.00914480686594

BP,"GO:0051299","centrosome separation",15,-0.666864751150942,-1.97616529068291,0.0007891

BP,"GO:0002710","negative regulation of T cell mediated immunity",27,0.561952672217034,1.95999

BP,"GO:0042100","B cell proliferation",99,0.372519742278637,1.68940677293899,0.000798479819

CC,"GO:0031519","PcG protein complex",34,-0.519275119121306,-1.95038585062703,0.000799122

BP,"GO:0086103","G protein-coupled receptor signaling pathway involved in heart process",14,0.680

BP,"GO:0007411","axon guidance",230,0.296585462315619,1.51755114827056,0.00080090117950

BP,"GO:0061180","mammary gland epithelium development",68,0.413786505612771,1.758933211;

BP,"GO:0033559","unsaturated fatty acid metabolic process",107,0.363162308892496,1.665794544

BP,"GO:0007040","lysosome organization",68,0.413455347732701,1.75752551818388,0.000811417

BP,"GO:0080171","lytic vacuole organization",68,0.413455347732701,1.75752551818388,0.0008114

BP,"GO:0002446","neutrophil mediated immunity",34,0.519965547830568,1.89531210694783,0.00

MF,"GO:0005254","chloride channel activity",72,0.407088551595631,1.75175769322099,0.0008154

BP,"GO:0002313","mature B cell differentiation involved in immune response",28,0.5568066012325

BP,"GO:0071548","response to dexamethasone",39,0.500383259750978,1.92036042542674,0.0008

BP,"GO:1901361","organic cyclic compound catabolic process",466,-0.245331506110349,-1.3910277

BP,"GO:0061098","positive regulation of protein tyrosine kinase activity",53,0.443860014819055,1.8

BP,"GO:0045625","regulation of T-helper 1 cell differentiation",10,0.742831047914621,2.015727345

BP,"GO:0070830","bicellular tight junction assembly",63,0.419164663701062,1.75542110884784,0.0

MF,"GO:0008376","acetylgalactosaminyltransferase activity",33,0.519754323630804,1.89853836750

MF,"GO:0008137","NADH dehydrogenase (ubiquinone) activity",35,-0.508424902349461,-1.9129279

CC,"GO:0098799","outer mitochondrial membrane protein complex",19,-0.631240056934029,-1.992

BP,"GO:0001911","negative regulation of leukocyte mediated cytotoxicity",25,0.591094899086118,2

CC,"GO:0044666","MLL3/4 complex",14,-0.678853696630762,-1.96911692149068,0.0008472629270

BP,"GO:0044272","sulfur compound biosynthetic process",141,0.338996732569148,1.62124250865

BP,"GO:0045064","T-helper 2 cell differentiation",15,0.661727855601535,1.99833606207752,0.0008

CC,"GO:0032587","ruffle membrane",93,0.386856929327192,1.73477670005658,0.0008690629820

CC,"GO:0045171","intercellular bridge",71,-0.393596593345209,-1.69900480940797,0.00087177050

BP,"GO:0035116","embryonic hindlimb morphogenesis",28,0.555626310065219,1.94718684700805

MF,"GO:0008484","sulfuric ester hydrolase activity",16,0.661268055325236,2.02508709562831,0.00

BP,"GO:0001977","renal system process involved in regulation of blood volume",15,0.659489886309

BP,"GO:0006446","regulation of translational initiation",81,-0.377743504144699,-1.6589929812649

CC,"GO:0005865","striated muscle thin filament",20,0.607898559693856,1.98298118664454,0.0008

BP,"GO:0035907","dorsal aorta development",10,0.741084893349862,2.01098902337957,0.000880

BP,"GO:0031669","cellular response to nutrient levels",200,0.306202835669033,1.54007079812701

BP,"GO:0000209","protein polyubiquitination",234,-0.281395639525394,-1.46728199036461,0.0008

BP,"GO:0031102","neuron projection regeneration",54,0.445132000615228,1.82720674910898,0.00

BP,"GO:0045664","regulation of neuron differentiation",184,0.309883105806427,1.5474567318586

BP,"GO:0050806","positive regulation of synaptic transmission",145,0.326948036840514,1.5733740

MF,"GO:0005516","calmodulin binding",199,0.308356014361895,1.54867088753358,0.0009064510

BP,"GO:0030224","monocyte differentiation",35,0.509611501693559,1.88198083661906,0.0009151

BP,"GO:0045732","positive regulation of protein catabolic process",223,0.295466461469868,1.5034

MF,"GO:0061650","ubiquitin-like protein conjugating enzyme activity",36,-0.496132199532653,-1.8

BP,"GO:0006882","cellular zinc ion homeostasis",38,0.507528978307468,1.92860290351025,0.0009

BP,"GO:0046887","positive regulation of hormone secretion",119,0.353019694850397,1.642247137

BP,"GO:0062208","positive regulation of pattern recognition receptor signaling pathway",43,0.48189

BP,"GO:2000573","positive regulation of DNA biosynthetic process",73,-0.389008064975236,-1.6790

BP,"GO:0035988","chondrocyte proliferation",20,0.606178066983453,1.97736889389918,0.000944

MF,"GO:0106310","protein serine kinase activity",350,-0.264165552418094,-1.45703118375589,0.00

BP,"GO:0000462","maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, 1

BP,"GO:0086009","membrane repolarization",46,0.46762828524903,1.84401442507626,0.00094930

BP,"GO:0044154","histone H3-K14 acetylation",20,-0.602748283492613,-1.93392092860789,0.0009

BP,"GO:0060767","epithelial cell proliferation involved in prostate gland development",10,0.7371930

BP,"GO:1904894","positive regulation of receptor signaling pathway via STAT",48,0.46125424247714

BP,"GO:2000272","negative regulation of signaling receptor activity",60,0.422410349526516,1.7604

BP,"GO:0030104","water homeostasis",66,0.415405254012974,1.76101817711106,0.000970031602

MF,"GO:0016407","acetyltransferase activity",82,-0.379691369657713,-1.67091390725818,0.00097

BP,"GO:0042886","amide transport",278,0.281947503831267,1.46681110605654,0.0009726286439

BP,"GO:2000107","negative regulation of leukocyte apoptotic process",48,0.460394143183128,1.84
MF,"GO:0008237","metallopeptidase activity",179,0.3124595286065,1.5573385547677,0.00098049
CC,"GO:0005875","microtubule associated complex",148,-0.319177136431525,-1.56782173789539,
CC,"GO:0070775","H3 histone acetyltransferase complex",10,-0.750459943134304,-1.94173757391
MF,"GO:0140223","general transcription initiation factor activity",43,-0.471491021236878,-1.82543
BP,"GO:0002088","lens development in camera-type eye",83,0.382560976820295,1.6923852741505
BP,"GO:0033617","mitochondrial cytochrome c oxidase assembly",21,-0.594118793658377,-1.92169
BP,"GO:0007187","G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide secon
BP,"GO:0048592","eye morphogenesis",151,0.332818004589923,1.61806810095467,0.0010064583
BP,"GO:0010566","regulation of ketone biosynthetic process",17,0.646026882308104,2.0087896459
BP,"GO:0051770","positive regulation of nitric-oxide synthase biosynthetic process",17,0.645833627
BP,"GO:0042269","regulation of natural killer cell mediated cytotoxicity",45,0.465574751269479,1.8
BP,"GO:0046470","phosphatidylcholine metabolic process",68,0.409826683558782,1.742100708908
BP,"GO:0046639","negative regulation of alpha-beta T cell differentiation",25,0.586492587372979,2
BP,"GO:0042632","cholesterol homeostasis",80,0.393085737322358,1.71992879650969,0.0010196
MF,"GO:0015485","cholesterol binding",50,0.453561215952123,1.83366399638638,0.00102163706
BP,"GO:0002921","negative regulation of humoral immune response",16,0.655075516243506,2.006
BP,"GO:0016446","somatic hypermutation of immunoglobulin genes",12,-0.722526021494679,-2.00
BP,"GO:0070227","lymphocyte apoptotic process",74,0.403235080068407,1.74755987556064,0.001
BP,"GO:0050871","positive regulation of B cell activation",73,0.391164304011971,1.6867985880012
BP,"GO:0048806","genitalia development",46,0.465843295651813,1.8369756152572,0.0010578551
BP,"GO:0002827","positive regulation of T-helper 1 type immune response",18,0.621747815604735
BP,"GO:0001765","membrane raft assembly",10,0.733911737084721,1.99152412989486,0.0010696
BP,"GO:0072110","glomerular mesangial cell proliferation",10,0.733857180968129,1.991376087811
MF,"GO:0023026","MHC class II protein complex binding",25,0.58431019424587,2.00672570383992
BP,"GO:0086065","cell communication involved in cardiac conduction",56,0.44169230589482,1.819
MF,"GO:0043138","3'-5' DNA helicase activity",13,-0.700387304296372,-1.98526390813782,0.00108
MF,"GO:0070492","oligosaccharide binding",15,0.652539720977756,1.97058903494772,0.0010866
BP,"GO:0043331","response to dsRNA",54,0.442980859193495,1.81837660407639,0.001086389517
BP,"GO:0071071","regulation of phospholipid biosynthetic process",16,0.654476839258077,2.00428
MF,"GO:0005035","death receptor activity",13,0.694671745092833,2.03170666770998,0.00109402
BP,"GO:0001516","prostaglandin biosynthetic process",28,0.551099364103303,1.93132221015685,0
BP,"GO:0046457","prostanoid biosynthetic process",28,0.551099364103303,1.93132221015685,0.0
MF,"GO:0032451","demethylase activity",38,-0.492740690199556,-1.86321122503384,0.00109402
BP,"GO:0035137","hindlimb morphogenesis",35,0.505831696019498,1.8680221213603,0.00109597
BP,"GO:0006970","response to osmotic stress",79,0.397745677072613,1.73748972829757,0.00109
BP,"GO:0006775","fat-soluble vitamin metabolic process",43,0.474837362336357,1.8641513301769
BP,"GO:1904358","positive regulation of telomere maintenance via telomere lengthening",37,-0.485
BP,"GO:0003143","embryonic heart tube morphogenesis",70,0.409602059104637,1.7527431858559
BP,"GO:0031342","negative regulation of cell killing",28,0.550655261474129,1.92976585693422,0.0
BP,"GO:0019079","viral genome replication",124,0.337467015879114,1.5804111764436,0.0011115
BP,"GO:0070059","intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress
MF,"GO:0061608","nuclear import signal receptor activity",18,-0.606042707033423,-1.89184467443
BP,"GO:0045738","negative regulation of DNA repair",28,-0.558153709948915,-1.95719711398706,
BP,"GO:0042130","negative regulation of T cell proliferation",64,0.430712732230331,1.8149886912
BP,"GO:0008300","isoprenoid catabolic process",10,0.73131297274974,1.98447218942367,0.00112
MF,"GO:0005237","inhibitory extracellular ligand-gated ion channel activity",15,0.650460330658849
BP,"GO:0055002","striated muscle cell development",66,0.41367015473758,1.75366260966568,0.0
BP,"GO:0072189","ureter development",18,0.61956214151801,1.95484981152681,0.001134290992
BP,"GO:0033622","integrin activation",26,0.554792752943081,1.92054912568723,0.001134661439

BP,"GO:1902305","regulation of sodium ion transmembrane transport",63,0.414455792324714,1.73

BP,"GO:0042446","hormone biosynthetic process",64,0.428267977800426,1.80468669340442,0.00

BP,"GO:0051279","regulation of release of sequestered calcium ion into cytosol",76,0.39534962318

BP,"GO:0055094","response to lipoprotein particle",29,0.545496675721653,1.9355552271481,0.00

BP,"GO:0070528","protein kinase C signaling",29,0.545432369769046,1.93532705394697,0.001143

MF,"GO:0005261","cation channel activity",319,0.268262888213782,1.42642402092283,0.0011479

MF,"GO:0016279","protein-lysine N-methyltransferase activity",43,-0.467252807600189,-1.8090241

BP,"GO:0060291","long-term synaptic potentiation",82,0.385640006448814,1.69547249415297,0.0

BP,"GO:0071357","cellular response to type I interferon",55,0.441278008799044,1.8018453058319

MF,"GO:0016896","exoribonuclease activity, producing 5'-phosphomonoesters",37,-0.48257287003

BP,"GO:0070979","protein K11-linked ubiquitination",28,-0.55736025757538,-1.95441482898583,0.

CC,"GO:0000421","autophagosome membrane",48,0.45571790821414,1.82503545760567,0.00115

MF,"GO:0097493","structural molecule activity conferring elasticity",11,0.731296232240282,2.0538

BP,"GO:0055119","relaxation of cardiac muscle",17,0.642061075337727,1.99645815915214,0.0011

BP,"GO:0031579","membrane raft organization",23,0.577142794809038,1.94286623521411,0.0011

MF,"GO:0005504","fatty acid binding",47,0.4634602662201,1.83745218276972,0.00117516173549

MF,"GO:0032396","inhibitory MHC class I receptor activity",10,0.729816083813575,1.98041026986

BP,"GO:0002291","T cell activation via T cell receptor contact with antigen bound to MHC molecule

BP,"GO:0030239","myofibril assembly",65,0.418686631643676,1.76880166410139,0.001176051107

BP,"GO:0003208","cardiac ventricle morphogenesis",71,0.402473837538783,1.72181970399565,0.0

BP,"GO:0061687","detoxification of inorganic compound",17,0.641188714604437,1.9937455952379

BP,"GO:0001701","in utero embryonic development",380,0.263384973289377,1.42607459656614,0

MF,"GO:0043175","RNA polymerase core enzyme binding",39,-0.48214186279648,-1.817539349577

BP,"GO:1903975","regulation of glial cell migration",13,0.693187273680979,2.02736503371264,0.0

BP,"GO:2000209","regulation of anoikis",23,0.576558779049719,1.94090023215591,0.0011867740

MF,"GO:0070696","transmembrane receptor protein serine/threonine kinase binding",23,0.5764141

CC,"GO:0014704","intercalated disc",49,0.447995256039871,1.79905765632154,0.0011861391552

BP,"GO:0030834","regulation of actin filament depolymerization",49,0.447865213573068,1.798535

BP,"GO:0090050","positive regulation of cell migration involved in sprouting angiogenesis",20,0.601

BP,"GO:0002369","T cell cytokine production",38,0.501998381196012,1.90758671309908,0.001194

BP,"GO:0002724","regulation of T cell cytokine production",38,0.501998381196012,1.90758671309

MF,"GO:0015923","mannosidase activity",15,0.648018763216898,1.95693630316051,0.001196230

BP,"GO:0045069","regulation of viral genome replication",82,0.384841434566054,1.6919615600196

BP,"GO:0034614","cellular response to reactive oxygen species",132,0.336333434770229,1.5924610

BP,"GO:0034035","purine ribonucleoside bisphosphate metabolic process",21,0.600407840273825,

BP,"GO:0050427","3'-phosphoadenosine 5'-phosphosulfate metabolic process",21,0.600407840273

BP,"GO:0051984","positive regulation of chromosome segregation",14,-0.668621794159533,-1.939

BP,"GO:0014897","striated muscle hypertrophy",78,0.398555177378498,1.73708619535602,0.0012

BP,"GO:1904872","regulation of telomerase RNA localization to Cajal body",18,-0.602783687792692

CC,"GO:0043034","costamere",16,0.651939241777552,1.99651825764982,0.00124328705349466,0

BP,"GO:0097485","neuron projection guidance",231,0.291824582661267,1.49327953423199,0.0012

MF,"GO:0003714","transcription corepressor activity",180,-0.301942168634671,-1.5337574181768

BP,"GO:0050931","pigment cell differentiation",34,0.512327440713071,1.8674706529239,0.001247

BP,"GO:0072594","establishment of protein localization to organelle",406,-0.249172131918466,-1.3

MF,"GO:0080025","phosphatidylinositol-3,5-bisphosphate binding",27,0.551465655738591,1.92337

BP,"GO:0008203","cholesterol metabolic process",131,0.332828650605678,1.57333490825412,0.00

BP,"GO:0043371","negative regulation of CD4-positive, alpha-beta T cell differentiation",21,0.59912

MF,"GO:0016278","lysine N-methyltransferase activity",44,-0.465904226390031,-1.8224687755743

BP,"GO:2000008","regulation of protein localization to cell surface",38,0.500164632894474,1.90061

BP,"GO:0045620","negative regulation of lymphocyte differentiation",52,0.435306435199769,1.771

CC,"GO:0036464","cytoplasmic ribonucleoprotein granule",234,-0.277404543942545,-1.4464712106
BP,"GO:0090280","positive regulation of calcium ion import",20,0.597167124420792,1.9479749608
BP,"GO:0050685","positive regulation of mRNA processing",31,-0.522983192476887,-1.8960408102
CC,"GO:0034719","SMN-Sm protein complex",17,-0.63324471029444,-1.94288967478913,0.001305
BP,"GO:0097300","programmed necrotic cell death",41,0.474792333803811,1.84254604318508,0.0
BP,"GO:0050927","positive regulation of positive chemotaxis",24,0.572625932591839,1.940532989
BP,"GO:0008228","opsonization",16,0.64968226513993,1.98960642480507,0.00131921154819966,
BP,"GO:0045981","positive regulation of nucleotide metabolic process",39,0.487114675641331,1.86
BP,"GO:1900544","positive regulation of purine nucleotide metabolic process",39,0.4871146756413
BP,"GO:0006910","phagocytosis, recognition",29,0.54127237974289,1.92056639490289,0.0013267
BP,"GO:0046653","tetrahydrofolate metabolic process",18,-0.598921065835734,-1.8696135035664
BP,"GO:0030042","actin filament depolymerization",54,0.439052944925379,1.80225304645595,0.0
BP,"GO:0007005","mitochondrion organization",475,-0.23526888727146,-1.3380919752411,0.0013
BP,"GO:0002027","regulation of heart rate",101,0.366918110513473,1.67134470793342,0.0013435
BP,"GO:0034122","negative regulation of toll-like receptor signaling pathway",34,0.50871498373386
BP,"GO:0046661","male sex differentiation",158,0.324623858437389,1.58930357968173,0.0013472
BP,"GO:0071825","protein-lipid complex subunit organization",47,0.461057797876151,1.827927265
BP,"GO:0042487","regulation of odontogenesis of dentin-containing tooth",11,0.728718939317595,
MF,"GO:0004065","arylsulfatase activity",13,0.69020624981843,2.01864643229992,0.00136525944
BP,"GO:1902563","regulation of neutrophil activation",13,0.68999468790113,2.01802767709496,0.0
BP,"GO:1903978","regulation of microglial cell activation",17,0.63806574072235,1.98403485754144
MF,"GO:0045236","CXCR chemokine receptor binding",17,0.636525227514046,1.97924470551053,(
CC,"GO:0005697","telomerase holoenzyme complex",21,-0.583548417032572,-1.88750080253036,(
BP,"GO:0001755","neural crest cell migration",58,0.418120999091786,1.72559314798062,0.001379
BP,"GO:1901978","positive regulation of cell cycle checkpoint",10,-0.740187341667522,-1.91515827
BP,"GO:0007020","microtubule nucleation",36,-0.489320208707784,-1.84788304753697,0.0013893
BP,"GO:0008212","mineralocorticoid metabolic process",14,0.666846641010098,1.98961981709242
BP,"GO:0001886","endothelial cell morphogenesis",11,0.727337380444115,2.04272988993128,0.00
BP,"GO:0003306","Wnt signaling pathway involved in heart development",11,0.727329046323281,2
BP,"GO:0042659","regulation of cell fate specification",13,0.689404107196617,2.01630040552582,(
BP,"GO:0008211","glucocorticoid metabolic process",23,0.568981719034018,1.91539317532508,0.0
BP,"GO:0072311","glomerular epithelial cell differentiation",23,0.568888559926396,1.91507956890
BP,"GO:0045953","negative regulation of natural killer cell mediated cytotoxicity",19,0.61604165574
BP,"GO:0098869","cellular oxidant detoxification",88,0.377660011463858,1.67735167508209,0.001
BP,"GO:0002833","positive regulation of response to biotic stimulus",168,0.312210746816457,1.540
MF,"GO:0031994","insulin-like growth factor I binding",13,0.689022583021431,2.01518456165267,(
BP,"GO:0036003","positive regulation of transcription from RNA polymerase II promoter in response
BP,"GO:1902041","regulation of extrinsic apoptotic signaling pathway via death domain receptors",4
BP,"GO:0035329","hippo signaling",40,0.479938824908689,1.85534115415643,0.001434760143470
BP,"GO:0090670","RNA localization to Cajal body",19,-0.61418665296083,-1.93855376186005,0.001
BP,"GO:0090671","telomerase RNA localization to Cajal body",19,-0.61418665296083,-1.938553761
BP,"GO:0090672","telomerase RNA localization",19,-0.61418665296083,-1.93855376186005,0.0014
BP,"GO:0090685","RNA localization to nucleus",19,-0.61418665296083,-1.93855376186005,0.00144
BP,"GO:2000780","negative regulation of double-strand break repair",26,-0.542175570940143,-1.85
CC,"GO:0005776","autophagosome",107,0.349716756740285,1.6041209428968,0.00145346660748
BP,"GO:0071402","cellular response to lipoprotein particle stimulus",32,0.521131410782203,1.8886
BP,"GO:0070203","regulation of establishment of protein localization to telomere",11,-0.698719524
BP,"GO:0070831","basement membrane assembly",15,0.643492239635165,1.94326676328449,0.00
BP,"GO:0060038","cardiac muscle cell proliferation",45,0.4577898533481,1.80297147118078,0.001
BP,"GO:0014741","negative regulation of muscle hypertrophy",28,0.541820038845237,1.898802907

BP,"GO:0010573","vascular endothelial growth factor production",34,0.507003872755489,1.848065

BP,"GO:0006721","terpenoid metabolic process",96,0.366078222044451,1.65231784744141,0.0014

BP,"GO:0032274","gonadotropin secretion",15,0.643333316371891,1.94278683473771,0.00148843

CC,"GO:0002102","podosome",29,0.536733439399011,1.90446112772287,0.00149140512626697,0.0014

BP,"GO:0120255","olefinic compound biosynthetic process",24,0.569502128344133,1.92994694268

MF,"GO:0071813","lipoprotein particle binding",29,0.535935279763217,1.90162906270045,0.0015

MF,"GO:0071814","protein-lipid complex binding",29,0.535935279763217,1.90162906270045,0.001

BP,"GO:0032042","mitochondrial DNA metabolic process",22,-0.572969975499818,-1.87178559750

BP,"GO:0003085","negative regulation of systemic arterial blood pressure",20,0.591222873632233,0.0014

MF,"GO:0044325","transmembrane transporter binding",125,0.343750811829134,1.612366118551

CC,"GO:0031089","platelet dense granule lumen",13,0.686752769075209,2.00854603610218,0.0014

BP,"GO:1904994","regulation of leukocyte adhesion to vascular endothelial cell",29,0.535797372943

BP,"GO:0046425","regulation of receptor signaling pathway via JAK-STAT",98,0.356701732431946,1

MF,"GO:0005548","phospholipid transporter activity",57,0.426520508984758,1.76090310065514,0.

BP,"GO:0034111","negative regulation of homotypic cell-cell adhesion",14,0.66072596724136,1.971

BP,"GO:0019511","peptidyl-proline hydroxylation",14,0.660658533516005,1.97115682943772,0.0014

BP,"GO:1903115","regulation of actin filament-based movement",39,0.482279653077635,1.850882

MF,"GO:0070063","RNA polymerase binding",55,-0.420737870400474,-1.73645181377334,0.00154

BP,"GO:0071901","negative regulation of protein serine/threonine kinase activity",111,0.349211824

BP,"GO:0050768","negative regulation of neurogenesis",134,0.335173204954105,1.5920008361086

BP,"GO:0035590","purinergic nucleotide receptor signaling pathway",33,0.505219245497213,1.8454

CC,"GO:0097197","tetraspanin-enriched microdomain",10,0.722565607369825,1.9607355623242,0.

BP,"GO:2000104","negative regulation of DNA-templated DNA replication",14,-0.662832863490882,

BP,"GO:0070734","histone H3-K27 methylation",14,-0.661884200308262,-1.91989435332371,0.001

BP,"GO:0010498","proteasomal protein catabolic process",478,-0.234787652881867,-1.3355993221

BP,"GO:0030903","notochord development",18,0.611984939803902,1.93094213487886,0.0015655

MF,"GO:0008409","5'-3' exonuclease activity",16,-0.633976416614041,-1.93867954718307,0.00158

BP,"GO:0072077","renal vesicle morphogenesis",18,0.61175049160113,1.93020240113096,0.00158

MF,"GO:0000287","magnesium ion binding",210,-0.281102913449995,-1.46169647628072,0.00158

CC,"GO:0031092","platelet alpha granule membrane",17,0.633509963276148,1.9698688857934,0.0

BP,"GO:1904869","regulation of protein localization to Cajal body",11,-0.6967372677232,-1.851135

BP,"GO:1904871","positive regulation of protein localization to Cajal body",11,-0.6967372677232,-1

BP,"GO:0010508","positive regulation of autophagy",132,0.333235249881897,1.57779186816403,0

BP,"GO:0090594","inflammatory response to wounding",15,0.64199481171527,1.93874471666463,

BP,"GO:0071456","cellular response to hypoxia",126,0.333073433166125,1.55989587500034,0.001

BP,"GO:0045807","positive regulation of endocytosis",96,0.36372332808093,1.64168888048723,0.0

BP,"GO:0045623","negative regulation of T-helper cell differentiation",17,0.632587941105702,1.967

BP,"GO:0002830","positive regulation of type 2 immune response",17,0.632352534594259,1.96626

BP,"GO:0055007","cardiac muscle cell differentiation",106,0.351529939236088,1.6125823338313,0

BP,"GO:0003181","atrioventricular valve morphogenesis",23,0.563791666442629,1.8979216275045

MF,"GO:0008227","G protein-coupled amine receptor activity",47,0.457299137482673,1.813025537

BP,"GO:0048103","somatic stem cell division",10,0.720693095917495,1.95565436311129,0.001644

MF,"GO:0016746","acyltransferase activity",226,-0.277783700412616,-1.44621665892508,0.001656

MF,"GO:0016705","oxidoreductase activity, acting on paired donors, with incorporation or reduction

BP,"GO:0045806","negative regulation of endocytosis",49,0.441028703902891,1.77108140257505,0

BP,"GO:0045986","negative regulation of smooth muscle contraction",14,0.659463187773378,1.967

BP,"GO:0035521","monoubiquitinated histone deubiquitination",28,-0.545462292260878,-1.912693

BP,"GO:0035522","monoubiquitinated histone H2A deubiquitination",28,-0.545462292260878,-1.91

MF,"GO:0033038","bitter taste receptor activity",20,-0.58382402206114,-1.87320233969926,0.0016

BP,"GO:0097178","ruffle assembly",42,0.471406281522421,1.83025719241434,0.00169877821539

BP,"GO:0032930","positive regulation of superoxide anion generation",19,0.60930900177573,1.956

BP,"GO:0150078","positive regulation of neuroinflammatory response",14,0.659315897021275,1.96

BP,"GO:0051055","negative regulation of lipid biosynthetic process",53,0.428278616723683,1.7515

BP,"GO:0036363","transforming growth factor beta activation",11,0.720952274754683,2.02479729

BP,"GO:0046716","muscle cell cellular homeostasis",19,0.609257753916796,1.95638430067263,0.0

MF,"GO:0001848","complement binding",19,0.609055776809385,1.95573573306805,0.001717853

BP,"GO:1904427","positive regulation of calcium ion transmembrane transport",68,0.399952901071

BP,"GO:1902547","regulation of cellular response to vascular endothelial growth factor stimulus",21

BP,"GO:0090308","regulation of DNA methylation-dependent heterochromatin assembly",16,-0.632

BP,"GO:0035025","positive regulation of Rho protein signal transduction",31,0.53397456614753,1.9

BP,"GO:0060337","type I interferon signaling pathway",53,0.427192303379455,1.74709262399217,

BP,"GO:0003209","cardiac atrium morphogenesis",27,0.542542949926674,1.89225810272433,0.00

BP,"GO:1903829","positive regulation of protein localization",431,0.25049544400042,1.3739983984

BP,"GO:0032836","glomerular basement membrane development",11,0.720710669016814,2.02411

BP,"GO:0002604","regulation of dendritic cell antigen processing and presentation",11,0.720503187

CC,"GO:0043296","apical junction complex",136,0.325484511015835,1.54875391495834,0.0017361

BP,"GO:0045842","positive regulation of mitotic metaphase/anaphase transition",15,-0.6486663215

BP,"GO:1901970","positive regulation of mitotic sister chromatid separation",15,-0.6486663215258

CC,"GO:0032994","protein-lipid complex",38,0.490703903213481,1.86466785730609,0.001750256

BP,"GO:0061564","axon development",465,0.24613392718073,1.36214911568317,0.001758631141

BP,"GO:1901184","regulation of ERBB signaling pathway",74,0.390253222095242,1.6912984657143

MF,"GO:0030695","GTPase regulator activity",474,0.246939223118302,1.36964344885174,0.00176

MF,"GO:0060589","nucleoside-triphosphatase regulator activity",474,0.246939223118302,1.369643

MF,"GO:0030169","low-density lipoprotein particle binding",18,0.608437423561399,1.91974896958

BP,"GO:0051570","regulation of histone H3-K9 methylation",24,-0.553127066190957,-1.853119903

BP,"GO:0032814","regulation of natural killer cell activation",38,0.489343616691629,1.8594987878

BP,"GO:0007140","male meiotic nuclear division",48,-0.437366079119106,-1.75018257703821,0.00

BP,"GO:0030539","male genitalia development",24,0.563484178260143,1.90955312185899,0.0017

BP,"GO:0010755","regulation of plasminogen activation",14,0.658772768615352,1.9655304155278

BP,"GO:0043031","negative regulation of macrophage activation",16,0.642312476667213,1.967036

BP,"GO:0032341","aldosterone metabolic process",13,0.67882732263559,1.98536648044917,0.001

BP,"GO:0090527","actin filament reorganization",11,0.71842053907756,2.01768690592829,0.0018

BP,"GO:0120192","tight junction assembly",68,0.398753028152197,1.69502855936854,0.00182495

BP,"GO:0060428","lung epithelium development",36,0.492845547575573,1.83477445434621,0.001

BP,"GO:0001562","response to protozoan",24,0.56158924100564,1.90313149816542,0.001831760

BP,"GO:0045019","negative regulation of nitric oxide biosynthetic process",13,0.676559163045889,

BP,"GO:1904406","negative regulation of nitric oxide metabolic process",13,0.676559163045889,1.9

BP,"GO:0032868","response to insulin",245,0.28518991088587,1.46728062948835,0.001859424366

BP,"GO:0051152","positive regulation of smooth muscle cell differentiation",10,0.716877594590283

CC,"GO:0042627","chylomicron",13,0.674855828939968,1.97375105160934,0.00187175258605412

BP,"GO:0042362","fat-soluble vitamin biosynthetic process",13,0.674813536901804,1.97362736007

CC,"GO:0001401","SAM complex",11,-0.692982313150055,-1.84115867715008,0.00187273261865

CC,"GO:0140275","MIB complex",11,-0.692982313150055,-1.84115867715008,0.001872732618653

CC,"GO:0000314","organellar small ribosomal subunit",26,-0.534131958185659,-1.82877559486775

CC,"GO:0005763","mitochondrial small ribosomal subunit",26,-0.534131958185659,-1.82877559486

BP,"GO:0090175","regulation of establishment of planar polarity",56,0.430086588691089,1.771563

MF,"GO:0005544","calcium-dependent phospholipid binding",53,0.424828043641656,1.737423487

BP,"GO:0051656","establishment of organelle localization",386,-0.249545789311647,-1.3894838946

MF,"GO:0005217","intracellular ligand-gated ion channel activity",30,0.52370962691931,1.8801511

BP,"GO:0001953","negative regulation of cell-matrix adhesion",35,0.491942668467285,1.816730336

BP,"GO:0061318","renal filtration cell differentiation",22,0.586915804551603,1.95475626177984,0.
BP,"GO:0072112","glomerular visceral epithelial cell differentiation",22,0.586915804551603,1.9547!
BP,"GO:0032928","regulation of superoxide anion generation",22,0.586211100919987,1.952409206
BP,"GO:0006353","DNA-templated transcription, termination",19,-0.604893565678644,-1.90922204
BP,"GO:0070741","response to interleukin-6",36,0.49122142293801,1.82872813332264,0.00188474
BP,"GO:0043090","amino acid import",52,0.427322599206301,1.73929490937726,0.001888565060
CC,"GO:0030686","90S preribosome",25,-0.55696116383397,-1.88837517443161,0.0018903955400
BP,"GO:1904037","positive regulation of epithelial cell apoptotic process",29,0.527510639414008,1.
BP,"GO:0045666","positive regulation of neuron differentiation",87,0.372130368493293,1.6549878:
BP,"GO:0051492","regulation of stress fiber assembly",85,0.383147188401923,1.69726228909564,C
BP,"GO:0046546","development of primary male sexual characteristics",136,0.323444064661677,1.!
BP,"GO:1901550","regulation of endothelial cell development",17,0.626841308284752,1.949133022
BP,"GO:1903140","regulation of establishment of endothelial barrier",17,0.626841308284752,1.949
MF,"GO:0042056","chemoattractant activity",30,0.52335425320412,1.87887537248884,0.00191326
BP,"GO:0033137","negative regulation of peptidyl-serine phosphorylation",26,0.540622578222283,:
BP,"GO:0002407","dendritic cell chemotaxis",26,0.540203299800496,1.87004420952059,0.0019156
BP,"GO:0051058","negative regulation of small GTPase mediated signal transduction",55,0.4326495!
BP,"GO:1904851","positive regulation of establishment of protein localization to telomere",10,-0.72
BP,"GO:0072310","glomerular epithelial cell development",13,0.674510270821175,1.972740397672
BP,"GO:0086002","cardiac muscle cell action potential involved in contraction",50,0.4353737287816
BP,"GO:1904816","positive regulation of protein localization to chromosome, telomeric region",12,-!
BP,"GO:0031047","gene silencing by RNA",105,-0.340174283925341,-1.56822114188724,0.0019520
BP,"GO:0032411","positive regulation of transporter activity",110,0.337990159826436,1.554183140
BP,"GO:0034471","ncRNA 5'-end processing",20,-0.576836129194492,-1.85078164994901,0.001961
BP,"GO:0045779","negative regulation of bone resorption",16,0.638569359091998,1.955573928525
BP,"GO:2001185","regulation of CD8-positive, alpha-beta T cell activation",18,0.603556621075402,1
BP,"GO:0072015","glomerular visceral epithelial cell development",12,0.712072706833888,2.01300.
BP,"GO:0043301","negative regulation of leukocyte degranulation",14,0.654003769868154,1.95130
BP,"GO:0034433","steroid esterification",16,0.638002255775009,1.95383721434459,0.0020029083
BP,"GO:0034434","sterol esterification",16,0.638002255775009,1.95383721434459,0.00200290839
BP,"GO:0034435","cholesterol esterification",16,0.638002255775009,1.95383721434459,0.0020029
BP,"GO:0006706","steroid catabolic process",27,0.539974646382704,1.88330048343909,0.0020045
MF,"GO:0032934","sterol binding",60,0.405403872540185,1.68957650428993,0.002014326764319.
MF,"GO:0019957","C-C chemokine binding",24,0.554993584343985,1.88077992689707,0.00201658
BP,"GO:1903317","regulation of protein maturation",65,0.409543988217879,1.7301772570064,0.00
BP,"GO:0035148","tube formation",151,0.32410494183914,1.57570762554701,0.002022856802028
CC,"GO:0001527","microfibril",12,0.711140953305761,2.01037092587411,0.0020247120499567,0.(
BP,"GO:1905063","regulation of vascular associated smooth muscle cell differentiation",15,0.633799
CC,"GO:0030992","intraciliary transport particle B",17,-0.623299425680654,-1.91237605110646,0.0
BP,"GO:0051894","positive regulation of focal adhesion assembly",26,0.538561051020814,1.864359
BP,"GO:0010273","detoxification of copper ion",14,0.652005224911693,1.94533860794008,0.00206
BP,"GO:1990169","stress response to copper ion",14,0.652005224911693,1.94533860794008,0.002
BP,"GO:2001234","negative regulation of apoptotic signaling pathway",218,0.289048674353466,1.4
MF,"GO:0008013","beta-catenin binding",85,0.379513484750989,1.68116573831002,0.0020804333
BP,"GO:0090263","positive regulation of canonical Wnt signaling pathway",103,0.357153887828963
BP,"GO:0043393","regulation of protein binding",188,0.302273057801104,1.5124486900311,0.0020
BP,"GO:0070863","positive regulation of protein exit from endoplasmic reticulum",13,0.6704461205
BP,"GO:0040037","negative regulation of fibroblast growth factor receptor signaling pathway",18,0.(
BP,"GO:0010759","positive regulation of macrophage chemotaxis",18,0.603058206232179,1.902776
BP,"GO:0071404","cellular response to low-density lipoprotein particle stimulus",18,0.60277464033

BP,"GO:0046831","regulation of RNA export from nucleus",12,-0.704973266858159,-1.95562269811

BP,"GO:0034616","response to laminar fluid shear stress",12,0.710252770737596,2.0078600644146

MF,"GO:0140297","DNA-binding transcription factor binding",461,0.24663042578235,1.3663683255

BP,"GO:0071453","cellular response to oxygen levels",149,0.318892747058979,1.54264758561602,(

BP,"GO:0061517","macrophage proliferation",11,0.713315603082367,2.00334967313379,0.002113

BP,"GO:0009953","dorsal/ventral pattern formation",91,0.363383740865651,1.62943702271621,0.(

BP,"GO:0050891","multicellular organismal water homeostasis",59,0.416270937158398,1.73248633

BP,"GO:1904029","regulation of cyclin-dependent protein kinase activity",95,-0.350850690623296,-

CC,"GO:0000124","SAGA complex",18,-0.587145566358639,-1.83285468159562,0.00213720933079

BP,"GO:0060795","cell fate commitment involved in formation of primary germ layer",32,0.5113399

MF,"GO:0016709","oxidoreductase activity, acting on paired donors, with incorporation or reduction

CC,"GO:0000803","sex chromosome",25,-0.552939208140793,-1.87473874558013,0.002147334917

BP,"GO:0071470","cellular response to osmotic stress",39,0.475676753679406,1.82554231233874,(

BP,"GO:0051653","spindle localization",54,-0.415450384707433,-1.69512123839502,0.0021555064

BP,"GO:0070423","nucleotide-binding oligomerization domain containing signaling pathway",23,0.5

BP,"GO:0003171","atrioventricular valve development",26,0.537251072175828,1.85982436048092,

CC,"GO:1904724","tertiary granule lumen",55,0.431331190655616,1.76123003105658,0.002171066

BP,"GO:0007007","inner mitochondrial membrane organization",33,-0.496362615080298,-1.837666

CC,"GO:0035371","microtubule plus-end",23,-0.556053170415334,-1.83252878959939,0.00217331

CC,"GO:0071006","U2-type catalytic step 1 spliceosome",11,-0.687209760266964,-1.825821798230

CC,"GO:0071012","catalytic step 1 spliceosome",11,-0.687209760266964,-1.82582179823076,0.002

BP,"GO:0016233","telomere capping",38,-0.476482342143241,-1.80173317541962,0.00219884546

BP,"GO:0030878","thyroid gland development",26,0.535738926905702,1.85458970436646,0.00220

BP,"GO:0046456","icosanoid biosynthetic process",50,0.430582896669453,1.74076690711993,0.00

BP,"GO:0033673","negative regulation of kinase activity",213,0.287164587617055,1.456429271089

BP,"GO:1903405","protein localization to nuclear body",12,-0.702712375959025,-1.9493509006348

BP,"GO:1904867","protein localization to Cajal body",12,-0.702712375959025,-1.9493509006348,0.

CC,"GO:0031616","spindle pole centrosome",12,-0.70226260546577,-1.94810322015257,0.0022396

BP,"GO:0003300","cardiac muscle hypertrophy",76,0.383371187096725,1.6681716550076,0.00225

BP,"GO:0014015","positive regulation of gliogenesis",59,0.414205985542396,1.72389217474549,0.(

BP,"GO:0006694","steroid biosynthetic process",167,0.306895396317556,1.51323461822194,0.002

BP,"GO:0016579","protein deubiquitination",137,-0.323444181233607,-1.56788604296055,0.00228

BP,"GO:0000963","mitochondrial RNA processing",19,-0.600233908117314,-1.8945147944317,0.00

BP,"GO:0060742","epithelial cell differentiation involved in prostate gland development",10,0.71065

MF,"GO:0001846","opsonin binding",15,0.630446448853815,1.9038700929524,0.00229415777598

BP,"GO:0014856","skeletal muscle cell proliferation",15,0.630342099762475,1.90355497163704,0.C

BP,"GO:0042573","retinoic acid metabolic process",34,0.498348452380761,1.81651622730925,0.00

BP,"GO:0009147","pyrimidine nucleoside triphosphate metabolic process",23,-0.554630040312641,

BP,"GO:0046688","response to copper ion",38,0.478920159232346,1.81988979767287,0.00232660

BP,"GO:0060601","lateral sprouting from an epithelium",11,0.71012076883024,1.9943769685875,0

BP,"GO:0051573","negative regulation of histone H3-K9 methylation",12,-0.699279173009952,-1.93

BP,"GO:0071372","cellular response to follicle-stimulating hormone stimulus",12,0.70709365543121

CC,"GO:0030687","preribosome, large subunit precursor",23,-0.553048950475364,-1.822628082574

BP,"GO:0043550","regulation of lipid kinase activity",66,0.396916167638275,1.68263780789454,0.C

BP,"GO:0000966","RNA 5'-end processing",22,-0.561390909792693,-1.83395895850516,0.0023818

BP,"GO:1901019","regulation of calcium ion transmembrane transporter activity",79,0.38258992661

BP,"GO:0045616","regulation of keratinocyte differentiation",34,0.497777277565021,1.8144342537

BP,"GO:0014823","response to activity",64,0.410917591892628,1.73157356751989,0.00239374078

BP,"GO:2000108","positive regulation of leukocyte apoptotic process",27,0.536520363281298,1.871

BP,"GO:0050732","negative regulation of peptidyl-tyrosine phosphorylation",51,0.43014902503296:

BP,"GO:0001892","embryonic placenta development",86,0.367039482685259,1.62835191731894,0.000291", "nuclear-transcribed mRNA catabolic process, exonucleolytic",19,-0.598575180761

BP,"GO:0030166","proteoglycan biosynthetic process",56,0.421074672577695,1.73444253643667,0.00097720", "calcineurin-mediated signaling",46,0.447924296112364,1.76631501863379,0.0006109", "regulation of carbohydrate metabolic process",167,0.306068001477545,1.50915

BP,"GO:0019835","cytolysis",24,0.548837156908639,1.85991682961373,0.00249758772544616,0.01904814", "regulation of protein localization to chromosome, telomeric region",13,-0.67815

BP,"GO:0008593","regulation of Notch signaling pathway",86,0.36613371051305,1.6243335053419,0.0006907", "pinocytosis",21,0.576348832925293,1.89907707512763,0.00252291822976103,0.0061430", "bone trabecula morphogenesis",13,0.663759898577463,1.94129878064655,0.002000191", "regulation of fatty acid transport",31,0.525497029143628,1.89859833876104,0.0051349", "positive regulation of lyase activity",49,0.431820591203969,1.73410349839431,0.0061631", "ubiquitin conjugating enzyme activity",33,-0.493925450884982,-1.82864346419

MF,"GO:0032393","MHC class I receptor activity",14,0.646492352589749,1.9288902683275,0.002540140115", "export across plasma membrane",63,0.397125843957519,1.66312466131261,0.0098505", "G-rich strand telomeric DNA binding",10,-0.71971377738351,-1.8621850463736

BP,"GO:0060271","cilium assembly",305,-0.258656915480284,-1.40424438528149,0.0025755475550001736", "establishment of planar polarity",71,0.386102777072945,1.65178281747959,0.0007164", "establishment of tissue polarity",71,0.386102777072945,1.65178281747959,0.0007033", "vacuole organization",177,0.302663058389622,1.50530311871095,0.002591242

CC,"GO:0035580","specific granule lumen",62,0.404583356181235,1.69626402367353,0.002595052001021", "negative regulation of response to DNA damage stimulus",72,-0.3847657634599

BP,"GO:0051495", "positive regulation of cytoskeleton organization",187,0.303789557088041,1.521

BP,"GO:0062098", "regulation of programmed necrotic cell death",23,0.549390927561917,1.849443

MF,"GO:0032452", "histone demethylase activity",28,-0.531813789437934,-1.86483471365211,0.000140457", "protein demethylase activity",28,-0.531813789437934,-1.86483471365211,0.00090322", "regulation of superoxide metabolic process",29,0.519527820963108,1.84341139

BP,"GO:0021700", "developmental maturation",281,0.267323671878968,1.39127476954164,0.00260010614", "negative regulation of cardiac muscle hypertrophy",26,0.530820187861237,1.83

MF,"GO:0005179", "hormone activity",115,0.338736483577721,1.56675044127125,0.00264488462

MF,"GO:0003727", "single-stranded RNA binding",84,-0.360532701376019,-1.5975588142291,0.00260674", "placenta blood vessel development",30,0.515176687082784,1.84951738504876,

BP,"GO:0033262", "regulation of nuclear cell cycle DNA replication",13,-0.676481931063749,-1.9175

CC,"GO:0000812", "Swr1 complex",13,-0.676104356451991,-1.91643333447819,0.00266162417346

MF,"GO:0070700", "BMP receptor binding",13,0.662435356526495,1.93742489210046,0.002671314

BP,"GO:0048143", "astrocyte activation",21,0.572672083137762,1.88696213564377,0.00267242183

BP,"GO:0045017", "glycerolipid biosynthetic process",237,0.277717620639484,1.42209972122098,0.0002675", "positive regulation of acute inflammatory response",26,0.530454203331212,1.8

BP,"GO:0071827", "plasma lipoprotein particle organization",44,0.457068502728017,1.79404684208

BP,"GO:0010894", "negative regulation of steroid biosynthetic process",23,0.548223267800823,1.84

BP,"GO:0000079", "regulation of cyclin-dependent protein serine/threonine kinase activity",92,-0.34

BP,"GO:0072070", "loop of Henle development",10,0.706433408736194,1.91695964047459,0.00272

BP,"GO:0008584", "male gonad development",135,0.31862676193059,1.51527495765753,0.002727

MF,"GO:0035325", "Toll-like receptor binding",12,0.701890969312751,1.98422154044229,0.002730

BP,"GO:0014874", "response to stimulus involved in regulation of muscle adaptation",13,0.66184072

BP,"GO:0060976", "coronary vasculature development",46,0.446374085977457,1.76020202260502,0.0009110", "vitamin biosynthetic process",20,0.567972364038004,1.85274087997279,0.0027

BP,"GO:0071636", "positive regulation of transforming growth factor beta production",20,0.5679115

BP,"GO:0006482", "protein demethylation",32,-0.498149747117134,-1.83543300872407,0.0027675

BP,"GO:0008214", "protein dealkylation",32,-0.498149747117134,-1.83543300872407,0.002767562

BP,"GO:0014857","regulation of skeletal muscle cell proliferation",13,0.661445773788399,1.934530

BP,"GO:0045776","negative regulation of blood pressure",46,0.44614398057804,1.75929464020494

MF,"GO:1990226","histone methyltransferase binding",11,-0.680405540369032,-1.80774392197247

BP,"GO:2000810","regulation of bicellular tight junction assembly",20,0.566999026356849,1.849565

BP,"GO:0006469","negative regulation of protein kinase activity",194,0.298155847120118,1.494678

BP,"GO:2000515","negative regulation of CD4-positive, alpha-beta T cell activation",30,0.514019432

CC,"GO:0031527","filopodium membrane",18,0.590350057179,1.86267949681955,0.002807327136

BP,"GO:0032890","regulation of organic acid transport",67,0.402450241632109,1.71099927216384,

BP,"GO:0043691","reverse cholesterol transport",17,0.613699027328122,1.9082677294033,0.00281

BP,"GO:0045833","negative regulation of lipid metabolic process",93,0.364452293814673,1.6343071

BP,"GO:0001738","morphogenesis of a polarized epithelium",93,0.36427993217229,1.63353501184

CC,"GO:1990752","microtubule end",32,-0.496405957600184,-1.82900801531958,0.0028389820061

BP,"GO:0032957","inositol trisphosphate metabolic process",12,0.7014595630348,1.9830019697861

BP,"GO:1903018","regulation of glycoprotein metabolic process",49,0.427591910916889,1.7171219

CC,"GO:0098831","presynaptic active zone cytoplasmic component",15,-0.635447387080845,-1.883

BP,"GO:0009148","pyrimidine nucleoside triphosphate biosynthetic process",18,-0.57867314664005

BP,"GO:0006119","oxidative phosphorylation",103,-0.343339104621879,-1.568471617887,0.002860

MF,"GO:0005049","nuclear export signal receptor activity",10,-0.716197133340582,-1.85308609321

BP,"GO:0014820","tonic smooth muscle contraction",10,0.704948739971943,1.91293088126622,0.00287

CC,"GO:0034707","chloride channel complex",50,0.424109965904872,1.71459804682795,0.002874

BP,"GO:0050926","regulation of positive chemotaxis",25,0.557716161942549,1.91539248953463,0.00288

BP,"GO:0051341","regulation of oxidoreductase activity",90,0.35635748285924,1.59575213647278,

BP,"GO:1902369","negative regulation of RNA catabolic process",68,-0.37898795577986,-1.6296895

MF,"GO:0004875","complement receptor activity",11,0.699582089119647,1.96477904522476,0.00289

BP,"GO:0035878","nail development",10,0.703896598320484,1.91007581657511,0.0029446420305

CC,"GO:0005669","transcription factor TFIIID complex",32,-0.495550392787113,-1.82585568630987,

MF,"GO:0031418","L-ascorbic acid binding",20,0.565731113849556,1.84542986255486,0.00295201

BP,"GO:0030318","melanocyte differentiation",24,0.541751291052344,1.83590402182072,0.002971

BP,"GO:0071466","cellular response to xenobiotic stimulus",165,0.306777162023395,1.5103441489

CC,"GO:0005732","sno(s)RNA-containing ribonucleoprotein complex",23,-0.546282273432009,-1.80

BP,"GO:0006644","phospholipid metabolic process",353,0.257739163857712,1.38155784547866,0.00298

BP,"GO:0034505","tooth mineralization",25,0.556571070608184,1.91145984513351,0.00300353481

BP,"GO:0098883","synapse pruning",11,0.698830087271939,1.96266704508164,0.00301690228897

BP,"GO:1901890","positive regulation of cell junction assembly",102,0.356569910532269,1.6295091

MF,"GO:0046332","SMAD binding",78,0.381011662923624,1.66062351588956,0.003035998637428

BP,"GO:0010042","response to manganese ion",21,0.567986300484437,1.87152241943789,0.00304

BP,"GO:0072330","monocarboxylic acid biosynthetic process",198,0.297657065507412,1.499271424

CC,"GO:0005687","U4 snRNP",10,-0.713621633721982,-1.84642225402012,0.00305237283653274,

BP,"GO:0032633","interleukin-4 production",32,0.501449342583583,1.81730598732501,0.0030521

BP,"GO:0032673","regulation of interleukin-4 production",32,0.501449342583583,1.81730598732501

BP,"GO:0070166","enamel mineralization",18,0.588294886140703,1.85619499680309,0.003071099

BP,"GO:0000722","telomere maintenance via recombination",15,-0.632759977183567,-1.875100311

BP,"GO:0009209","pyrimidine ribonucleoside triphosphate biosynthetic process",14,-0.64095246562

BP,"GO:2000404","regulation of T cell migration",42,0.462020603768444,1.79381685445485,0.00306

BP,"GO:0060907","positive regulation of macrophage cytokine production",12,0.69939460985197,1.8

MF,"GO:0016747","acyltransferase activity, transferring groups other than amino-acyl groups",201,-1.8

MF,"GO:0140416","transcription regulator inhibitor activity",21,0.567441095302604,1.86972596110

BP,"GO:0060433","bronchus development",11,0.698222903864768,1.96096176809761,0.00312529

BP,"GO:0044062","regulation of excretion",24,0.540168974512292,1.8305418171566,0.0031265994

BP,"GO:0060973","cell migration involved in heart development",20,0.563830772293594,1.8392308

BP,"GO:0071639","positive regulation of monocyte chemotactic protein-1 production",13,0.6567778

BP,"GO:0072498","embryonic skeletal joint development",15,0.617371711042574,1.8643860061798

BP,"GO:0002418","immune response to tumor cell",23,0.542805125833559,1.82727352878434,0.00

MF,"GO:0051393","alpha-actinin binding",28,0.522583344491743,1.83138810460642,0.0031941869

MF,"GO:0008139","nuclear localization sequence binding",25,-0.540602728238477,-1.83291194705

MF,"GO:0033612","receptor serine/threonine kinase binding",27,0.529104706472746,1.845388771

BP,"GO:0000470","maturation of LSU-rRNA",27,-0.531184776640785,-1.83884654858627,0.003218

CC,"GO:0031463","Cul3-RING ubiquitin ligase complex",36,-0.467822708322099,-1.76669926272654

BP,"GO:2000831","regulation of steroid hormone secretion",18,0.586585868842806,1.85080268517

MF,"GO:0047485","protein N-terminus binding",105,-0.33133579856342,-1.52747526466547,0.003

MF,"GO:0022836","gated channel activity",333,0.261349260898772,1.39346066678342,0.00324704

BP,"GO:0044342","type B pancreatic cell proliferation",18,0.585898969267796,1.848635371491,0.0

MF,"GO:0004114","3',5'-cyclic-nucleotide phosphodiesterase activity",23,0.542029857277567,1.824

MF,"GO:0050321","tau-protein kinase activity",22,-0.552673867120903,-1.80548201272507,0.0032

BP,"GO:0070231","T cell apoptotic process",50,0.420447119954448,1.69978983901083,0.00326750

MF,"GO:0046625","sphingolipid binding",27,0.528610177795684,1.84366397582278,0.0032917732

BP,"GO:0050650","chondroitin sulfate proteoglycan biosynthetic process",23,0.541597116126426,1

BP,"GO:0008156","negative regulation of DNA replication",30,-0.497853863726088,-1.78256637724

BP,"GO:0016577","histone demethylation",30,-0.497620946475974,-1.78173241673878,0.00329560

BP,"GO:0110020","regulation of actomyosin structure organization",93,0.361484572221752,1.62099

BP,"GO:0002437","inflammatory response to antigenic stimulus",67,0.398472644871597,1.6940886

BP,"GO:0033688","regulation of osteoblast proliferation",24,0.537920585218195,1.8229224039390

CC,"GO:0031904","endosome lumen",35,0.477594425742078,1.76374268228969,0.0033137199265

BP,"GO:0010524","positive regulation of calcium ion transport into cytosol",54,0.417387739651684,

BP,"GO:0051567","histone H3-K9 methylation",38,-0.466716835029436,-1.76480664827363,0.0033

BP,"GO:0090657","telomeric loop disassembly",11,-0.676453850290099,-1.79724482504002,0.0033

BP,"GO:0090022","regulation of neutrophil chemotaxis",31,0.5158305768703,1.86367385924921,0.

BP,"GO:0006704","glucocorticoid biosynthetic process",15,0.615044358182089,1.85735768915958,

BP,"GO:1904036","negative regulation of epithelial cell apoptotic process",46,0.440662438949045,1

BP,"GO:0051149","positive regulation of muscle cell differentiation",58,0.400171693925886,1.6515

CC,"GO:0031233","intrinsic component of external side of plasma membrane",24,0.5362397604769

BP,"GO:0006140","regulation of nucleotide metabolic process",77,0.372378173644128,1.61804106

BP,"GO:0090231","regulation of spindle checkpoint",17,-0.605844837140145,-1.85882275756647,0

BP,"GO:0090266","regulation of mitotic cell cycle spindle assembly checkpoint",17,-0.605844837140

BP,"GO:1903504","regulation of mitotic spindle checkpoint",17,-0.605844837140145,-1.8588227575

BP,"GO:0060382","regulation of DNA strand elongation",17,-0.605387050769724,-1.8574182003741

BP,"GO:1904646","cellular response to amyloid-beta",39,0.466756345638994,1.79130775663439,0.

BP,"GO:0033273","response to vitamin",82,0.365994354868897,1.60910007083988,0.00345932518

BP,"GO:0035812","renal sodium excretion",22,0.566443659200423,1.88657262452397,0.00346184

BP,"GO:0060351","cartilage development involved in endochondral bone morphogenesis",31,0.5154

BP,"GO:0009896","positive regulation of catabolic process",487,0.239920347304736,1.33569640997

BP,"GO:0007494","midgut development",11,0.693094162183423,1.94655767694004,0.0034865944

BP,"GO:1903587","regulation of blood vessel endothelial cell proliferation involved in sprouting angi

BP,"GO:0035930","corticosteroid hormone secretion",16,0.622254849051969,1.90561188440823,0.

MF,"GO:0001098","basal transcription machinery binding",58,-0.393561997109157,-1.63773208603

MF,"GO:0001099","basal RNA polymerase II transcription machinery binding",58,-0.3935619971091

BP,"GO:0016441","post-transcriptional gene silencing",83,-0.360546714343546,-1.58555560921874

BP,"GO:0038063","collagen-activated tyrosine kinase receptor signaling pathway",12,0.6950587933

BP,"GO:0089718","amino acid import across plasma membrane",44,0.44940281166857,1.76395811

MF,"GO:0005048","signal sequence binding",46,-0.431873829787955,-1.72484284058196,0.003555

BP,"GO:0046460","neutral lipid biosynthetic process",43,0.447015158284807,1.75492488170214,0.00011111111111111111

BP,"GO:0046463","acylglycerol biosynthetic process",43,0.447015158284807,1.75492488170214,0.00011111111111111111

CC,"GO:0008023","transcription elongation factor complex",42,-0.443938169586476,-1.7229713838

CC,"GO:0033276","transcription factor TFC complex",14,-0.635858245811157,-1.84440217046819,

BP,"GO:0048709","oligodendrocyte differentiation",92,0.353640945489547,1.58315256618998,0.00011111111111111111

BP,"GO:0045823","positive regulation of heart contraction",37,0.466400071436778,1.755267993441

BP,"GO:0050851","antigen receptor-mediated signaling pathway",163,0.298776457751619,1.463911

BP,"GO:0032088","negative regulation of NF-kappaB transcription factor activity",84,0.35629587882

BP,"GO:0000244","spliceosomal tri-snRNP complex assembly",13,-0.666889706702353,-1.89031419

BP,"GO:0060261","positive regulation of transcription initiation from RNA polymerase II promoter",4

BP,"GO:0002181","cytoplasmic translation",142,-0.300579057607417,-1.46330282662886,0.003681

BP,"GO:1901741","positive regulation of myoblast fusion",14,0.634430580966497,1.8929024738701

BP,"GO:2000177","regulation of neural precursor cell proliferation",79,0.371579640258432,1.62318

BP,"GO:0045927","positive regulation of growth",235,0.275907235964151,1.41446751567542,0.00011111111111111111

BP,"GO:0060068","vagina development",10,0.696579694029979,1.89022085212317,0.00373986171

BP,"GO:0009409","response to cold",48,0.43287360191734,1.73354976383637,0.003746365847708

BP,"GO:0030183","B cell differentiation",138,0.316716767632682,1.50622767437561,0.0037526481

MF,"GO:0004115","3',5'-cyclic-AMP phosphodiesterase activity",16,0.618477716443955,1.89404468

BP,"GO:0000012","single strand break repair",11,-0.672436053248683,-1.78657009100214,0.00376

MF,"GO:0043047","single-stranded telomeric DNA binding",11,-0.672219936961338,-1.7859958997

BP,"GO:0001709","cell fate determination",43,0.445601122954424,1.74937355813088,0.003810381

BP,"GO:0060536","cartilage morphogenesis",10,0.696166091971645,1.88909851214995,0.0038124

BP,"GO:0007130","synaptonemal complex assembly",22,-0.547256462237683,-1.78778436560589,0.0038124

CC,"GO:0005767","secondary lysosome",17,0.604733778535028,1.88039071771498,0.00384834395

BP,"GO:0010847","regulation of chromatin assembly",28,-0.520663594115582,-1.82573593187155,

BP,"GO:2000622","regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated de

CC,"GO:0017053","transcription repressor complex",75,-0.35744166778287,-1.54948521346135,0.00384834395

BP,"GO:0014888","striated muscle adaptation",43,0.445172686541471,1.74769157104972,0.00388

MF,"GO:0140303","intramembrane lipid transporter activity",40,0.457685762660485,1.7693155607

BP,"GO:0033555","multicellular organismal response to stress",73,0.369115091101675,1.591716851

BP,"GO:0048066","developmental pigmentation",45,0.436066159650074,1.71741431061954,0.00391

BP,"GO:0045063","T-helper 1 cell differentiation",21,0.559285237517901,1.84285230116052,0.00391

BP,"GO:0090136","epithelial cell-cell adhesion",16,0.615797350582313,1.88583624771199,0.00394

BP,"GO:0032147","activation of protein kinase activity",139,0.307792234313853,1.46856038589583

BP,"GO:2000243","positive regulation of reproductive process",83,0.35688429049728,1.5787959421

BP,"GO:0006665","sphingolipid metabolic process",149,0.311879092864959,1.50871894719908,0.00394

BP,"GO:0034381","plasma lipoprotein particle clearance",40,0.457478828702677,1.7685155982303

BP,"GO:0071230","cellular response to amino acid stimulus",66,0.382560526214034,1.62178025915

BP,"GO:0030656","regulation of vitamin metabolic process",12,0.691686847046393,1.95537483904

MF,"GO:0001637","G protein-coupled chemoattractant receptor activity",26,0.519945722990586,1.

MF,"GO:0004950","chemokine receptor activity",26,0.519945722990586,1.79991771413214,0.00399

BP,"GO:0002262","myeloid cell homeostasis",153,0.312057698712857,1.52041391657595,0.00399

BP,"GO:0045649","regulation of macrophage differentiation",22,0.563628650206136,1.8771970779

MF,"GO:0102545","phosphatidyl phospholipase B activity",11,0.690011968564724,1.937901324055

BP,"GO:0072203","cell proliferation involved in metanephros development",10,0.694614968491155

BP,"GO:0021545","cranial nerve development",54,0.413069244478366,1.6955934651228,0.004031

BP,"GO:0035725","sodium ion transmembrane transport",173,0.299321235816082,1.486970934980

MF,"GO:0015144","carbohydrate transmembrane transporter activity",38,0.463247627900509,1.76

BP,"GO:0043473","pigmentation",98,0.339928257455293,1.53722531829697,0.0041031522778401

BP,"GO:0036294","cellular response to decreased oxygen levels",134,0.31929597848129,1.5165874

BP,"GO:0097066","response to thyroid hormone",28,0.51599621809692,1.8083035860312,0.004111

MF,"GO:0004653","polypeptide N-acetylgalactosaminyltransferase activity",18,0.578353519190159,

CC,"GO:0070160","tight junction",124,0.320209546759788,1.49959173101642,0.004142114690482

MF,"GO:0015929","hexosaminidase activity",12,0.688607857960504,1.94667064319249,0.0041440

BP,"GO:0042976","activation of Janus kinase activity",15,0.6080122739896,1.83612166695731,0.00

CC,"GO:1905286","serine-type peptidase complex",11,0.688723594578288,1.9342829206536,0.004

MF,"GO:0042887","amide transmembrane transporter activity",34,0.479212252763845,1.74676339

CC,"GO:0010494","cytoplasmic stress granule",77,-0.363378220324332,-1.58905068129842,0.00418

BP,"GO:0002888","positive regulation of myeloid leukocyte mediated immunity",19,0.580064797961

BP,"GO:1904063","negative regulation of cation transmembrane transport",78,0.373652878630947,

BP,"GO:0099172","presynapse organization",51,0.415132452864857,1.67614620398125,0.0042233

BP,"GO:0034063","stress granule assembly",27,-0.522063709302874,-1.80727139069148,0.0042505

BP,"GO:0009408","response to heat",103,0.339038850036698,1.55762901978221,0.004257334686

BP,"GO:1901739","regulation of myoblast fusion",19,0.578828186204616,1.85867207925954,0.004

MF,"GO:0008146","sulfotransferase activity",52,0.410257031009541,1.66983437547293,0.0042924

BP,"GO:0019646","aerobic electron transport chain",67,-0.380202554756081,-1.62428420771918,0

MF,"GO:0004559","alpha-mannosidase activity",14,0.629667160597251,1.87869021728735,0.00429

CC,"GO:0030863","cortical cytoskeleton",105,0.333979449491059,1.5288147659463,0.0042974982

BP,"GO:0046058","cAMP metabolic process",22,0.562593557654073,1.87374964370142,0.0043072

BP,"GO:0071880","adenylate cyclase-activating adrenergic receptor signaling pathway",25,0.545117

BP,"GO:1902476","chloride transmembrane transport",66,0.381415275006648,1.61692522139728,(

BP,"GO:0051451","myoblast migration",13,0.647072569320666,1.89249334360841,0.00434636097

BP,"GO:0060347","heart trabecula formation",13,0.64643842924839,1.89063867394291,0.0043463

BP,"GO:0030730","sequestering of triglyceride",18,0.576667133700471,1.81950697449983,0.00435

BP,"GO:0045624","positive regulation of T-helper cell differentiation",21,0.557042341624453,1.835

CC,"GO:0031902","late endosome membrane",139,0.306940614214369,1.46449707499157,0.00444

BP,"GO:0034763","negative regulation of transmembrane transport",108,0.335797353043286,1.536

BP,"GO:0042058","regulation of epidermal growth factor receptor signaling pathway",69,0.3843143

MF,"GO:0005096","GTPase activator activity",265,0.274655111519375,1.42808823062675,0.004465

BP,"GO:0042276","error-prone translesion synthesis",10,-0.69951085586765,-1.80991207408642,0.

BP,"GO:0015074","DNA integration",10,-0.699092560898776,-1.80882977906792,0.0044788719823

BP,"GO:1901216","positive regulation of neuron death",84,0.352253351548249,1.5596244038071,0

BP,"GO:0046580","negative regulation of Ras protein signal transduction",49,0.416120571992209,1.

BP,"GO:0010165","response to X-ray",31,-0.488490268512589,-1.77098900659628,0.004538644310

BP,"GO:1905048","regulation of metallopeptidase activity",13,0.644880026034135,1.886080811580

BP,"GO:0035813","regulation of renal sodium excretion",20,0.553961267769043,1.80703631321151

CC,"GO:0016460","myosin II complex",22,0.560808455050318,1.8678042585788,0.0046018063583

BP,"GO:0032429","regulation of phospholipase A2 activity",11,0.686749530144872,1.928738752938

BP,"GO:0061365","positive regulation of triglyceride lipase activity",10,0.68902237312291,1.869713

BP,"GO:0001541","ovarian follicle development",57,0.40453220159209,1.67012369415469,0.00461

BP,"GO:1900152","negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation

MF,"GO:0070888","E-box binding",49,0.415515882315435,1.66862711005193,0.0046474274666720

BP,"GO:0034332","adherens junction organization",49,0.414727730628333,1.66546205348513,0.00

BP,"GO:0030833","regulation of actin filament polymerization",128,0.313043776075866,1.46828035

MF,"GO:0008135","translation factor activity, RNA binding",78,-0.361217353765767,-1.5842019800

CC,"GO:0046658","anchored component of plasma membrane",61,0.395768151255651,1.65109632

BP,"GO:0002026","regulation of the force of heart contraction",25,0.541007813040799,1.85801017

MF,"GO:0008395","steroid hydroxylase activity",36,0.475559481395003,1.77042156975535,0.00470

BP,"GO:1902652","secondary alcohol metabolic process",141,0.307927573688715,1.4726551146001

BP,"GO:0014037","Schwann cell differentiation",35,0.469016704378424,1.73206540033156,0.00470

BP,"GO:1900542","regulation of purine nucleotide metabolic process",75,0.370959289968502,1.614
BP,"GO:0060353","regulation of cell adhesion molecule production",11,0.685785837898574,1.9260:
BP,"GO:2000644","regulation of receptor catabolic process",11,0.685702688627223,1.92579869442
BP,"GO:2000846","regulation of corticosteroid hormone secretion",15,0.605376900184546,1.82816
BP,"GO:0032695","negative regulation of interleukin-12 production",18,0.574605048437844,1.8130
BP,"GO:2001214","positive regulation of vasculogenesis",12,0.682489583040684,1.9293744912016:
MF,"GO:0008429","phosphatidylethanolamine binding",10,0.687401365098616,1.86531477334655,
BP,"GO:0042368","vitamin D biosynthetic process",10,0.686834947905815,1.86377775813062,0.00:
BP,"GO:0090184","positive regulation of kidney development",10,0.686362979383099,1.862497036
MF,"GO:0015291","secondary active transmembrane transporter activity",237,0.270981680784018,
BP,"GO:0036005","response to macrophage colony-stimulating factor",13,0.640875915683786,1.87:
BP,"GO:0036006","cellular response to macrophage colony-stimulating factor stimulus",13,0.640875
MF,"GO:0042834","peptidoglycan binding",16,0.61155018842586,1.87282961113426,0.0048690334
BP,"GO:0015908","fatty acid transport",96,0.345997580792821,1.56168256806632,0.00486932071:
BP,"GO:0032908","regulation of transforming growth factor beta1 production",12,0.6820650929841
BP,"GO:1901203","positive regulation of extracellular matrix assembly",10,0.685192485967734,1.85
CC,"GO:0098862","cluster of actin-based cell projections",152,0.307394719979524,1.494074998807
MF,"GO:0051010","microtubule plus-end binding",21,-0.548332714840052,-1.77359480225697,0.00
BP,"GO:2001053","regulation of mesenchymal cell apoptotic process",13,0.639950138721626,1.871
MF,"GO:0005024","transforming growth factor beta-activated receptor activity",13,0.639582627622
BP,"GO:0042407","cristae formation",14,-0.624781208621795,-1.81227156342015,0.004945475669
CC,"GO:0030990","intraciliary transport particle",24,-0.526266946259308,-1.76313149783904,0.004
BP,"GO:0061384","heart trabecula morphogenesis",30,0.497355100875776,1.78553674627869,0.00
CC,"GO:0001533","cornified envelope",44,0.443252907301771,1.73981902897225,0.004964610745
BP,"GO:0019369","arachidonic acid metabolic process",56,0.404050996375967,1.66432056032719,
BP,"GO:0032414","positive regulation of ion transmembrane transporter activity",99,0.34128758169
BP,"GO:0034367","protein-containing complex remodeling",32,0.489220679399066,1.77298800555
MF,"GO:0003954","NADH dehydrogenase activity",38,-0.456119168229052,-1.72473345737549,0.0
BP,"GO:0001101","response to acid chemical",116,0.32579981624758,1.51222692533004,0.005015
MF,"GO:0017124","SH3 domain binding",121,0.322417227319697,1.50481889046436,0.005015189
MF,"GO:0017070","U6 snRNA binding",14,-0.624479820295784,-1.81139734139612,0.00501984233
CC,"GO:0005667","transcription regulator complex",473,-0.226821647882947,-1.28956406675954,0
BP,"GO:0043266","regulation of potassium ion transport",100,0.340308272488904,1.544887718593
BP,"GO:0022904","respiratory electron transport chain",94,-0.337400063957716,-1.5282539229739
BP,"GO:1903524","positive regulation of blood circulation",38,0.457712912688007,1.739302562245
BP,"GO:0150146","cell junction disassembly",21,0.55397209715924,1.82534543296604,0.00507075
BP,"GO:1903828","negative regulation of protein localization",183,0.283423787041591,1.41205011
BP,"GO:1903564","regulation of protein localization to cilium",10,-0.695761558186921,-1.80021115
BP,"GO:1904779","regulation of protein localization to centrosome",10,-0.695474469029259,-1.799
BP,"GO:0051293","establishment of spindle localization",50,-0.404577345950252,-1.6330466807934
BP,"GO:0010975","regulation of neuron projection development",411,0.243936995672931,1.333884
BP,"GO:0007095","mitotic G2 DNA damage checkpoint signaling",30,-0.487522333050883,-1.745574
BP,"GO:0030540","female genitalia development",18,0.569955145319288,1.79832922921382,0.005
CC,"GO:0005844","polysome",64,-0.385768489955338,-1.6317171929473,0.00519445887623157,0
BP,"GO:0031670","cellular response to nutrient",40,0.448469369632796,1.73368695065798,0.0052
BP,"GO:0046479","glycosphingolipid catabolic process",13,0.636899277092403,1.86273951268218,
BP,"GO:0032785","negative regulation of DNA-templated transcription, elongation",18,-0.55358462:
BP,"GO:0032092","positive regulation of protein binding",81,0.347038687323358,1.5246818746497
BP,"GO:0000041","transition metal ion transport",95,0.343390806898607,1.54781856578688,0.005
CC,"GO:0035869","ciliary transition zone",62,-0.377929829654383,-1.59054235637525,0.00528516:

BP,"GO:0150117","positive regulation of cell-substrate junction organization",31,0.49884661291266

BP,"GO:0010574","regulation of vascular endothelial growth factor production",31,0.498364473838

MF,"GO:0032404","mismatch repair complex binding",10,-0.693793892570338,-1.79512002216597,

BP,"GO:0045581","negative regulation of T cell differentiation",43,0.437756874426841,1.71857803

CC,"GO:1990204","oxidoreductase complex",106,-0.318762853475657,-1.47058624556575,0.00530

BP,"GO:0033173","calcineurin-NFAT signaling cascade",42,0.446825880925665,1.73482262408541,(

BP,"GO:0014904","myotube cell development",34,0.473342243395326,1.72536678320338,0.00535

BP,"GO:0040001","establishment of mitotic spindle localization",35,-0.460991942496088,-1.734463

BP,"GO:0031111","negative regulation of microtubule polymerization or depolymerization",38,-0.45

BP,"GO:0002726","positive regulation of T cell cytokine production",26,0.512454430860062,1.77398

BP,"GO:2000826","regulation of heart morphogenesis",11,0.682136162636895,1.91578209217101,(

BP,"GO:0006631","fatty acid metabolic process",369,0.248048708480492,1.33566327624461,0.005

MF,"GO:0004602","glutathione peroxidase activity",21,0.549456947025503,1.81046795318314,0.00

BP,"GO:0000154","rRNA modification",30,-0.485478584748259,-1.73825667549588,0.00545281409

BP,"GO:0043330","response to exogenous dsRNA",47,0.428892210474982,1.70040235538968,0.00

BP,"GO:0070228","regulation of lymphocyte apoptotic process",56,0.402023978085457,1.65597109

MF,"GO:0070513","death domain binding",10,0.681027621200715,1.84801914482743,0.005482663

BP,"GO:0045880","positive regulation of smoothened signaling pathway",33,0.475486270688596,1.

BP,"GO:0002673","regulation of acute inflammatory response",45,0.424954244721863,1.67365085

BP,"GO:0034766","negative regulation of ion transmembrane transport",84,0.34878069536252,1.54

BP,"GO:0006266","DNA ligation",16,-0.596658147240024,-1.82456147642252,0.0055303043511609

MF,"GO:0018024","histone-lysine N-methyltransferase activity",36,-0.45393170363528,-1.71424086

CC,"GO:0005778","peroxisomal membrane",61,-0.380314987859806,-1.59862466382724,0.005539

CC,"GO:0031903","microbody membrane",61,-0.380314987859806,-1.59862466382724,0.00553979

BP,"GO:0016575","histone deacetylation",92,-0.334656635777586,-1.51282506614125,0.00554763

BP,"GO:0032060","bleb assembly",10,0.680717166149881,1.84717670193717,0.005555280933258

BP,"GO:0035458","cellular response to interferon-beta",20,0.548715529488542,1.78992457613891

BP,"GO:0031453","positive regulation of heterochromatin assembly",13,-0.650518092625333,-1.843

BP,"GO:0120263","positive regulation of heterochromatin organization",13,-0.650518092625333,-1.

BP,"GO:1905269","positive regulation of chromatin organization",13,-0.650518092625333,-1.84390

BP,"GO:0072538","T-helper 17 type immune response",38,0.455689118350101,1.73161217252824,

BP,"GO:1904645","response to amyloid-beta",48,0.427129126831335,1.71054458776511,0.005601

BP,"GO:1902894","negative regulation of miRNA transcription",19,0.569304313723266,1.82809002

BP,"GO:0032351","negative regulation of hormone metabolic process",11,0.680341826100239,1.91

BP,"GO:0010660","regulation of muscle cell apoptotic process",58,0.385696428458529,1.59177634

BP,"GO:0050996","positive regulation of lipid catabolic process",27,0.51244712601472,1.787291174

BP,"GO:0010837","regulation of keratinocyte proliferation",34,0.470770494804473,1.715992573199

BP,"GO:0097581","lamellipodium organization",84,0.347978808037442,1.54069858707523,0.00566

BP,"GO:0046427","positive regulation of receptor signaling pathway via JAK-STAT",44,0.4378434434

BP,"GO:0009620","response to fungus",61,0.393051974769468,1.63976476562729,0.005689564969

MF,"GO:0004674","protein serine/threonine kinase activity",415,-0.228673967673241,-1.28309468

BP,"GO:0035966","response to topologically incorrect protein",151,0.306579121738431,1.49050198

BP,"GO:0060306","regulation of membrane repolarization",33,0.473652293219774,1.730138664842

BP,"GO:0086004","regulation of cardiac muscle cell contraction",33,0.473132576195462,1.7282402

CC,"GO:0090543","Flemming body",35,-0.458200157469691,-1.72395937810526,0.0057223263798

BP,"GO:0046503","glycerolipid catabolic process",66,0.373296140780838,1.58250595776031,0.005

BP,"GO:0060444","branching involved in mammary gland duct morphogenesis",23,0.526618215846

BP,"GO:0009314","response to radiation",414,-0.229789019297881,-1.28714989777686,0.00574998

BP,"GO:1900272","negative regulation of long-term synaptic potentiation",11,0.678723534491035,1

BP,"GO:0042045","epithelial fluid transport",10,0.678339795107827,1.84072552864654,0.0057731

BP,"GO:0021936","regulation of cerebellar granule cell precursor proliferation",10,0.6779919952052
MF,"GO:0042608","T cell receptor binding",10,0.677323214248231,1.83796696081123,0.00577313
CC,"GO:0016442","RISC complex",14,-0.620602399334444,-1.80015030059099,0.005763509956330
CC,"GO:0031332","RNAi effector complex",14,-0.620602399334444,-1.80015030059099,0.00576350
BP,"GO:0001776","leukocyte homeostasis",88,0.349601129630307,1.55273002858579,0.005771251
BP,"GO:0045103","intermediate filament-based process",88,0.349309743706809,1.5514358575005
BP,"GO:0046888","negative regulation of hormone secretion",58,0.384996893360502,1.5888893461
BP,"GO:0033032","regulation of myeloid cell apoptotic process",26,0.510696926350324,1.76790077
BP,"GO:2000193","positive regulation of fatty acid transport",24,0.521817594336617,1.7683520757
MF,"GO:0019783","ubiquitin-like protein peptidase activity",110,-0.321883734671762,-1.491858885
BP,"GO:0014854","response to inactivity",12,0.67686700822939,1.91347966630561,0.00586141662
CC,"GO:1990498","mitotic spindle microtubule",13,-0.648274037229465,-1.83754765513262,0.0058
BP,"GO:0006929","substrate-dependent cell migration",23,0.525889043888845,1.77032802978808,
BP,"GO:0042180","cellular ketone metabolic process",194,0.287994299829832,1.44373768197881,(
MF,"GO:0042800","histone methyltransferase activity (H3-K4 specific)",17,-0.585111438343604,-1.7
BP,"GO:0003337","mesenchymal to epithelial transition involved in metanephros morphogenesis",11
MF,"GO:0098641","cadherin binding involved in cell-cell adhesion",18,0.564704581782051,1.781766
BP,"GO:0051222","positive regulation of protein transport",286,0.258979229323272,1.35113392908
BP,"GO:2000045","regulation of G1/S transition of mitotic cell cycle",133,-0.299574275617475,-1.43
BP,"GO:0050858","negative regulation of antigen receptor-mediated signaling pathway",32,0.48607
BP,"GO:0032342","aldosterone biosynthetic process",11,0.677848721710452,1.90374079748818,0.0
BP,"GO:0007289","spermatid nucleus differentiation",17,-0.58397210572477,-1.79171393954474,0
MF,"GO:0097110","scaffold protein binding",66,0.371963174748209,1.5768551447524,0.00599913
BP,"GO:0002517","T cell tolerance induction",15,0.599816254800901,1.81137070540776,0.0060126
BP,"GO:0060644","mammary gland epithelial cell differentiation",18,0.564186133161703,1.7801267
BP,"GO:0044782","cilium organization",331,-0.246630871978256,-1.34623264788779,0.006023810
BP,"GO:0090224","regulation of spindle organization",43,-0.423915369348686,-1.64123813666992,
BP,"GO:0045939","negative regulation of steroid metabolic process",26,0.509358730144153,1.7632
MF,"GO:0140678","molecular function inhibitor activity",55,0.405217156844469,1.65460008734601
BP,"GO:0046348","amino sugar catabolic process",14,0.616482392749339,1.83935182404864,0.006
BP,"GO:0071695","anatomical structure maturation",232,0.270478616490833,1.38440231521868,0
BP,"GO:0061307","cardiac neural crest cell differentiation involved in heart development",15,0.5993
BP,"GO:0061308","cardiac neural crest cell development involved in heart development",15,0.59934
BP,"GO:0032801","receptor catabolic process",27,0.510090414557025,1.77907153746629,0.006098
MF,"GO:0016251","RNA polymerase II general transcription initiation factor activity",38,-0.44798144
BP,"GO:1903238","positive regulation of leukocyte tethering or rolling",11,0.676224044318769,1.89
BP,"GO:0016081","synaptic vesicle docking",10,-0.688096462432649,-1.7803785102781,0.00613489
BP,"GO:0062149","detection of stimulus involved in sensory perception of pain",24,0.520736148959
BP,"GO:2000615","regulation of histone H3-K9 acetylation",11,-0.649339669620365,-1.7252061769
MF,"GO:0032266","phosphatidylinositol-3-phosphate binding",42,0.442094973327628,1.716454651
BP,"GO:0070202","regulation of establishment of protein localization to chromosome",12,-0.670840
BP,"GO:0006839","mitochondrial transport",171,-0.28558688929254,-1.42764670319716,0.006186
BP,"GO:0048286","lung alveolus development",44,0.435772208059855,1.71045641752243,0.00619
CC,"GO:0043083","synaptic cleft",17,0.588181129848425,1.8289210494929,0.00621063117546952
BP,"GO:0007589","body fluid secretion",85,0.35630345364814,1.57835013190061,0.006219373532
MF,"GO:0005355","glucose transmembrane transporter activity",20,0.543988059394812,1.7745034
CC,"GO:0001931","uropod",13,0.630556752391869,1.84418952872901,0.00624557324601319,0.01
CC,"GO:0031254","cell trailing edge",13,0.630556752391869,1.84418952872901,0.00624557324601
BP,"GO:0006264","mitochondrial DNA replication",13,-0.644430627441358,-1.82665342177101,0.0
CC,"GO:0034364","high-density lipoprotein particle",27,0.509297077170427,1.7763045692508,0.00

MF,"GO:0070325","lipoprotein particle receptor binding",28,0.505468424392102,1.7714090382772

BP,"GO:0099550","trans-synaptic signaling, modulating synaptic transmission",11,0.6757064905526

BP,"GO:0002765","immune response-inhibiting signal transduction",11,0.674846935485001,1.89531

BP,"GO:0014841","skeletal muscle satellite cell proliferation",14,0.614934294111706,1.8347328793

BP,"GO:0071354","cellular response to interleukin-6",32,0.48402979329251,1.75417567976479,0.0

BP,"GO:0097186","amelogenesis",23,0.523282485623888,1.76155343520134,0.0063311074498819

CC,"GO:0031941","filamentous actin",28,0.505292827974842,1.77079366238907,0.0063457026768

BP,"GO:0017145","stem cell division",28,0.50508732198243,1.77007346869385,0.00634570267681

BP,"GO:0006972","hyperosmotic response",26,0.506874962361016,1.75467011894272,0.00634364

MF,"GO:0046943","carboxylic acid transmembrane transporter activity",159,0.295143193945932,1.7

BP,"GO:0002430","complement receptor mediated signaling pathway",12,0.674031214405963,1.90

BP,"GO:0070424","regulation of nucleotide-binding oligomerization domain containing signaling pat

BP,"GO:0071875","adrenergic receptor signaling pathway",30,0.491869088407232,1.765841609271

BP,"GO:0014044","Schwann cell development",29,0.489578616415098,1.73714431687152,0.00639

BP,"GO:0048265","response to pain",29,0.488878646514007,1.73466065297181,0.0063942921549

BP,"GO:0034219","carbohydrate transmembrane transport",119,0.318072896116857,1.4796746771

BP,"GO:0099625","ventricular cardiac muscle cell membrane repolarization",26,0.506398468889627

MF,"GO:0008503","benzodiazepine receptor activity",11,0.673619506265819,1.89186302929973,0.

BP,"GO:0030835","negative regulation of actin filament depolymerization",40,0.444516600307393,1

BP,"GO:0006368","transcription elongation from RNA polymerase II promoter",56,-0.397685386542

CC,"GO:0005871","kinesin complex",48,-0.404522507779017,-1.61875435461432,0.0064792358317

BP,"GO:0009208","pyrimidine ribonucleoside triphosphate metabolic process",17,-0.581444144178

BP,"GO:0072710","response to hydroxyurea",10,-0.685754248524838,-1.77431827376243,0.006511

BP,"GO:0007409","axonogenesis",422,0.236104547399362,1.29230305173046,0.006519551584971

BP,"GO:0035821","modulation of process of another organism",23,0.521800723579666,1.75656530

BP,"GO:0006687","glycosphingolipid metabolic process",58,0.382821222274156,1.57991031183017

BP,"GO:0060713","labyrinthine layer morphogenesis",21,0.543982179868593,1.79242852253733,0.

BP,"GO:0070301","cellular response to hydrogen peroxide",81,0.342010325699656,1.50259024018

MF,"GO:0004112","cyclic-nucleotide phosphodiesterase activity",25,0.532260489523022,1.8279688

CC,"GO:0055038","recycling endosome membrane",91,0.340743351511238,1.52791600106866,0.0

BP,"GO:0031644","regulation of nervous system process",130,0.322471364965262,1.519026576933

BP,"GO:0002228","natural killer cell mediated immunity",73,0.353996308488817,1.5265208690881

BP,"GO:0051923","sulfation",24,0.518555569997081,1.75729762387071,0.00673027982207119,0.0

BP,"GO:1900027","regulation of ruffle assembly",30,0.489600088452694,1.75769575374664,0.0067

BP,"GO:0070266","necroptotic process",34,0.463717704934736,1.69028464296495,0.00675852398

BP,"GO:0038034","signal transduction in absence of ligand",65,0.383189572755863,1.61883925287

BP,"GO:0097192","extrinsic apoptotic signaling pathway in absence of ligand",65,0.38318957275586

BP,"GO:0070099","regulation of chemokine-mediated signaling pathway",10,0.671513940881093,1.

BP,"GO:0035581","sequestering of extracellular ligand from receptor",10,0.671255407041759,1.821

BP,"GO:0044089","positive regulation of cellular component biogenesis",467,0.234580989772313,1.

BP,"GO:1903580","positive regulation of ATP metabolic process",32,0.481032829998605,1.7433143

BP,"GO:0010458","exit from mitosis",29,-0.480838669491713,-1.70348412118845,0.006837822091

BP,"GO:0033182","regulation of histone ubiquitination",12,-0.667296302973446,-1.8511053650027

BP,"GO:0032371","regulation of sterol transport",33,0.468054111045786,1.70968984284619,0.0068

BP,"GO:0032374","regulation of cholesterol transport",33,0.468054111045786,1.70968984284619,0.

BP,"GO:0035747","natural killer cell chemotaxis",10,0.669938613946884,1.81792829819469,0.0068

BP,"GO:0071364","cellular response to epidermal growth factor stimulus",41,0.433355261908462,1.

MF,"GO:0099106","ion channel regulator activity",131,0.306328450165629,1.44806417103788,0.00

MF,"GO:0000175","3'-5'-exoribonuclease activity",34,-0.463280370919242,-1.74007081610827,0.00

BP,"GO:0051353","positive regulation of oxidoreductase activity",55,0.401801892892598,1.6406547

MF,"GO:0008191","metalloendopeptidase inhibitor activity",16,0.59930401757254,1.835326570776

BP,"GO:1900745","positive regulation of p38MAPK cascade",29,0.484169880185944,1.71795280178

BP,"GO:0061081","positive regulation of myeloid leukocyte cytokine production involved in immune

BP,"GO:0006883","cellular sodium ion homeostasis",22,0.550409324123749,1.8331693652293,0.00

BP,"GO:1902101","positive regulation of metaphase/anaphase transition of cell cycle",16,-0.5895534

BP,"GO:1901993","regulation of meiotic cell cycle phase transition",10,-0.680535302640015,-1.7608

BP,"GO:0001710","mesodermal cell fate commitment",17,0.585263648647512,1.81984928144549,(

BP,"GO:0031345","negative regulation of cell projection organization",177,0.287128397629003,1.42

CC,"GO:0090533","cation-transporting ATPase complex",18,0.560844709281128,1.76958387345582

BP,"GO:0010575","positive regulation of vascular endothelial growth factor production",28,0.49952:

BP,"GO:0055008","cardiac muscle tissue morphogenesis",59,0.38940983238248,1.62069256902228

CC,"GO:0031074","nucleocytoplasmic transport complex",11,-0.643811563567831,-1.71051875959:

BP,"GO:0048640","negative regulation of developmental growth",102,0.338629815994993,1.54752:

BP,"GO:0043928","exonucleolytic catabolism of deadenylated mRNA",13,-0.640817046453766,-1.81

BP,"GO:0036037","CD8-positive, alpha-beta T cell activation",26,0.503472766738465,1.7428925969

BP,"GO:0051155","positive regulation of striated muscle cell differentiation",43,0.42715022678339,

BP,"GO:0055021","regulation of cardiac muscle tissue growth",51,0.396853880434542,1.602344313

BP,"GO:0006120","mitochondrial electron transport, NADH to ubiquinone",42,-0.424544581225488,

BP,"GO:0031573","mitotic intra-S DNA damage checkpoint signaling",16,-0.588293517469061,-1.798

BP,"GO:0034755","iron ion transmembrane transport",21,0.540714843965946,1.78166260725307,C

BP,"GO:0006691","leukotriene metabolic process",31,0.487775518434019,1.76231213047261,0.00:

CC,"GO:0000346","transcription export complex",10,-0.678503829713584,-1.75555856411875,0.00

BP,"GO:1902931","negative regulation of alcohol biosynthetic process",13,0.624022477218607,1.82

BP,"GO:0048340","paraxial mesoderm morphogenesis",10,0.665434142937978,1.8057050808058,0

MF,"GO:0047844","deoxycytidine deaminase activity",10,0.665430494737648,1.80569518114263,0

MF,"GO:0004435","phosphatidylinositol phospholipase C activity",26,0.502115369300727,1.738193

BP,"GO:0042558","pteridine-containing compound metabolic process",33,-0.458683980592565,-1.6

BP,"GO:0007006","mitochondrial membrane organization",103,-0.31928195751481,-1.45857166202

BP,"GO:0032816","positive regulation of natural killer cell activation",25,0.530322921150619,1.8213

BP,"GO:0062009","secondary palate development",26,0.501435312545058,1.73583945714575,0.00

BP,"GO:0018200","peptidyl-glutamic acid modification",28,-0.501316017051103,-1.7578925738175

BP,"GO:0050860","negative regulation of T cell receptor signaling pathway",25,0.529898880089078,

BP,"GO:0002920","regulation of humoral immune response",41,0.430320487612772,1.6699623294:

BP,"GO:0060560","developmental growth involved in morphogenesis",229,0.26739737673942,1.364

BP,"GO:0031649","heat generation",16,0.59403489613384,1.81919025548857,0.007476030486780

BP,"GO:0006026","aminoglycan catabolic process",31,0.486735671644998,1.7585552084032,0.0074

BP,"GO:0006450","regulation of translational fidelity",15,-0.599594164976677,-1.77681782592032,)

BP,"GO:0035066","positive regulation of histone acetylation",31,-0.470670492803391,-1.706384593

BP,"GO:0051153","regulation of striated muscle cell differentiation",77,0.357268604125462,1.55238

BP,"GO:1903514","release of sequestered calcium ion into cytosol by endoplasmic reticulum",33,0.4

BP,"GO:0035815","positive regulation of renal sodium excretion",13,0.622575975424322,1.8208481

BP,"GO:0019217","regulation of fatty acid metabolic process",80,0.350875378050677,1.5352392859

MF,"GO:0032182","ubiquitin-like protein binding",110,-0.315991933194404,-1.46455170794921,0.0

CC,"GO:0043218","compact myelin",11,0.668670471738323,1.87796364638964,0.00766260948573

BP,"GO:0070391","response to lipoteichoic acid",10,0.664937821920644,1.80435827677985,0.0076

BP,"GO:0071223","cellular response to lipoteichoic acid",10,0.664937821920644,1.80435827677985

CC,"GO:0031011","Ino80 complex",15,-0.597389589729682,-1.77028485941356,0.00766699266392

BP,"GO:0006760","folic acid-containing compound metabolic process",26,-0.492500511138262,-1.68

BP,"GO:0033574","response to testosterone",41,0.429096548697946,1.66521253958255,0.0077327

BP,"GO:1990173","protein localization to nucleoplasm",13,-0.636624780763425,-1.80452756999280

BP,"GO:0060416","response to growth hormone",38,0.447056067045205,1.69880670028053,0.007
MF,"GO:0140104","molecular carrier activity",71,-0.348626762753103,-1.50488738119325,0.00776
MF,"GO:0050700","CARD domain binding",15,0.592349902347305,1.78882324691119,0.007784722
BP,"GO:1902947","regulation of tau-protein kinase activity",11,0.668036880144044,1.87618420190
BP,"GO:0030890","positive regulation of B cell proliferation",42,0.435848293760353,1.6922016225:
BP,"GO:2000649","regulation of sodium ion transmembrane transporter activity",54,0.39861620853
BP,"GO:0042752","regulation of circadian rhythm",115,-0.312423018463439,-1.46657226017067,0.1
BP,"GO:0010644","cell communication by electrical coupling",32,0.476161529909854,1.7256602526
MF,"GO:0098847","sequence-specific single stranded DNA binding",13,-0.634532258704561,-1.7985
BP,"GO:0006241","CTP biosynthetic process",13,-0.634112129395712,-1.79740540195319,0.007894
BP,"GO:0090503","RNA phosphodiester bond hydrolysis, exonucleolytic",40,-0.437846566753987,-1
MF,"GO:0030371","translation repressor activity",28,-0.499226197331123,-1.75056450441337,0.00
MF,"GO:0004198","calcium-dependent cysteine-type endopeptidase activity",16,0.59237457466549
MF,"GO:0005523","tropomyosin binding",16,0.591857635447504,1.81252254716029,0.0079368454
BP,"GO:0010919","regulation of inositol phosphate biosynthetic process",16,0.591415025896191,1.1
BP,"GO:2000725","regulation of cardiac muscle cell differentiation",16,0.591381201440242,1.81106
BP,"GO:0019731","antibacterial humoral response",44,0.427856110171299,1.67938481592696,0.00
BP,"GO:0043300","regulation of leukocyte degranulation",47,0.419576960904746,1.6634707629675
BP,"GO:0032703","negative regulation of interleukin-2 production",27,0.502455594690503,1.75244
BP,"GO:1902235","regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling p
BP,"GO:0046598","positive regulation of viral entry into host cell",11,0.665698865841895,1.869617
BP,"GO:0075294","positive regulation by symbiont of entry into host",11,0.665698865841895,1.869
MF,"GO:0050136","NADH dehydrogenase (quinone) activity",36,-0.44150496467596,-1.6673121712
BP,"GO:0051339","regulation of lyase activity",73,0.349864973775704,1.50870551761261,0.007995
CC,"GO:0032391","photoreceptor connecting cilium",38,-0.44032651791572,-1.66501636089435,0.1
CC,"GO:0071682","endocytic vesicle lumen",23,0.518302111019768,1.74478773745013,0.00801739
BP,"GO:0010649","regulation of cell communication by electrical coupling",15,0.590506157730033,0.
BP,"GO:0030202","heparin metabolic process",15,0.590305208822388,1.78264852603138,0.008081
BP,"GO:0030325","adrenal gland development",27,0.500445960683053,1.74543402362182,0.00809
BP,"GO:0032735","positive regulation of interleukin-12 production",42,0.435155355214987,1.68951
BP,"GO:1902932","positive regulation of alcohol biosynthetic process",25,0.527715221415447,1.812
BP,"GO:0051132","NK T cell activation",13,0.621244031408115,1.81695261078773,0.00814839172:
BP,"GO:0009214","cyclic nucleotide catabolic process",13,0.621237814350819,1.81693442775834,C
BP,"GO:0016048","detection of temperature stimulus",24,0.512682966022397,1.73739635656641,C
BP,"GO:0002862","negative regulation of inflammatory response to antigenic stimulus",26,0.496120
BP,"GO:0010390","histone monoubiquitination",29,-0.472775953427831,-1.6749200524895,0.0082
BP,"GO:0002753","cytoplasmic pattern recognition receptor signaling pathway",53,0.392896584174
BP,"GO:0001676","long-chain fatty acid metabolic process",108,0.321413258552333,1.47037855209
BP,"GO:0042474","middle ear morphogenesis",20,0.532965001385667,1.73854593671024,0.008279
BP,"GO:0045724","positive regulation of cilium assembly",22,-0.524981027414973,-1.71501469204:
BP,"GO:0045687","positive regulation of glial cell differentiation",41,0.427074148035949,1.6573641
BP,"GO:0097306","cellular response to alcohol",86,0.338193824162122,1.50037962665735,0.00832
CC,"GO:1904813","ficolin-1-rich granule lumen",124,0.305072850763445,1.42870420008327,0.0083
BP,"GO:0006720","isoprenoid metabolic process",114,0.31409336143263,1.45244719819913,0.008
BP,"GO:0019377","glycolipid catabolic process",14,0.609683131132141,1.81906538212448,0.00834
BP,"GO:0051180","vitamin transport",44,0.425838417712746,1.67146513920025,0.0083759373088
BP,"GO:0080009","mRNA methylation",15,-0.591993546773251,-1.7542944014097,0.00841133853:
BP,"GO:0032413","negative regulation of ion transmembrane transporter activity",64,0.3781865673
BP,"GO:0003417","growth plate cartilage development",19,0.551141944534565,1.76976893736319
BP,"GO:0060711","labyrinthine layer development",46,0.419996233580332,1.65618534556221,0.00

BP,"GO:0006705","mineralocorticoid biosynthetic process",12,0.666817626339055,1.885070410613

BP,"GO:0055072","iron ion homeostasis",79,0.353921074042954,1.54604881014311,0.0084846234

BP,"GO:0032306","regulation of prostaglandin secretion",14,0.608510619574053,1.8155670481924

BP,"GO:0032308","positive regulation of prostaglandin secretion",14,0.608510619574053,1.8155670

CC,"GO:0000177","cytoplasmic exosome (RNase complex)",13,-0.631685256855447,-1.7905263759

BP,"GO:0022412","cellular process involved in reproduction in multicellular organism",366,-0.23237

BP,"GO:0048678","response to axon injury",77,0.354409324414833,1.53996361741215,0.00851305

BP,"GO:0032869","cellular response to insulin stimulus",193,0.283688277579232,1.4264777849935

BP,"GO:0021602","cranial nerve morphogenesis",29,0.479660509099422,1.7019524535428,0.00854

MF,"GO:0061575","cyclin-dependent protein serine/threonine kinase activator activity",11,-0.63440

BP,"GO:0006081","cellular aldehyde metabolic process",65,0.377323764638958,1.59405830603733

CC,"GO:0001673","male germ cell nucleus",14,-0.602741872543051,-1.74834316496483,0.0085945

MF,"GO:0005342","organic acid transmembrane transporter activity",160,0.290295757529219,1.42

MF,"GO:0015145","monosaccharide transmembrane transporter activity",23,0.515580407763288,1.

BP,"GO:0032410","negative regulation of transporter activity",72,0.358990795950577,1.544786474

BP,"GO:0099054","presynapse assembly",49,0.396883302527065,1.59380246654654,0.0086166798

BP,"GO:1902117","positive regulation of organelle assembly",75,-0.341739834631074,-1.481418839

BP,"GO:1905208","negative regulation of cardiocyte differentiation",11,0.662366119224135,1.8602

BP,"GO:0043567","regulation of insulin-like growth factor receptor signaling pathway",21,0.5339527

BP,"GO:0034454","microtubule anchoring at centrosome",11,-0.633159986838222,-1.68221898549

BP,"GO:0010826","negative regulation of centrosome duplication",11,-0.632558499304926,-1.6806

BP,"GO:0046606","negative regulation of centrosome cycle",11,-0.632558499304926,-1.680620915

BP,"GO:0031112","positive regulation of microtubule polymerization or depolymerization",36,-0.438

BP,"GO:0051580","regulation of neurotransmitter uptake",16,0.585782881737032,1.793919039476

BP,"GO:1900363","regulation of mRNA polyadenylation",17,-0.571166527383103,-1.752424506036

BP,"GO:0050951","sensory perception of temperature stimulus",26,0.494222761804633,1.7108714

BP,"GO:0030502","negative regulation of bone mineralization",17,0.573275386129505,1.782572353

BP,"GO:0014808","release of sequestered calcium ion into cytosol by sarcoplasmic reticulum",32,0.4

BP,"GO:0045104","intermediate filament cytoskeleton organization",87,0.342400877309235,1.5227

MF,"GO:0005253","anion channel activity",85,0.349641902082332,1.54884084512581,0.008827851

BP,"GO:0002886","regulation of myeloid leukocyte mediated immunity",57,0.391552697149132,1.6

BP,"GO:0060561","apoptotic process involved in morphogenesis",25,0.522582244408923,1.7947303

BP,"GO:0042594","response to starvation",184,0.2753755037527,1.37513684704474,0.0088646956

BP,"GO:0070839","metal ion export",46,0.419520442501693,1.65430914251802,0.0088824620286

BP,"GO:0120178","steroid hormone biosynthetic process",41,0.424826758024265,1.648642588151

BP,"GO:0035194","post-transcriptional gene silencing by RNA",79,-0.343818052544411,-1.51249731

BP,"GO:2000406","positive regulation of T cell migration",30,0.479613366628002,1.7218427811693

BP,"GO:1901617","organic hydroxy compound biosynthetic process",233,0.258931625781395,1.326

BP,"GO:0006813","potassium ion transport",232,0.265712308687556,1.36000671735771,0.008988

BP,"GO:0060420","regulation of heart growth",58,0.376428508794883,1.55352746427935,0.00903

BP,"GO:0070193","synaptonemal complex organization",25,-0.508572748612267,-1.724314396107

BP,"GO:0032276","regulation of gonadotropin secretion",11,0.6609414311634,1.85625660557559,0

BP,"GO:0045762","positive regulation of adenylate cyclase activity",36,0.461109246668278,1.71662

BP,"GO:0009267","cellular response to starvation",148,0.298036750109808,1.43983047137178,0.00

BP,"GO:0090026","positive regulation of monocyte chemotaxis",20,0.529359464009008,1.7267845

BP,"GO:1902337","regulation of apoptotic process involved in morphogenesis",12,0.6653034064947

BP,"GO:1904748","regulation of apoptotic process involved in development",12,0.66530340649471

BP,"GO:0051148","negative regulation of muscle cell differentiation",54,0.396128967143766,1.6260

MF,"GO:0015149","hexose transmembrane transporter activity",21,0.532379386409824,1.7541971

MF,"GO:0070717","poly-purine tract binding",29,-0.465083641075384,-1.64766822608904,0.00928

MF,"GO:0004532","exoribonuclease activity",39,-0.429433845702115,-1.6188449351339,0.0093045
BP,"GO:0035791","platelet-derived growth factor receptor-beta signaling pathway",14,0.606435459
BP,"GO:1904377","positive regulation of protein localization to cell periphery",65,0.3747542134303
MF,"GO:0005085","guanyl-nucleotide exchange factor activity",218,0.268096784616786,1.36198331
BP,"GO:0046036","CTP metabolic process",15,-0.585684293832538,-1.73559776667221,0.00945342
BP,"GO:0006643","membrane lipid metabolic process",192,0.279595680344502,1.40520255515355
MF,"GO:0017134","fibroblast growth factor binding",23,0.512456847604662,1.72511051887045,0.0
BP,"GO:0045332","phospholipid translocation",48,0.41098744706422,1.64590122530489,0.0095371
BP,"GO:0051281","positive regulation of release of sequestered calcium ion into cytosol",40,0.43449
BP,"GO:1900746","regulation of vascular endothelial growth factor signaling pathway",19,0.5470500
BP,"GO:0032212","positive regulation of telomere maintenance via telomerase",34,-0.45279703147
BP,"GO:0099623","regulation of cardiac muscle cell membrane repolarization",26,0.4906680524046
BP,"GO:0050852","T cell receptor signaling pathway",121,0.309154170375252,1.44291618507475,0
BP,"GO:0045746","negative regulation of Notch signaling pathway",35,0.44850633108602,1.656321
BP,"GO:0002887","negative regulation of myeloid leukocyte mediated immunity",12,0.66383594229
BP,"GO:0060603","mammary gland duct morphogenesis",30,0.47527651025539,1.70627318833121
BP,"GO:0003129","heart induction",10,0.655950637712492,1.77997088343819,0.009705916744568
BP,"GO:0072283","metanephric renal vesicle morphogenesis",15,0.581816077932624,1.7570124034
BP,"GO:0043489","RNA stabilization",56,-0.386711976047117,-1.59381188517369,0.009745799556
MF,"GO:0008081","phosphoric diester hydrolase activity",88,0.342541152244315,1.5213736113455
BP,"GO:1905897","regulation of response to endoplasmic reticulum stress",77,0.351375285906539,
BP,"GO:0045665","negative regulation of neuron differentiation",70,0.365456281296936,1.5638373
BP,"GO:0007567","parturition",15,0.581346192997982,1.75559340926232,0.00986059270862488,
MF,"GO:0004540","ribonuclease activity",106,-0.305027627576278,-1.40721990890787,0.00987744
BP,"GO:0072574","hepatocyte proliferation",21,0.528758549320256,1.74226645726894,0.0098896
BP,"GO:0072575","epithelial cell proliferation involved in liver morphogenesis",21,0.5287585493202
BP,"GO:1905515","non-motile cilium assembly",59,-0.368870853409907,-1.53298359669186,0.0098
BP,"GO:0032753","positive regulation of interleukin-4 production",25,0.51850064629465,1.7807126
BP,"GO:0045576","mast cell activation",62,0.371515587200615,1.55762345428776,0.00992014651
BP,"GO:0031113","regulation of microtubule polymerization",53,-0.382197279159358,-1.555917758
BP,"GO:0044743","protein transmembrane import into intracellular organelle",35,-0.445574944659
BP,"GO:0006865","amino acid transport",140,0.302430780304611,1.44862181170647,0.009929463
CC,"GO:0034451","centriolar satellite",103,-0.312268848938856,-1.42653376827042,0.0099620512
BP,"GO:1903793","positive regulation of anion transport",48,0.410145030154879,1.6425275577313
BP,"GO:0070232","regulation of T cell apoptotic process",34,0.453844386778584,1.6542956827056
BP,"GO:0106106","cold-induced thermogenesis",145,0.291962523442834,1.40501302553077,0.009
BP,"GO:0120161","regulation of cold-induced thermogenesis",145,0.291962523442834,1.40501302
BP,"GO:0070306","lens fiber cell differentiation",35,0.446598839782055,1.64927686155628,0.0099
BP,"GO:0071027","nuclear RNA surveillance",13,-0.62624948081159,-1.7751185438667,0.01000003
BP,"GO:0071028","nuclear mRNA surveillance",13,-0.62624948081159,-1.7751185438667,0.010000
BP,"GO:0002475","antigen processing and presentation via MHC class Ib",13,0.613725275779998,1.
MF,"GO:0004622","lysophospholipase activity",24,0.509242113529451,1.72573588609846,0.01008
BP,"GO:0033151","V(D)J recombination",16,-0.576009303222322,-1.76141797372901,0.010111286
BP,"GO:0072497","mesenchymal stem cell differentiation",11,0.658459733730255,1.849286748586
BP,"GO:2001242","regulation of intrinsic apoptotic signaling pathway",156,0.286730337206623,1.39
BP,"GO:0015748","organophosphate ester transport",137,0.309415024918382,1.46873986751803,
MF,"GO:0004601","peroxidase activity",50,0.391633328287185,1.58330101562516,0.01017007268
BP,"GO:0051895","negative regulation of focal adhesion assembly",17,0.568679866903418,1.76828
BP,"GO:0150118","negative regulation of cell-substrate junction organization",17,0.5686798669034
MF,"GO:0051117","ATPase binding",79,0.350806501006064,1.53244328537799,0.01019577115312

BP,"GO:0010460","positive regulation of heart rate",26,0.489499943046349,1.69452229261197,0.0

BP,"GO:2000310","regulation of NMDA receptor activity",22,0.538378149785556,1.7930988590480

BP,"GO:0090630","activation of GTPase activity",111,0.315313786485866,1.45387234491344,0.010

MF,"GO:0004659","prenyltransferase activity",17,-0.563920771128972,-1.73019343993599,0.01031

BP,"GO:0043470","regulation of carbohydrate catabolic process",51,0.385107635955479,1.5549174

BP,"GO:1904666","regulation of ubiquitin protein ligase activity",24,-0.498573238467382,-1.670350

BP,"GO:0031642","negative regulation of myelination",11,0.655409823419925,1.84072106350009,0.0

BP,"GO:1903027","regulation of opsonization",10,0.654043275582648,1.77479511431761,0.010435

BP,"GO:0032743","positive regulation of interleukin-2 production",34,0.45121220820636,1.6447012

CC,"GO:0031010","ISWI-type complex",13,-0.622328771179944,-1.76400520232232,0.01045115653

BP,"GO:0051445","regulation of meiotic cell cycle",49,-0.368008760464506,-1.47951932904337,0.0

BP,"GO:0009743","response to carbohydrate",204,0.273300705312508,1.37950899573591,0.01048

MF,"GO:0030247","polysaccharide binding",24,0.507129356187413,1.71857610675794,0.01053766

BP,"GO:0022011","myelination in peripheral nervous system",26,0.488982537716261,1.6927311690

BP,"GO:0032292","peripheral nervous system axon ensheathment",26,0.488982537716261,1.69273

BP,"GO:0034309","primary alcohol biosynthetic process",14,0.601210002087156,1.79378474873151

MF,"GO:0035925","mRNA 3'-UTR AU-rich region binding",26,-0.481120507346189,-1.647273540819

BP,"GO:0034204","lipid translocation",53,0.385755526053636,1.57762822246797,0.0105618970401

BP,"GO:0010872","regulation of cholesterol esterification",12,0.660746326799203,1.867907056400

BP,"GO:0060043","regulation of cardiac muscle cell proliferation",37,0.434629040842603,1.6356996

BP,"GO:0071397","cellular response to cholesterol",15,0.578488067072931,1.74696222340905,0.01

BP,"GO:1901223","negative regulation of NIK/NF-kappaB signaling",25,0.516848497874347,1.77503

BP,"GO:0099116","tRNA 5'-end processing",15,-0.582043765026571,-1.72480954214292,0.0106443

BP,"GO:0009395","phospholipid catabolic process",49,0.388916748113411,1.56181040743619,0.01

BP,"GO:0034427","nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'",11,-0.6198932

BP,"GO:0060544","regulation of necroptotic process",20,0.524076396655172,1.70955107288795,0.0

BP,"GO:0006110","regulation of glycolytic process",42,0.426647907468061,1.65648068742335,0.01

BP,"GO:0010803","regulation of tumor necrosis factor-mediated signaling pathway",50,0.391064247

BP,"GO:0043247","telomere maintenance in response to DNA damage",13,-0.62188888891582,-1.76

BP,"GO:0002065","columnar/cuboidal epithelial cell differentiation",87,0.337402863218101,1.50054

BP,"GO:0032305","positive regulation of icosanoid secretion",21,0.526465373879493,1.7347104136

BP,"GO:0000463","maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, L

MF,"GO:0015108","chloride transmembrane transporter activity",97,0.328867534876469,1.4864420

BP,"GO:0042117","monocyte activation",14,0.5980616189938,1.78439115654842,0.0108552830691

MF,"GO:0043395","heparan sulfate proteoglycan binding",18,0.545684921283729,1.721751530703

MF,"GO:0055106","ubiquitin-protein transferase regulator activity",21,-0.521587293251627,-1.6870

BP,"GO:0045747","positive regulation of Notch signaling pathway",41,0.418621059654841,1.624559

BP,"GO:1901020","negative regulation of calcium ion transmembrane transporter activity",31,0.473

MF,"GO:0015453","oxidoreduction-driven active transmembrane transporter activity",59,-0.3676611

BP,"GO:0071549","cellular response to dexamethasone stimulus",24,0.506832953870249,1.7175716

BP,"GO:1990440","positive regulation of transcription from RNA polymerase II promoter in response

MF,"GO:0016849","phosphorus-oxygen lyase activity",20,0.522468612801986,1.70430643941709,0

CC,"GO:0042788","polysomal ribosome",31,-0.459539494474329,-1.6660298992013,0.01101947611

BP,"GO:0048255","mRNA stabilization",48,-0.391074638208577,-1.5649407916881,0.01101903217

MF,"GO:0008514","organic anion transmembrane transporter activity",183,0.269732760952891,1.3

BP,"GO:0070201","regulation of establishment of protein localization",494,0.227322561852053,1.26

BP,"GO:0070525","tRNA threonylcarbamoyladenosine metabolic process",17,-0.561022866382397,-

BP,"GO:0009311","oligosaccharide metabolic process",62,0.368741298196866,1.54599191641939,0

BP,"GO:0097067","cellular response to thyroid hormone stimulus",17,0.566635083556764,1.761924

MF,"GO:0008525","phosphatidylcholine transporter activity",17,0.566275862911255,1.7608076712

BP,"GO:0070593","dendrite self-avoidance",17,0.566218065401774,1.76062795262289,0.01110417
BP,"GO:1900120","regulation of receptor binding",21,0.524781806954053,1.72916303824576,0.011
BP,"GO:0071371","cellular response to gonadotropin stimulus",20,0.521036099858856,1.69963354
BP,"GO:0006766","vitamin metabolic process",105,0.314627422037671,1.44022947913652,0.01116
BP,"GO:0055093","response to hyperoxia",18,0.544141045922891,1.71688027686799,0.011188267
BP,"GO:0098703","calcium ion import across plasma membrane",27,0.486994724237861,1.6985193
BP,"GO:0048009","insulin-like growth factor receptor signaling pathway",34,0.449248947705318,1.6
BP,"GO:0032309","icosanoid secretion",46,0.41250757059303,1.62665504765527,0.011231495010
BP,"GO:0032922","circadian regulation of gene expression",67,0.366217050411734,1.55695547396
CC,"GO:0030658","transport vesicle membrane",193,0.279590518176635,1.40587290556065,0.011
BP,"GO:0070585","protein localization to mitochondrion",119,-0.295514323658669,-1.39328454908
BP,"GO:0005976","polysaccharide metabolic process",99,0.324788543891895,1.47294197743094,0.
BP,"GO:0006650","glycerophospholipid metabolic process",287,0.254094709160598,1.32652800430
BP,"GO:0120163","negative regulation of cold-induced thermogenesis",46,0.411819454453222,1.62
BP,"GO:0007000","nucleolus organization",15,-0.577567321149322,-1.7115441941085,0.011388735
BP,"GO:0010769","regulation of cell morphogenesis involved in differentiation",92,0.332262828003
BP,"GO:1990542","mitochondrial transmembrane transport",83,-0.334249456969281,-1.469909668
BP,"GO:0045605","negative regulation of epidermal cell differentiation",13,0.608077313090217,1.7
BP,"GO:0045683","negative regulation of epidermis development",13,0.608077313090217,1.778443
BP,"GO:0042634","regulation of hair cycle",28,0.482118031050337,1.68957781832981,0.01156072
BP,"GO:0033120","positive regulation of RNA splicing",36,-0.426237065254673,-1.60965403247097
BP,"GO:0006707","cholesterol catabolic process",11,0.648583368176362,1.82154893713448,0.0116
BP,"GO:0016127","sterol catabolic process",11,0.648583368176362,1.82154893713448,0.01160328
BP,"GO:0086100","endothelin receptor signaling pathway",10,0.651100612585916,1.766809979228
BP,"GO:0034244","negative regulation of transcription elongation from RNA polymerase II promoter
BP,"GO:0019433","triglyceride catabolic process",30,0.469974779944427,1.68723963610179,0.0116
BP,"GO:0051646","mitochondrion localization",49,-0.366024320271649,-1.47154121021013,0.0116
BP,"GO:0016074","sno(s)RNA metabolic process",15,-0.575796618486855,-1.70629695149199,0.01
BP,"GO:0097193","intrinsic apoptotic signaling pathway",277,0.253714116949128,1.319538221101
CC,"GO:0031227","intrinsic component of endoplasmic reticulum membrane",157,0.287830125393
BP,"GO:0010799","regulation of peptidyl-threonine phosphorylation",42,0.423844388317387,1.645
BP,"GO:0042391","regulation of membrane potential",403,0.234564142029325,1.28132514804979,
BP,"GO:0000271","polysaccharide biosynthetic process",70,0.36167821924807,1.54767052598638,
MF,"GO:0019104","DNA N-glycosylase activity",13,-0.616037472267357,-1.74617237098764,0.0118
BP,"GO:0080111","DNA demethylation",27,-0.490311512381875,-1.6973521680672,0.01181172335
MF,"GO:0008188","neuropeptide receptor activity",43,0.417488219005065,1.63900585868433,0.01
BP,"GO:0001325","formation of extrachromosomal circular DNA",15,-0.574443387741583,-1.702280
BP,"GO:0090656","t-circle formation",15,-0.574443387741583,-1.70228683156216,0.01183534679
BP,"GO:0090737","telomere maintenance via telomere trimming",15,-0.574443387741583,-1.70228
BP,"GO:0007018","microtubule-based movement",356,-0.233596018670199,-1.29204336432225,0.
BP,"GO:0044331","cell-cell adhesion mediated by cadherin",26,0.485213102804262,1.67968235961
BP,"GO:0060236","regulation of mitotic spindle organization",39,-0.424619202096791,-1.60069508
BP,"GO:0033632","regulation of cell-cell adhesion mediated by integrin",11,0.645789697834293,1.8
MF,"GO:0097001","ceramide binding",18,0.541215778793564,1.70765043935335,0.011949362459
BP,"GO:0097035","regulation of membrane lipid distribution",59,0.374957160192485,1.5605417036
BP,"GO:0009411","response to UV",139,-0.283481347842648,-1.38055136668644,0.012038832918
BP,"GO:0032303","regulation of icosanoid secretion",22,0.528755503768336,1.76105009257905,0.
BP,"GO:0016051","carbohydrate biosynthetic process",197,0.271505972380811,1.36517848754874
BP,"GO:0120009","intermembrane lipid transfer",45,0.406847653922141,1.60233938732731,0.012
MF,"GO:0120013","lipid transfer activity",45,0.406847653922141,1.60233938732731,0.0121158170

MF,"GO:0008353","RNA polymerase II CTD heptapeptide repeat kinase activity",12,-0.638620541868
BP,"GO:0031103","axon regeneration",47,0.411864767261101,1.63289470698757,0.012163237065
CC,"GO:0031464","Cul4A-RING E3 ubiquitin ligase complex",10,-0.657487747302073,-1.7011816220
BP,"GO:0033687","osteoblast proliferation",29,0.468729988778993,1.66316830199198,0.01225744
BP,"GO:0010737","protein kinase A signaling",32,0.461207100869004,1.67146380427519,0.012329
BP,"GO:0016266","O-glycan processing",42,0.421349482147551,1.63590930042355,0.01233303794
BP,"GO:0070076","histone lysine demethylation",26,-0.47617420791562,-1.63033826565921,0.0123
BP,"GO:0071276","cellular response to cadmium ion",36,0.447319876113258,1.66529064866527,0.
CC,"GO:0055037","recycling endosome",184,0.269314904662353,1.34487216114956,0.0123834474
BP,"GO:0072393","microtubule anchoring at microtubule organizing center",13,-0.61321313241030
MF,"GO:0030228","lipoprotein particle receptor activity",18,0.540307733366463,1.7047853636602
CC,"GO:0000502","proteasome complex",58,-0.358997876920651,-1.4939001889658,0.0124569686
BP,"GO:0050773","regulation of dendrite development",96,-0.314243492729862,-1.4240111801819
BP,"GO:0060547","negative regulation of necrotic cell death",17,0.562181004023186,1.7480749036
BP,"GO:2000738","positive regulation of stem cell differentiation",20,0.515836186743595,1.682671
BP,"GO:0031281","positive regulation of cyclase activity",48,0.403666468058017,1.6165825480488
BP,"GO:0048259","regulation of receptor-mediated endocytosis",103,0.312908257266322,1.437578
BP,"GO:0090713","immunological memory process",17,0.561438893873259,1.74576734767643,0.0
BP,"GO:1900426","positive regulation of defense response to bacterium",12,0.654879777809658,1.
MF,"GO:0051371","muscle alpha-actinin binding",15,0.570625420462471,1.72321800570376,0.012
BP,"GO:0035584","calcium-mediated signaling using intracellular calcium source",20,0.51507638302
BP,"GO:0060231","mesenchymal to epithelial transition",20,0.515029095295389,1.6800385364618
BP,"GO:0043970","histone H3-K9 acetylation",13,-0.611841745605012,-1.73427948735016,0.01270
BP,"GO:0006516","glycoprotein catabolic process",25,0.511936129758547,1.75816783692554,0.01
MF,"GO:0005031","tumor necrosis factor-activated receptor activity",10,0.645295811009207,1.751
BP,"GO:0051918","negative regulation of fibrinolysis",10,0.64483790093728,1.74981564498279,0.0
BP,"GO:0032892","positive regulation of organic acid transport",43,0.416329516202728,1.63445693
MF,"GO:0016493","C-C chemokine receptor activity",23,0.502020877322208,1.68997936159734,0.0
BP,"GO:0010893","positive regulation of steroid biosynthetic process",21,0.519557411329541,1.711
BP,"GO:0032608","interferon-beta production",54,0.384097041158218,1.5766664830816,0.012979
BP,"GO:0032648","regulation of interferon-beta production",54,0.384097041158218,1.5766664830
BP,"GO:0098661","inorganic anion transmembrane transport",90,0.325453111452891,1.457363807
MF,"GO:0008022","protein C-terminus binding",174,-0.267687735331258,-1.34778337494997,0.01
BP,"GO:1902373","negative regulation of mRNA catabolic process",57,-0.366183910295813,-1.5151
BP,"GO:0032535","regulation of cellular component size",334,0.24789571529958,1.3228183167846
CC,"GO:0000176","nuclear exosome (RNase complex)",12,-0.634834119893263,-1.76105403249621
BP,"GO:0060041","retina development in camera-type eye",146,0.29135706075716,1.40327052291
BP,"GO:0072173","metanephric tubule morphogenesis",10,0.643119920023188,1.74515377588842
BP,"GO:0010763","positive regulation of fibroblast migration",14,0.591334339701108,1.764319482
BP,"GO:0042176","regulation of protein catabolic process",379,0.23692906540549,1.282766443113
BP,"GO:1902808","positive regulation of cell cycle G1/S phase transition",55,-0.368542928054867,-1
MF,"GO:0016684","oxidoreductase activity, acting on peroxide as acceptor",54,0.383696841378967
BP,"GO:0007141","male meiosis I",27,-0.483904665379924,-1.67517305259751,0.01314888284537
BP,"GO:0048711","positive regulation of astrocyte differentiation",12,0.65352676850685,1.8474976
BP,"GO:0030513","positive regulation of BMP signaling pathway",36,0.444245572984812,1.6538455
BP,"GO:0048643","positive regulation of skeletal muscle tissue development",18,0.53661435855656
BP,"GO:0042574","retinal metabolic process",18,0.536354721194163,1.69231277280593,0.0133193
BP,"GO:0000478","endonucleolytic cleavage involved in rRNA processing",15,-0.570966549475923,-
BP,"GO:0000479","endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSI
BP,"GO:0034374","low-density lipoprotein particle remodeling",16,0.569447851814294,1.74389415

BP,"GO:1902806","regulation of cell cycle G1/S phase transition",157,-0.27691483333355,-1.374946

BP,"GO:0015833","peptide transport",243,0.257778526871666,1.32612321713796,0.013344826325

MF,"GO:0043121","neurotrophin binding",10,0.642585147138176,1.74370262985723,0.013354698

CC,"GO:0000109","nucleotide-excision repair complex",11,-0.606383679396769,-1.61107802005591

BP,"GO:1904353","regulation of telomere capping",26,-0.473225372832453,-1.6202419635175,0.01

MF,"GO:0032036","myosin heavy chain binding",13,0.601697788710574,1.75978570872529,0.0134

BP,"GO:0010657","muscle cell apoptotic process",62,0.363177257694723,1.52266401232781,0.0134

BP,"GO:2000737","negative regulation of stem cell differentiation",23,0.50095209603471,1.6863814

BP,"GO:0097048","dendritic cell apoptotic process",11,0.639878202791505,1.79710044595755,0.01

BP,"GO:2000668","regulation of dendritic cell apoptotic process",11,0.639878202791505,1.7971004

BP,"GO:0034145","positive regulation of toll-like receptor 4 signaling pathway",11,0.6398215280509

CC,"GO:0000242","pericentriolar material",21,-0.509188410426222,-1.64698164756569,0.01352711

BP,"GO:0035195","miRNA-mediated gene silencing",73,-0.333657482015601,-1.44017145732627,0.0

BP,"GO:0030889","negative regulation of B cell proliferation",17,0.559221137804943,1.7388713414

MF,"GO:0017166","vinculin binding",12,0.65099621327135,1.84034382203855,0.013581574267015

BP,"GO:0051302","regulation of cell division",176,-0.268398233792415,-1.35702601036469,0.01358

BP,"GO:0051702","biological process involved in interaction with symbiont",95,0.325006076038164

BP,"GO:0031943","regulation of glucocorticoid metabolic process",10,0.640273105178803,1.737428

BP,"GO:0097320","plasma membrane tubulation",19,0.535323206174661,1.71897347159388,0.013

BP,"GO:0006656","phosphatidylcholine biosynthetic process",28,0.476702547744391,1.6705993112

BP,"GO:0006633","fatty acid biosynthetic process",146,0.290299751962573,1.39817817930978,0.01

BP,"GO:0045761","regulation of adenylate cyclase activity",56,0.370713114772176,1.526998978921

BP,"GO:0048593","camera-type eye morphogenesis",120,0.314729096461329,1.46869977690786,0.0

BP,"GO:0006486","protein glycosylation",213,0.259829089346133,1.31779024128481,0.013786951

BP,"GO:0043413","macromolecule glycosylation",213,0.259829089346133,1.31779024128481,0.013

BP,"GO:0006957","complement activation, alternative pathway",16,0.568489385489023,1.7409589

CC,"GO:0120103","centriolar subdistal appendage",10,-0.654018734503575,-1.6922059097832,0.01

BP,"GO:0000027","ribosomal large subunit assembly",25,-0.493597219593982,-1.67353990937796,0

BP,"GO:1903727","positive regulation of phospholipid metabolic process",13,0.6007279218856,1.75

BP,"GO:1901623","regulation of lymphocyte chemotaxis",26,0.482293457357952,1.6695753016595

BP,"GO:0031331","positive regulation of cellular catabolic process",425,0.232619140158357,1.2757

BP,"GO:0070296","sarcoplasmic reticulum calcium ion transport",37,0.423489182079338,1.5937754

CC,"GO:0030315","T-tubule",49,0.382582566738594,1.53637362580678,0.0139748494586647,0.03

BP,"GO:0060736","prostate gland growth",12,0.649977613631365,1.83746427601914,0.014031787

BP,"GO:0036315","cellular response to sterol",20,0.511978892195669,1.67008869324253,0.014051

BP,"GO:0030101","natural killer cell activation",91,0.329505354096017,1.47752406827076,0.01405

BP,"GO:0051782","negative regulation of cell division",17,-0.552243542739194,-1.69436595318429

BP,"GO:0051100","negative regulation of binding",155,0.289335812558084,1.41181572277242,0.01

BP,"GO:0015732","prostaglandin transport",19,0.533278790670568,1.71240865995128,0.01409659

BP,"GO:0006525","arginine metabolic process",19,0.532821928379497,1.71094163190268,0.01409

MF,"GO:0070034","telomerase RNA binding",21,-0.507564850135453,-1.6417302043909,0.0141121

BP,"GO:0015669","gas transport",21,0.515648924496591,1.69907006899869,0.0141171738233594

BP,"GO:0021885","forebrain cell migration",59,0.370563971497431,1.54225760371502,0.01413431

CC,"GO:0000782","telomere cap complex",11,-0.603025243938124,-1.60215511903954,0.01414586

CC,"GO:0000783","nuclear telomere cap complex",11,-0.603025243938124,-1.60215511903954,0.0

BP,"GO:0050862","positive regulation of T cell receptor signaling pathway",15,0.564052697183767,0

BP,"GO:0010457","centriole-centriole cohesion",13,-0.608210774761233,-1.72398741705786,0.014

MF,"GO:0016423","tRNA (guanine) methyltransferase activity",13,-0.608144628000667,-1.72379991

MF,"GO:0140102","catalytic activity, acting on a rRNA",18,-0.520631165001608,-1.62522093809853

MF,"GO:0046965","nuclear retinoid X receptor binding",15,0.563314497839591,1.70113992602087,

BP,"GO:0071715","icosanoid transport",54,0.380944294969013,1.56372488574153,0.01441389971

BP,"GO:0055010","ventricular cardiac muscle tissue morphogenesis",47,0.407832256000497,1.6169

MF,"GO:0036041","long-chain fatty acid binding",14,0.585493574979316,1.74689283550202,0.0145

BP,"GO:0045655","regulation of monocyte differentiation",19,0.531808801636016,1.707688386059

BP,"GO:0072175","epithelial tube formation",136,0.289857826635785,1.37923135691593,0.014653

MF,"GO:0005041","low-density lipoprotein particle receptor activity",15,0.562372759288716,1.6982

BP,"GO:0034370","triglyceride-rich lipoprotein particle remodeling",12,0.64652660669341,1.827708

BP,"GO:0034372","very-low-density lipoprotein particle remodeling",12,0.64652660669341,1.82770

BP,"GO:0014842","regulation of skeletal muscle satellite cell proliferation",12,0.64549044222588,1

BP,"GO:0060272","embryonic skeletal joint morphogenesis",11,0.63411020150008,1.780900991674

BP,"GO:0070944","neutrophil-mediated killing of bacterium",11,0.632715272240779,1.7769833273

MF,"GO:0055056","D-glucose transmembrane transporter activity",11,0.62949802852497,1.767947

BP,"GO:1903573","negative regulation of response to endoplasmic reticulum stress",39,0.430116298

BP,"GO:0006826","iron ion transport",54,0.380158879291404,1.5605008604524,0.01484557487170

BP,"GO:0071676","negative regulation of mononuclear cell migration",21,0.513299947558628,1.691

BP,"GO:0051099","positive regulation of binding",166,0.283007575099148,1.39239204384981,0.014

BP,"GO:0000028","ribosomal small subunit assembly",17,-0.549391627162071,-1.6856158487806,0

MF,"GO:0016874","ligase activity",127,-0.286607786883971,-1.37069033013699,0.0149341119865

BP,"GO:0042733","embryonic digit morphogenesis",55,0.379405594748678,1.54920520912612,0.014

CC,"GO:0005838","proteasome regulatory particle",19,-0.53243281271188,-1.68051459119899,0.014

BP,"GO:1905820","positive regulation of chromosome separation",18,-0.519417892409995,-1.62143

BP,"GO:0002861","regulation of inflammatory response to antigenic stimulus",39,0.4292071226180

MF,"GO:0140666","annealing activity",13,-0.603736483139771,-1.71130493464265,0.01511275546

MF,"GO:0005212","structural constituent of eye lens",23,0.497846284198264,1.67592620854888,0

BP,"GO:0007588","excretion",64,0.362335180280874,1.526851206022,0.0152404972998789,0.034

MF,"GO:0140658","ATP-dependent chromatin remodeler activity",13,-0.602134685694068,-1.70676

MF,"GO:0051011","microtubule minus-end binding",13,-0.600068847699908,-1.70090893771024,0

MF,"GO:0034185","apolipoprotein binding",18,0.530550691696393,1.67399983014935,0.01529818

CC,"GO:0043073","germ cell nucleus",18,-0.518515143172829,-1.61861548838137,0.015310833345

MF,"GO:0001530","lipopolysaccharide binding",31,0.460484044135986,1.66370919859871,0.01535

BP,"GO:0030004","cellular monovalent inorganic cation homeostasis",105,0.306952958336875,1.40

BP,"GO:1902883","negative regulation of response to oxidative stress",18,0.529945539462398,1.67

MF,"GO:0048027","mRNA 5'-UTR binding",26,-0.468373811085614,-1.60363105382817,0.01550272

BP,"GO:0010642","negative regulation of platelet-derived growth factor receptor signaling pathway"

BP,"GO:0051898","negative regulation of protein kinase B signaling",38,0.429416619640979,1.6317

BP,"GO:0048741","skeletal muscle fiber development",31,0.459603535359876,1.6605279579696,0

BP,"GO:0010454","negative regulation of cell fate commitment",11,0.625176622785156,1.75581100

MF,"GO:0015101","organic cation transmembrane transporter activity",25,0.502020831866874,1.72

BP,"GO:2000179","positive regulation of neural precursor cell proliferation",48,0.397461104961106

BP,"GO:0010506","regulation of autophagy",325,0.243490260240908,1.29462885061109,0.0157140

BP,"GO:1990776","response to angiotensin",28,0.472176125835823,1.6547365109309,0.015740395

BP,"GO:0050901","leukocyte tethering or rolling",33,0.436458427485983,1.59427835946175,0.0157

MF,"GO:0016247","channel regulator activity",136,0.288357329898988,1.37209153883905,0.01577

MF,"GO:0015276","ligand-gated ion channel activity",145,0.28358240826703,1.3646853463526,0.0

MF,"GO:0022834","ligand-gated channel activity",145,0.28358240826703,1.3646853463526,0.0157

MF,"GO:0031543","peptidyl-proline dioxygenase activity",12,0.641409929830702,1.8132437296775

BP,"GO:0090331","negative regulation of platelet aggregation",12,0.641282231999294,1.812882732

BP,"GO:0051952","regulation of amine transport",89,0.331022518542621,1.47485397237348,0.015

BP,"GO:0030852","regulation of granulocyte differentiation",15,0.560067653812461,1.69133485970

BP,"GO:0042267","natural killer cell mediated cytotoxicity",70,0.35587355083337,1.5228315565918

BP,"GO:1905477","positive regulation of protein localization to membrane",99,0.317140327522652, BP,"GO:0035994","response to muscle stretch",24,0.496403694205215,1.68222864198022,0.01607 BP,"GO:0010719","negative regulation of epithelial to mesenchymal transition",34,0.440665001640 BP,"GO:1901844","regulation of cell communication by electrical coupling involved in cardiac conduc BP,"GO:0070723","response to cholesterol",25,0.498840708627257,1.71319357762705,0.01630733 BP,"GO:0061515","myeloid cell development",71,0.342038702104311,1.46327269472652,0.016318 BP,"GO:1902656","calcium ion import into cytosol",28,0.470807386262019,1.64993977678277,0.01 BP,"GO:0072089","stem cell proliferation",64,0.35990898021067,1.51662739474215,0.0163590356 BP,"GO:0035872","nucleotide-binding domain, leucine rich repeat containing receptor signaling path BP,"GO:0036314","response to sterol",30,0.45795624662056,1.64409232978413,0.0164388428537, BP,"GO:1905476","negative regulation of protein localization to membrane",32,0.451393290913682 BP,"GO:0051348","negative regulation of transferase activity",247,0.253347198198657,1.30565549, BP,"GO:0099622","cardiac muscle cell membrane repolarization",36,0.435562144793558,1.6215187 BP,"GO:0045109","intermediate filament organization",68,0.352064182044178,1.49656253661812, MF,"GO:0004954","prostanoid receptor activity",11,0.622865130018876,1.74931916424891,0.0165 BP,"GO:0043568","positive regulation of insulin-like growth factor receptor signaling pathway",11,0. CC,"GO:0031672","A band",34,0.440092444222831,1.60416885540192,0.0165705854560713,0.036 BP,"GO:0034976","response to endoplasmic reticulum stress",243,0.254481649856761,1.30916266 MF,"GO:0000900","mRNA regulatory element binding translation repressor activity",15,-0.55765318 BP,"GO:0032728","positive regulation of interferon-beta production",37,0.419542925846994,1.578 BP,"GO:0034650","cortisol metabolic process",12,0.639509274563008,1.80787064284785,0.016740 BP,"GO:0047484","regulation of response to osmotic stress",14,0.580806856933413,1.7329094298 BP,"GO:0015837","amine transport",97,0.316625607383594,1.43111002476032,0.01683093086052 CC,"GO:0036019","endolysosome",27,0.471416929279145,1.64418780911344,0.016872005814520 BP,"GO:0031440","regulation of mRNA 3'-end processing",27,-0.474369746119198,-1.64216522905 CC,"GO:0032039","integrator complex",17,-0.542902652885683,-1.66570670320605,0.0169614031 BP,"GO:0032239","regulation of nucleobase-containing compound transport",14,-0.5771347658127 BP,"GO:0043649","dicarboxylic acid catabolic process",18,0.527961635504884,1.66583080937024,0 BP,"GO:0010818","T cell chemotaxis",26,0.476429851408423,1.64927701329873,0.0170346127672 BP,"GO:0035589","G protein-coupled purinergic nucleotide receptor signaling pathway",14,0.58057 MF,"GO:0045028","G protein-coupled purinergic nucleotide receptor activity",14,0.5805724351261 BP,"GO:0003376","sphingosine-1-phosphate receptor signaling pathway",14,0.580089548357472,1. CC,"GO:0005811","lipid droplet",97,0.31552618266591,1.42614075601434,0.0171186321341117,0. BP,"GO:0032769","negative regulation of monooxygenase activity",11,0.620007736362865,1.74129 BP,"GO:0070861","regulation of protein exit from endoplasmic reticulum",25,0.495191961285207,1 BP,"GO:0018027","peptidyl-lysine dimethylation",22,-0.500617329313016,-1.63542305345765,0.01 BP,"GO:2001198","regulation of dendritic cell differentiation",12,0.638454639844841,1.804889226 BP,"GO:0006541","glutamine metabolic process",23,-0.491930005098471,-1.62120449045796,0.01 BP,"GO:0008306","associative learning",79,0.338122453285491,1.47703500843597,0.01733964258 BP,"GO:0010452","histone H3-K36 methylation",13,-0.593630173046801,-1.68265836645253,0.017 BP,"GO:2000052","positive regulation of non-canonical Wnt signaling pathway",15,0.554606895013 CC,"GO:0005859","muscle myosin complex",15,0.554443956041289,1.67435198983886,0.0174344 BP,"GO:0023035","CD40 signaling pathway",15,0.554198707696046,1.67361137024983,0.0174344 BP,"GO:0031114","regulation of microtubule depolymerization",29,-0.444013239881456,-1.573021 CC,"GO:0000791","euchromatin",53,-0.360860498643809,-1.46905613632475,0.017464617588997 BP,"GO:0072331","signal transduction by p53 class mediator",162,-0.264845788788702,-1.3175382 BP,"GO:2000242","negative regulation of reproductive process",61,0.368469569451978,1.53720997 BP,"GO:0106056","regulation of calcineurin-mediated signaling",35,0.429934487111321,1.5877358 CC,"GO:0140672","ATAC complex",12,-0.620555935484387,-1.72144580502066,0.01759227017734 BP,"GO:0010765","positive regulation of sodium ion transport",33,0.432019144313378,1.57806271

BP,"GO:0009755","hormone-mediated signaling pathway",182,0.275375807291938,1.36977401215

BP,"GO:1902043","positive regulation of extrinsic apoptotic signaling pathway via death domain rece

BP,"GO:0003283","atrial septum development",21,0.506950645483038,1.67040912388346,0.01775

BP,"GO:0072655","establishment of protein localization to mitochondrion",115,-0.29788154200509

BP,"GO:0050961","detection of temperature stimulus involved in sensory perception",19,0.5253187

BP,"GO:0060037","pharyngeal system development",28,0.468682554736615,1.64249332595166,0.0

BP,"GO:0051930","regulation of sensory perception of pain",28,0.468229978308678,1.64090727638

BP,"GO:0051931","regulation of sensory perception",28,0.468229978308678,1.640907276386,0.017

BP,"GO:0008645","hexose transmembrane transport",106,0.301406795184048,1.38265114563706,0

MF,"GO:0001217","DNA-binding transcription repressor activity",322,0.239194904831039,1.273091

BP,"GO:0002467","germinal center formation",14,0.576584511074228,1.72031153628388,0.017958

MF,"GO:0004407","histone deacetylase activity",20,-0.491388993121989,-1.57662407992211,0.017

CC,"GO:0001772","immunological synapse",43,0.403693344430035,1.58484892869437,0.01798173

BP,"GO:2000758","positive regulation of peptidyl-lysine acetylation",37,-0.406157111265065,-1.538

BP,"GO:0051123","RNA polymerase II preinitiation complex assembly",28,-0.472176455521299,-1.6

MF,"GO:0008330","protein tyrosine/threonine phosphatase activity",10,0.629629809588845,1.7085

BP,"GO:0045657","positive regulation of monocyte differentiation",10,0.629434919591205,1.70801

BP,"GO:0048147","negative regulation of fibroblast proliferation",29,0.452592109528188,1.605907

BP,"GO:0006361","transcription initiation from RNA polymerase I promoter",10,-0.64465566518055

BP,"GO:0021548","pons development",10,-0.644617975457008,-1.66788241692925,0.01809286323

BP,"GO:0097428","protein maturation by iron-sulfur cluster transfer",11,-0.591852496281405,-1.57

BP,"GO:1904668","positive regulation of ubiquitin protein ligase activity",11,-0.591632007621397,-1

MF,"GO:0061629","RNA polymerase II-specific DNA-binding transcription factor binding",341,0.2415

BP,"GO:0060333","interferon-gamma-mediated signaling pathway",25,0.489814507105581,1.68219

BP,"GO:0070918","primary sncRNA processing",51,-0.358769908710319,-1.45708197513201,0.0182

CC,"GO:0005923","bicellular tight junction",117,0.305525399588134,1.4200515280346,0.01827597

BP,"GO:0010977","negative regulation of neuron projection development",129,0.299068238068976

MF,"GO:0120020","cholesterol transfer activity",22,0.515168580582281,1.71579807692315,0.0182

BP,"GO:1904948","midbrain dopaminergic neuron differentiation",17,0.546227390012862,1.698467

BP,"GO:0036376","sodium ion export across plasma membrane",15,0.551167067708525,1.6644561

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214700193424e-09,7.86317825511555e-10,2835,"tags=60%, list=16%, signal=50%","54921/56897/2
4e-09,7.86317825511555e-10,2539,"tags=62%, list=14%, signal=54%","9531/7205/11346/10398/40
-10,1.57214700193424e-09,7.86317825511555e-10,2539,"tags=62%, list=14%, signal=54%","9531/7
14700193424e-09,7.86317825511555e-10,2835,"tags=60%, list=16%, signal=50%","54921/56897/25
e-10,1.57214700193424e-09,7.86317825511555e-10,3087,"tags=57%, list=17%, signal=47%","8520/7
1.57214700193424e-09,7.86317825511555e-10,2643,"tags=51%, list=15%, signal=44%","90627/2246
114700193424e-09,7.86317825511555e-10,3327,"tags=51%, list=19%, signal=42%","3550/23113/912
193424e-09,7.86317825511555e-10,2344,"tags=69%, list=13%, signal=60%","8467/7158/29980/107
10,1.57214700193424e-09,7.86317825511555e-10,3123,"tags=46%, list=17%, signal=39%","84159/8
1700193424e-09,7.86317825511555e-10,3950,"tags=48%, list=22%, signal=39%","301/79148/728/64
415027808117,1e-10,1.57214700193424e-09,7.86317825511555e-10,953,"tags=60%, list=5%, signal:
,1.57214700193424e-09,7.86317825511555e-10,5511,"tags=79%, list=31%, signal=55%","10250/165
81204576555379,1e-10,1.57214700193424e-09,7.86317825511555e-10,3035,"tags=61%, list=17%, s
0193424e-09,7.86317825511555e-10,4101,"tags=59%, list=23%, signal=46%","4240/2246/3913/7094
6,1e-10,1.57214700193424e-09,7.86317825511555e-10,953,"tags=59%, list=5%, signal=56%","7517/
8,1e-10,1.57214700193424e-09,7.86317825511555e-10,2585,"tags=54%, list=14%, signal=46%","644
193424e-09,7.86317825511555e-10,2585,"tags=53%, list=14%, signal=46%","64431/57492/5931/645
0193424e-09,7.86317825511555e-10,3084,"tags=45%, list=17%, signal=38%","8658/11144/7517/25
14700193424e-09,7.86317825511555e-10,3950,"tags=51%, list=22%, signal=40%","301/79148/728/
14700193424e-09,7.86317825511555e-10,2861,"tags=49%, list=16%, signal=41%","4052/64285/3490
7214700193424e-09,7.86317825511555e-10,2405,"tags=57%, list=13%, signal=50%","7994/4300/501
,1e-10,1.57214700193424e-09,7.86317825511555e-10,4657,"tags=68%, list=26%, signal=51%","5694
..57214700193424e-09,7.86317825511555e-10,4657,"tags=68%, list=26%, signal=51%","56943/5592
2.79322487800855,1e-10,1.57214700193424e-09,7.86317825511555e-10,953,"tags=47%, list=5%, si
,1e-10,1.57214700193424e-09,7.86317825511555e-10,3669,"tags=72%, list=20%, signal=58%","5694
2128,1e-10,1.57214700193424e-09,7.86317825511555e-10,4016,"tags=56%, list=22%, signal=44%","
3723,1e-10,1.57214700193424e-09,7.86317825511555e-10,6750,"tags=66%, list=38%, signal=42%","
6,1e-10,1.57214700193424e-09,7.86317825511555e-10,4711,"tags=76%, list=26%, signal=56%","548
087047,1e-10,1.57214700193424e-09,7.86317825511555e-10,953,"tags=59%, list=5%, signal=56%","
57214700193424e-09,7.86317825511555e-10,4016,"tags=56%, list=22%, signal=44%","2246/2152/80
0193424e-09,7.86317825511555e-10,3352,"tags=46%, list=19%, signal=38%","90627/1793/2246/301
07,1e-10,1.57214700193424e-09,7.86317825511555e-10,3327,"tags=61%, list=19%, signal=50%","35
1.57214700193424e-09,7.86317825511555e-10,3892,"tags=51%, list=22%, signal=40%","301/728/20
114700193424e-09,7.86317825511555e-10,3347,"tags=53%, list=19%, signal=44%","25937/2246/39:
,1.57214700193424e-09,7.86317825511555e-10,3295,"tags=47%, list=18%, signal=39%","301/7914:
114700193424e-09,7.86317825511555e-10,3123,"tags=47%, list=17%, signal=39%","860/861/64764/

57214700193424e-09,7.86317825511555e-10,4794,"tags=56%, list=27%, signal=42%","54971/26240,
316,1e-10,1.57214700193424e-09,7.86317825511555e-10,3454,"tags=57%, list=19%, signal=46%","
214700193424e-09,7.86317825511555e-10,2822,"tags=59%, list=16%, signal=50%","1387/55693/75
57,1e-10,1.57214700193424e-09,7.86317825511555e-10,2191,"tags=41%, list=12%, signal=36%","90
517626251391,1e-10,1.57214700193424e-09,7.86317825511555e-10,2191,"tags=50%, list=12%, sig
424e-09,7.86317825511555e-10,3199,"tags=45%, list=18%, signal=38%","25937/9902/2274/1052/86
1700193424e-09,7.86317825511555e-10,4039,"tags=51%, list=23%, signal=40%","90627/1793/2246/
214700193424e-09,7.86317825511555e-10,4039,"tags=52%, list=23%, signal=41%","90627/1793/22
983,1e-10,1.57214700193424e-09,7.86317825511555e-10,2712,"tags=82%, list=15%, signal=70%","2
-10,1.57214700193424e-09,7.86317825511555e-10,2712,"tags=82%, list=15%, signal=70%","2303/8
57214700193424e-09,7.86317825511555e-10,1826,"tags=76%, list=10%, signal=69%","79003/51112
93424e-09,7.86317825511555e-10,3065,"tags=40%, list=17%, signal=34%","7205/824/79026/1465/
-10,1.57214700193424e-09,7.86317825511555e-10,5263,"tags=73%, list=29%, signal=52%","51639/2
14700193424e-09,7.86317825511555e-10,4599,"tags=65%, list=26%, signal=49%","7107/728/7057/
193424e-09,7.86317825511555e-10,3993,"tags=55%, list=22%, signal=43%","3074/2239/3920/5159,
7214700193424e-09,7.86317825511555e-10,4892,"tags=57%, list=27%, signal=42%","2152/3597/72
14700193424e-09,7.86317825511555e-10,4631,"tags=65%, list=26%, signal=48%","301/2152/27202
00193424e-09,7.86317825511555e-10,4600,"tags=52%, list=26%, signal=39%","558/1465/5327/103
214700193424e-09,7.86317825511555e-10,3803,"tags=45%, list=21%, signal=36%","7205/824/79026
11,-2.73355903410543,1e-10,1.57214700193424e-09,7.86317825511555e-10,953,"tags=45%, list=5
1.57214700193424e-09,7.86317825511555e-10,3123,"tags=53%, list=17%, signal=44%","860/861/6
49208504,1e-10,1.57214700193424e-09,7.86317825511555e-10,953,"tags=58%, list=5%, signal=55%
89214223,1e-10,1.57214700193424e-09,7.86317825511555e-10,3343,"tags=72%, list=19%, signal=5
581,1e-10,1.57214700193424e-09,7.86317825511555e-10,3035,"tags=59%, list=17%, signal=49%","
424e-09,7.86317825511555e-10,4600,"tags=52%, list=26%, signal=39%","558/1465/5327/10398/215
89,1e-10,1.57214700193424e-09,7.86317825511555e-10,4631,"tags=66%, list=26%, signal=49%","30
7214700193424e-09,7.86317825511555e-10,3672,"tags=60%, list=20%, signal=48%","9697/9902/86
93424e-09,7.86317825511555e-10,2552,"tags=56%, list=14%, signal=48%","10413/6237/677/2022/2
700193424e-09,7.86317825511555e-10,3700,"tags=48%, list=21%, signal=39%","7205/30008/7414/
205418465,1e-10,1.57214700193424e-09,7.86317825511555e-10,3244,"tags=46%, list=18%, signal=
-10,1.57214700193424e-09,7.86317825511555e-10,2565,"tags=53%, list=14%, signal=46%","64769/1
424e-09,7.86317825511555e-10,4600,"tags=52%, list=26%, signal=39%","558/1465/5327/10398/215
10,1.57214700193424e-09,7.86317825511555e-10,4001,"tags=50%, list=22%, signal=40%","90627/1
10,1.57214700193424e-09,7.86317825511555e-10,3409,"tags=54%, list=19%, signal=44%","7132/74
24e-09,7.86317825511555e-10,2539,"tags=56%, list=14%, signal=49%","9531/7205/11346/10398/40
00193424e-09,7.86317825511555e-10,4757,"tags=58%, list=27%, signal=43%","5253/5897/51460/11
894,1e-10,1.57214700193424e-09,7.86317825511555e-10,1155,"tags=87%, list=6%, signal=81%","54
214700193424e-09,7.86317825511555e-10,4261,"tags=54%, list=24%, signal=42%","2303/5592/6649
0,1.57214700193424e-09,7.86317825511555e-10,5263,"tags=82%, list=29%, signal=58%","51639/57
1e-10,1.57214700193424e-09,7.86317825511555e-10,4631,"tags=56%, list=26%, signal=42%","2152,
93424e-09,7.86317825511555e-10,3027,"tags=55%, list=17%, signal=46%","1303/7373/80781/1295/
00193424e-09,7.86317825511555e-10,3084,"tags=43%, list=17%, signal=36%","8658/10059/11144/
825255,1e-10,1.57214700193424e-09,7.86317825511555e-10,3153,"tags=48%, list=18%, signal=40%
1.57214700193424e-09,7.86317825511555e-10,4261,"tags=54%, list=24%, signal=42%","2303/5592
6,1e-10,1.57214700193424e-09,7.86317825511555e-10,4261,"tags=54%, list=24%, signal=42%","230
14700193424e-09,7.86317825511555e-10,3286,"tags=51%, list=18%, signal=42%","2770/79441/107
7214700193424e-09,7.86317825511555e-10,2245,"tags=44%, list=13%, signal=39%","5327/2152/710
e-10,1.57214700193424e-09,7.86317825511555e-10,2422,"tags=46%, list=13%, signal=40%","25937
10,1.57214700193424e-09,7.86317825511555e-10,3802,"tags=56%, list=21%, signal=45%","1051/10
2.66477696411071,1e-10,1.57214700193424e-09,7.86317825511555e-10,3769,"tags=67%, list=21%

932920859,1e-10,1.57214700193424e-09,7.86317825511555e-10,4001,"tags=56%, list=22%, signal=74,1e-10,1.57214700193424e-09,7.86317825511555e-10,3232,"tags=45%, list=18%, signal=37%", "905073207617,1e-10,1.57214700193424e-09,7.86317825511555e-10,3454,"tags=55%, list=19%, signal=1,1.57214700193424e-09,7.86317825511555e-10,4068,"tags=52%, list=23%, signal=41%", "7107/301,7214700193424e-09,7.86317825511555e-10,5263,"tags=84%, list=29%, signal=60%", "51639/57819/514700193424e-09,7.86317825511555e-10,4018,"tags=73%, list=22%, signal=57%", "6830/6603/8028/59,1e-10,1.57214700193424e-09,7.86317825511555e-10,4051,"tags=46%, list=23%, signal=36%", "67002891848,1e-10,1.57214700193424e-09,7.86317825511555e-10,4039,"tags=61%, list=23%, signal=1.57214700193424e-09,7.86317825511555e-10,3871,"tags=49%, list=22%, signal=39%", "687/2246/2011179,1e-10,1.57214700193424e-09,7.86317825511555e-10,3625,"tags=50%, list=20%, signal=40%140605719411,1e-10,1.57214700193424e-09,7.86317825511555e-10,3584,"tags=67%, list=20%, signal=29911945845243,-2.65102553976712,1e-10,1.57214700193424e-09,7.86317825511555e-10,2565,"tags=375,1e-10,1.57214700193424e-09,7.86317825511555e-10,4024,"tags=48%, list=22%, signal=38%", "1,1.57214700193424e-09,7.86317825511555e-10,3932,"tags=55%, list=22%, signal=44%", "8767/5420106304,1e-10,1.57214700193424e-09,7.86317825511555e-10,3932,"tags=55%, list=22%, signal=44%00193424e-09,7.86317825511555e-10,2819,"tags=63%, list=16%, signal=53%", "114991/55693/1117657214700193424e-09,7.86317825511555e-10,3993,"tags=53%, list=22%, signal=42%", "301/1051/870144082,1e-10,1.57214700193424e-09,7.86317825511555e-10,3605,"tags=45%, list=20%, signal=36%083,1e-10,1.57214700193424e-09,7.86317825511555e-10,6047,"tags=66%, list=34%, signal=44%", "11,1e-10,1.57214700193424e-09,7.86317825511555e-10,4583,"tags=50%, list=26%, signal=38%", "1791,1e-10,1.57214700193424e-09,7.86317825511555e-10,5014,"tags=50%, list=28%, signal=37%", "424092540528,1e-10,1.57214700193424e-09,7.86317825511555e-10,3123,"tags=48%, list=17%, signal=1,1.57214700193424e-09,7.86317825511555e-10,2245,"tags=44%, list=13%, signal=39%", "5327/2151e-10,1.57214700193424e-09,7.86317825511555e-10,5202,"tags=84%, list=29%, signal=60%", "5781e-10,1.57214700193424e-09,7.86317825511555e-10,4016,"tags=57%, list=22%, signal=45%", "2246/118469493,1e-10,1.57214700193424e-09,7.86317825511555e-10,4016,"tags=57%, list=22%, signal=47214700193424e-09,7.86317825511555e-10,4039,"tags=57%, list=23%, signal=44%", "30008/861/9503424e-09,7.86317825511555e-10,3327,"tags=51%, list=19%, signal=42%", "3550/91272/90799/849424e-09,7.86317825511555e-10,4828,"tags=64%, list=27%, signal=47%", "197335/1639/4682/9857/97-10,1.57214700193424e-09,7.86317825511555e-10,5263,"tags=76%, list=29%, signal=54%", "51639/1124555968915,1e-10,1.57214700193424e-09,7.86317825511555e-10,6047,"tags=66%, list=34%, signal=14700193424e-09,7.86317825511555e-10,2736,"tags=45%, list=15%, signal=38%", "2246/1051/5154,10,1.57214700193424e-09,7.86317825511555e-10,4196,"tags=48%, list=23%, signal=38%", "824/558,06047,1e-10,1.57214700193424e-09,7.86317825511555e-10,3153,"tags=46%, list=18%, signal=38%", "14700193424e-09,7.86317825511555e-10,3511,"tags=46%, list=20%, signal=37%", "2246/23529/3621e-10,1.57214700193424e-09,7.86317825511555e-10,4549,"tags=66%, list=25%, signal=49%", "2303,e-10,1.57214700193424e-09,7.86317825511555e-10,4039,"tags=60%, list=23%, signal=47%", "30008e-10,1.57214700193424e-09,7.86317825511555e-10,3150,"tags=49%, list=18%, signal=40%", "79971095297,1e-10,1.57214700193424e-09,7.86317825511555e-10,5263,"tags=77%, list=29%, signal=55%07214700193424e-09,7.86317825511555e-10,3295,"tags=41%, list=18%, signal=34%", "2246/2152/500193424e-09,7.86317825511555e-10,4128,"tags=52%, list=23%, signal=41%", "90990/5905/27436/9000193424e-09,7.86317825511555e-10,3695,"tags=49%, list=21%, signal=39%", "558/1465/10398/51038,1e-10,1.57214700193424e-09,7.86317825511555e-10,4598,"tags=49%, list=26%, signal=38%", "57214700193424e-09,7.86317825511555e-10,2831,"tags=46%, list=16%, signal=39%", "824/1051/876869,1e-10,1.57214700193424e-09,7.86317825511555e-10,2831,"tags=46%, list=16%, signal=39%", "800193424e-09,7.86317825511555e-10,3667,"tags=50%, list=20%, signal=40%", "1051/4256/90/1893/4700193424e-09,7.86317825511555e-10,3625,"tags=57%, list=20%, signal=46%", "301/10344/1843/07214700193424e-09,7.86317825511555e-10,4109,"tags=58%, list=23%, signal=45%", "301/7376/72857214700193424e-09,7.86317825511555e-10,4632,"tags=61%, list=26%, signal=45%", "55929/7994/093424e-09,7.86317825511555e-10,4715,"tags=57%, list=26%, signal=42%", "4052/7132/135228/2/3

59,1e-10,1.57214700193424e-09,7.86317825511555e-10,3248,"tags=42%, list=18%, signal=35%","23
-10,1.57214700193424e-09,7.86317825511555e-10,2422,"tags=43%, list=13%, signal=37%","25937/
.0,1.57214700193424e-09,7.86317825511555e-10,3659,"tags=53%, list=20%, signal=42%","7376/293
0706816575,1e-10,1.57214700193424e-09,7.86317825511555e-10,4786,"tags=57%, list=27%, signal=
-10,1.57214700193424e-09,7.86317825511555e-10,3667,"tags=50%, list=20%, signal=40%","1051/4.
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00193424e-09,7.86317825511555e-10,3454,"tags=47%, list=19%, signal=38%","7107/558/64114/86:
,1.57214700193424e-09,7.86317825511555e-10,2544,"tags=40%, list=14%, signal=35%","5327/301/
14700193424e-09,7.86317825511555e-10,3635,"tags=52%, list=20%, signal=41%","23133/1017/148
'214700193424e-09,7.86317825511555e-10,3244,"tags=42%, list=18%, signal=35%","2246/8767/467
,1e-10,1.57214700193424e-09,7.86317825511555e-10,3232,"tags=43%, list=18%, signal=36%","9062
00193424e-09,7.86317825511555e-10,5056,"tags=62%, list=28%, signal=45%","5976/317781/9785/
1e-09,7.86317825511555e-10,3649,"tags=45%, list=20%, signal=36%","805/55201/23331/79029/347
.0,1.57214700193424e-09,7.86317825511555e-10,3667,"tags=56%, list=20%, signal=45%","1051/425
7,1e-10,1.57214700193424e-09,7.86317825511555e-10,3253,"tags=44%, list=18%, signal=36%","791
-10,1.57214700193424e-09,7.86317825511555e-10,3416,"tags=58%, list=19%, signal=48%","80254/
.57214700193424e-09,7.86317825511555e-10,3669,"tags=55%, list=20%, signal=44%","54556/5429,
'214700193424e-09,7.86317825511555e-10,3057,"tags=44%, list=17%, signal=37%","558/117854/29
7141,2.57745843498008,1e-10,1.57214700193424e-09,7.86317825511555e-10,3365,"tags=57%, list
e-10,1.57214700193424e-09,7.86317825511555e-10,3401,"tags=53%, list=19%, signal=44%","83871
'214700193424e-09,7.86317825511555e-10,3644,"tags=55%, list=20%, signal=44%","860/4038/425
.0,1.57214700193424e-09,7.86317825511555e-10,4685,"tags=49%, list=26%, signal=37%","558/1465
257269138,1e-10,1.57214700193424e-09,7.86317825511555e-10,3829,"tags=43%, list=21%, signal=
7214700193424e-09,7.86317825511555e-10,3060,"tags=45%, list=17%, signal=38%","11144/256006
155,1e-10,1.57214700193424e-09,7.86317825511555e-10,4196,"tags=51%, list=23%, signal=39%","8
.4700193424e-09,7.86317825511555e-10,4633,"tags=54%, list=26%, signal=40%","301/728/7057/27
7854,1e-10,1.57214700193424e-09,7.86317825511555e-10,3153,"tags=54%, list=18%, signal=45%","
08701279,1e-10,1.57214700193424e-09,7.86317825511555e-10,1997,"tags=40%, list=11%, signal=3
700193424e-09,7.86317825511555e-10,6728,"tags=64%, list=37%, signal=41%","54433/55011/1529
7638322,1e-10,1.57214700193424e-09,7.86317825511555e-10,3667,"tags=56%, list=20%, signal=45
14700193424e-09,7.86317825511555e-10,3605,"tags=54%, list=20%, signal=43%","8767/54209/931
31,1e-10,1.57214700193424e-09,7.86317825511555e-10,2904,"tags=40%, list=16%, signal=34%","2
57214700193424e-09,7.86317825511555e-10,6634,"tags=71%, list=37%, signal=45%","23016/55152
700193424e-09,7.86317825511555e-10,2401,"tags=44%, list=13%, signal=39%","710/135228/2/515
7022,1e-10,1.57214700193424e-09,7.86317825511555e-10,3127,"tags=53%, list=17%, signal=44%","
,1.57214700193424e-09,7.86317825511555e-10,3871,"tags=53%, list=22%, signal=42%","2152/8742
37,1e-10,1.57214700193424e-09,7.86317825511555e-10,3327,"tags=42%, list=19%, signal=35%","17
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44,1e-10,1.57214700193424e-09,7.86317825511555e-10,3669,"tags=49%, list=20%, signal=40%","54
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3e-09,2.79073681164507e-08,1.3958021092226e-08,4802,"tags=45%, list=27%, signal=34%", "1859/2
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5353339697474,2.90726250539248e-09,3.58033782482273e-08,1.790725326288e-08,5047,"tags=4
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095845e-07,1.04590792914744e-06,5.23116507248164e-07,2844,"tags=41%, list=16%, signal=35%",
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34256108048,1.20968642905625e-07,1.07810650168522e-06,5.3922079743943e-07,2316,"tags=38
06,1.21287781031739e-07,1.07976679542823e-06,5.40051202334208e-07,1388,"tags=55%, list=8%
1,1.22228637436873e-07,1.08695225939486e-06,5.43645050997586e-07,2973,"tags=51%, list=17%,
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2,4.1389773641818,1.31474657212315e-07,1.16281394322274e-06,5.81587682439676e-07,4041,"t
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1708125798106e-07,1.18882480617482e-06,5.94597156217254e-07,3906,"tags=48%, list=22%, sign
6185948210752e-07,1.20056332652602e-06,6.0046824065524e-07,4118,"tags=44%, list=23%, signa
318199202e-07,1.21375626469273e-06,6.07066760029438e-07,3867,"tags=53%, list=22%, signal=4
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4690910658e-07,1.35151866924603e-06,6.75969371714175e-07,4007,"tags=56%, list=22%, signal=
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4630169e-07,1.36586312166919e-06,6.83143827171362e-07,4041,"tags=63%, list=23%, signal=49%
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716242843e-07,1.86511563540253e-06,9.32847671975312e-07,4643,"tags=51%, list=26%, signal=38
.23230729353037e-07,1.88609081931547e-06,9.43338523647475e-07,2813,"tags=38%, list=16%, si
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5,2.29598898676372e-07,1.9358712120763e-06,9.68236456309401e-07,3565,"tags=59%, list=20%, s
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3,2.02697695878472,3.61624615725347e-07,2.92175435051254e-06,1.46133123985695e-06,3713,'
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4539501142e-07,5.69941272280571e-06,2.85059209690682e-06,1818,"tags=64%, list=10%, signal=5
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4360021e-07,5.88065041693866e-06,2.94123910979811e-06,5144,"tags=47%, list=29%, signal=34%
4e-07,5.90059530064935e-06,2.95121465125204e-06,5306,"tags=56%, list=30%, signal=40%","9877
97,7.86336746353871e-07,5.94543727847839e-06,2.97364260897787e-06,4051,"tags=63%, list=23%
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7.90524392140136e-07,5.96816205749884e-06,2.98500853010523e-06,3622,"tags=47%, list=20%, s
570538948176e-07,5.97035527393028e-06,2.98610547916478e-06,2439,"tags=34%, list=14%, signa
444773465,7.92319282665543e-07,5.97035527393028e-06,2.98610547916478e-06,6506,"tags=64%
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537014037e-07,6.02762657987983e-06,3.01475003257044e-06,2616,"tags=50%, list=15%, signal=4
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148299996582e-07,6.41651910433228e-06,3.20925673188604e-06,5202,"tags=81%, list=29%, signal
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e-07,6.53809914129281e-06,3.27006564490168e-06,2245,"tags=42%, list=13%, signal=37%","824/8
1087788875e-07,6.62340105980655e-06,3.31272986077664e-06,4631,"tags=81%, list=26%, signal=6
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194936613214e-07,6.71664622253837e-06,3.35936693320596e-06,4240,"tags=53%, list=24%, signal
3008e-07,6.93368519405875e-06,3.46792014860326e-06,3066,"tags=31%, list=17%, signal=26%", "31
9.44199378047713e-07,6.96411301703431e-06,3.4831387888244e-06,2164,"tags=49%, list=12%, si
34880988633e-07,7.07743854277027e-06,3.53981916340898e-06,4758,"tags=46%, list=27%, signal=
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7,9.68863075610829e-07,7.12662360051115e-06,3.56441933604098e-06,3836,"tags=34%, list=21%
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07,7.29864503188729e-06,3.65045678527102e-06,2342,"tags=71%, list=13%, signal=62%", "4162/46
.00219291929249e-06,7.33889727283767e-06,3.67058916127475e-06,962,"tags=52%, list=5%, sign
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07351844751e-06,7.6542814703244e-06,3.8283302733103e-06,4220,"tags=36%, list=24%, signal=28
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.26946022790294,1.11924302165346e-06,8.11526073148913e-06,4.05889154385245e-06,2316,"tag
1846002,1.18819337909574e-06,8.60751852521404e-06,4.30509694161529e-06,4425,"tags=53%, lis
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17,0.777609813289173,2.4179404670519,1.23633526851178e-06,8.94033190610656e-06,4.471555
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264204,1.27288649141921e-06,9.17200478923342e-06,4.58742779942233e-06,3151,"tags=28%, list
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57692803e-06,1.13976206976145e-05,5.70058163258744e-06,3733,"tags=41%, list=21%, signal=32%
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7e-06,1.24878648998532e-05,6.24587316660187e-06,2405,"tags=79%, list=13%, signal=68%","5931/
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1,1.78791545572577e-06,1.25928741976942e-05,6.29839413482891e-06,1985,"tags=63%, list=11%,
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16,1.90875833050244e-06,1.33514524185231e-05,6.67780113452344e-06,4504,"tags=48%, list=25%
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02519135,1.97908270367673e-06,1.37580715987974e-05,6.88117391661772e-06,1846,"tags=40%,
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icing 5'-phosphomonoesters",56,-0.509375043201756,-2.09936088911533,1.3625465969157e-05,7.
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0944e-05,9.79977128816789e-05,4.90140860895467e-05,3024,"tags=53%, list=17%, signal=44%","4

97,2.23196716820662,1.75604856469655e-05,9.85035385359111e-05,4.92670775261201e-05,5020
2,1.79077023536485e-05,0.000100381934296865,5.02065673247117e-05,4070,"tags=38%, list=23%
8,1.82642438568421e-05,0.000102309975236673,5.11708874279984e-05,2787,"tags=39%, list=16%
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64,2.04611662378908e-05,0.000113366298010618,5.67007670582529e-05,2265,"tags=47%, list=13
16687562444e-05,0.000114503926242856,5.7269757971134e-05,3815,"tags=30%, list=21%, signal=2
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020416615328e-05,0.000115990459096664,5.80132554174415e-05,4764,"tags=37%, list=27%, signa
33,2.10843988646483e-05,0.000116264582070462,5.81503595053001e-05,3758,"tags=37%, list=21%
85,2.11641401909131e-05,0.000116625173879147,5.83307114485684e-05,1941,"tags=56%, list=11
943e-05,0.000116809818023073,5.84230622157466e-05,769,"tags=85%, list=4%, signal=81%", "107:
217830155503,2.12263904060137e-05,0.000116809818023073,5.84230622157466e-05,2753,"tags=
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-05,0.000117767820768277,5.8902212469836e-05,1858,"tags=50%, list=10%, signal=45%", "2934/26
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109819596e-05,0.000122719697477306,6.13789203866239e-05,3533,"tags=88%, list=20%, signal=7
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847527,2.35384003458828e-05,0.000128402763765997,6.42213367261033e-05,3066,"tags=45%, li
n of immune receptors built from immunoglobulin superfamily domains",99,0.429078138374173,1.9
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67540566e-05,0.000133040800972612,6.65410761184504e-05,3026,"tags=69%, list=17%, signal=57

391e-05,0.000134023383452182,6.70325200596154e-05,4520,"tags=52%, list=25%, signal=39%","64
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773303,2.2473566196792,2.48354142424926e-05,0.000134485174525636,6.72634873624647e-05,;
3341,2.27096358834839,2.48950132494873e-05,0.000134718154255548,6.73800134343823e-05,3;
2147737e-05,0.000134974980610566,6.75084665248142e-05,3565,"tags=46%, list=20%, signal=37%
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3008e-05,0.00013943742986422,6.97403846528722e-05,3962,"tags=32%, list=22%, signal=25%",'3C
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693722e-05,0.000141578787035573,7.0811396023024e-05,4121,"tags=50%, list=23%, signal=39%",'
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42,2.73240977413341e-05,0.000145920017372906,7.29826858545074e-05,5194,"tags=60%, list=29
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512834091,2.87754477072026e-05,0.000153067302987004,7.65574394083882e-05,2191,"tags=82%
329627,2.92340205790305e-05,0.000155404917767403,7.77266100831061e-05,2308,"tags=80%, lis
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9123397945186e-05,0.000163684363420096,8.18676196032442e-05,2562,"tags=32%, list=14%, sigr
1333,1.79999779667276,3.10301363820145e-05,0.000164201138354827,8.21260873816748e-05,41
124421980156e-05,0.000165121731850818,8.25865271974539e-05,2138,"tags=31%, list=12%, signa
7225967205,3.18623622619919e-05,0.000168385748026963,8.42190425404234e-05,4801,"tags=51
536682,3.20465377663964e-05,0.000169249031166517,8.46508182714839e-05,2924,"tags=41%, lis
24,3.2082040954484e-05,0.000169326512258471,8.46895708586583e-05,2745,"tags=55%, list=15%
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,0.000173205919956037,8.66298775992303e-05,3998,"tags=78%, list=22%, signal=61%",'6629/516
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285845771e-05,0.000184016921396305,9.20370584376981e-05,3095,"tags=41%, list=17%, signal=3
516163835e-05,0.000184016921396305,9.20370584376981e-05,4512,"tags=38%, list=25%, signal=2
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3265497e-05,0.000186659914569908,9.3358965767326e-05,2743,"tags=31%, list=15%, signal=27%",
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75,0.0184756992147421,0.0401925032928345,0.0201024978912307,6827,"tags=86%, list=38%, sign
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93,0.0193662407734957,0.0418084475450127,0.0209107211483163,4945,"tags=57%, list=28%, sigr
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%, list=24%, signal=29%", "1410/710/135228/2/7057/4803/831/334/9314/2621/1471/183/7078/5627
", "118460/22894/27327/1655/6741/90806/207/60493/56006/8087/23381/57819/56915/339345/5
%, signal=40%", "54209/10344/2296/1906/10519/2840/57007/2920/6387/6360/6355/6376/2921/10
33%", "2274/54209/9454/5350/3270/1906/8877/845/29995/683/477/6444/6548/10519/5027/1910
%", "6741/9877/54888/23381/84248/5976/23049/56943/23293/10212/91746/8021/6830/728343/9
6, list=22%, signal=37%", "7132/54209/284207/9314/7538/10769/7130/11221/9572/9021/7010/504
%, list=22%, signal=44%", "8767/10417/10865/11027/3556/7098/2149/10392/148022/5027/7292/880
%, 3215, "tags=36%, list=18%, signal=30%", "6788/84159/117854/8767/5587/367/92565/8061/183/810
", "55614/1303/3624/677/1847/4323/1843/4313/1295/64321/3678/2335/1290/1289/4851/3915/39:
07/79026/79901/64114/83547/10581/10410/2683/3920/2040/112770/11010/1601/4758/5476/709
7107/79026/79901/64114/83547/10581/10410/2683/3920/2040/112770/11010/1601/4758/5476/7:
=54%, list=20%, signal=43%", "9510/6678/7057/7058/23166/90993/9314/183/1969/10769/2296/505
%, 31/861/2303/367/26524/10413/1893/183/5159/4208/2296/1906/7042/4851/85301/57493/4488/2
%, list=26%, signal=35%", "301/8767/23529/1435/3280/8744/2214/3133/4208/3592/683/604/3105/70
t=18%, signal=42%", "91272/10726/4926/91782/81929/56776/10540/79003/51112/23636/81620/28
signal=31%", "860/2303/121227/10413/90/2022/116039/4323/3280/2295/64321/3217/1746/1969/4
%, signal=35%", "8531/467/90/4209/26508/7040/4208/26471/858/7026/10791/1959/23764/84466/4
%, 3244, "tags=55%, list=18%, signal=45%", "301/5587/9261/64094/5159/2296/3592/8877/4851/3164,
7854/2934/3956/6484/4774/10581/10410/3673/4124/2621/2040/81603/3356/1969/3678/7538/85
gs=49%, list=20%, signal=40%", "5154/56034/54209/80310/183/2260/5159/2335/5155/2149/7042/7
signal=34%", "10847/84851/79718/2023/9063/23414/6837/10987/607/1859/5253/4863/51460/113
st=23%, signal=31%", "11346/25802/2934/5154/51429/2059/389/148170/2316/10174/51474/90102
ignal=41%", "5327/710/10544/5154/308/7057/5592/5627/5155/7056/5054/5328/1906/4846/11489
4%", "7132/7414/1903/80781/91663/1306/57493/8985/1910/5175/1909/26084/6781/10411/4478/7:
%, signal=33%", "23588/27101/51343/116138/23008/11146/440590/81545/79699/196394/54800/1
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6, list=20%, signal=36%", "7107/1051/861/3624/677/54209/1435/7040/4286/4853/10272/7130/7098
", "728/27202/10344/3958/54210/7130/1906/7042/683/1441/2920/57580/3680/23604/6360/6355/
=52%", "91272/10726/4926/91782/81929/10540/79003/51112/23636/81620/283489/8379/4292/86
", "25913/51377/10856/10714/7528/8607/54107/64710/5425/10445/5426/86/64858/3978/4176/170
l%, signal=34%", "558/6788/2152/5154/7057/6237/2022/57333/1839/7040/7162/2621/3488/2260/7:
l=33%", "83716/2246/5154/10413/10252/57333/4323/3280/4124/3488/4054/5159/5241/7043/273:
st=18%, signal=28%", "6788/2246/4739/5154/56034/51429/7057/283/23328/6556/80310/1839/905
ignal=46%", "3913/2297/3280/5159/5155/2668/6662/1958/5156/30812/3976/7484/6943/947/1499
signal=31%", "301/861/8767/3956/9580/1326/3280/8744/7070/3707/3133/11221/2737/3592/567/
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:=27%, signal=38%", "5253/5897/10498/56893/80764/30827/4300/124930/23613/51035/6872/2332
=45%", "54460/54938/55005/51373/51067/80324/64951/115416/51095/5442/54931/65080/6832/!
15%, signal=29%", "301/8767/23529/54209/6556/7040/10865/5321/196/3133/4208/11221/3592/30

signal=30%","8531/467/90/4209/26508/7040/4208/26471/858/7026/10791/1959/23764/84466/48
ags=50%, list=14%, signal=43%","9510/7057/80310/1839/4209/3673/7040/3488/8013/4313/183/51!
","54556/1487/11143/51147/8520/322/51230/55683/64769/10856/84148/84289/339287/9767/28.
signal=44%","9510/6678/7057/7058/23166/90993/9314/183/1969/10769/2296/5054/28984/7042/
604/301/3801/7414/7094/83872/1009/83478/182/126374/11135/4643/7791/9124/57477/6282/1:
6, signal=30%","6788/79971/25937/3487/4038/83439/57664/26524/2300/10413/27185/8324/5732
, signal=87%","84296/64785/4174/4176/8318/4171/51659/9837/4172/4175/4173"
ignal=31%","6788/79971/25937/3487/4038/83439/57664/26524/10413/27185/4929/8324/2308/95
'2934/4162/9429/4643/2621/183/5155/6446/2013/1906/5125/2149/54885/5641/2771/4883/1910.
st=5%, signal=68%","84296/64785/6117/9401/4174/4176/8318/641/4171/51659/9837/4172/4175/!
ist=27%, signal=37%","10111/79897/55629/55720/5168/22803/64782/54464/23293/65095/10775/
39%","2246/2297/3280/183/3217/4208/2737/4070/2668/7481/84445/6662/51804/30812/7484/69.
il=31%","3801/7414/7094/1009/389/2316/7040/183/1969/7043/6615/654/2149/7042/5872/6591/!
s=53%, list=23%, signal=41%","2246/55614/860/7057/677/10252/90993/64094/2260/7538/3164/1.
. signal=40%","2246/55614/860/7057/677/10252/90993/64094/2260/7538/3164/1373/1960/53834,
057/3488/4313/3489/10272/7130/6385/1514/3690/3685/3688/1513/151887/284297/59339/3676/
6788/79971/25937/3487/4038/83439/57664/26524/2239/2300/10413/27185/4929/8324/57326/2:
38%","5592/3673/143872/183/3356/80005/1906/8877/2149/477/2668/5743/3363/323/59/1910/1
3913/54587/23529/728/54209/7223/9580/7040/3280/1745/1746/23500/11221/9572/2737/1959/3
5%, signal=54%","51230/55683/64769/10856/51105/84148/339287/284058/6944/8607/1386/54799
5, list=18%, signal=31%","100101267/961/23511/284439/29072/8658/87178/10204/84271/55051/9
l=32%","83716/2246/5154/10413/10252/57333/4323/3280/4124/3488/4054/5159/5241/7043/273
ags=52%, list=22%, signal=41%","8767/9261/7057/10417/10865/11027/3133/7098/10392/148022/7
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0%","2246/2303/10252/116039/2297/3280/183/3217/2296/2737/6385/4070/2668/7481/84445/924
%","6788/79971/25937/3487/4038/83439/57664/26524/2239/2300/10413/27185/4929/8324/5732
52%, list=13%, signal=45%","25937/3913/2303/10413/182/4643/3280/4208/5155/4853/2737/4851/
8,2369,"tags=47%, list=13%, signal=41%","117854/2934/3956/10581/10410/81603/9023/5806/1047
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3,3327,"tags=68%, list=19%, signal=55%","3550/7517/7756/25906/84861/7175/81620/8379/9319/5!
ignal=40%","4437/54556/126549/56941/51750/3836/29072/5531/9984/64769/56154/10856/2334
1%, list=7%, signal=56%","79003/81620/283489/8379/9184/9212/147841/891/1062/10615/3192/47
360/4209/116039/4323/4054/4208/7043/2296/2690/2737/654/871/85301/4488/7048/309/10370/!
54/117854/100507436/10581/8061/10410/10417/81603/7098/3592/84282/10577/197259/10475/3
9%, signal=34%","7107/1051/861/3624/677/54209/182/1435/7040/4286/3707/4208/7538/4853/10
0%","2246/2303/10252/2297/3280/183/3217/2296/2737/6385/4070/2668/7481/84445/9244/4091/
l=47%","7132/182/26508/7040/6615/4853/4846/7042/4851/11117/6591/23493/1942/4091/6662/7
%, list=17%, signal=32%","558/301/861/8767/677/54209/1435/9580/4323/7040/8744/2621/3707/4
signal=32%","558/301/861/8767/677/54209/1435/9580/4323/7040/8744/2621/3707/4853/11221/
28%","1410/3913/2303/3624/147912/10252/182/57381/631/116039/9314/10848/4124/2295/4286
ignal=32%","2274/861/2303/10413/90/4000/2022/8324/10848/7040/2139/183/5159/10512/4208/
=67%, list=19%, signal=54%","3550/7517/7756/25906/84861/7175/81620/8379/9319/55755/9184/9
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7,"tags=67%, list=19%, signal=54%","3550/7517/7756/25906/84861/7175/81620/8379/9319/55755/
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%, list=7%, signal=44%","81620/1111/8379/27085/9319/55755/9184/5885/348654/5347/9735/549C
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25898/10014/64783/8175/163486/23451/80764/10521/30827/113246/988/7994/10212/10421/102
%, signal=38%","2246/2303/10252/2297/3280/183/3217/2296/2737/6385/4070/2668/7481/84445/
ignal=38%","2246/2303/10252/2297/3280/183/3217/2296/2737/6385/4070/2668/7481/84445/924

s=42%, list=26%, signal=32%","6311/92170/1975/1636/54464/8892/192670/10922/5499/2935/115:
, list=21%, signal=28%","6324/79026/5587/23704/54209/2316/2040/7070/183/4208/5350/3779/32
%, list=21%, signal=38%","558/6788/2152/5154/7057/2022/1839/7040/7162/2621/3488/2260/388
:=13%, signal=44%","117854/2934/3956/10581/10410/81603/9023/5806/10475/8519/3685/857/20
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il=36%","2152/1051/2/90/2683/2214/54210/2335/3133/9180/26471/5743/1910/445/7292/3569/50
;716/2246/5154/10413/10252/57333/4323/3280/4124/3488/4054/5159/5241/7043/2737/4846/48!
7030/5378/5887/23186/4437/2071/5395/7507/2547/2072/7158/79840/1161/7520/4292/79728/55
9070939e-08,3875,"tags=51%, list=22%, signal=40%","8767/9261/7057/10417/10865/11027/3133/7
signal=32%","2274/861/2303/10413/90/4000/2022/8324/10848/7040/183/5159/4208/5350/4853/2
16176/10575/25876/81027/112714/2009/1759/1155/22832/324/79848/90990/27436/10694/19638
7%, list=28%, signal=34%","301/8767/23529/3956/6284/6810/54209/6556/7040/3958/11027/8013/
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ist=28%, signal=42%","367/143872/2621/183/5155/2013/1906/4846/7026/5125/2149/146/1910/20
gnal=32%","9531/7132/2934/7057/4055/2022/8061/3673/4323/4313/183/3356/355/7098/1906/65
ial=28%","1793/4739/79365/4038/7132/23529/7414/10413/27185/4803/54209/2316/706/10501/1
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, list=7%, signal=59%","3550/7517/7756/25906/84861/7175/81620/8379/9319/55755/9184/9232/5
%","4052/3074/7376/5587/2934/54209/2316/706/10226/7070/3356/4681/4481/5350/11015/3270,
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89/100101267/23511/29072/8658/10204/84271/9883/53371/10128/57187/3178/8106/81929/642:
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%","90/182/26508/7040/4208/6615/4853/4846/7042/4851/11117/6591/23493/7048/53834/1942/
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0/6002/8520/22944/55660/4926/5687/11331/4137/9984/7175/4670/9360/10274/10856/22880/2:
=16%, signal=45%","9510/5154/80310/5592/3673/3488/8013/183/5159/4208/5155/6282/80005/50
28%","1410/3913/2303/3624/147912/10252/182/57381/631/116039/9314/10848/4124/2295/4286
55781/23481/10412/10436/84946/57050/84294/2091/55127/23195/84261/27340/10813/79954/6
signal=28%","1410/5327/7376/710/135228/2/7057/4803/1893/831/334/9314/2621/1471/183/7078
st=28%, signal=34%","301/8767/23529/3956/6284/6810/54209/6556/7040/3958/11027/8013/4853
"282973/10059/114791/9217/85459/26153/7756/4926/10844/9448/84056/10128/27072/4137/795
:39%","710/2/5154/6678/7057/5768/7040/2621/5627/2335/3671/5155/7043/5054/7076/7042/216
signal=43%","9575/84126/51720/197342/29086/545/80198/80254/988/65975/5781/51499/1432/5
107/25937/7414/10413/57333/1435/4054/2296/54360/4846/2149/567/4851/3915/284/5743/3908
signal=62%","7517/4137/25913/3159/3184/5892/7528/5932/4221/3146/56852/57697/9401/3149/
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%, signal=42%","81620/1111/5810/8379/27085/9319/55755/9184/286151/5885/348654/5347/973
al=39%","5327/710/5154/7057/5592/5627/5155/7056/5054/5328/1906/4846/114897/2191/5156/5
:signal=79%","79003/51112/81620/283489/27085/55166/9184/9735/54908/9212/983/55920/55055
%, list=10%, signal=79%","79003/51112/81620/283489/27085/55166/9184/9735/54908/9212/983/5
t=17%, signal=40%","860/2303/116039/4323/3217/1746/7043/2737/7048/4188/3201/3204/5396/3
al=70%","5000/4999/5001/1663/4174/5422/8318/4171/1660/55388/4998/990"
"7205/7414/7057/90102/395/3673/6281/4323/7070/11170/79834/1307/29984/6385/7010/123720,
:93%, list=5%, signal=89%","10714/54107/5425/5426/3978/4176/1763/5422/5984/9837/4172/5983
4/85360/3490/367/5069/8061/3673/7005/3488/4313/639/183/3726/3678/5241/1307/7043/7056/
%, list=20%, signal=51%","25937/1052/860/1051/5587/10413/90/182/4208/2737/654/4488/4921/8:
al=61%","6635/11157/6637/24148/10594/27258/26121/6634/153527/6628/9128/51691/6632/66:
gnal=61%","6635/11157/6637/24148/10594/27258/26121/6634/153527/6628/9128/51691/6632/66

l%","91272/10726/4926/91782/81929/56776/10540/79003/51112/23636/81620/283489/8379/429
58%","50485/51750/259282/6419/54465/9984/546/84083/1325/10189/1663/55345/4796/64710/5
/2934/23704/2316/1839/10848/183/5350/9096/3270/1906/4846/7042/30845/845/23493/477/644
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list=21%, signal=50%","54386/5394/100134934/27000/4297/2074/9400/80169/359787/4968/24144
13%, list=13%, signal=38%","824/85461/26509/135228/54209/30846/8754/4627/975/3688/22904/7
461/26509/135228/54209/30846/8754/4627/975/3688/22904/7305/4773/3566/10411/9518/58494
=27%, signal=42%","301/861/8767/639/3707/3133/2737/3592/3077/604/3105/7048/975/4092/801
465/10398/7414/7094/2316/5592/10627/2335/4627/114897/5912/3690/3569/5156/3572/3315/40
il=30%","55023/23636/81620/1111/5810/8379/27085/8697/51434/8452/79866/9319/55755/9184/
signal=43%","5327/710/135228/5154/7057/5592/90102/5627/5155/7056/5054/5328/1906/4846/11
nal=38%","90627/2059/25959/148170/11135/395/57381/143872/23189/5159/388/10161/29984/1
0/3913/2303/3624/147912/10252/182/57381/631/116039/9314/10848/4124/2295/4286/1745/707
","860/5654/90/2022/11167/2297/7040/3280/1745/4681/51232/7043/4853/10272/7130/10468/6
nal=27%","56548/9469/6484/2300/1839/2683/374378/30815/4124/117248/1471/25825/84752/54
./1051/8767/2615/6556/3280/3958/8744/3133/11326/6385/3105/7048/8654/975/2697/5027/1604
:=27%, signal=46%","706/9314/183/1906/4846/1373/5806/10365/5743/1728/148022/80149/857/4
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08,3327,"tags=64%, list=19%, signal=52%","3550/7517/7756/25906/84861/7175/81620/8379/9319/
9%","7107/4739/85360/51429/5592/83478/10252/395/57326/57139/6281/10344/143872/81565/7
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gs=43%, list=13%, signal=38%", "5154/367/183/3217/59277/6591/4070/2668/6662/3082/51804/232
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al=34%","1051/367/3673/1435/3488/1969/5241/7043/2737/6239/6778/4488/7048/3398/2697/537
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%","6169/26065/207/6125/8440/5914/8087/10131/1938/9470/3872/6199/56915/339345/5976/66
7%, list=27%, signal=42%","6284/6810/54209/11027/8013/2242/148022/22904/3162/7305/8291/34
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signal=35%","10847/84851/23414/10987/607/1859/5253/4863/11315/114803/10498/56943/1002
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344/58191/2920/6387/6360/6355/6376/2921/6354/6358/3576/6347/6357/6351/6368/414062/38
list=19%, signal=43%","7376/1435/7040/183/4481/3690/5322/3685/19/4790/5468/4023/5583/185
5%, list=27%, signal=40%","10111/545/54464/23293/10575/65057/54984/5981/170506/10694/556
al=28%","7798/2303/90/2022/182/10848/26508/7040/3280/639/10512/4208/2296/4846/8321/70
=10%, signal=25%","9656/11200/79184/1027/7976/1386/81620/91603/1111/54962/79960/79035/
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%, list=23%, signal=29%", "6324/79026/23704/54209/2040/4208/5350/3270/1906/30845/845/6236/
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57%", "1295/1307/1290/1289/1278/85301/50509/4060/1284/1281/1287/1277/1282/1300"
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l=38%", "79971/5154/7040/59277/10512/7043/23129/2296/7042/6591/7052/1956/6662/3082/1896
7,"tags=40%, list=11%, signal=36%", "84159/5327/2152/5154/56034/80310/64651/25976/4643/8013
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6%", "7414/7094/1009/389/183/1969/6615/5872/6591/57493/9948/7481/2697/79778/90952/2701/4
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3", "5836/55214/8309/5351/54749/2752/4846/7026/1373/5660/8985/8974/5066/283208/2350/640
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1%", "6879/5440/9519/64210/5442/7015/2962/10623/9533/5438/129685/2068/5434/728340/6917
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signal=37%", "117854/2934/10581/10410/81603/7538/9023/5806/3428/9636/8519/8091/684/1031
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3%", "5154/7040/59277/10512/7043/23129/7042/6591/7052/1956/3082/1896/4824/3911/2252/16
2%", "3065/53615/57459/6599/3183/3066/9219/6598/6601/3150/86/1104/6597/1108/6605/5928/5
al=30%", "100507436/2214/54210/3133/2013/3592/135250/567/3105/3106/3140/3916/5027/7305
l=49%", "367/4313/4851/3400/6662/4824/23213/5916/9420/2099/7474/652/6469/3169/3371/8621
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9%", "824/558/1051/23529/4803/54209/4929/1435/1745/8013/4208/7043/2690/26471/8321/2149
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l=29%", "2355/301/135228/10413/677/182/9314/3280/1969/7538/23022/2296/8754/23764/4851/
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0%, signal=25%", "79971/7376/3624/6810/283/54209/7040/5321/93664/183/1601/7043/9367/8754
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01/860/861/8767/677/8324/9580/8744/639/3707/11221/2737/567/6778/604/1960/7048/1514/31.
gnal=43%","90/26508/3280/4846/8321/7042/4851/23493/7049/7048/7481/10370/53834/2535/409
34%","5587/7070/3356/5350/3270/2149/845/477/309/80024/53373/22821/5027/3708/3710/3357
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%","2274/90/4000/10252/182/8324/7040/3280/183/64321/5159/10512/4208/9096/1906/7042/485
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=13%, signal=32%","301/861/8767/9580/8744/3707/11221/2737/604/1960/7048/7292/8808/10288
3%","824/253827/558/1410/301/5587/6810/22925/54209/4929/11030/80310/6649/5445/8061/230
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","558/64114/2303/2316/182/7040/1471/183/10512/4208/2296/4846/1909/3976/84870/3200/94,
list=23%, signal=30%","90627/2059/25959/4803/83478/10252/1435/143872/23189/5159/3707/101
gs=45%, list=13%, signal=39%","301/861/8767/3707/2737/7048/7292/114548/64332/3142/51043/9
st=25%, signal=40%","65975/51499/57551/51343/60561/1017/6419/5514/80279/8883/5884/26058
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gnal=46%","51095/5442/56903/7015/10623/9533/5438/349565/5434/1040/54974/390637/548644
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, list=22%, signal=39%","8767/6284/11027/10392/3428/5027/1958/7305/3569/114548/351/91662/
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gs=35%, list=19%, signal=29%","6788/8767/4055/23328/8324/344558/4616/7164/3489/7098/8877,
3%, signal=38%","2246/3490/706/183/1601/6615/9572/654/6591/158219/1958/5978/4790/50846/
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;/1051/23529/4803/54209/4929/840/1435/1745/8013/4208/7043/2690/355/26471/8321/2149/70:
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. list=10%, signal=36%","7057/182/90102/395/8324/4323/23189/11170/5054/4851/4070/604/3204,
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;, signal=46%","2246/367/10252/2668/7481/10370/23213/1499/7474/652/6469/22943/650/6495/2
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, "tags=49%, list=24%, signal=38%","9443/6872/170506/9282/26036/2071/6908/10629/5436/9439/5
, "301/1893/6778/604/975/7292/3569/602/114548/3142/3566/64127/91543/3586/942/972/9655/
021/55379/79041/23039/3631/23592/23353/64328/23190/114880/163087/23588/5905/27101/64:
=30%, signal=56%","904/6432/7936/1859/10921/708/11338/56853/6429/6431/9646/6433/57060/5
=27%, signal=34%","7132/23529/3280/183/2690/3592/9021/2149/4851/6778/1489/9244/1647/857
44/83716/84159/6237/64651/25976/4313/7043/4487/5156/1277/83690/7122/5083/22943/51176/
=21%, signal=37%","79148/27202/79890/1843/4681/7130/11117/23143/3204/347/3162/6387/134/
!0%, signal=35%","55904/134353/1978/284001/5514/23476/51529/11331/26073/440/57504/57521

%","54209/9636/3082/7292/7305/3569/602/27242/9308/947/64127/29108/85480/3123/28514/352%, signal=38%","54209/9636/3082/7292/7305/3569/602/27242/9308/947/64127/29108/85480/312%, signal=80%","5154/5159/5155/1289/1278/1281/5156/1277/1282/1291"
539,"tags=40%, list=20%, signal=33%","54209/11027/7098/9572/857/51296/3430/4814/11213/4067=30%","4502/6649/5445/9429/2052/4499/196/5159/493869/4493/26471/4846/4489/84203/1373/130%","558/117854/2934/3956/10581/10410/81603/9023/4851/5806/10475/3428/9636/8519/80912636736e-06,1944,"tags=50%, list=11%, signal=45%","127435/633/1462/150356/3339/4060/54829/7057/3673/3075/4811/2335/10468/1289/1514/50509/1513/1508/10457/4023/6386/4035/348/331381e-06,3566,"tags=68%, list=20%, signal=54%","3107/3133/3077/567/3105/3106/3140/6890/68921291, signal=47%","23405/6419/7517/284131/2072/1775/1773/84083/22909/1677/328/5932/55345/644211291, list=22%, signal=42%","54209/9636/3082/7292/3569/602/9308/947/64127/29108/85480/353514/1291, signal=46%","3673/1906/8877/2149/5743/151/6915/3784/9446/387/6869/59341/255743/6865/1291/966/51429/51226/11037/1839/6517/4643/3107/3133/1601/11015/1906/567/5872/3105/5045/781291, list=23%, signal=49%","3673/1906/8877/2149/5743/151/6915/387/6869/255743/6865/93649/601291, signal=40%","8767/54209/11027/9572/23643/3430/929/4814/4067/9111/4792/338382/2150/7121291, signal=20%, signal=35%","5350/3270/3164/30845/845/477/6548/8654/4092/80149/857/54795/6781/134/1291, tags=55%, list=19%, signal=45%","7376/1435/183/4481/3690/5322/3685/19/4790/5468/4023/551291, signal=3%","860/1893/871/5744/85301/4488/7048/6662/4092/23213/5916/8817/9451/55959/2131/25981291, signal=3e-05,2562,"tags=78%, list=14%, signal=67%","3107/3133/3077/567/3105/3106/6890/6892/3123/6891291, signal=1836661160952e-05,3769,"tags=71%, list=21%, signal=57%","567/5641/1514/8722/1509/3115/3108, signal=43%","1303/3624/4323/4313/1295/64321/3678/2335/1290/1289/3914/1284/8091/3685/3912/31291, signal=5378/4437/8313/29072/5395/4595/10714/3146/4292/6996/6117/10535/9156/3978/6119/6118/21291, list=13%, signal=74%","5154/56034/80310/3678/5159/5155/3554/3690/5156/4067/2081"1291, signal=7%,"79897/55720/22803/54464/23293/65095/10775/131870/9271/79033/55651/4841291, signal=6.6%, list=21%, signal=36%","80310/3958/2621/5054/3592/5641/6387/351/58494/29108/387/6354/631291, signal=18%","84168/5154/2059/389/2683/4643/7040/4651/9936/7010/284/10519/3690/7408/3685/59/361291, signal=446497e-05,2342,"tags=56%, list=13%, signal=49%","2621/183/5155/2013/5125/2149/1910/134/181291, signal=11, signal=44%","3624/183/1601/654/2149/114897/3625/2697/668/4824/185/81285/2150/6865/5443/251291, signal=1%","558/117854/2934/3956/10581/10410/2040/81603/7538/9023/4851/29969/5806/10475/3428/1291, signal=7994/23522/257218/54556/221656/64769/10856/50809/6944/8607/54799/26122/57634/10902/841291, signal=23%, signal=34%","558/301/3958/2621/3707/4208/10461/1831/604/1942/5027/6387/4254/4067/631291, signal=7,"7486/7015/54386/100134934/80169/23381/5976/10111/23049/65986/23293/65057/3104/65111291, signal=11, signal=41%","10922/1153/79066/9238/1432/2332/170506/56339/27257/23185/4848/9698/129563/481291, signal=1signal=39%","6147/23481/10412/4869/115416/23195/51121/6135/2971/4839/65008/55052/818871291, signal=77/7040/11027/3107/3133/3105/3106/6890/958/6892/3115/28/3123/6891/3135/3122/4239/55080, signal=35%, list=14%, signal=30%","8767/23529/54209/6556/7040/10865/5321/3133/3592/3554/567/67781291, signal=19261/5154/121227/26020/182/116039/3280/5159/7043/54360/9096/1906/2737/6385/7042/4851291, signal=1%,"9902/79148/4323/1471/4313/4327/5045/1514/5653/2191/3688/1513/1508/8751/4320/140761291, signal=64%, list=7%, signal=59%","30008/2022/3280/4851/23493/133/1909"
,"8861/26036/51562/11143/51147/10629/9913/7862/64769/6885/6878/84148/84289/56970/6871291, signal=ags=49%, list=31%, signal=35%","9131/118460/22894/27327/1655/81892/84153/6741/90806/207/11291, signal=1l=41%","434/9869/23133/1017/1487/8085/11176/9646/7175/55729/22880/23347/3065/10155/501291, signal=1list=17%, signal=30%","8767/728/283/2634/1969/3133/3592/3105/10392/3140/5027/3569/284297, signal=8,"tags=35%, list=10%, signal=31%","1793/4739/2316/6281/91663/23189/1601/80005/6239/4070/51291, signal=ags=68%, list=28%, signal=49%","9314/183/1906/5806/10365/5743/148022/445/4088/5025/64581/51291, signal=1%,"list=17%, signal=23%","1410/11346/25802/30008/2934/51429/2059/389/54209/148170/2316/101291, signal=,"3913/728/54209/9572/7431/3569/351/10319/4919/712/28514/4035/5354/4504/7099/6608/3551291, signal=tags=43%, list=24%, signal=33%","1410/7057/706/2308/7040/183/5159/5155/683/7048/2771/47801291, signal=al=40%","301/8767/6556/10865/5321/3554/6778/7292/602/9173/3142/3566/3123/7099/9655/2461291, signal=1%,"signal=30%","10865/196/3133/3592

5,"tags=46%, list=25%, signal=35%","192670/94103/1153/79066/10313/2332/170506/56339/6470/2
t=11%, signal=31%","29980/9656/11200/79184/1027/1386/91603/1111/54962/5591/835/90381/5
s=46%, list=26%, signal=35%","54209/2316/7070/183/3779/1906/2149/30845/6548/5348/5027/34
53%, list=14%, signal=46%","9510/80310/3673/3488/8013/183/5159/5155/6282/80005/1545/3037/
, list=20%, signal=33%","301/7376/8013/5743/5468/5467/972/3553/51085/344/9104/5465/335/72
513/51116/6132/6173/6181/6202/9349/6168/54460/6228/6142/56945/6235/6189/6147/51373/6
gs=67%, list=9%, signal=61%","3280/1745/1746/23500/11221/4851/3400/1499"
i1/677/54209/5187/23328/1843/4616/7538/11221/8877/80149/3082/1647/5606/6688/652/4217/
nal=30%","11346/4739/5358/800/2059/389/2316/10174/51474/90102/395/6281/11170/7791/912
signal=30%","11346/4739/5358/800/2059/389/2316/10174/51474/90102/395/6281/11170/7791/9
-05,4192,"tags=43%, list=23%, signal=33%","2332/170506/56339/6470/27257/25904/4848/9698/12
5","301/22925/7223/9429/5321/183/1906/8273/6542/81031/56606/6515/89874/4915/477/5660/9
1656/10930/11176/4595/56154/55729/10419/546/8846/7874/10155/53615/51010/200424/10919
, "7376/1435/7040/183/4481/3690/5322/3685/19/4790/5468/4023/5583/185/4792/6646/1401/546
signal=45%","92797/90121/404672/115939/6193/25879/55226/6202/10607/55781/6229/10436/48
, "7334/5980/9100/26073/10714/83932/51455/55339/7336/56852/5425/201973/5424/51514/5427
%, signal=42%","10111/23049/545/54464/23293/10575/65057/51548/54984/170506/10694/6714/5
4%, list=22%, signal=35%","54209/11027/7098/9572/857/3430/4814/11213/4067/64127/2099/5692
80258474e-05,5644,"tags=47%, list=31%, signal=32%","2316/1903/5141/5350/1906/5744/5660/277
%, signal=40%","7414/7057/90102/395/6281/4323/7070/11170/79834/1307/6385/7010/6548/347/
list=23%, signal=40%","7414/7057/90102/395/6281/4323/7070/11170/79834/1307/6385/7010/654
%","9314/3488/6615/10468/7042/4851/8985/2736/1499/2252/94234/2131/6608/6469/8626/4804
072/55660/5289/84501/55958/11021/9094/91782/26073/4628/5300/56776/285643/57448/54627
492/64919/6599/196528/6598/605/6601/51412/86/55193/6597/8289/6602/6605"
%","301/22925/7223/9429/5321/183/1906/8273/6542/89874/4915/477/5660/9121/5322/2697/50
list=28%, signal=41%","1839/2535/1956/2209/8322/1950/2069/374/3115/3123/685/10618/348/934
ignal=45%","84545/65003/64976/29088/219927/65080/28998/122704/9801/55052/57129/78988/
%, signal=45%","84545/65003/64976/29088/219927/65080/28998/122704/9801/55052/57129/789
signal=52%","10116/5514/54465/7517/25906/9984/7175/8563/11200/57805/81620/79621/8379/5
1%, signal=28%","7376/117854/710/2/54209/100507436/3075/11027/3133/11326/11221/3592/84
list=22%, signal=43%","2303/1969/5054/8754/5328/7042/6591/10519/9780/1942/1545/3976/4067
, list=23%, signal=38%","7414/7057/90102/395/6281/4323/7070/11170/79834/1307/6385/7010/65
2078e-05,2652,"tags=48%, list=15%, signal=41%","3624/90/2022/11030/7040/1601/7043/654/3077
7048/6662/340419/1896/3202/5916/1499/7477/5604/652/6469/6722/51176"
gs=35%, list=14%, signal=30%","3133/3592/135250/567/3105/3106/3140/3916/5027/7305/5817/31
list=14%, signal=34%","2934/22925/7057/10413/677/831/2621/7538/5054/26471/28984/7010/511
list=14%, signal=41%","301/8767/6556/10865/5321/3554/7292/9173/3142/3566/9655/246778/355
i4%","3556/7098/3554/683/148022/8808/9173/26280/7097/7096/11141/7099/7100/59307/35337
624/5321/183/1601/1906/654/114897/5027/4824/8322/1588/185/3784/5025/9536/6696/3553/35
4%, list=27%, signal=33%","54209/2316/8013/7070/183/3779/1906/2149/30845/6548/5348/4780/5
, "tags=58%, list=25%, signal=44%","558/2260/1969/5159/51232/10461/7010/4915/4921/2050/5383
gnal=51%","5592/114897/3569/3572/4067/10019/5580/170692/84034/1511/928/10630/51206/84
1/79971/55614/301/56937/10981/10410/79890/3107/388/3133/30846/7098/3077/8877/29984/21
18%, signal=27%","79971/79365/2303/8553/26508/3280/64321/3217/10512/2296/9096/2737/702
signal=48%","7414/3915/284/5743/3908/2697/90952/3688/3569/5175/58494/1003/7122/83700/9
signal=36%","1893/23143/80024/347/6387/351/6793/58494/29108/326/387/4478/6354/8764/747
ial=32%","6324/2934/23704/2316/122786/4643/5350/2013/54749/4627/477/6444/6548/2697/59/
45%","8767/3133/3105/7048/975/1604/7292/51043/3659/2000/8764/3965/29126/653499/64926/
ial=35%","56548/9469/2300/54360/633/79586/81031/1634/337876/10090/23213/3425/1499/8179
91181/8021/23039/64328/5905/8498/10527/9972/100101267/3843/3836/23511/8658/10204/988

=25%, signal=34%", "301/8767/3280/8744/3133/3105/7048/975/1604/7292/3569/10288/1947/35729/3691/83742/4915/7851/5653/3400/3082/443/5339/50846/10397/8560/5916/27242/58494/1499%, signal=44%", "25937/3913/10413/3280/6662/30812/3976/7484/7477/130497/55366/5311"496097e-05,5785,"tags=51%, list=32%, signal=35%", "1903/5141/5350/5744/2771/146/7432/151/190tags=54%, list=26%, signal=40%", "861/677/54209/1435/7040/4853/2242/3398/146433/2353/7305/3al=33%", "5914/8087/1938/9470/85476/9617/10987/1975/8892/2935/1153/1964/2332/6470/8661, list=25%, signal=42%", "4052/558/90/2022/2260/1969/5159/51232/10461/8425/7010/4915/4921/170506/56339/27257/4848/9698/129563/1797/4849/27161/196513/124245/5436/10492/9924/342nal=31%", "7798/90/26508/3280/639/4846/8321/7042/4851/57493/23493/7049/7048/7481/10370%, signal=31%", "51116/6132/6173/6181/6202/9349/6168/54460/6228/6142/56945/6235/6189/614, "9510/2/3624/4313/5241/4327/7043/7130/4846/7042/5806/5066/5156/8204/8322/2069/2099/33signal=46%", "55870/7799/56950/51409/11105/2091/79091/55209/4297/51108/54093/2145/15119il=54%", "7132/182/26508/4853/4846/7042/4851/23493/4091/23462/4772/652/2702"%, "64769/10856/6944/8607/54799/26122/57634/10902/55257/8295/86/79829/8089"05,3728,"tags=45%, list=21%, signal=36%", "4803/1435/5159/3707/10161/4853/2149/4851/7052/284=38%", "9314/91663/7070/3678/965/3690/3685/3688/10288/4814/3586/342035/83700/3557/35536%, signal=64%", "2246/5587/7057/64094/2260/4851/5641/3315/8817/5025/8823/2247/9037/105627%", "55062/7376/5587/467/2/25959/706/2308/3673/1611/2621/3920/11170/7538/2690/355/27515%, signal=29%", "301/861/8767/6778/604/7048/1514/975/4092/80149/1604/7292/3569/602/188305,"tags=46%, list=13%, signal=40%", "301/8767/7048/975/1604/7292/114548/64332/3142/510430/2/3624/4313/5241/4327/7043/7079/7130/4846/7042/5806/1958/5066/5176/5156/1545/8204/8301/3624/6810/2297/183/1601/8425/1906/9572/2752/654/3077/114897/5208/3625/80024/7432/2list=15%, signal=31%", "301/861/8767/6778/604/1514/4092/80149/7292/3569/602/1880/114548/6%, signal=51%", "56548/9469/633/79586/1634/337876/3425/29940/166012/2131/55454/133584/22%", "29072/55660/5289/55958/26073/5300/57448/54627/11113/80179/23636/201161/79187/6683list=12%, signal=46%", "25937/3913/10413/3280/6662/30812/3976/7477/130497/55366/5311"l=60%", "114991/55693/222229/546/11335/9682/23310/1786/1058/3070/157570/2146/10951/361045168304e-05,2522,"tags=34%, list=14%, signal=30%", "117854/23529/6810/10417/7040/10865/80nal=39%", "90/2022/182/26508/6615/4846/7042/4851/6591/4488/23493/7048/10370/221662/666al=39%", "301/11135/3673/9124/6282/23022/302/4059/11117/91624/90952/3688/27255/27020/48al=34%", "9843/301/6810/728/7223/2683/5155/302/56606/7010/6548/10392/10351/975/1956/8487819/27288/79066/51690/6629/124790/25929/6627/134353/51574/55285/64852/11189/10594/2ags=59%, list=27%, signal=43%", "100131801/27235/118980/5498/790955/23761/285521/55750/794038/135228/3624/5154/3488/6615/10468/7042/4851/4488/1956/6662/2736/9079/26018/1896/88/135228/3624/5154/3488/6615/10468/7042/4851/4488/1956/6662/2736/9079/26018/1896/83239%, signal=36%", "10734/11144/256006/388649/51547/56154/56776/4439/10919/7917/256126/898gnal=47%", "7376/8061/9314/7040/5155/7042/84913/2353/4091/6662/1958/2908/5978/4776/688/51%, list=19%, signal=41%", "558/117854/8767/54209/1435/2621/1906/3554/837/81844/10555/8303%, signal=44%", "1893/7040/2621/4054/4846/4851/23493/54829/5552/6662/54795/5167/23462"nal=29%", "6788/8767/4055/8324/344558/4616/7164/7098/10392/1647/351/64127/29108/6386/7i,4736,"tags=56%, list=26%, signal=41%", "545/54464/23293/10575/65057/54984/170506/10694/67il=36%", "114907/7132/4000/2308/3488/8013/90523/183/6442/84676/1906/4846/4851/29995/65410/54209/3673/1471/4481/7042/9445/3339/323/10288/5621/2892/8322/773/712/8301/4035/709al=32%", "25937/3624/11030/7040/1601/7043/654/81031/7042/7431/84913/3625/2353/4091/40926915301e-05,3566,"tags=44%, list=20%, signal=35%", "558/27202/54209/706/2621/671/80149/602%, signal=36%", "6284/6810/10417/8013/2214/54210/3133/2242/9948/148022/3162/7305/3569/213%, signal=55%", "5154/5592/5155/7056/4846/114897/5156/10019/5580/170692/348/928"gs=30%, list=14%, signal=26%", "23529/6810/54209/7040/10865/3133/3592/3554/135250/567/6778ignal=31%", "221656/10930/11176/56154/55729/10419/546/8846/7874/10155/53615/200424/10915649/9429/4499/493869/4493/4846/4489/84203/5742/5743/1728/4780/216/10516/57016/4501/9

signal=38%","7376/22925/5321/1601/1906/654/302/114897/5027/4824/5580/1588/5025/4035/3425%, signal=39%","2246/3490/706/1601/6615/9572/654/6591/1958/5978/4790/50846/27120/2712:ags=43%, list=20%, signal=34%","54556/126549/51147/6419/165918/7334/84501/1054/55693/647nal=26%","3074/2683/53947/374378/117248/84752/2992/79586/23127/79623/8985/337876/72790%, signal=42%","1051/90/116039/7040/4208/7043/654/9636/5027/4088/7020/130497/7475/2824, list=23%, signal=31%","444/2152/8767/2934/1611/55075/355/2149/5641/10392/3428/1942/5371,ags=47%, list=25%, signal=35%","100507436/196/3133/3077/604/3105/3106/4092/1604/64127/3136","51095/6227/54931/2091/5394/118460/6741/56915/79033/80789/55520/51574/79650/3028/6nal=61%","182/26508/4853/4846/7042/4851/23493/4091/23462/4772/652/2702"
"10344/3958/3269/23604/6355/6376/6354/6347/6357/6351/388372/6348/6356/6352"
gs=40%, list=21%, signal=32%","64114/367/6810/54209/4323/7040/3958/1969/5525/1601/10519/8al=54%","51742/55209/23411/4297/57343/54093/4800/5926/23067/55904/8085/23476/9739/290gs=44%, list=25%, signal=33%","5048/636/246176/25876/146057/57551/324/5563/27124/4733/552s=50%, list=8%, signal=46%","1893/7040/2621/4054/4846/4851/23493/54829/5552/6662/54795/51:17%, signal=24%","25802/2934/51429/2059/283/148170/51474/11135/395/10344/91663/23189/1%, signal=27%","26058/51379/55367/245711/1032/8454/57695/25799/57521/1019/6198/1977/112tags=58%, list=30%, signal=40%","100131801/27235/118980/790955/23761/285521/55750/79135/.signal=35%","23529/54209/7040/3280/1745/1746/23500/11221/9572/1959/4851/9948/3398/1464gna=25%","56548/9469/6484/2300/1839/2683/374378/30815/4124/117248/25825/84752/54360/.i6%, list=30%, signal=47%","55968/22924/49856/9857/1453/51104/636/246176/146057/324/9851/.1%","2068/23411/728340/3981/2074/2968/10463/4968/1643/56949/85015/5887/4331/11143/58ags=44%, list=20%, signal=35%","558/27202/54209/706/2621/671/80149/602/10457/11213/947/63nal=62%","8189/10978/53981/642843/23283/11052/51692/55339/81608/11051/1478/10898/1477764/9092/50628/4863/23379/10285/51602/2332/2483/25988/55651/79664/1017/55341/6606/92:%","558/84159/1051/9510/2/3624/283/25976/4323/4313/5241/4327/10461/7130/2296/26471/10i7436/3075/2214/54210/3133/2013/3592/135250/567/3105/3106/3140/3916/5027/1604/7305/22i nal=27%","26058/11331/322/51379/55367/245711/1032/8454/57695/25799/57521/1019/6198/19signal=55%","8767/54209/79155/4067/64127/2150/7097/7096/1535/7128"
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, list=4%, signal=42%","861/2022/90993/3673/7040/5159/7043/28984/2149/7431"
signal=49%","54209/3105/10392/3106/23643/284297/64127/3123/7097/7096/64581/7099/721/1i367/10252/2668/7481/1499/7474/652/22943/650/6495/2247/3207"
e-05,1858,"tags=34%, list=10%, signal=31%","1793/4739/2316/6281/91663/1601/80005/6239/5567i%, signal=47%","710/54209/3426/1604/715/716/713/712/4153/735/51279/714/732/721/729/730/1signal=32%","1465/10398/25802/389/10174/122786/90102/395/6281/7791/5159/9124/2037/7043i83,"tags=33%, list=17%, signal=28%","6788/2246/5154/56034/7057/23328/80310/7040/3356/2260i.6/6132/6173/6181/6202/9349/6168/8667/54460/689/6228/6142/56945/6235/6189/6147/51373/6i, signal=71%","2303/80310/5159/5155/4851/59/1958/947/8837/652/2828/3570/8710"
i344/3958/3269/23604/6355/6376/6354/5734/6347/6357/6351/388372/6348/6356/11314/6352"
it=20%, signal=55%","728/7057/54209/1435/4323/146433/6376/5919/5025/59341/1436/719/6348,i, signal=32%","824/558/1410/301/80310/6649/8061/8013/4313/5159/388/8754/1906/4846/8877/92%, list=16%, signal=77%","64852/53981/642843/23283/11052/81608/4686/11051/22916/1478/1list=20%, signal=24%","11031/5327/2303/677/4929/2308/6517/23189/5791/81565/23371/8013/1i list=21%, signal=36%","7376/710/2/100507436/3133/11326/11221/3105/3106/3428/9636/6737/54signal=45%","7376/22925/7057/54209/158219/3690/3685/19/4790/3569/5468/1066/5467/4792/5i it=9%, signal=33%","114907/687/5327/301/677/90/11170/7538/1906/54541/2908/5176/445/5978/

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.91055624266488e-05,3.95650748668304e-05,5565,"tags=71%, list=31%, signal=49%","254528/2016
376/8061/9314/7040/5155/7042/84913/2353/4091/6662/1958/2908/5978/4776/688/5468/4088/2
;nal=53%","30008/2022/25976/6662/7763/1281/4638/130497/5311/652/6608/6469/6722/6495"
tags=75%, list=21%, signal=59%","10921/708/11338/56853/6429/6431/6433/57060/27316/10772/8
=31%","84159/30008/2303/2022/7040/2296/8321/7042/4851/57493/23493/7049/2535/4092/1901
67%, list=15%, signal=56%","51230/9646/55683/22938/84148/23168/4602/284058/26053/1789/30!
152/3673/3958/5155/284/2668/7424/3082/1901/6387/6360/10457/6376/4088/2252/3576/2150/7.
3,"tags=61%, list=18%, signal=50%","25937/90/2022/182/7040/1601/7043/6615/2296/28984/7042/
. list=26%, signal=43%","5654/1745/4681/51232/10272/7130/8321/4851/2200/94031/4091/4092/9!
6, signal=22%","11031/83871/196383/64114/7132/367/6810/2239/54209/2316/6281/4323/91663/
46%","10468/27120/27122/27123/100463488/100463482/4043/100463498/22943/100463486/355
6, list=16%, signal=24%","117854/8767/5587/4803/7040/2621/3270/4915/284/8412/5743/1956/545
;","7376/54209/10226/4481/158219/3690/3685/80149/19/4790/3569/5468/4023/1066/5467/4792
5,2787,"tags=80%, list=16%, signal=68%","8189/53981/642843/23283/11052/51692/55339/81608/1
gnal=48%","25937/10413/3280/6662/30812/3976/7484/7477/130497/55366/5311"
nal=33%","9131/118460/22894/27327/1655/81892/84153/6741/90806/207/1149/60493/6999/5600
signal=60%","2246/10413/10252/6662/51804/157506/374/2099/10253/7474/652/6469/6495"
=47%, list=21%, signal=37%","4803/1435/5159/3707/10161/4853/2149/4851/2840/2151/1281/112:
05,4069,"tags=53%, list=23%, signal=41%","710/54209/3426/975/1604/715/602/716/713/64127/71
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/83547/10581/10410/6517/3920/388/9367/11342/3592/302/10791/2149/5641/5660/1514/309/53:
1/728/6484/4803/54209/8061/6517/7162/11170/183/3356/3678/4208/57477/10769/6446/1959/5
73649e-05,5859,"tags=69%, list=33%, signal=47%","9811/5394/56006/23381/5976/55629/23049/23
6","23481/10412/23016/6227/10799/27340/5394/10200/10438/81887/117246/65095/80135/7903:
nal=43%","90/116039/7040/4208/7043/654/7042/9636/5027/10766/4088/7020/6869/130497/2824
gs=77%, list=25%, signal=58%","10575/65057/10694/25836/25913/10856/10576/222229/1736/720:
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3%, list=25%, signal=40%","1153/79066/51594/1432/2332/23185/10921/79048/708/11338/56853/6
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list=14%, signal=34%","10865/3133/3592/3554/567/3105/3106/3140/975/5027/1604/7292/3569/1:
/301/5358/7169/395/9124/57477/23022/7010/10634/7171/6525/8826/4641/27295/8522/9260/54
.2%","100507436/3133/2013/3592/567/3105/3106/3140/5027/5817/3123/1075/3135/2213/3122/3
%, signal=55%","57343/359787/5253/4300/9869/23133/1017/134353/9739/9646/7175/55729/228:
6","4038/135228/3624/5154/3488/6615/10468/7042/4851/4488/1956/6662/2736/9079/1896/8323
l=27%","23529/3624/677/4323/7040/30011/196/4208/6778/683/604/3398/148022/975/7292/730:
=19%, signal=38%","30008/27185/6237/1435/6281/7070/1307/54453/2013/6385/7010/10519/398
, "311/140576/7057/3726/3707/4208/3779/8754/1906/845/5641/3625/5027/2353/5179/2354/857
=28%, signal=37%","966/3107/3133/567/3105/89866/3106/351/374/3115/23423/149111/3123/152
30008/2022/182/3280/5159/7042/4851/23493/60681/1281/4638/23462/56999/94/4035/54567/67
st=23%, signal=31%","3074/4124/3556/4758/7098/2720/3554/4126/141/683/148022/3073/8808/1:
signal=31%","2303/10413/90/2022/3280/64321/4208/4853/2296/8463/1906/9645/4851/7048/103
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21%, signal=30%","1839/9052/4208/5054/5328/1906/3077/729993/80863/3460/151/3688/4061/27
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67%, list=8%, signal=62%","5587/2316/2013/7076/81031/683/55679/967/3987/1495"
34%, list=15%, signal=29%","7376/5654/710/2/100507436/11027/196/3133/11326/11221/3105/104
s=51%, list=27%, signal=38%","1051/2615/11326/6385/8654/7305/10288/5621/10457/27242/51043
%, list=26%, signal=46%","4853/2242/7010/90952/5156/10788/10411/1436/7226/1440/51225/9535
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8%","558/1051/54209/4055/2621/4853/7048/3106/10288/4067/55365/6688/2150/3135/2213/289
.274/9510/4313/7010/4488/23493/7049/1277/23462/1101/133522/6722/6422/2201/5950/2280/70
st=20%, signal=46%","860/649/2737/654/6662/4092/4088/8200/8817/94/7474/652/650/7704/4017
=24%, signal=49%","4052/2615/7057/4054/2335/7042/5045/7481/5743/4060/3685/7305/1281/947
:30%","4038/135228/3624/5154/3488/6615/10468/7042/4851/4488/1956/6662/2736/9079/1896/8
t=32%, signal=43%","2068/22828/55209/2074/9400/54623/904/6919/23160/7936/56943/9150/902
%","558/1051/23529/4803/54209/4929/840/1745/4208/7043/355/26471/2149/7042/4170/4915/2
%, list=16%, signal=38%","117854/10581/10410/3428/9636/8519/8091/684/10318/5359/57169/848
6%","3800/10513/3796/347240/9493/1062/9585/56992/9928/10112/9126/24137/146909/81930/3
i%, signal=41%","301/1893/6778/604/975/7292/3569/114548/3142/3566/64127/91543/942/972/90
24%","3074/83468/6484/5836/2683/53947/25976/374378/30815/117248/84752/2992/79586/2312
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5%, list=27%, signal=35%","9131/118460/22894/27327/1655/81892/84153/6741/90806/207/1149/6
3%","2683/3920/2040/11010/4126/5660/2357/3916/967/684/10043/84061/5547/54918/23385/71
%, list=28%, signal=33%","301/7376/8013/1601/9572/654/5743/5166/6662/1958/857/5978/27120/
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%, signal=29%","558/1051/23529/4803/4929/1435/1745/8013/4208/7043/2690/8321/2149/4915/2
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gs=52%, list=20%, signal=42%","1051/90/116039/7040/4208/7043/654/9636/5027/4088/7020/1304
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70%","11143/51147/51230/55683/64769/84148/84289/9767/284058/79960/3054/10445/54934/11
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."254528/9941/201626/5394/22894/54840/90806/83940/81875/56915/10111/5168/22803/64782/
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it=20%, signal=49%","4437/126549/51750/9984/23347/2187/7158/84083/55183/7014/4292/641/64
st=17%, signal=37%","114907/687/5327/301/677/90/11170/7538/6446/1906/54541/2908/5176/44
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%, list=19%, signal=26%","84159/8531/1051/9510/2/3624/5154/367/10046/283/25976/4323/4313/
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%, list=23%, signal=39%","170506/56339/27257/4848/9698/129563/4849/27161/196513/5436/104
"3913/54587/728/54209/9572/3691/4915/7431/3400/443/3569/5339/10397/351/10319/4919/406
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t=32%, signal=42%","1018/892/2068/728340/79616/2968/8408/904/1147/81669/1020/5257/51719
6, list=26%, signal=30%","11315/114803/56943/85015/8078/10869/51035/51138/10868/54764/205
11/3624/6810/2297/183/1601/8425/1906/9572/2752/654/3077/114897/5208/3625/80024/7432/26
.5%, signal=47%","5327/3624/5069/1906/4851/7049/1909/1545/2730/2492"
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},","tags=48%, list=13%, signal=42%","10413/10252/6662/340419/3202/157506/1499/1522/2131/102
1717e-05,4487,"tags=67%, list=25%, signal=50%","7040/7043/3077/7042/604/284/684/4092/3162/1
, list=23%, signal=44%","25825/5125/5045/1514/2028/1359/1889/4311/1522/590/1511/10159/136
st=17%, signal=40%","860/2303/4323/1746/7043/2737/7048/5396/3198/51804/3199/157506/5156
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3%","216/57016/151056/9249/220/339761/157506/1545/29785/10170/5467/8644/5919/54884/83
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, signal=51%","9857/1453/636/324/9851/50855/26005/11190/10540/79648/5108/64770/23636/29
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=69%, list=21%, signal=55%", "3107/3133/3105/3106/6892/3115/3123/3135/972/3122/5311/3113/3
gnal=56%", "65980/23140/4297/26009/10498/80764/4300/23613/6872/23476/11176/54454/8019/
3%, signal=56%", "65980/23140/4297/26009/10498/80764/4300/23613/6872/23476/11176/54454/8

%, list=20%, signal=33%", "7376/54209/5360/29116/183/4481/302/5322/3162/19/4023/185/348/33
ignal=39%", "7132/4000/2308/3488/8013/90523/183/84676/1906/4851/29995/6548/8654/5468/35
%", "2648/6883/27097/6881/8464/171023/9960/6879/10600/8314/158880/51720/114803/56943/9
=45%, list=13%, signal=40%", "54209/11027/9572/3430/4814/4067/338382/2150/7128/57162"
33%", "301/8767/6778/604/4092/80149/7292/3569/602/1880/114548/64332/3142/51043/3566/31
5, signal=33%", "2355/5154/56034/80310/2621/183/5159/2335/5155/26471/8877/4921/1956/5371/
tags=51%, list=27%, signal=38%", "7132/23529/3280/2690/3592/9021/1489/9244/857/3569/5008/3.
l=31%", "2052/196/54498/1728/2329/5446/2987/1545/29785/2948/9446/316/2327/874/57552/27.
l=32%", "60493/11201/54888/8087/9470/57819/9575/339345/27067/5976/6128/6175/23589/9898,
al=40%", "64321/2737/4851/2735/3398/7481/1956/2736/348093/5156/3142/6943/4088/1499/513:
!8%", "11343/3673/3356/1906/2149/6548/7432/5743/5027/5179/1910/56925/6387/5028/55273/3:
=44%, list=23%, signal=34%", "2246/55614/860/7057/10252/90993/64094/2260/53834/8826/81848,
6", "2274/9510/2022/4313/7042/4851/7010/57493/4488/23493/7049/22904/1901/1277/23462/38:
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93%, list=26%, signal=69%", "5587/64094/2260/5641/3315/8817/5025/8823/2247/9037/3791/4233/
l=31%", "301/2687/7132/9261/11343/2052/5321/1906/27306/5742/5743/5322/8605/1545/29785/
1413/10252/7481/6662/51804/157506/374/2099/10253/7474/652/6469/6495/6423/6422"
49%, list=30%, signal=35%", "100131801/27235/9927/637/118980/5498/790955/23761/23456/2855
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gs=43%, list=28%, signal=31%", "301/8767/23529/3956/6556/7040/3958/4853/6778/604/975/3916/
3%, signal=37%", "2295/2737/5125/7042/3398/2736/348093/5156/3142/6943/5915/5919/3576/646
6", "26509/4038/54209/7223/3356/30846/858/4846/2149/477/7048/5743/5348/161742/857/8487:
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signal=32%", "79148/7057/27202/10501/79890/1843/4681/10512/7130/4851/1588/56920/1991/74
!246/10398/4739/9322/800/5587/2934/51429/2059/83872/389/7223/2316/90102/79083/631/464:
=20%, signal=43%", "90/116039/7040/4208/7043/654/9636/5027/4088/7020/130497/2824/338773/
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0%, list=27%, signal=30%", "54998/51657/10201/57662/10111/1859/4682/375189/8678/54464/509:
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i, signal=36%", "2246/367/10252/4208/2737/2668/7481/1499/2131/7474/652/22943/650/6495/224
ial=44%", "3280/3958/5159/5155/5350/6387/162514/5621/6781/1950/1499/7779/2641/5311/6347
gnal=35%", "861/2303/10413/147912/4208/2296/84466/7042/4851/23493/284/2735/7049/7048/10
l=31%", "216/57016/151056/9249/220/339761/157506/1545/29785/10170/5467/8644/5919/54884
i1/5836/706/355/7098/26471/197259/857/4814/8837/427/329/4504/4217/57162/9181/9825/653:
21%, signal=28%", "7376/56937/8767/367/25959/10413/5187/4929/26508/8013/196/5241/1601/9:
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%, list=16%, signal=72%", "64852/53981/642843/23283/11052/81608/4686/11051/22916/1478/108:
%, signal=59%", "3678/8754/9780/3688/255743/5420/23075/3676/83706/6352/100/10563"
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i4%", "4240/558/7094/7057/54209/54843/2621/302/309/85477/312/341359/4311/91683/79792/5:
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:22%, signal=38%", "706/1601/654/1910/1958/5978/27122/133/10170/8644/1583/1586/650/6718/3
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8,"tags=48%, list=11%, signal=43%","57551/54984/51343/60561/55743/80279/8883/5884/29980/793%","10208/5394/118460/6621/56915/55756/23379/79066/55651/80789/79664/55596/51574/796%","87178/64852/8189/9646/55149/10978/53981/10914/6626/56254/9810/11052/51692/55339/8',"87178/64852/8189/9646/55149/10978/53981/10914/6626/56254/9810/11052/51692/55339/816nal=62%","567/6892/3115/3108/3123/3122/55080/3113/3119/3111/3117/3109/3127/2923/3120"igs=83%, list=25%, signal=62%","567/6892/3115/3108/3123/3122/55080/3113/3119/3111/3117/3109;signal=47%","4038/1893/4054/4208/4851/5552/4091/6662/4092/54795/5167/796/22943/22856/631209/706/1435/3280/4851/146433/5179/3569/2629/5583/374/6376/4067/163175/1436/3953/355s=59%, list=22%, signal=46%","56548/9469/54360/633/79586/1634/337876/3425/29940/166012/238%, list=26%, signal=29%","6311/92170/1975/54464/8892/192670/94103/5499/2935/1153/79066,signal=26%","301/3624/6810/183/1601/1906/9572/2752/654/3077/114897/5208/3625/80024/2697ral=56%","5423/3980/8505/328/5426/3978/5424/2237/5111"=:21%, signal=43%","54209/26471/9572/8877/5743/3569/6376/120892/1075/3479/3553/2896/63413%, signal=38%","301/8767/604/4092/80149/7292/114548/64332/3142/51043/3566/3123/942/31,"3399/55214/5351/2752/4846/7026/1373/8985/8974/5066/283208/2350/445/339761/5468/5033,gnal=32%","860/4038/116039/4853/2737/7042/4851/4488/4154/2697/5396/340419/157506/832320%, signal=32%","860/4038/116039/4853/2737/7042/4851/4488/4154/2697/5396/340419/157506nal=49%","301/4851/2771/3162/5978/6688/2213/6814/11141/3965/5906/3134/7879/29091/1131=:30%, signal=43%","2246/1601/654/3269/5978/4790/5028/27122/348/23541/650/1581/2185/28527%","10607/10436/57050/84294/2091/55127/27340/10813/79954/6201/10199/51602/9724/5109=38%","7107/4054/3690/5166/5027/1901/3569/796/3635/133522/1436/338773/7128/6696/53832=:21%, signal=47%","1601/654/1958/5978/4790/27122/133/8614/2865/650/3091/1609/653"signal=32%","728/27202/7130/1906/3554/683/391/23604/64127/3576/972/83700/2526/7060/355:gs=76%, list=22%, signal=60%","54209/148022/22904/7305/8291/3430/9111/84868/2896/1524/53:,"54617/29844/93973/54891/79913/10847/125476/55929/54556/10428/64431/51377/10856/7528.2,3605,"tags=67%, list=20%, signal=53%","51429/257364/152503/8754/5045/348/29763/3553/713:5,4803,"tags=70%, list=27%, signal=52%","79897/10775/131870/27161/23405/55520/10556/284131',"11031/4240/1793/2934/51429/7057/54209/257364/3673/4481/84466/4627/19/51454/391/2209signal=27%","301/861/8767/9580/8744/639/3707/11221/2737/604/1960/7048/4092/80149/7292/;', "10856/3065/53615/57459/29803/6599/3183/29841/328/3066/9219/6598/54107/55206/6601/5l%, list=25%, signal=48%","3399/7040/4851/144165/6662/9573/30812/5467/28514/652/116173/16l1%","80789/79650/64852/55656/57508/26173/11340/51010/23404/25896/5393/114034"14%","3624/1435/7040/3398/146433/351/3976/2629/133396/3123/6688/7097/1436/375387/652/:64297392,1979,"tags=45%, list=11%, signal=40%","824/54209/30846/8754/7305/4773/3566/10411,% , signal=45%","183/7026/3398/146/151/6915/134/387/6869/81285/1535/147/5144/153/80852/1353,"tags=41%, list=19%, signal=34%","85450/64114/367/7057/10413/90/4000/3958/2139/8682/504785,"tags=75%, list=27%, signal=55%","996/51433/51343/1017/64682/27338/8697/51434/8452/5:99,3004,"tags=52%, list=17%, signal=44%","183/3217/4070/2668/6662/51804/30812/55366/652/66nal=32%","23049/51366/11315/56943/55929/55437/8841/23293/4659/10212/91746/57506/5781/23049/51366/11315/56943/55929/55437/8841/23293/4659/10212/91746/57506/5781/8021/3728%, signal=47%","3913/2303/182/4643/4853/2296/1910/8826/5175/1909/947/2131/652/5420"ral=27%","9531/467/64764/7057/23645/90993/9709/3316/871/23471/27129/11080/4780/5611/26=:21%, signal=26%","9843/79901/4502/6556/4499/4493/654/3077/4489/4501/3162/2512/64116/50s=57%, list=16%, signal=48%","5592/3488/4208/5054/4780/5467/387/4035/93649/10221/199/3486)%","11031/79890/302/284/3690/975/967/3688/57007/857/6401/133/3357/6424/1950/6386/830104309,3253,"tags=28%, list=18%, signal=23%","8767/728/27202/3958/11027/8013/7070/4208/7000!8%, list=18%, signal=23%","8767/728/27202/3958/11027/8013/7070/4208/7006/123920/1997/31027%, signal=29%","79971/7376/6810/283/54209/7040/7043/8754/2752/654/7042/5208/5027/74244,"tags=71%, list=19%, signal=58%","9014/11137/51547/4691/2475/6949/6598/1663/25926/6597"4695/1349/4718/4712/4723/192286/10975/4702/4713/1350/125965/6390/7386/4700/1345/56901

=19%, signal=73%","7376/54209/158219/19/5468/1066/5467/5465/9619"
s=32%, list=15%, signal=27%","64114/367/6810/2239/54209/4323/7040/3958/1969/5525/2037/160
:70%","30827/84332/9070/5929/29915/23067/259282/91272/9739/54554/80335/84661/3054/110
4939165,3253,"tags=27%, list=18%, signal=23%","8767/728/27202/3958/11027/8013/7070/2214/42
478/90102/1839/3678/6239/1289/4488/84962/10979/387/94"
:27%","7376/1051/2303/56034/2308/3356/63976/9572/7030/4851/6778/4883/5743/8878/2697/21
"7376/706/51474/4481/302/5045/10577/10351/857/19/4790/1066/4035/348/26119/3990/114879
,1979,"tags=41%, list=11%, signal=36%","824/54209/30846/8754/7305/4773/3566/10411/9518/88
%","92797/90121/404672/115939/25879/55226/6202/10607/55781/57050/84294/6227/10799/55
0370/5743/4693/1508/3976/6781/5467/8614/6696/7421/2706"
, list=23%, signal=36%","11346/389/2316/10174/90102/395/6281/7043/28984/6385/29109/4070/6
:25%","2246/51474/80271/5321/8871/3707/1601/654/8877/9023/3269/10577/158219/26002/854
%, signal=54%","5893/6419/7334/84464/51444/5932/56916/7336/55218/1763/641/83990"
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27547,1650,"tags=44%, list=9%, signal=40%","1435/183/4481/5322/4790/4023/5583/185"
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ist=29%, signal=27%","23291/26001/64207/10477/84133/152006/1643/7332/25820/84085/55298/
nal=38%","5154/4000/7048/7481/6662/5396/4487/1499/2252/2719/130497/7474/652/8646/6608/
st=22%, signal=36%","5154/56034/2022/80310/5155/5912/9961/7424/857/91662/5167/10457/372
444/83716/84159/6237/90102/64651/25976/4313/7043/4487/5156/1277/83690/2719/7122/5083/
477,3153,"tags=36%, list=18%, signal=30%","9531/6788/85450/64114/7132/467/6810/7057/4803/3
","132949/10352/10056/5188/57038/57176/80222/92935/2193/79731/23395/23438/55278/57470
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gs=43%, list=19%, signal=35%","301/7376/5743/972/3553/51085/344/9104/335"
5301/4488/4921/7048/309/6662/5916/6781/2121/5915/54796/2131/3953/25987/2261"
ist=15%, signal=31%","4739/1839/9052/2621/7070/183/5155/9467/5912/146433/1942/84632/996
ist=18%, signal=53%","8082/6641/6442/6444/8910/7402/5239/1605/1756/6645/54212"
t=13%, signal=64%","301/604/7292/114548/3142/3566/942/9655"
il=55%","3556/3554/683/8808/9173/26280/7097/7096/11141/7099"
i2%, list=13%, signal=55%","3556/3554/683/8808/9173/26280/7097/7096/11141/7099"
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:55%","10799/54931/51367/7257/81887/79897/192670/10775/80746/27161/23405/3028/10556/1
tags=86%, list=21%, signal=68%","6742/1017/546/25792/81620/58525/10926/2021/80174/144455/
%, list=18%, signal=31%","79971/57664/10413/27185/57326/7040/23189/23500/1601/9839/1956/8
=44%","3678/4851/6591/4170/4915/5166/3688/857"
=43%","824/117854/10581/10410/7098/3428/8519/684/5359/3659/4332/3455/4938/54739"
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%, signal=26%","6788/8531/861/2303/367/26524/10413/27185/4803/10501/1435/81565/2335/105
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, "9572/4846/5742/5743/1593/3162/339761/6948/1545/29785/9420/6392/6916/79689/1588/5564
57%","6446/1906/1910/5446/1909/3784/525"
, signal=46%","6484/80310/7070/3554/683/6403/6387/6401/5734/1991/83700/3383/23236/2526/
signal=39%","10344/6360/6355/6376/6354/9034/6358/6347/6357/6351/6368/414062/10763/3883
t=19%, signal=56%","7132/2022/90993/183/28984/4851/650/7133/57589"

6, signal=26%", "6788/5327/85360/3624/367/2683/1843/6615/26471/7076/27306/4851/4627/4488,
29/3956/3624/677/4323/7040/30011/196/4208/4853/1316/8935/6778/683/604/3398/148022/975,
3%, signal=42%", "3280/5159/2668/6662/30812/3976/7484/1499/55366/5311/652/6608"
al=34%", "7376/11343/1373/7148/857/151056/4023/150763/376497/348/64788/338328/6583/287
926/285643/54627/9212/9493/24137/9055/29127"
367, "tags=39%, list=13%, signal=34%", "301/861/8767/604/4092/80149/7292/114548/64332/3142/5
=30%", "1051/22925/5321/183/1906/2564/477/5027/3688/6529/8501/5621/5205/6424/6781/1066,
,"tags=54%, list=22%, signal=43%", "51755/4331/1017/10983/8621/8851/1032/1019/1164/645121/8
6, list=26%, signal=57%", "9314/1969/347/3569/3586/2150/4210/1991/9655/3965/4938/140885/593
22%, signal=29%", "51594/51690/9238/1432/200035/2332/131870/170506/56339/27257/23185/25
46%", "677/3488/196/1373/3625/5179/445/358/351/1545/6781/10411/3784/3709/3309/2230/5311
tags=29%, list=14%, signal=25%", "23529/54209/7040/10865/3133/3592/3554/135250/567/6778/31
=9%, signal=48%", "3720/1789/6598/9682/11091/22823/54880/1786/55170/23028/672"
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"6324/79026/7414/10791/29109/5912/477/6548/53834/5348/2697/3688/1495/6330/58494/1499/
s=42%, list=25%, signal=31%", "7040/3280/183/2690/9021/2149/4851/1647/857/3569/602/5468/15
l=42%", "25825/5125/5045/1514/2028/1359/1889/1522/590/1511/10159/1363/5126/1215/10699/!
%, list=19%, signal=43%", "7107/10272/7130/7098/2200/10766/10234/1499/3635/9935/7099/1102
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3494, "tags=29%, list=19%, signal=24%", "10205/2239/83872/1009/90/9314/91663/91179/3678/3556
%", "55062/51429/11037/1839/6517/4643/1601/1906/5872/5045/7851/2535/1956/2209/7450/832
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48%", "5784/2303/1969/2296/7026/57493/79987/161198/7424/79652/7075/94/54345/85329/2324
19%, signal=39%", "7132/4000/2308/8013/90523/183/84676/1906/4851/29995/6548/8654/5468/35
gs=47%, list=15%, signal=40%", "654/28984/4851/10076/9647/4855/7474/3169/7082"
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2%, list=25%, signal=54%", "301/307/9314/671/602/284297/3586/1991/945/56957/10333/5607/711
3767/148170/5187/4055/8324/344558/4616/7164/7098/11221/29969/9459/10392/1956/1647/479
;nal=34%", "4739/117854/4038/5784/54209/90/2621/284/2668/8878/2697/3688/399694/57605/10
signal=37%", "54209/706/3280/1745/1746/23500/11221/9572/4851/3400/1499/1600/430/1030/92
44%, list=25%, signal=33%", "196/3077/604/4092/80149/1604/7292/9173/51043/3566/64127/8764/
23%, signal=53%", "10417/7040/8013/7043/7042/604/148022/3162/11213/23586/7805/3135/972/7
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3674,3321, "tags=69%, list=19%, signal=56%", "7376/3690/3685/19/5468/4792/1401/5465/9619"
16%, signal=43%", "5980/56897/9100/26073/1032/10714/83932/51455/5425/201973/5426/5424/54
4/23704/79073/7223/94015/3779/2564/302/3775/309/53373/22821/9780/5348/8542/2697/5027/
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=42%, signal=43%", "51079/4706/28976/29078/4716/4695/4718/4712/4702/4713/4700/4715/4722/
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s=58%, list=13%, signal=50%", "57381/5159/196740/4693/22899/5156/1545/8322/1282/94/25932"
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4503, "tags=31%, list=25%, signal=24%", "79971/64285/301/7376/6810/283/54209/57333/7040/7043
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," list=18%, signal=45%", "2246/9314/3678/6271/28514/3586/168667/7082/221074/2247/3716"
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29%, signal=27%", "23291/26001/64207/10477/84133/152006/1643/7332/25820/84085/55298/5113
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7%, list=20%, signal=22%", "6324/23704/7223/6556/3779/302/3775/8273/477/309/80024/6548/533

3%", "728/8061/3688/3959/23601/8808/7305/10288/23643/10312/10871/4332/3135/4046/4688/2
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ó, signal=43%", "860/116039/4488/340419/157506/4487/1499/7020/130497/6469/8626/2019/6052
al=33%", "23122/284001/10142/114791/7756/4926/10844/6904/4137/8851/23332/2258/11075/104
13/5321/116236/196463/63874/5337/5322/79887/2151/5333/3162/151056/8605/1909/23659/402
l=44%", "7040/183/1906/2771/7305/5446/5580/2150/285590/1535/64581/3684/4689/4688/2358/!
%, signal=49%", "3356/2149/3269/146/5743/857/6915/54795/6916/387/6869/147/2702/342527/55
gnal=23%", "558/301/3624/677/11167/1435/3707/4208/7538/10461/355/4846/2149/567/4851/183
signal=70%", "2621/5155/2013/2149/134/2150/1535/2702"
.6%, signal=42%", "8531/90/7040/3488/4208/84466/2697/4015/4534/4088/1499/28514/57158/652,
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al=23%", "25802/2934/51429/2059/283/148170/11135/395/10344/91663/23189/11170/23500/936
gnal=32%", "7376/283/11343/5321/1373/7148/857/151056/23659/4023/145447/51196/150763/376
", "10352/10056/5188/57038/57176/80222/92935/2193/79731/23395/23438/55278/57470/25973/
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%", "301/861/8767/9454/11326/7538/5621/9308/947/64127/2633/5142/7805/6711/942/64581/48
5%, signal=30%", "301/861/8767/9454/11326/7538/5621/9308/947/64127/2633/5142/7805/6711/9
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7%", "64285/55614/1839/9052/7040/183/8412/5641/1956/84632/9961/5329/2549/6662/8826/796!
gnal=28%", "5587/2934/706/7070/3356/5350/11015/3270/2149/6672/845/477/309/80024/53373/2
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gnal=45%", "119504/996/51433/51343/51529/25906/64682/27338/8697/51434/11065/701/991"
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, signal=37%", "710/966/2/54209/3075/11326/1604"
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;76/54209/4481/158219/19/5468/4023/1066/5467/6646/5465/9619"
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, list=15%, signal=46%", "2355/5154/56034/80310/2621/183/5159/2335/5155/8877/4921/1956/537
=40%, list=17%, signal=33%", "2296/5054/654/4851/84913/2668/6662/55273/694/6424/3976/5583,
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6", "6837/10025/9443/9282/112950/9439/9412/90390/10001/80306/9862/219541/9477/55090/54
l=23%", "3074/5836/2683/53947/374378/117248/84752/2992/79586/23127/79623/8985/337876/3
324/23704/2316/183/5350/9096/3270/30845/845/477/6548/2697/857/54795/493/6330/79191/48
49%", "3107/3133/5476/3105/3106/6892/3115/3123/3135/972/3122/5311/3113/3134/3119/10134
gnal=36%", "639/3726/7026/10370/5743/4693/1508/3976/6781/5467/8614/6696/7421/2706"
signal=51%", "55599/51639/27288/10081/154007/23451/51690/10992/55285/6635/6637/23450/66
gnal=30%", "9510/79148/7092/5069/4323/4313/649/4327/8754/9507/8751/81792/11174/170692/!
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signal=46%","367/157506/23213/1499/7474/652/6469/8626"
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=79%, list=20%, signal=63%","7057/6556/10392/64127/3123/2213/972/3122/10875/968/50856"
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gs=53%, list=26%, signal=39%","545/54464/23293/10575/65057/54984/10694/6714/8658/167227/5
%, signal=26%","558/301/5587/6810/22925/54209/4929/80310/6649/2308/8013/4313/388/49386
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signal=38%","389/2316/83478/90102/1839/3678/6239/1289/4488/84962/10979/387/94"
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057/5627/7056/5054/5328/2191"
signal=29%","6324/5187/2040/4846/477/6548/5348/5027/286183/493/6330/5349/154043/482/37
, list=28%, signal=35%","3958/7070/1997/975/5621/2633/7805/8934/10385/3783/56940/5795/597
21%, signal=30%","558/1051/23529/4803/54209/4929/1745/4208/7043/26471/2149/7042/4170/49
","444/7057/55214/79073/6517/5350/3270/845/51655/6444/6271/3708/3710/202333/817/6345/
","5563/1017/5579/1111/9212/7443/9031/6790/983"
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, signal=53%","23383/23244/23126/27127/25836/91272/8658/23047/54921/546/5885/79075/1131
st=30%, signal=41%","2033/9575/10847/7994/23522/6872/11143/8520/9913/1387/79969/9862/11
, list=30%, signal=29%","6324/23704/79073/7223/94015/3779/2564/302/3775/309/53373/22821/9
gs=46%, list=19%, signal=37%","558/3624/2621/80149/7292/9173/5621/64127/7805/3123/3586/70
","5980/9100/26073/10714/83932/51455/5425/201973/5424/51514/5427/5111"
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ist=24%, signal=27%","6556/183/1906/477/2771/6548/5166/1910/6560/23682/1203/55647/10312,
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%, list=27%, signal=34%","3597/2059/90/3673/3678/9180/3077/3691/567/11117/729993/7048/36
=45%","311/567/975/10288/3115/3108/3123/972/3122/55080/3113/3119/3111/3117/3109/3127/
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26%, signal=55%","1906/5606/10135/64127/120892/7097/7099/6347/90865/3458/9590/3791/371
ags=74%, list=26%, signal=55%","1906/5606/10135/64127/120892/7097/7099/6347/90865/3458/95
3%, list=20%, signal=55%","860/2737/654/6662/4092/4088/8200/8817/94/7704/4017/3207/392255
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4,"tags=78%, list=28%, signal=56%","347/64127/59341/64581/9655/3965/3553/4938/7291/6850/49
al=48%","7376/54209/4481/158219/19/5468/4023/1066/5467"
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, signal=30%","1793/4739/23529/27185/4803/2316/706/6281/91663/7040/3280/4124/81565/2335
39/2022/7049/3690/3685/3688/57007/23643/1464/10082/4919/942/3676/4804/4920/7852/3547,
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igs=64%, list=13%, signal=55%","57381/4693/22899/1545/8322/1282/25932"
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;nal=49%","9133/994/995/7272/10403/993"
gnal=34%","283/6556/10417/3133/3105/602/2920/2921/64127/5919/3576/1991/6590/6039/1511/
signal=29%","117854/10413/182/3280/4054/2296/8463/7042/4851/4070/2668/144165/4780/2216
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7,4882,"tags=49%, list=27%, signal=36%","57662/1639/1859/246176/25876/146057/57551/324/271
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%, signal=32%","2152/6484/7057/7056/5054/2149/4780/6915"
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ist=24%, signal=66%","7057/5045/4060/7305/1281/6376/375387/25987/5678/10159/8710/2627/23
8940521,4815,"tags=56%, list=27%, signal=41%","83860/10025/6872/170506/9282/26036/6908/56
2%, signal=52%","56548/9469/79586/337876/29940/166012/55454/22856/83539/7358/54480/505
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, signal=43%","8324/7040/64321/4208/7042/23493/144165/1956/28514/652/93649/22943/650/28
587/3490/2/3624/2059/706/8061/6517/7040/196/3779/6446/2720/978/7049/7048/10365/3625/11
502/706/4499/4493/4489/23498/1373/5027/5066/4501/445/7779/5025/4504/7780/7412/57817/6
signal=56%","5394/255374/6741/5976/54464/27257/134353/167227/55149/53981/7884/51692/25
3%, list=21%, signal=27%","7223/302/309/80024/53373/22821/3685/3708/84876/93129/80036/162
85,"tags=48%, list=18%, signal=40%","5587/7040/5159/5155/388121/7010/5156/4067/64127/2321/
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%","7223/302/309/53373/22821/3685/3708/84876/93129/80036/162514/54795/3710/117531/574
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list=10%, signal=36%","143872/183/3356/80005/1906/59/1910/151/1909/387"
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0%","27030/5378/4437/5395/4595/4439/4292/6996/2956/5111/4436"
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gnal=29%","1410/3624/10501/7040/183/64321/10512/1601/978/29948/7042/604/29946/11007/7
st=23%, signal=35%","389/10174/90102/395/6281/7791/9124/7043/28984/6385/29109/4070/6548
"389/10174/90102/395/6281/7791/9124/7043/28984/6385/29109/4070/6548/7481/1901/3693/22
6","84168/1969/26499/23129/9780/2191/3690/7408/3685/1464/10979"
st=39%, signal=42%","4716/4695/4718/4712/4723/4702/4713/4700/4715/4722/4725/4726/4714/4
nal=42%","4716/4695/4718/4712/4723/4702/4713/4700/4715/4722/4725/4726/4714/4705/4731/4
=42%","4716/4695/4718/4712/4723/4702/4713/4700/4715/4722/4725/4726/4714/4705/4731/470
signal=39%","79148/728/7057/1435/146433/1588/5919/59341/1436/719/2185/1240/6352"
%, signal=39%","966/3107/3133/567/3105/89866/3106/374/3115/149111/3123/22872/3135/972/3
:49%","51230/55683/84148/339287/284058/26053/3054/10445/54934/11091/672"
signal=45%","10623/9533/2971/7629/2074/84265/6621/112495/171568/23451/23379/170506/25
40%","90/2022/26508/6615/7042/4851/6591/4488/23493/7048/55273/4487"
=74%, list=30%, signal=52%","4851/2771/3162/5978/6688/2213/6814/3965/5906/3134/11314/2294

, "2934/4627/6840/85477/23380/11034/9535"
2153433238,3135,"tags=64%, list=17%, signal=53%", "8767/51296/64127/4792/7128/3304/7099/330
31%, signal=38%", "1655/10146/3508/5976/317781/9785/79039/10521/10212/64848/56919/91646
22%, signal=34%", "2274/54209/9454/29995/683/6548/10519/3708/55273/5621/493/2633/120892
7%", "3624/183/1601/654/114897/4824/8322/185/3784/5443/2587/1408/56729"
gnal=46%", "404672/80349/2963/5430/246721/2648/4646/6883/27097/6881/2965/8464/81488/68
=32%", "546/4602/10919/3720/79813/55183/1111/1789/6598/4089/9682/57673/2625/1786/79723
nal=45%", "47/55229/80025/54677/80347/11332/3156/79646/53354/79877"
01/7057/2335/633/7052/2162/1634/1281/2312/133584/79625/1832/6698/3713/5266/3848/9806/1
372987,2649,"tags=43%, list=15%, signal=37%", "8851/1032/1019/1164/836/645121/8900/905/1027
934/5592/5350/3270/477/8654/5028/134/5142/817/5025/5997/3759/5144/6588/6833/89/390594
=45%", "7040/5155/7130/4790/1950/80760/8692/3037/3553/3699/3036/2247/160/347365/3373/30
01928601/10609/317761/100507650/56159/10388/27127/50511/27030/10734/7329/256126/4292
01928601/10609/317761/100507650/56159/10388/27127/50511/27030/10734/7329/256126/429
6, signal=38%", "10392/23643/929/64127/81035/85363/7097/64581/7099/1755/5724/8685/51284"
ignal=43%", "7798/367/1956/157506/23213/1499/7474/652/6469/8626/3091/653/25928"
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1%, signal=62%", "567/3115/3108/3123/3122/3113/3119/3111/3117/3109/3127"
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15%, list=18%, signal=37%", "57664/2239/8324/1601/8321/7481/144165/2535/8323/10082/7484/49
10%", "4716/4695/1349/4718/4712/4723/10975/4702/4713/1350/125965/6390/7386/4700/1345/56
9%, signal=60%", "10116/5514/54465/9984/8563/11200/57805/79621/55159/6118/79968"
signal=36%", "301/11135/9124/6282/23022/302/91624/90952/27255/27020/152330/342035/54538
", "1993/1153/2332/170506/23185/55651/25929/10921/9698/79048/64852/23367/7073/26135/57
/83478/51474/23189/81565/4070/857/391/1464/10312/26084/1436/22871/3383/51225/199/2319
", "100507436/9314/196/4853/3592/4851/3105/3140/8751/5817/7805/3123/6688/51225/84868/99
371,"tags=41%, list=30%, signal=29%", "207/6125/8440/26574/8408/5914/8087/10131/1938/9470/3
al=28%", "3074/11343/56898/5321/4758/8309/8877/1373/196463/5322/79887/57016/3073/15105
11031/55062/79971/56548/9469/5587/6810/51429/7045/2316/10981/6517/25825/9367/5125/58
ags=67%, list=20%, signal=54%", "79135/25813/56993/401505/10452/84303/10989/139322/54927/5
ial=32%", "3726/3707/4208/1906/5641/3625/2353/2354/8826/341359/8644/817/3725/3309/91683
/1576/79068/8239/1577/1595/80853/359787/1558/5253/1565/55818/8242/10765/121642/79831/
s=44%, list=26%, signal=33%", "7376/83643/54209/1893/9314/2621/9636/857/3569/7850/5468/112
gs=67%, list=32%, signal=46%", "22828/55209/2074/9400/904/6919/23160/7936/9025/7469/6830/8
85461/1051/4803/54209/8061/6517/7162/183/3356/3678/4208/10769/6446/1959/567/3269/4915
27%, signal=49%", "100131801/51204/1355/285521/1352/51241/6341/79072/100303755/493753/1
2066,0.000689221846708324,6672,"tags=83%, list=37%, signal=52%", "23481/23016/6227/10799/27
, list=27%, signal=42%", "10111/545/10575/65057/51548/170506/10694/51750/5514/8658/5609/31
l=59%", "11176/8467/7528/22893/23378/23512/11335/6839/2146"
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s=36%, list=21%, signal=29%", "3074/4124/4758/2720/4126/3073/4121/1486/2632/57134/2629/55
47%", "5440/51095/5442/7015/10623/9533/5438/5434/548644/5432/171568/55718/27297/5436/1
", "5440/51095/5442/7015/10623/9533/5438/5434/548644/5432/171568/55718/27297/5436/10621
", signal=26%", "9531/1410/8531/80303/7132/10413/677/79073/4055/2022/706/3673/6517/4313/18
ist=21%, signal=26%", "9531/1410/8531/80303/7132/10413/677/79073/4055/2022/706/3673/6517/
%", "6688/306/6814/3684/84106/6813/5724/3689/6850/57126"
8/10627/4643/4651/4627/55930/92922/4629/4641/79784/4635/4636/4642/103910/84952/4634/9
%", "5784/2303/1969/2296/79987/161198/7424/7075/94/54345/85329/2324/10630"

ist=25%, signal=40%", "6387/351/58494/29108/387/6354/8764/7474/284114/199/6351/3676/6348/
33/7048/3106/10288/11213/4067/326/3135/7128/3965/84868/5678/29126"
ignal=31%", "84501/11021/9094/91782/26073/4628/56776/285643/55521/11113/23636/54784/112
6", "8175/23451/51690/11338/51631/55660/55015/6637/25766/51747/6628/10291/6631"
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6", "860/4209/4323/4208/2296/654/1277/8817/2131/338773/652/162466/2261/1749/4665/3636"
, "860/4209/4323/4208/2296/654/1277/8817/2131/338773/652/162466/2261/1749/4665/3636"
, signal=35%", "221908/7517/85459/4591/56890/23636/10432/7514/7840/79959/55835/55755/229
list=36%, signal=46%", "5440/5442/10623/9533/5438/5434/548644/5432/171568/55718/27297/543
ignal=44%", "10468/4061/27120/27122/116372/27123/100463488/100463482/4043/100463498/22
=53%", "23636/137886/1111/5902/4751/6790/64793/3832"
%", "8767/728/54209/3569/11213/64127/245937/3663/5970"
nal=43%", "5360/183/5322/4023/185/348/3990/3931/9388/344/9619/335/4353/336/338/341/5320
%, signal=43%", "5360/183/5322/4023/185/348/3990/3931/9388/344/9619/335/4353/336/338/341,
list=17%, signal=36%", "25937/10413/182/2308/7040/4488/3400/11007/122953/3569/7041/5167/4
;nal=30%", "90780/25942/4801/26155/6418/26053/1111/6598/84656/55677/6871/4089/4802/2625
37%", "2033/9575/10847/55140/7994/23522/80018/6872/57106/11143/26151/79612/340562/852
218/9364/207/8636/11158/284076/5314/285331/49856/164395/27077/57662/55717/55212/1453,
273/81031/56606/9121/6560/6529/51296/6512/64116/57419/26503/6507/8671/28968/6583/912:
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,"2303/90/182/10501/3280/2335/10512/2296/1906/6591/309/2668/10370/1910/6662/1947/1575
nal=25%", "79971/64285/7376/6810/283/54209/7040/7043/8754/9572/2752/3592/654/2149/7042/
%", "8767/7057/7098/3106/7292/4790/11213/958/64127/7805/3659/353514/3586/7097/3135/421
0%, signal=32%", "8767/7057/7098/3106/7292/4790/11213/958/64127/7805/3659/353514/3586/70
:41%, list=20%, signal=33%", "5587/7040/5159/5155/388121/9021/7010/5156/113791/4067/64127/
, "11031/83871/10981/8406/5322/5027/23682/55647/10312/338382/339122/57192/7879/55207"
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39884/3276/10009/10419/222229/79084/53615/200424/80319/80312/26097/2079/1786/29128"
t=22%, signal=47%", "706/1601/654/1958/5978/27122/133/1583/650/1609/653/1585"
6, list=15%, signal=25%", "5587/54209/6556/54210/5054/3140/671/3569/358/6403/284297/29108/!
l=34%", "4502/4499/4493/4489/4780/4501/358/5621/351/4504"
st=11%, signal=45%", "2934/10581/10410/81603/9023/5806/8519/4061/85363/8724/11043"
5343,3700,"tags=64%, list=21%, signal=51%", "6484/3569/6403/6401/2113/387/1991/2526/3676/94
38,"tags=44%, list=28%, signal=31%", "3958/7070/123920/1997/975/5621/5583/4067/2633/7805/89
56%", "285643/54627/4292/9212/9493/24137/3619/9055/29127"
=72%, list=22%, signal=56%", "11027/7305/6688/306/6814/3684/2207/84106/6813/5724/3689/6850
s=73%, list=12%, signal=64%", "654/4851/84913/55273/694/1499/94/652"
st=24%, signal=44%", "5154/4000/7048/7481/6662/5396/1499/7474/652/8646/6608/6469/4609/649
=36%", "117854/10581/10410/9023/6672/9636/8519/3429/81844/4599/3434/11274/7474/3455/11
22%, signal=32%", "3913/861/4803/1959/3691/4915/1960/2668/10370/1910/5339/10397/30812/16
%, list=27%, signal=32%", "5587/7070/5350/3270/2149/845/477/5027/5371/857/5621/6376/4067/94
ignal=34%", "1839/1601/2535/1956/2209/8322/1950/2069/374/3115/3123/685/10618/348/9341/8
:39%, list=25%, signal=29%", "100507436/3133/3592/135250/3105/3106/3916/5817/3135/3965/313
%, signal=49%", "1051/4929/8013/3164/6867/8204/4088"
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38,0.000815276660986688,3102,"tags=34%, list=17%, signal=28%", "2152/2934/1611/55075/355/21.
%", "216/57016/151056/9249/220/339761/157506/1545/10170/8644/54884/57104/195814/126/92

gnal=27%", "183/2564/6542/89874/477/6548/8542/2697/253512/6560/3688/6529/2350/8501/5710/54209/5360/10577/158219/10351/857/19/5468/1950/1066/6256/4792/4035/348/6469/25987/664
 , list=23%, signal=40%", "7057/2621/5054/28984/7010/51129/284/4780/57124/641700/958/79155/
s=33%, list=18%, signal=28%", "64285/55614/1839/9052/7040/183/8412/1956/84632/9961/5329/25
13/10413/183/4208/2296/1906/7042/4851/57493/23493/2735/7049/7048/10370/1901/1848/11214
 , list=6%, signal=39%", "710/966/2/11326/1604"
t=39%, signal=40%", "4716/4695/4718/4712/4723/4702/4713/1350/7386/4700/341947/4715/4722/
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 , "6284/6810/8013/2242/3916/3162/8773/3566/4067/6688/2150/2213/306/6814/3684/284021/39
3%", "5327/5054/5328/5269/1508/114769/834"
1410/301/5154/3673/7040/4313/183/5159/7026/4488/6751/5743/1728/1956/5179/5066/10095/6
46%, list=10%, signal=41%", "2022/7040/7043/7042/7049/7048/4091/4092/4088/10979/25805"
367/8324/2139/64321/9096/2737/7004/4851/7481/6662/3688/50846/2736/1499/6657/28514/747
6, signal=32%", "6649/9429/493869/4846/84203/5742/5743/1728/4780/216/10516/57016/9446/425
14%, signal=33%", "4853/9096/4851/4488/23493/3398/84525/2697/4487/23462/79191/652/2702/9
14, signal=44%", "54496/29104/84193/196074/55870/55621/56950/60487/51409/11105/2091/79091/5520
.0491/444/55214/5351/8985/8974/283208/60681/5033/5352/64175/54583"
9026/2246/311/6282/302/6271/6277/8826"
; ", "860/5744/4488/23314/23601/2736/3199/4088/6469/8994/3727"
9124/23022/79778/4790/5468/27295/9260/8572/9499/5311/1605/129446/64236/5970/84665/77
%", "122961/55140/4682/10539/4728/51654/51218/51750/80224/374291/441250/5980/54901/459
122961/55140/4682/10539/4728/51654/51218/51750/80224/374291/441250/5980/54901/4595/47
38%", "1051/9580/284207/6517/63976/11221/6239/7030/5743/3914/51043/64641/59341/338557/
%", "4502/4499/4493/4489/4501/7779/3309/4504"
s=49%, list=25%, signal=37%", "54209/5187/148022/347/80149/3569/7850/64127/29108/4210/645
524,4496,"tags=49%, list=25%, signal=37%", "54209/5187/148022/347/80149/3569/7850/64127/291
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list=27%, signal=40%", "151987/51366/80764/55818/6830/26036/1487/55611/5531/55693/3720/25
1363293,5799,"tags=72%, list=32%, signal=49%", "5394/100134934/80169/54464/65057/54984/671
63899/55699/91801/55226/90353/26024/54938/55152/51067/55621/80324/54920/60487/51095/
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6, signal=45%", "55968/22924/49856/84687/9857/1453/51104/636/246176/146057/324/9851/5085
50%, list=19%, signal=49%", "1435/7040/3398/146433/3976/10221/3059/4920/8737"
l=43%", "2934/10581/10410/81603/9023/5806/8519/684/4061/85363/8724/11043"
"8013/6793/58494/4478/3037/3553/6279/6280"
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%, list=23%, signal=50%", "30008/2022/5155/23493/4773/348093/2069/4772/652/93649/6469/430
gnal=53%", "55229/80025/80347/11332/79646/53354/79877"
49/493869/84203/5742/5743/1728/9446/4258/2878/348/2876/4504/9536/241/847/9588/4257/11
', "5327/861/7057/6281/5054/5328/302/7123/1522"
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52/53981/642843/23283/11052/51692/81608/4686/11051/22916/1478/10898/1479/79869"
ags=70%, list=19%, signal=57%", "7132/183/28984/4851/650/7133/57589"

, list=17%, signal=66%","8883/5884/91603/90381/11073/4998/990/63967"
st=23%, signal=43%","3280/1745/1746/23500/11221/4851/9948/146433/3400/443/27242/1499/70
169/7171/8736/7140/7170/58/7134/7136/7125/343263/442721/4607/56203"
57%, list=25%, signal=42%","8767/3133/3105/7048/975/1604/7292/3965/64926/10148/6850/7297,
al=32%","7376/283/11343/5321/1373/7148/857/151056/23659/4023/145447/51196/150763/376
'192670/2332/9698/29066/27161/23264/87178/3178/192669/26523/23369/23567/5936/6895/199
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9589/80324/55783/54931/54517/54888/79066/83480/23070/56339/51726/23091/27079/57721/10
6%, list=21%, signal=38%","6484/9314/3688/3569/6403/6387/6401/64116/58494/2113/387/2131/195
'5327/3399/2308/3280/1906/1373/5743/5166/6662/80149/445/4023/6916/8644/81285/7097/286:
t=18%, signal=31%","3280/5350/4846/845/6236/477/5743/401152/10288/2669/28954/6781/9446/
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1656/11176/56154/55729/10419/546/10155/53615/200424/10919/79813/9219/64863/1789/8493,
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ignal=27%","10856/57609/90780/25942/4801/26155/3066/6418/2932/26053/1111/6598/84656/55
signal=41%","301/3707/4208/1514/3569/80301/64127/5291/3665/1234/3661"
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'1655/10146/3508/5976/317781/9785/79039/10521/10212/64848/56919/91646/170506/8886/971
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6%, list=22%, signal=43%","3399/3488/51232/7130/4851/7424/4091/6662/3199/54795/5468/374/40:
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303/1969/2296/161198/7424/7075/94/54345/2324/10630"
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%, list=25%, signal=60%", "5329/3569/3572/84034/1511/3716/10630/51206/6352/22915/50848/37
31%", "2152/6484/7057/7056/5054/2149/4780/6915"
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signal=57%", "9314/4313/4208/7980/10365/5743/4780/445/5339/3037/5311/9655/2185"
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, list=13%, signal=40%", "25937/11030/7040/1601/7043/654/81031/5468/79674/8200/4035/6711/6
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","94015/2564/5348/8542/57101/55107/5349/2555/57348/1192/25932/54102/50636/2569/1193/
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.5%","114907/5327/387758/1906/1373/54541/2908/5176/445/358/1545/2629/8837/54206/9076/2
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=45%, list=20%, signal=36%","4739/1839/2621/183/5155/146433/1942/84632/5621/2209/1950/20
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%, signal=38%","374378/117248/79586/79623/337876/11227/55568/79695/26301/28/2590/55454
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3%, list=20%, signal=51%","79135/25813/56993/401505/10452/84303/10989/139322/54927/55735
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32/9070/5929/8085/58508/84661/79447/11091/22976/23054"
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34/9657/51335/14/79650/79441/200942/11021/9094/7507/84861/22826/63935/92400/11103/229
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26%","143941/10612/51343/5987/867/23295/55743/25831/9781/81545/997/3093/7326/89890/54
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","677/1435/2242/4627/146433/3428/3204/5153/5468/3725/133396/3123/3635/1436/972/652/46
%, list=17%, signal=23%","8742/51429/27185/54209/257364/83547/152503/29116/2308/25976/970
%, list=29%, signal=38%","10477/7332/55585/6872/65264/997/3093/7326/7334/63893/7329/5744
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%, list=17%, signal=34%","8658/5609/54921/3178/25913/11232/10576/63922/1736/2671/7203/55:
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18%, list=23%, signal=37%", "558/2621/3707/10461/1831/604/1942/6387/4254/64127/972/652/305
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ignal=30%", "3831/55083/1639/7802/547/23095/55860/5048/2009/2342/10120/90990/196385/854
5%, signal=75%", "23522/11143/51147/7862/64769/84289/9678/27154/23774"
, list=38%, signal=39%", "10302/54700/6879/9519/2962/387332/129685/2968/6621/83860/6872/69
, signal=26%", "1410/147912/10252/631/1969/1414/7431/8412/7048/10370/4094/2697/161742/21
5, list=23%, signal=51%", "100131801/51204/285521/51241/6341/79072/100303755/493753/116228
5801,0.00169384410483856,5941,"tags=53%, list=33%, signal=36%", "301/183/3356/3269/6751/336
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40%, list=25%, signal=30%", "100507436/3133/3592/135250/3105/3106/3916/5817/3135/3965/3134
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/10577/309/975/347/857/19/54762/5375/114876/6820/950/80765/114879/6646/6342/57655/961
, list=11%, signal=33%", "710/966/2/11326/1604/2213"
, list=5%, signal=63%", "5423/5395/4292/7374/9156/10721/2956/4436"
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367/2295/10461/654/5156/7484/1499/1588/2099/55366/7474/6469/8626/4920/5950/653/3209/5
=28%, list=3%, signal=27%", "8767/6556/10865/5321/3554"
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, signal=65%", "80310/5159/5155/1958/8837/652/3570/8710"
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374197004409,3631,"tags=41%, list=20%, signal=33%", "1051/23645/90993/9709/837/5371/3708/84
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52,"tags=70%, list=33%, signal=47%","201626/5394/22894/90806/81875/56915/22803/54464/79033
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68/5467/5375/338557/241/6809/6342/165140/6279/2173/6280/116362/2938/2169/2946/57834/1
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781338664206,0.00193950933734092,4841,"tags=90%, list=27%, signal=66%","3958/975/3383/396
/10398/25802/5159/1906/9948/3688/5339/51804/4629/11214/5156/8837/7140/5239/58529/825/
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ignal=43%","4502/4499/4493/4489/4501/7779/4504/847/4494"
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414/10791/29109/477/6548/5348/2697/3688/1495/6330/1499/5239/2702/3759/1674/57817/2911
it=23%, signal=28%","25802/2934/2059/51474/9948/6840/85477/130271/11034/2150/6711/11344/
97,1089,"tags=40%, list=6%, signal=38%","301/2303/57381/10769/27286/10519/5743/3162"
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=62%, list=30%, signal=44%","84836/8459/5167/9060/6820/27233/6817/6822/8460/27284/6799/67
tags=62%, list=30%, signal=44%","84836/8459/5167/9060/6820/27233/6817/6822/8460/27284/679
5, list=17%, signal=54%","4926/79677/81620/56852/9212/891/3192/55920/990"
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ags=67%, list=25%, signal=50%","10575/10694/55651/167227/10856/10576/1736/7203/8607/22948
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","10981/4286/4208/2737/9839/967/1910/23682/5167/4254/56999/81285"
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list=12%, signal=33%","55062/55614/57664/26499/23612/53373/8724/11152/285590/57158"
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57,2265,"tags=48%, list=13%, signal=42%","301/861/604/4092/80149/7292/3142/51043/3566/9659
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9%, list=27%, signal=36%", "54209/3356/4846/5027/351/8671/5957/3479/4609/51085/5465/3091/6
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tags=32%, list=12%, signal=29%", "54209/11027/9572/11213/4067/64127/56927/338382/2150/55366
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20%, signal=33%", "7376/51429/5360/183/5322/19/4023/185/348/3990/3931/6646/9388/84879/34
s=73%, list=22%, signal=57%", "860/1435/340419/652/650/4804/4982/147495"
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=17%, signal=58%", "7517/7175/57805/8379/348654/4085/10403"
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39, "tags=63%, list=23%, signal=49%", "100507436/3133/3105/3106/3135/3965/3134/84868/6318/52
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51%", "10575/10694/55651/167227/10856/10576/1736/7203/8607/55135/22948/10574/908"
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9%, list=12%, signal=61%", "2074/9400/4968/24144/51366/56893/55611/23347/2187/7158/78990/5
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, list=22%, signal=44%", "54209/148022/975/3688/19/5468/4023/1066/348/928/7099/9655/2207/9
1459,"tags=82%, list=25%, signal=62%", "10575/10694/10576/1736/7203/55135/22948/10574/908"
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3624/2297/3625/2697/668/6865/1081"
3022/9948/6840/85477/7171/134265/7984/285590/7082/7412/5782/83706/64147"
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%", "7057/54209/5360/23166/4481/8578/4023/81035/23780/348/338328/3990/1401/335/336"
12%", "7057/54209/5360/23166/4481/8578/4023/81035/23780/348/338328/3990/1401/335/336"
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68", "tags=40%, list=23%, signal=31%", "26524/10252/1843/183/11221/7026/57493/1647/857/81848,
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6, list=24%, signal=39%", "2771/5027/140/5028/134/5025/9934/1511/2857/5029/64805/5724/100/5
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s=71%, list=11%, signal=64%", "29980/84083/81620/91603/54962/675/641/26271/51053/8914"
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, "2668/6662/30812/3976/7484/1499/652/6608"
", "22983/60496/83983/57026/129563/5566/84618/3417/1017/283629/1797/5635/79077/2770/48
l=46%", "135228/6678/334/3690/6403/9749/5175/10184/928"
it=25%, signal=62%", "10575/10694/51574/10576/1736/7203/22948/10574/908"
=82%, list=25%, signal=62%", "10575/10694/51574/10576/1736/7203/22948/10574/908"
al=24%", "9531/55062/117854/8767/5587/2308/81603/10769/10475/53373/10392/1634/148022/1
ial=54%", "7040/7076/2149/3162/5468/7099/2896/3552/240/3091"
9%", "677/54209/4000/6517/3779/1906/28984/4851/6548/10370/5743/4780/1263/1958/3162/358
=28%", "11031/558/54209/3673/1601/5054/3077/302/567/284/967/6401/929/6424/1950/120892/2
", list=13%, signal=46%", "301/604/4092/80149/7292/3142/51043/3566/9655"
ist=12%, signal=47%", "975/7292/3569/114548/3566/64127/91543/942/972"
al=24%", "2274/90/4000/8324/7040/183/5159/4208/9096/1906/23493/6444/6548/3688/5339/462
gnal=36%", "90/26508/7042/4851/23493/7048/1942/4091/23462"
3%, signal=36%", "3356/3269/146/3363/151/3357/147/153/1128/148/3352/3274/26538/9038/2653
, "8324/7042/4851/3214/84750/678/3815/81606"
", "55140/1375/64172/653082/64840/204219/1376/54675/80168/7051/55146/6785/7994/165679/
548162754695,0.00260354978833225,3914,"tags=33%, list=22%, signal=26%", "444/55214/254295/5
=28%", "7376/5587/257364/79890/3958/302/3690/3685/857/6386/8301/2042/4043/29763/79772/
%, list=14%, signal=49%", "5592/143872/80005/5743/796/134/10203/5997"
st=41%, signal=49%", "2648/6883/27097/6881/8464/171023/6879/10600/8314/114803/56943/1062
2%, list=41%, signal=49%", "2648/6883/27097/6881/8464/171023/6879/10600/8314/114803/56943/
0%", "50834/259292/259296/259290/50837/50836/50838/50835/54429/259293/259289/50831/259
478/23189/81565/4070/857/391/1464/26084/22871/3383/51225/199/23191/64787/83543/5962/3

6, list=22%, signal=57%", "7040/183/2771/7305/5580/2150/1535/64581/3684/2358/1401/3689/6854%, list=20%, signal=52%", "54209/26471/3569/120892/1075/3553/6348/90865/5336"
list=25%, signal=34%", "83643/5154/5155/6615/8877/6591/5978/4790/27120/27122/8644/376497, =28%, signal=72%", "4052/2615/4054/5045/3685/375387/5678/2627/3696/3694/3326"
=38%", "9531/3920/4015/4534/1134/825/6722/1756/3091"
6/11326/84466/22918/5806/3684/629/721/1401/3689/731/720"
;,"tags=46%, list=27%, signal=34%", "7070/2149/30845/6548/6376/9446/81671/5354/5311/57158/8: 252404699,2776,"tags=48%, list=15%, signal=40%", "64094/3592/1634/967/4641/493/81792/28514 44728,2305,"tags=50%, list=13%, signal=44%", "55729/22880/10155/80312/51535/90378/1786/230: 3%, list=21%, signal=38%", "5159/10161/2149/2840/2151/1281/11214/2150/2828/9002/137735/335 nal=34%", "117854/10581/10410/6672/9636/8519/3429/81844/11274/7474/3455/11140/4939/493 5%", "90/2022/4853/7042/4851/57493/23493/7474/54567/6608/650"
, signal=22%", "9531/7107/79971/25937/7376/4038/5587/6810/10413/283/54209/2316/257364/70 :=11%, signal=48%", "3913/4811/4643/23213/55959/2131"
7,"tags=73%, list=17%, signal=60%", "7057/6556/10392/64127/2213/972/10875/968"
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'tags=60%, list=7%, signal=56%", "996/51433/51529/81620/8697/51434/8452/9787/9700"
60/4481/8542/4023/348/3990/3931/344/3250/3069/335/336/1191/350/338/51599/341/3949/628 /3913/4038/91653/7414/1009/27185/4803/2316/4929/706/10501/2297/334/9314/81565/4313/70 signal=29%", "64285/1839/9052/183/8412/5641/1956/84632/9961/5329/79651/1950/2069/2537/5: ;", "90627/1793/85360/83478/395/57139/79890/143872/79658/7070/6004/57514/4924/54453/800 st=25%, signal=25%", "90627/1793/85360/83478/395/57139/79890/143872/79658/7070/6004/5751 %, signal=42%", "7057/54209/5360/23166/4481/8578/81035/3990/1401"
%, signal=42%", "55693/546/4602/10919/3720/55183/1789/6598/9682/1786/23028/672"
signal=31%", "558/100507436/2621/639/2214/3133/3592/148022/3916/7305/3601/3134/84868/2: 35%", "56155/56159/10388/192670/50511/91646/11022/27030/11144/400629/643376/245711/56 %", "367/654/5156/7484/1499/55366/6469/4920/653/3209/7490/3293"
ignal=45%", "861/7057/6281/5054/302/7123/1522"
4%, signal=48%", "11326/9572/671/80149/6376/133396/145581/2213/2896"
8%", "1601/654/1910/5978/27122/650/653/1585"
%", "4739/2934/83872/123720/54857/116985/57091/9564"
1969/6615/5872/6591/7481/79778/90952/23562/5175/4641/1366/5010/5583/1003/7122/4867/40 5%", "10413/57333/10365/6662/3202/7068/2252/7477/60485/5604/652/6469/3169/54206/9719"
56/2634/602/958/3566/3586/64581/115361/163351"
s=77%, list=20%, signal=62%", "706/80149/857/493/947/2717/3586/140885/9104/5740"
77%, list=20%, signal=62%", "706/80149/857/493/947/2717/3586/140885/9104/5740"
/2303/677/2308/6517/23189/5791/81565/23371/183/2690/858/9021/1959/5872/8412/2771/3625 gs=90%, list=23%, signal=69%", "30008/2022/93649/6469/1491/2852/6648/3815/93145"
44/335/336/350/338/51599/341"
, signal=36%", "5360/6615/6591/1593/4790"
5813/84303/10989/139322/54927/55735/10651"
5813/84303/10989/139322/54927/55735/10651"
gnal=46%", "51116/54460/56945/51373/64951/51023/28973/23107/64965/65993/51650/60488/63 %, signal=46%", "51116/54460/56945/51373/64951/51023/28973/23107/64965/65993/51650/60488: =18%, signal=35%", "57664/2239/8324/1601/8321/7481/144165/2535/8323/10082/7484/4919/848: 0%, signal=30%", "301/311/308/307/5321/302/309/312/8291/8605/341359/91683/306/11199/5748 0%, signal=28%", "27183/2241/4430/55968/85440/29082/5314/23291/9696/80208/283446/1020/79 21%, signal=34%", "53373/22821/3708/358/3710/3709/5311/7226/1259/57192/55283/6263/6261"
10%, signal=31%", "7057/182/90102/395/4323/11170/5054/604/3204/347/8751/94"

al=43%","3913/2303/182/4643/4853/1910/8826/1909/2131/652/5420"
list=13%, signal=43%","3913/2303/182/4643/4853/1910/8826/1909/2131/652/5420"
2%, signal=53%","7040/183/2771/7305/5446/5580/2150/1535/64581/3684/2358/1401/3689/6850/
=26%, signal=62%","6607/23064/22828/22803/29101/80298/57466/6606/7270/10419/54797/51728/
10413/22904/4790/3569/3572/6688/3570/57817/5970/3716/1116/6997/8737/5740/6774/11122/4/
542/477/3688/6529/8501/81855/6507/6583/2055/6520/8140/8864/5997/6582/54716/23428/653/
/23481/55127/27340/27341/10199/65095/88745/51096/134430/55813/79050/9790/10885/55759/
48%, list=17%, signal=40%","2934/22925/7057/28984/57124/3569/641700/6424/958/8644/3135/63/
=20%, signal=30%","4803/26508/1745/2260/1746/4681/4208/654/604/9638/151/5978/10362/2213/
al=35%","389/10174/90102/395/6281/7043/28984/6385/29109/4070/6548/7481/1901/22899/582/
1%, list=18%, signal=26%","84159/8531/3624/5154/367/10046/4323/5159/7098/26471/7042/5872/
5%, signal=39%","7132/7414/1903/1003/7122/23236/3553/3551"
list=16%, signal=39%","7132/7414/1903/1003/7122/23236/3553/3551"
958/5155/2668/7424/3082/6360/10457/6376/2252/7474/652/4908/6348/2247/6352"
=50%, list=16%, signal=42%","54541/4092/3082/1647/857/154043/9647/624/22943/51085/5144/17/
2621/3592/1880/54795/6688/7984/7226/3965/5294/7852/6352/3579/1230/1234"
4399,"tags=49%, list=25%, signal=37%","83478/10252/143872/23189/7042/57493/604/22821/3688/
35273,4459,"tags=90%, list=25%, signal=68%","10575/10694/10576/1736/7203/55135/22948/10574/
signal=47%","3913/182/4643/4853/8826/652/5420"
tags=40%, list=20%, signal=32%","6324/23704/2316/2697/857/54795/6330/3784/3762/3752/3753/
887961597,4459,"tags=75%, list=25%, signal=56%","10575/10694/10576/1736/7203/55135/22948/
1646/2332/11022/9271/56339/4087/25904/4848/9698/79753/29066/4849/27161/55571/23405/23/
2%, signal=30%","54209/6446/1906/30845/6548/3460/3736/1909/126755/6256/154043/482/5580/
","10557/54913/10607/10799/54931/51367/27340/54974/6741/79897/10775/29777/3028/10556/
signal=50%","7107/5027/3569/796/3635/338773/7128/57817/84959/4982"
6%, list=25%, signal=42%","861/3133/3077/3105/51043/3659/29126/10859/3071/8651"
list=13%, signal=51%","3913/182/4643/4853/8826/652/5420"
st=28%, signal=52%","3162/6688/2213/3965/3134/11314/2294/3071/3598/8832"
3/185/348/3931/6646/9619/335/336/55004/341/20/8435"
185/348/3931/6646/9619/335/336/55004/341/20/8435"
183/185/348/3931/6646/9619/335/336/55004/341/20/8435"
1593/8578/1588/348/4504/6696/3290/412/51302/51171/6718/1581/1591"
7/309/975/347/857/19/1880/54762/5375/114876/6820/950/80765/114879/6646/6342/57655/961/
38/57007/9034/1524/7852/3579/1230/1234/1232/10663/51554/2532/1238/3577"
=28%","861/2934/7057/831/6281/4323/5054/302/4627/7123/5621/7850/83596/120892/1522/114/
8/7040/79812/8463/8321/6385/7042/4851/7052/84913/2668/10370/144165/2535/7408/6662/319/
425/339366/2200/79875/4239/81794/8076/2201"
4,4011,"tags=80%, list=22%, signal=62%","30008/2022/5155/23493/4773/4772/93649/1491/2852/6/
=51%","11020/92104/23059/79989/28981/64792/51098/150737/57560/51668"
st=19%, signal=41%","6281/7070/1307/6385/7010/3987/4088/9647/10979/5795/9270/6422/4653"
%","4502/4499/4493/4489/4501/4504"
8%","4502/4499/4493/4489/4501/4504"
2%, list=20%, signal=26%","85450/8531/64114/367/7057/10413/90/4000/4929/90993/9709/3958/
439/367/7414/7223/4929/2308/9314/23189/64321/2737/9351/2697/6662/4092/30851/5829/1495/
gs=37%, list=18%, signal=30%","79971/57664/10413/7040/23189/23500/9839/1956/857/4790/3404/
3%","6788/8767/27185/5155/1601/23129/3077/302/567/284/7049/165904/84525/148022/4015/34/
96,"tags=69%, list=27%, signal=51%","161291/89866/975/55741/10134/123264/9695/56681/55754/
8786543,3871,"tags=67%, list=22%, signal=52%","7057/10252/90993/81848/23213/55959/10253/7/
list=20%, signal=45%","728/7057/1435/146433/5919/59341/1436/719/1240/6352"
4,"tags=78%, list=29%, signal=55%","975/3688/19/5468/4023/1066/928/9655/2207/3689/6850/394

, signal=65%", "6830/9972/29072/55051/7175/11052/22916/55677/1660/10657"
gnal=63%", "9314/7043/10365/4780/4091/4092/445/19"
5%, signal=22%", "7205/55062/2274/7376/860/1051/117854/3399/79365/367/4774/10413/2316/51
nal=28%", "677/54209/4000/2308/6517/3779/355/1906/28984/4851/6548/10370/5743/4780/1263,
, "54209/1435/146433/2629/6376/1436/90865/1191/5595"
25%", "4038/90/7092/649/4681/1906/2737/2735/4188/4091/2736/3199/1499/94/652/54567/8646,
=31%, signal=40%", "5339/358/388697/2629/6337/8692/59341/3037/525/2131/2312/7466/8626/90
s=44%, list=23%, signal=34%", "324/51654/10527/124790/4331/7023/6714/80279/10983/3843/245
9913/6878/56970/55578/117143/23326/6871/8295"
2,3123,"tags=41%, list=17%, signal=34%", "2303/8324/9314/2139/64321/2114/1499/6657/79577/65:
4235666524,1.79414073404524,0.0021438743310726,0.00643241438278262,0.0032172068413679
/80714/1017/79677/23347/7703/7341/6599/55791/6045/6598/23512/1788/3192/157570/10733"
nal=37%", "8531/80303/677/706/6517/5743/5269/358/4638/624/59341/5311/825/54206/92241/59
122/3996/4926/84501/5080/84327/23332/56776/6993/79648/29899/137886/55755/5347/54908/1
835851,3135,"tags=48%, list=17%, signal=40%", "8767/51296/64127/4792/329/7128/3304/7099/578
ial=37%", "90/26508/7042/4851/23493/7048/1942/4091/23462/2702/650"
68/1471/7130/978/567/51646/5806/1265/7077/1509/427/79792/23191/116844/25840/1476/1260
t=34%, signal=44%", "140823/4580/26517/3954/158234/790955/1678/26520/29928/55750/79135/2
126/23332/122060/22919/55755/10615/146909/9793/90417/11004"
signal=62%", "57703/9775/10594/27339/22794/23020/55110/9939"
2%", "57703/9775/10594/27339/22794/23020/55110/9939"
i/100134934/80169/24144/10111/23293/65057/51750/8658/5609/25913/2072/7874/3184/7014/7
6", "1906/3202/1909/4088/3200/5604/3213/6469/6722/6495/1081/8820/7849"
26%", "301/2687/5321/1906/27306/5742/5743/5322/6916/8644/4258/972/9536/3553/241"
signal=26%", "25937/26524/10252/9052/1843/7070/4616/183/5525/11221/7026/57493/9467/5787
al=63%", "10575/10694/51574/10576/1736/7203/55135/22948/10574/908"
63%", "10575/10694/51574/10576/1736/7203/55135/22948/10574/908"
926/10101/137886/9212/6790/9787"
,"7132/4000/2308/8013/90523/183/84676/1906/4851/29995/23493/6548/8654/11214/5468/335
il=41%", "23529/706/7040/3280/1959/4851/3398/146433/443/3569/3572/30812/3976/5583/4067/
4%", "2246/3490/706/1601/6615/9572/654/9023/6591/1593/1958/5978/4790/50846/27120/27122
6", "57599/9098/401447/51720/29086/10987/11315/114803/56943/85015/8078/10869/51035/108
54%", "80324/51095/54931/6832/60493/10922/9238/51654/3028/87178/79072/22868/54802/5500
26,2452,"tags=60%, list=14%, signal=52%", "367/4851/5660/1499/3169/8626"
66/22918/5806/3685/64581/3684/1401/3689/720"
i0%", "147912/84466/284/5467/2047/8837/6469/6495/2247"
i1%", "220/339761/157506/29785/10170/8644/83875/126/340665/1592/56603/59342/125/1381"
gs=70%, list=30%, signal=49%", "50808/4833/10201/54963/347736/29922/79077/4830/790/7371/83
i02/6649/4499/4493/4489/4780/5066/4501/358/5621/351/4504/3931/3552/4017"
ial=47%", "367/23213/7474/652/6469/8626"
3%, list=6%, signal=55%", "55693/1789/6598/9682/1786/23028/672"
igs=58%, list=15%, signal=50%", "5327/3624/1906/4851/1909/2730/2492"
signal=46%", "23481/10412/23195/84261/81887/22884/10969/56342/117246/80135/8568/51018/5
6", "5587/7040/5159/5525/5155/388121/9021/7010/975/5156/113791/4067/64127/23533/9655/23
1557/54913/10607/10799/54931/51367/27340/54974/6741/79897/10775/29777/3028/87178/1055
i2,"tags=33%, list=18%, signal=27%", "79026/5350/3270/30845/845/6236/477/6548/401152/2669/2
i%, signal=32%", "135228/677/7538/2296/4851/4488/3204/5583/54206/8626/130120/7421/2118"
3/284207/23371/4313/183/1906/654/1284/3569/53632/5467/3586/2641/1535/825/2730/847/121
i, list=20%, signal=33%", "301/4208/5027/4067/3586/7474/3965/5291/29124/29126/6352"
ags=41%, list=18%, signal=34%", "9052/7070/9021/9467/9961/857/54625/57732/10019/5580/8692/

l=33%","6788/1051/677/3280/639/3726/5155/6615/7026/9021/23493/4188/10370/1956/133/3976
!,"tags=74%, list=31%, signal=51%","118460/22894/56915/9652/129563/5436/167227/29883/11340
al=32%","56548/9469/2300/54360/79586/81031/337876/10090/1499/29940/166012/2131/3479/3
4%","2274/9454/29995/6548/10519/4776/4773/5621/493/4772/64581/3479/58529/2494/2065/53
list=22%, signal=26%","3487/2308/7040/3356/5155/4837/26471/3269/114897/5208/5166/5027/54
)/4814/4277/735/732/729/730/3002/2999/731/10670/3001/3929/5320"
52,4459,"tags=69%, list=25%, signal=52%","10575/10694/10576/1736/7203/55135/22948/10574/90
gnal=27%","10413/182/4323/3280/1745/1746/4846/7042/4851/23493/604/221336/23555/27255/5
51/257364/30844/857/29108"
:59%","4313/4488/22904/1277/1101/133522/6422/2201/7059/7480"
il=42%","22925/7057/5321/1906/5027/5025/9536/3553/51703/3552/553/5465/8660/6850/6754/2
al=35%","4846/84876/140/1909/796/5957/55366/2492/59350/6786/153/23479/122042/10487/49/
signal=39%","10477/7332/55585/6872/65264/997/3093/7326/7334/63893/57448/118424/27338/!
","11027/3140/10288/353514/10990/11025/11024/79168/10859"
il=27%","23704/9429/477/6548/5348/2697/19/482/3784/8671/376497/3752/3753/3737/6582/864!
signal=59%","3178/25913/7014/79035/6117/6118/3181"
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=34%","57664/2239/8324/2295/1601/8321/9948/7481/144165/2535/8323/10082/7484/4919/8487
=34%","57664/2239/8324/2295/1601/8321/9948/7481/144165/2535/8323/10082/7484/4919/8487
531/55062/83871/3074/4124/8406/26471/302/141/5322/9638/5027/25978/19/1203/4693/643246
414/5768/4758/567/5806/1265/7077/671/4790/1509/1522/79792/1991/6590/23191/8566/116844
'tags=33%, list=14%, signal=29%","9984/1032/2072/8563/51616/23347/2187/7158/11200/57805/78
5, list=19%, signal=25%","11346/25802/2934/51429/389/148170/10174/11135/6281/10344/7043/1!
=22%, signal=41%","8531/26471/857/8837/427/329/57162/9181/9825/8737/8326/11035"
2%","5253/55818/8242/10765/79831/23133/23210/54620/221656/55693/84678/3720/23030/517!
2%","5253/55818/8242/10765/79831/23133/23210/54620/221656/55693/84678/3720/23030/517!
22%, signal=48%","7040/183/683/2771/4780/10516/7305/5446/5580/2150/1535/64581/3684/235!
5","558/860/4774/27185/283/4929/10981/631/3280/4313/59277/5241/1906/7042/4488/10365/26
%, list=19%, signal=47%","7132/4000/2308/90523/84676/4851/5468/493/4088/5025/54206/5997/!
/284207/183/1906/5744/2200/3625/7432/5179/885/133/6781/796/79006/4828/2641/8614/3479/
0%","124540/11338/23210/27161/5436/9716/87178/3178/9775/284131/3187/51663/192669/998!
al=36%","8061/3280/3726/4853/7026/9021/23493/23462/5604/5311/113026/100506013/9394"
, list=12%, signal=47%","546/81620/58525/54962/10926/80174/8317"
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54/9518/29108/1003/652/651/650/222663/653/656"
/54209/9572/3569/351/712/4035/6608/3553/3459/2896/2358"
al=26%","824/7376/5154/283/80271/5321/8871/3356/3707/5155/9021/129303/63874/5337/1269
8%, list=17%, signal=32%","3133/9180/5743/3569/5008/3572/2865/3553/241/5294"
, signal=33%","7376/5360/183/5322/19/4023/185/348/3990/3931/6646/9388/84879/344/9619/33!
%, list=24%, signal=43%","6615/6591/5978/4790/27120/27122/348/650/340895/653/190/10613/11
115344,4199,"tags=45%, list=23%, signal=34%","324/51654/10527/124790/4331/7023/6714/80279/
","182/79191/153572/28514/7477/5311"
34159/8531/3624/5154/367/10046/4323/5159/7098/26471/7042/5872/3625/10370/2697/6662/50
',"23643/81622/7097/7096/6279/6280/6850/10333"
08,"tags=46%, list=13%, signal=40%","114907/183/6442/84676/53632/1605"
=34%","639/5159/23129/4851/23493/7049/6444/144165/161742/4091/11174/2719/652/3340/936.
i%","5360/6615/6591/1593/4790/27010/8566/9104/3458"
L,3714,"tags=60%, list=21%, signal=48%","7057/5045/7481/5743/4060/947/6376/4088/3965/10159,
'5253/55818/8242/10765/79831/23133/23210/54620/221656/55693/84678/3720/54784/23030/51
'53/55818/8242/10765/79831/23133/23210/54620/221656/55693/84678/3720/54784/23030/5178

:17%, signal=51%","147912/284/5467/2047/8837/6469/6495/2247"
ignal=34%","143872/4846/7424/9424/796/5547/134/2865/2702/153/5465/9283/6648/5724/9365/8
ial=51%","58525/11335/254251/10528/84458/10951"
ist=16%, signal=42%","1969/6615/6591/4641/5583/7122/4867/9076/7082/3551"
st=20%, signal=26%","25937/26524/10252/9052/1843/7070/4616/183/11221/7026/57493/9467/57
04,"tags=47%, list=21%, signal=37%","301/861/604/4092/80149/7292/3142/51043/3566/9655/3965
8/4651/3690/7408/3685/3135/7402/57348/1756/3675/10630/8326"
ignal=35%","22925/7057/5321/183/1906/477/5027/3688/6529/8501/134/5025/9536/3553/51703/8
%","19/1066/348/3990/3931/9388/344/9619/335/336/1191"
st=20%, signal=27%","83643/5154/5525/5155/6615/8877/6591/6662/347/5978/4790/27120/27122,
6, signal=29%","57664/2239/8324/2295/1601/8321/9948/7481/144165/2535/2195/8323/10082/74
2/122060/22919/55755/259266/10615/146909/9793/90417/11004"
ignal=57%","3707/3269/5028/23236/2185/2852/5336/5724/5031"
t=22%, signal=34%","1839/1471/25825/81031/9445/5806/1499/3479/4504/23236/9452/6646/2338
, list=21%, signal=53%","27445/1487/9699/23085/8927/23025/10497/8541/1488/9783"
tags=72%, list=28%, signal=52%","4833/10201/54963/347736/29922/4830/790/7371/83549/56474/
","4716/4695/4718/4712/4723/538/4702/4713/1350/125965/7386/201626/4700/341947/4715/47
%, signal=68%","8021/23039/64328/23214/57510/56478/7514/1434/5901"
=46%","183/3356/1906/4638/1909"
,"94015/2564/57101/55107/2555/57348/1192/25932/54102/28962/2569/1193/2557/2742/9022/8
30%","2152/3673/7424/1901/6387/4088/3576/2150/4908"
ignal=31%","183/1906/2771/2668/10392/4883/1956/6271/857/4790/3357/493/2717/64127/185/12
t=25%, signal=37%","1153/79066/51594/1432/2332/170506/23185/79048/8313/10492/55051/2336
52%","728/27202/2357/2358/719/2359/1240"
488/3655/8323/4487"
ial=43%","6879/2962/129685/2068/6917/2968/83860/6872/2071/6908/10629/2958/2967/51616/2
5214/5351/8985/8974/5066/283208/5033/5352/64175/54583"
,"4286/4208/2737/9839/1910/5167/4254/56999/81285"
6, signal=29%","5141/2052/2621/196/4208/54498/7098/1906/1728/4780/2329/5978/5621/5446/29
3%, list=26%, signal=61%","10557/54913/54433/10799/2091/51367/10199/10775/51602/55651/105
al=23%","824/3074/7376/5154/80271/5321/8871/3356/5159/3707/5155/10903/388121/166929/25
8/54829/10312/1277/54757/7020/7475/9313/6786/123041/5465/56975/6522"
6376/713/712/3684/714/22943/1524/718/2043"
=24%, signal=29%","7058/6281/7162/7070/183/1969/3556/1307/6385/7010/79953/4915/27286/85
0/90993/1290/1601/28984/1278/7049/7048/10370/8091/2353/5371/4091/4092/1281/7041/5468/
%","706/387758/8754/5743/351/120892/3309/9451/468"
19%, signal=23%","301/7376/11343/5321/1906/9572/27306/5742/5743/1593/5166/84532/220/157
5121/6634/6628/6632/6636"
L051/3133/3556/7292/114548/9308/3123/942/3965/2207/8140/84868/51176/1649"
ignal=36%","1051/3133/3556/7292/114548/9308/3123/942/3965/2207/8140/84868/51176/1649"
88/10312/54757/9313/6786/123041/5465/56975/6522"
7%, signal=55%","7517/2072/79677/5892/51002/7014/7515/5889/675/5888"
70,"tags=79%, list=28%, signal=57%","4833/10201/54963/347736/29922/4830/790/7371/83549/56
3%","1893/23143/347/6387/351/29108/326/387/8764/7474/284114/199/3676/6364/6352/10563/1
=83%, list=23%, signal=64%","10417/7805/3135/972/7474/7099/51704/5336/8482/10859"
7319592,4968,"tags=40%, list=28%, signal=29%","10847/55140/1375/64172/653082/64840/204219
ignal=35%","3399/3398/3400/4188/4091/3397/4092/4824"
7048/6662/3202/7477/652/6722/9719"
:/1906/2771/1910/6781/134/185/6869/4881"
t=20%, signal=40%","2022/5159/10512/1906/4851/6591/1909/652/5308/7291"

7,5014,"tags=77%, list=28%, signal=55%","64127/59341/64581/3965/3553/4938/7291/6850/4940/8
signal=48%","116039/81031/1499/7483/130497/2131/652/3207/3373"
=36%","100507436/196/3592/3105/3140/8751/5817/3123/84868/29126"
'4/23022/5468/27295/9260/8572/9499/5311/1605/129446/64236/84665/775/3741/11122/4892"
. signal=45%","8021/3841/9972/30000/23633/100101267/3843/3836/9883/9221/3842/8315/26953
%, signal=43%","3624/654/4091/9518/29108/1003/60485/652/651/650/222663/6997/653/656/498
'23481/10412/4839/65008/81887/23560/117246/80135/55651/8886/84365/51018/79707/28585!
ignal=40%","7126/10016/23510/64410/9817/9978/90293/11146/54800/89890/57542/84078/55958
%, signal=42%","183/1601/654/114897/4824/185/5443/2587/1408/56729"
6%","25836/4331/805/6812/2071/6804/11331/8815/84313/2072/27043/2967/1459/3065/6882/16
6324/23704/79073/94015/3779/2564/3775/309/53373/22821/9780/5027/3685/3708/358/57101/8
=46%","3487/3488/8013/26471/9572/3164/51092/1992/54206/6422"
%, list=15%, signal=41%","5136/5141/27115/8654/5153/5142/8622/5151/5139/5137/5144"
5","84446/9344/4140/1020/1859/1453/4139/146057/57551/5261/2931/2011/9024/2534/84630/29
3958/355/2737/1831/1942/7474/652/3965/57864/10018/29124/29126/8737/3091/6352/100/1550
50/5321/54749/5660/1901/6403/81631/4067/51228/4099/375298/2055"
=57%, list=22%, signal=44%","56548/9469/54360/79586/337876/29940/166012/55454/22856/8353
%, signal=44%","3980/5884/7270/146059/29980/84083/3060/81620/91603/54962/675/641/26271/
'5253/55818/8242/10765/79831/23133/23210/54620/221656/55693/84678/3720/23030/51780/96
list=23%, signal=34%","389/10174/90102/395/6281/7043/1906/28984/6385/29109/4070/6548/748
:=13%, signal=27%","2/54209/2214/3133/10769/4853/4851/5045/975/79651/2209/4067/64127/13
signal=43%","4883/3685/4330/30812/4088/387/338773/650/115908/6422/51374/25/63923/4057/1
3592/567/5641/1514/967/1513/1508/351/8572/4043/5618/1520/6440/4036/338/3717"
:=46%, list=27%, signal=34%","7070/2149/5027/857/6376/9446/5025/5311/57158/825/9002/799/28
%","546/4602/10919/3720/79813/55183/1789/6598/9682/57673/1786/79723/6839/23028/672"
51750/7517/25913/84464/7014/9401/641"
al=33%","728/27202/7130/1906/683/23604/64127/3576/972/83700/7060/719"
ignal=52%","5978/27122/1583/1586/650/1609/653/1585/1589/1392/9563"
:=50%, list=24%, signal=38%","10413/831/2621/5054/26471/7010/51129/284/4780/3162/79155/88
list=23%, signal=32%","30008/2022/4323/7040/4208/1906/9780/84525/221662/3479/652/93649/6
tags=42%, list=11%, signal=37%","2152/966/7070/8754/2159/2350/5621/929/8692/338328"
, signal=29%","54209/3356/26471/4846/978/5166/5027/54541/351/8671/5957/51341/3479/4609/
al=49%","7517/25906/7175/81620/8379/55755/348654/891/4085/10403"
5,"tags=59%, list=17%, signal=49%","7517/25906/7175/81620/8379/55755/348654/891/4085/10403
7%, signal=49%","7517/25906/7175/81620/8379/55755/348654/891/4085/10403"
signal=53%","54617/29844/93973/54891/79913/125476/25913/51377/10856/7528/8607/64710/10
al=37%","54209/5641/837/2697/5621/351/773/4035/2213/3479/3383/7099/3676/2358/7412/1001
/706/3673/2621/2242/6591/5743/5179/4330/2350/1277/6781/6256/5467/8614/590/2876/10631/1
33/1906/2771/1910/134/185/6869/525/4881"
51,2414,"tags=42%, list=13%, signal=36%","2690/871/85301/7048/309/6662/1277/5916/6781/5915
, signal=22%","9531/55062/117854/8742/8767/5587/51429/27185/677/54209/257364/83547/1525
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0.00490691855944428,3083,"tags=56%, list=17%, signal=47%","7057/79812/3592/3162/185/54567,
l=45%","183/1601/654/114897/185/3784/5443/2587/1408"
%, signal=39%","58506/23160/9150/51602/6872/6925/55250/27161/57466/6908/23476/6827/9221
"tags=53%, list=28%, signal=39%","58506/23160/9150/51602/6872/6925/55250/27161/57466/6908
gnal=36%","2332/56339/4087/9698/79753/29066/27161/23405/23264/55051/23019/26058/29883
43,"tags=83%, list=25%, signal=63%","4921/1284/1287/1277/1282/84959/1285/1288/6850/780"
17%, signal=34%","183/6542/477/3688/8501/6507/6583/2055/6520/8140/8864/5997/6582/54716,
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al=37%","7376/283/5321/23659/4023/51196/150763/376497/57104/84879/9104/150094/64900/96
il=37%","7376/283/5321/23659/4023/51196/150763/376497/57104/84879/9104/150094/64900/96
%, signal=43%","2074/54623/904/6919/7936/23379/4300/7469/6830/51755/3899/55250/79664/42
ial=38%","51616/6878/6873/8295/6874/6877"
33%","7223/9580/3280/1745/1746/23500/11221/2737/4851/9948/4915/146433/3400/6662/443/31
signal=37%","3270/1906/7042/23493/477/146/54795/133/3784/147/100506013/5997/5144/153/1
st=18%, signal=22%","8767/3958/7070/4208/7006/123920/1997/3105/975/80149/4773/10384/562
l,"tags=33%, list=20%, signal=27%","307/9314/1611/3656/80149/602/114548/140/6737/1545/9166
:33%, signal=67%","7375/57819/10421/25980/24148/10594/27339/26121/11218/9733/10772/1352
26897197471,4815,"tags=52%, list=27%, signal=39%","83860/10025/6872/170506/9282/6908/9039
"728689/6139/6210/6157/8668/79727/6193/1983/1974/285381/7458/6132/6173/6181/6202/9349
ignal=38%","824/30846/4773/3566/9518/92304"
st=21%, signal=33%","27185/2308/2737/4851/2735/2771/3398/55679/7424/7832/1495/1950/6376
%","8531/10413/27185/4803/1839/1435/4323/81565/58191/2335/4208/2690/1906/8877/7042/48
10461/2099/7474/5950/578/4036"
207/6548/5611/2353/133/4023/2766/4792/376497/9451/153/3306/37/7425/1734/6648/65084/44
:9/3956/3624/677/4323/4853/1316/604/3398/3688/3569/602/112616/1880/10312/3087/28514/66
15%, signal=53%","5136/5141/27115/5153/5142/8622/5151/5139/5137/5144"
23411/3981/54840/2074/1161/7014/7515/55775/142"
signal=77%","54386/80169/10111/3178/25913/7014/79035/6117/6118/3181"
:2/9314/3280/64321/4208/4853/4170/5396/3199/1499/64641/28514/4855/652/8643/10660/5660
5615/6591/340419/3202/4487/6781/7477"
al=43%","10609/56159/10388/192670/27030/10734/388649/56154/10919/7917/256126/9319/588
8878/5322/3916/2512/120892/4689/4688/1393/2495/84557"
al=45%","57343/359787/5253/9869/23133/1017/9646/7175/55729/22880/10155/25942/80312/51
0538979093589862,4312,"tags=64%, list=24%, signal=48%","51594/79048/9775/4116/22794/3182/
:32%","161882/6667/4084/23186/23013/56980/5926/7023/1487/56998/221895/3065/57649/9611
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6, signal=37%","161291/57088/57194/19/23120/5205/5359/81671/148229/57205/84879/79895/96
1%, signal=22%","824/7057/4929/706/4208/64856/477/5179/1910/2701/4862/116372/796/6869/5
%","10981/4286/4208/2737/9839/967/1910/23682/5167/4254/4935/56999/81285/1638/10018/10
%","301/8767/6778/7292/3142/3566/9655/246778/51176/5971/84766"
3801/7414/3693/1545/1495/5271/7060/6722/29119/1832/3815"
l=28%","2246/56034/283/6556/9052/2621/183/5155/2690/2013/7098/28984/7042/284/7048/748
%, signal=26%","5327/85360/3624/367/4488/3625/7432/8654/10370/10519/1910/6662/151056/50
:26%","3074/5587/53947/30815/4758/2720/285362/166929/259230/8877/5660/10351/5027/3073,
gnal=43%","54209/29116/4481/302/3162/348/338328/26119/4043/3990/57552/6646/9388/344/33
signal=35%","824/1051/56034/80310/4313/1307/1290/1278/4915/1956/445/1281/5156/1277/128
signal=47%","6615/6591/4790/157506/8644/171425/3458"
54%, list=31%, signal=37%","2840/57007/9034/1524/1240/7852/3579/1230/1234/1232/10663/5155
6","2840/57007/9034/1524/1240/7852/3579/1230/1234/1232/10663/51554/1238/3577"
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6, signal=41%","3624/1435/7040/3398/146433/3976/714/10221/3059/4920/8737"
signal=58%","5321/151056/8605/23659/3990/10908/375775/374569"
s=60%, list=13%, signal=52%","5159/1958/2719/130497/6469/4609"
3280/2737/1959/10370/3198/57007/51804/10312/5205/1499/6507/3200/7020/2047/104/2131/99
signal=19%","6324/2040/3775/477/80024/6548/53373/5348/6529/54795/57419/493/6330/6337/5
list=28%, signal=32%","6517/81031/56606/6515/55314/358/26503/154091/6527/144195/200010/6
33/4286/4208/2737/6591/9839/967/1910/23682/1896/5167/129880/4254/3257/4935/56999/8934
:20%, signal=28%","677/54209/4000/6517/3779/1906/28984/4851/6548/10370/5743/4780/1263/19

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;=39%, list=12%, signal=34%","374378/117248/79623/11227/55568/79695/2590"
31/54587/1969/117583/54532/5872/5912/2697/79778/51421/7408/90952/57125/23562/1366/501
074/3073/8692/51172/4668/3373/57214/6677/2760/4669"
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9%, signal=38%","9429/2697/51296/6890/6892/6891/376497/64849/81034/6563/84976/215/1025
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,"tags=63%, list=22%, signal=49%","6810/3133/148022/7305/23586/6688/2150/3684/5724/3689/71
;=32%, list=18%, signal=26%","23704/5350/845/6236/477/401152/857/8501/2669/28954/9446/817
4038/728/2239/3556/8321/10082/351/6386/145581/26280/22871/7474/11141/22943"
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246/3490/9261/7057/100507436/3316/4846/5743/11080/51278/3162/6387/162514/929/55107/3
5","824/30846/4773/3566/9518/8837/92304"
5548/9469/10090/8459/4166/166012/9956/9957/6820/3340/27233/9394/9435/83539/6817/50515
39%","4716/4695/4718/4712/4723/4702/4713/1350/7386/4700/341947/4715/4722/4725/9167/47
,"4124/4121/57134/55741/4125/23324/4122/11253/9695/4123"
'800/2934/51429/7223/79083/4643/91663/2995/2037/57477/4627/9948/7171/130271/8826/1121
41/1969/5744/27115/196883/5142/8622/5151/109/5144"
7,3171,"tags=44%, list=18%, signal=36%","5350/2771/146/151/11214/493/5142/147/5144/153/1812
al=33%","2564/8542/6560/6529/57101/55107/6507/2555/50636/2569/1193/2557/2742/84561/80
4466/51804/6608/7060/55909/6495/9270"
2274/9510/7010/23493/7049/23462/6722/5950/2280"
209/10226/5468/5167/4023/57104/3553/123/5465"
,"list=13%, signal=37%","301/8767/7292/114548/64332/3142/3566/942/9655"
,"6556/83547/10581/10410/3920/388/11342/302/309/5337/3140/3916/967/25978/9741/23555/23
,"list=20%, signal=25%","23704/7057/8682/5350/845/6236/477/401152/857/8501/2669/28954/516
212,"tags=35%, list=18%, signal=29%","64285/1839/9052/183/8412/1956/84632/9961/5329/79651/
90627/1793/85360/83478/395/79890/143872/79658/7070/6004/57514/54453/80005/93663/5488
l=56%","5429/5980/10714/51455/5425/201973/5427"
6419/8815/114821/79725/6598/7644/81931"
al=35%","824/26471/7042/4170/1728/2353/1958/54541/5978/7305/5621/1499/134/7020/387/712
47%, list=24%, signal=36%","83478/10252/143872/23189/7042/57493/604/22821/3688/81848/549
7158/836/79184/1161/7520/64710/2625/675/641/7516/595/5888/4436"
gnal=49%","84168/7078/7076/7077/8301/4035/4155/6774"
gnal=35%","183/1906/2771/1910/134/185/6869/4881"
627/4627/4629/79784/4635/4636/103910/4634/4620/8735/4626/4622/4619/4632/4625"
ignal=52%","301/22925/283/185/4035/553/5538"
t=27%, signal=51%","7376/338328/344/335/5406/350/51099"
"1051/3624/283/4323/4313/4327/7130/2296/5806/3625/668/1495/2069/4254/2099"
7976349329,0.00629635521991696,3125,"tags=60%, list=17%, signal=50%","10492/3184/10642/490
7/8553/3280/4286/196/6615/9572/6591/84913/5468/6943/6886/344018/406/4609/430"
11%","3801/7414/1009/654/4092/5339/1499/10979/1003/80139/28513/83700/1004/1016/7082/59
17%, signal=20%","25802/2934/51429/2059/148170/11135/10344/91663/23189/23500/93663/684
6, signal=43%","1984/1937/728689/143244/8668/54516/1983/1974/7458/9669/8667/10480/1981/4
3%, signal=33%","966/2239/7070/51299/10392/1942/2350/27255/5621/929/10082/64127/8692/27
5%, signal=37%","5350/4846/477/6548/857/133/493/4635/817/4634/153"
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ignal=30%","2246/51474/9023/10577/158219/8542/1593/19/8578/351/2629/9420/1066/6256/546
,"3913/1959/3691/4915/5339/10397/163175/57716/1605/400746/79628/9639/4665/4653/2065"

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ist=19%, signal=59%","4851/857/81035/3576/4855/93649/3553/335"
, signal=49%","29116/302/5045/7805/151636/348"
:=21%, signal=42%","183/1601/654/114897/185/5443/2587/1408"
st=11%, signal=35%","7057/4790/11213/64127/353514/3586/4210"
;nal=50%","6237/54453/51666/55273/133/947/5906"
=40%","4240/311/54209/5360"
%","6615/6591/1593/4790"
7%, signal=59%","2297/6662/30812/652/4609/5979/186/5076"
=25%, list=20%, signal=20%","6556/8273/81031/56606/80024/6548/9121/253512/6560/6529/5129
6, list=20%, signal=49%","54209/1435/5153/7097/1436/7099/81501/1796"
8,3671,"tags=62%, list=20%, signal=49%","54209/1435/5153/7097/1436/7099/81501/1796"
.09/10392/114548/64127/7097/130120"
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:ags=83%, list=24%, signal=63%","7057/5045/4060/7305/6376/25987/10159/8710/2627/23607"
, list=18%, signal=66%","90102/7040/28984/11117/6662/4088/1605/23187"
signal=17%","79901/2059/389/2316/51474/9429/2683/4643/3775/4627/85477/2317/2028/151056
,"23291/22924/1639/5048/146057/324/23122/4926/23332/22919/9793/81930/90417/11004"
, list=27%, signal=51%","4488/6662/4487/8200/6469/3091/7849/3209/5076"
"tags=54%, list=10%, signal=48%","4052/90/2022/8425/7049/7048/94"
90955/79135/25813/57143/10939/84303/10989/139322/54927/55735"
3%","57728/112752/55764/79809/11020/92104/23059/9742/57539/79989/28981/64792/51098/15
4%","2274/9510/2022/7042/4851/7010/57493/23493/7049/1901/23462"
74/388697/7062/2312/11187/1824/1832/388698/6698/1041/3713/126638/6703/5266/3848/35313
al=34%","11343/2052/5321/5742/5743/8605/1545/29785/6916/8644/2876/4051/240/113612/574
l,"tags=44%, list=26%, signal=33%","54209/1906/30845/6548/3460/3736/1909/126755/154043/482
signal=40%","5360/183/5322/4023/185/348/3990/3931/9388/344/9619/335/4353/336/338/341/53
45%","4716/4695/4718/4712/4723/4702/4713/4700/9131/4715/4722/4725/4726/4714/4705/4731
"824/1051/56034/80310/4313/1307/1290/1906/1278/1373/4915/10365/1728/1956/445/5339/128
93/395/30011/57514/57088/8871/6451/8754/9467/6450/26578/84632/7408/392/5359/134265/87
/57819/79066/51690/51574/64852/10594/27258/9128/51691/9733/25804"
=26%","9282/161882/4087/9421/6667/8861/4084/23186/23013/53635/25929/4331/112950/5698
gnal=25%","23704/54209/2316/3356/3779/4846/845/7432/967/3688/857/5621/3736/126755/134,
gnal=36%","4716/4695/4718/2819/4712/4723/4702/4713/1350/6390/2108/7386/4700/2820/7975:
nal=36%","3270/1906/7042/23493/477/146/54795/133/3784/147/100506013/5997/5144/153/100,
09/7043/6591/6376/713/712/3684/714/22943/1524/6833/9922/718"
signal=22%","9531/64285/64114/26524/257364/7040/5525/1601/3592/2149/6672/29969/284/36:
!9%, signal=50%","9696/285331/84455/56623/2622/55704/2932"
, list=30%, signal=63%","55968/636/324/50855/11190/23636/2932/137886/55722"
nal=36%","23122/3996/4926/84501/5080/84327/23332/56776/6993/79648/29899/137886/55755/5:
=18%, signal=21%","6324/4038/5587/64764/27185/4803/2316/10501/29116/9314/3280/23189/81:
t=11%, signal=33%","29980/79184/1111/90381/5347/641/51514/983/11073/672/63967"
6","558/10461/1588/2099/7474/8626/5950/578/4036"
l32/6173/5682/8667/689/6228/6142/6235/1981/6227/6135/6231/6143/6169/8087/1938/6128/63:
6","25959/2621/2242/6591/5179/4330/2350/3162/1277/4023/6256/10631/1030/6722/7421/1591/
l=42%","3074/4758/3073/2629/2717/5580"
l80,"tags=72%, list=31%, signal=50%","9400/7936/9025/7469/51574/165918/6827/10915/7428/259
nal=29%","6788/8767/23129/3077/302/567/148022/857/6737/351/120892/51339/25805/151636/4
%","9843/79901/7223/6556/3077/567/392/2512/64116/6948/79689/7779/55640/91252/7225/573
13/79867/27077/283232/9742/146057/51259/9657/56123/56121/80184/10210/5108/1070/23322/

gs=48%, list=22%, signal=38%", "6281/7070/1307/6385/7010/3987/4088/9647/10979/5795/9270/64
tags=52%, list=19%, signal=42%", "728/7040/5743/57447/3569/23213/1545/3572/9451/55959/468/
al=66%", "254394/545/5395/4595/4292/84515/2956/5111/4436"
3%, signal=32%", "301/861/2737/604/4092/80149/7292/3142/51043/3566/3659/972/652/441478/9
, "4716/4695/4718/2819/4712/4723/4967/5162/10975/4702/4713/6390/594/2108/124056/7386/4
al=36%", "2274/9454/29995/6548/10519/4776/4773/5621/493/4772/64581/3479/58529/2065/533
, "858/4773/5339/2876/3479/6608/58/55909/6495/131377/89/6261/1827/9456/56203/4618/7480
=17%, signal=41%", "4926/5080/23332/6993/79648/29899/137886/55755/5347/54908/1058/4085/
69066,4882,"tags=55%, list=27%, signal=40%", "57662/1859/25876/146057/57551/324/27124/2312:
ist=13%, signal=37%", "10865/3554/567/3105/975/1604/7292/3569/114548/91543/3553"
al=47%", "7481/7474/652/6608/22943/650"
%", "301/7376/2687/7132/11343/2052/56898/5321/8013/8309/1906/27306/5742/5743/51084/532
53%", "493869/4258/2878/2876/9536/241/9588/4257/1193/373156/2938/2879/2946/4259/2950"
1/91893/29063/51106/115939/63899/55226/285367/196074/54433/10436/2091/4839/117246/27:
%", "8767/7098/148022/130132/857/11213/64127/81035/23586/3434/4792/64135/5899/6520/366
%, signal=32%", "3958/1831/604/1942/5027/4067/3586/972/7474/652/3965/57864/29124/29126/
1/4170/92196/8717/8737/598"
5%, list=20%, signal=37%", "83871/2735/5396/1495/2121/2719/64927/3340/6608/6469/3169/2285
, signal=27%", "3133/9180/5743/1910/3569/5008/114548/3572/134/2213/2865/9536/3553/241"
list=18%, signal=24%", "23704/5350/845/6236/477/401152/857/8501/2669/28954/9446/817/7779/
0/24144/3980/2547/79840/3146/7515/3978/5888/7153"
32%, signal=46%", "55209/4297/54093/2145/30827/9070/9869/5929/9757/23067/84444/6419/8085
'8800/5195/8799/10478/1610/57506/8443/84896/84188/55825/5189/4077/55670/54332/3156/11
800/5195/8799/10478/1610/57506/8443/84896/84188/55825/5189/4077/55670/54332/3156/110
1547/11176/10013/5931/57504/3065/53615/9112/57459/1810/25942/3066/56916/64426/9219/10
2013/5027/4638/5376"
al=34%", "824/117854/10581/7098/3428/3659/4332/4938"
6, list=22%, signal=54%", "9869/1017/7175/55729/22880/10155/25942/51535/1786"
59%, list=22%, signal=54%", "9869/1017/7175/55729/22880/10155/25942/51535/1786"
it=22%, signal=54%", "9869/1017/7175/55729/22880/10155/25942/51535/1786"
al=41%", "10865/4851/4092/80149/3569/64332/51043/64581/10758/23765/3570/3558/6774/8480
;4209/4313/5641/837/2697/5621/351/773/4035/2213/3479/3383/7099/3676/2358/7412/10018/48
1%, signal=50%", "7040/5155/6662/5978/4776/5468/5467/652/6722/5970/5465/2627"
6, list=21%, signal=43%", "5978/4790/27122/8644/650/653"
3%, signal=37%", "9531/824/183/26471/1906/3592/23493/4780/80149/3162/5468/8837/817/3479/
7%, signal=38%", "134/5580/57104/3553/344/5465/335/7291/8660/336/215/13/51099/440503"
signal=35%", "687/5587/135228/10413/677/7538/4853/6591/374/2252/3037/8626/130120/7421"
, "7414/23189/1969/6239/29984/123720/9459/3688/1901/84962/23380/51196/11344/29780/512:
4,"tags=52%, list=29%, signal=37%", "3280/183/2690/2149/4851/3569/1545/3586/3588/3587/3570/
'/5806/5322/5919/6688/64581/1991/1511/7099/23765/57817/6279/6280/1524/6283/23406/5336,
%, signal=27%", "1198/8999/1859/1024/23049/8491/545/51265/1453/984/657/7786/1454/9113/39
19%, signal=23%", "9531/467/64764/7057/23645/90993/9709/3316/871/23471/27129/11080/4780/
signal=31%", "6324/23704/2316/845/9948/2697/857/6330/3784/3753/2702/3759"
20%, signal=36%", "5350/477/857/54795/6781/134/5142/817/2702/3759/5144/29119/1824/1832/7
;5770/285331/55763/7251/23265/5898/11064/116986/57448/23636/283489/54536/9493/9928/55
%", "11343/5321/1373/5322/151056/8605/23659/4023/145447/338328/57104/3990/23236/10908/
ags=48%, list=16%, signal=40%", "367/1435/1969/5241/4488/5371/374/2099/7474/7421/6356"
.1190/1387/10276/55693/1965/9094/7507/8704/4852/1196/1032/2547/2072/10856/1258/7158/70
=82%, list=26%, signal=61%", "11170/7305/5621/351/134/348/1524/2043/25"
06/1910/3708/358"

ags=60%, list=19%, signal=49%","2735/1950/6608/6469/2247/9283"
33/3105/3140/3123/3122/1794/54869"
405/167227/27044/192669/57510/1977/26523/6895/1660"
7161/23405/167227/27044/192669/57510/1977/26523/6895/1660"
8/301/3707/4208/10461/355/1831/5027/3569/1880/10312/4254/4067/10019/5142/972/7128/837
gnal=32%","631/81565/7431/286077/5339/4534/7062/3861/3881/3885/2055/6469/81493/1674/10
%, signal=29%","3624/1906/3625/2697/26056/5978/5008/3976/134/4828/338557/6865/5211/3553
25%, signal=35%","301/3707/4208/23601/4254/64127/5291/3665/1234/5728/350/23657"
%, signal=41%","22925/5321/1906/5027/5025/9536/3553/51703/3552/553/6754/2180/2170"
%, signal=32%","55031/9960/392188/84640/10600/100288520/83844/8239/8314/7375/158880/38
07/6442/3586/1605/847/89"
%","79441/85459/55142/23354/54801/115106/7283/3192/93323"
ial=32%","3673/2335/6591/7424/1464/6386/22801/9270/64805"
al=26%","301/7376/8013/1601/9572/654/5743/5166/1910/6662/1958/57016/857/5978/27120/157
%, list=39%, signal=58%","84193/55870/11105/4297/54093/30827/9070/5929/9757/23067/6419/80
511628698,4800,"tags=75%, list=27%, signal=55%","2668/3976/7484/1499/652/6608/7849/6299/50
it=18%, signal=41%","301/11135/9124/6282/302/1266/3875/11187/29091"
), signal=25%","9531/79971/7376/5587/6810/283/54209/2316/7040/161291/2621/2040/7043/8754
%, list=10%, signal=21%","11200/5356/1027/328/51692/55626/79960/10197/27085/5591/835/7027
14,3232,"tags=34%, list=18%, signal=28%","3958/7070/1997/5621/2633/7805/10385/2213/56940/57
50%","1601/654/5978/27122/650/653/1585"
l=36%","50511/9025/55818/9271/83983/90780/6732/3148"
38/54209/54210/858/4846/7431/5660/2697/5028/3572/9332/493/4067/3784/28514/5604/3709/27
048/3106/10288/326/3135"
=19%, signal=45%","1051/3398/3202/80139/6608/2066/5618/2247/3664/3091"
32/4218/92104/8636/23059/11158/5314/200894/9696/285331/49856/2302/79867/582/27077/283
ial=34%","2770/4926/91782/7175/126731/29899/23636/79187/79598/8480/79866/5347/84722/10
list=24%, signal=38%","6615/6591/5978/4790/27120/27122/348/650/340895/653/190/10613/1116
gnal=27%","6324/3399/5350/3398/3400/4188/4091/3397/4092/3708/857/4824/817/7779/29763/5
l%","216/4245/1486/5973/80896/1116/5016"
il=23%","558/860/283/4929/631/3280/4313/59277/5241/1906/7042/4488/10365/26468/2697/1910
44,3531,"tags=60%, list=20%, signal=48%","182/3280/10512/1906/10370/1909/652/5308/7291"
4,3531,"tags=60%, list=20%, signal=48%","182/3280/10512/1906/10370/1909/652/5308/7291"
,"55614/29116/7040/302/5045/5641/7805/151636/348"
7214,"tags=66%, list=40%, signal=39%","6883/6881/10302/6879/9519/2962/387332/129685/2968/1
%, list=20%, signal=58%","6484/6403/6401/1991/2526/3676/9435/5724"
i804/23025/10497/8541/1488"
ags=38%, list=9%, signal=34%","3673/3356/56925/6387/3736/55107/796/134/2047"
signal=43%","1111/6598/4089/2625/672"
%, signal=30%","55062/55614/57664/5321/26499/23612/57732/129880/90203/8724/11152/28559
i,4459,"tags=75%, list=25%, signal=56%","10575/10694/10576/1736/7203/55135/22948/10574/908'
.468/8314/131474/9026/89941/64112/10948/26517/9131/10425/9927/292/158234/637/7332/104
',"5154/4124/3488/4054/5241/7043/84525/3202/3976/6943/652/93649/3169/54206/9394/2324/1
911/9211/348/22871/133584"
06/7432/4883/2697/5066/857/358/51043/353/134/6869/3783/6776/6583/1535/4881/10758/4939,
:18%, signal=37%","6517/81031/56606/6515/154091/6527/144195/200010/6514"
95/3384/7430/9051/6404/10211/388325"
/4478/8395/3384/7430/9051/6404/10211/388325"
%","6742/3980/11232/64863/92667/201973/2021/1763/6240"
%","5360/8542/348/3990/3931/344/3250/3069/335/336/1191/350/338/341/6289/5444"

gnal=40%","1601/3339/8301/5649/4035/348/26119/4043/22943/1401/335/336/160/1191/338"
gs=36%, list=7%, signal=34%","5327/2149/4915/27020"
=23%, signal=49%","10288/4067/3135/945/5678/387837/10859"
signal=47%","147912/84466/284/5467/2047/8837/6495/2247"
50%","10413/22904/4790/3569/3572/6688/3570/57817/5970/3716/6997/8737/5740/6774/11122/
2/54757/9313/84957/6786/123041/9622/5465/56975/6522/64065/25818/3694"
525/4641/27295/9260/8572/254102/83700/64236/56940/92521/83715/342527"
324/64321/7042/4851/3214/2131/84750/7704/678/6423/4674/3815/10263/2124"
531/80303/7098/358/59341/23308/54206/9076/92241/9181/553"
%, list=20%, signal=22%","9429/8273/6542/89874/9121/253512/6529/8501/6512/81855/28965/65
6, list=18%, signal=48%","728/27202/2357/2358/719/2359/1240"
821037053160104,2990,"tags=58%, list=17%, signal=49%","51296/329/7128/3304/7099/57864/330:
signal=36%","5350/2771/146/151/11214/493/5142/3784/147/5997/5144/153/1812"
,"3913/3691/4915/5339/10397/163175/57716/1605/400746/79628/9639"
7/706/64856/1910/2701/796/6869/5025/5649/7060"
%, signal=27%","6517/8013/8682/1906/81031/56606/6515/55314/4780/358/1909/5167/26503/546
s=38%, list=13%, signal=33%","6324/23704/9948/2697/6330/3784/3762/3752/3753/2702"
=51%","706/2564/2555/2557/2554/2566/2559/2567"
=32%, list=19%, signal=26%","25802/2934/2059/51474/6840/85477/130271/6711/11344/23075/596
"tags=57%, list=31%, signal=40%","2074/9400/54623/904/23160/7936/56943/9150/9025/7469/683
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'tags=71%, list=30%, signal=50%","50808/4833/10201/54963/347736/29922/4830/790/7371/83549,
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3/4038/91653/7414/1009/27185/4803/4929/10501/2297/334/81565/7070/1969/2335/10512/4853
!%, signal=51%","5027/79792/64581/6590/130120/6280/3458/598/6850/84659/4843/5068/4057/5:
al=31%","3074/53947/30815/4758/2720/285362/3073/2629/2717/5580/51228/8705/81849/7357/:
l=38%","677/9021/133/84870/7477/3586/51176/6768/6692/653"
signal=26%","558/301/80310/8013/388/1906/8877/6778/10365/1728/4780/3082/3569/358/1545/
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31/6820/3340/22856/27233/6817/2132/9953/6822/8460/27284/6799/6783"
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/5836/355/7098/197259/857/8837/329/57162/9181/9825/8737/8326/11035"
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s=46%, list=23%, signal=36%","9531/3624/2139/8406/2260/355/6591/4170/2668/3685/1495/2537/
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list=19%, signal=41%","4052/4681/2200/375387/2201"
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27%, signal=41%","54209/3356/26471/5027/351/8671/3479/4609/51085/5465/3091/65018/89/34:
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46%, list=19%, signal=38%","677/7538/1601/2296/6591/1956/6662/3397/8826/1277/8837/5151/54
6","6324/23704/2316/5592/3779/6446/6236/5348/3708/857/2669/28954/126755/493/6330/5349/
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23%, signal=34%","183/1906/2771/2668/10392/4883/6271/3357/64127/185/348/2230/1535/3553/

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%","183/477/6548/6337/482/6507/3552/483"
.1331,"tags=56%, list=7%, signal=52%","996/51433/51529/81620/8697/51434/8452/9787/9700"
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l=34%","2303/9314/2139/652/22943/3207/6423"
list=14%, signal=21%","4038/10413/2316/83478/10501/29116/3280/23189/7070/10512/1601/567/
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signal=44%","23633/3836/57510/5901/3838/3837"
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%, list=17%, signal=51%","167227/29883/11340/51010/23404/57472/5393/115024"
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3%, signal=35%","861/10413/4208/1906/4851/23493/2735/7049/7048/10370/60485/3479/5997/96
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, signal=33%","140823/7755/9026/89941/64112/4580/26517/9927/808/292/3954/158234/637/572
ist=14%, signal=34%","558/2621/2214/3133/3592/148022/3916/7305/3601/3134"
6","2615/7043/8321/7042/7049/7048/7481/2535"
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, signal=27%","710/966/2/54209/3075/11326/1604/64127/2213/3553/5650/2627/10563/718"
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%","7040/2720/1486/3425/8692/10894/60495/2247/1116/5016/3373/2799/57214/6677/4669/342
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9844/93973/54891/79913/125476/51377/10856/7528/8607/10445/86"
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%, signal=37%", "3270/845/477/2697/857/3736/79191/482/817/2702/5144/2706/10345/775/57165
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gs=44%, list=15%, signal=37%", "824/826/11131/825/10753/92291/726"
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", "4846/2771/4883/1910/84876/140/1909/796/10886/5957/55366/2492/59350/6786/153/23479/12
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23%, signal=42%", "23529/7040/3280/1959/4851/3398/146433/443/3572/3976/7097/4099/1605/64
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'861/10413/4208/1906/4851/23493/2735/7049/7048/10370/1848/60485/3479/32/5997/9686/578:
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=40%","3624/3625/2697/668/6865"
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%","55062/5587/467/2308/1611/2621/3920/355/2752/3625/10634/3428/4780/5166/80149/64324
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gs=34%, list=18%, signal=28%","6810/54209/3958/1969/2037/10519/8878/1956/3688/391/5621/493%, signal=24%","1793/57139/79890/4924/54453/80005/23348/57480/29984/152273/163259/94610201/54963/347736/29922/4830/7371/83549/56474/1503"
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=24%","8767/3958/7070/7006/1997/3105/975/80149/10384/5621/64332/27242/11118/3115/2633.2%, signal=35%","4323/1745/1746/23493/604/221336/23555/51162/23462/28514/4792/51341/54"tags=75%, list=28%, signal=54%","3162/6688/2213/3965/1524/11314/2294/3598/8832"
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s, signal=47%","2668/3976/7484/1499/652/6608/7849/6299/5076/342184"
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013/2242/3162/10397/8773/5359/3566/4067/85480/284021/3965/5169/3937/64109/2268/6813/!%, signal=27%","10142/4926/6904/4137/8851/23332/11075/2288/1027/157922/122060/22919/557:ags=69%, list=41%, signal=41%","10440/3329/51555/100287932/84134/9804/51025/5190/140823/183/6542/4915/477/2697/5027/3688/6529/8501/6512/81855/26503/134/6507/6583/57030/2055/9/283254/57600/9851/64743/23265/50855/8045/26005/284001/23177/80184/9043/117178/5144:al=29%","1051/22925/5321/183/1906/5027/3688/6529/5025/468/9536/3553/3552/553/5724/524al=34%","3958/1831/1942/7474/652/3965/57864/29124/29126/3091/6352/100/155038/11035/8176","7376/1051/2303/56034/63976/9572/7030/4851/6778/4883/2697/216/3397/857/3910/51043/3%, signal=24%","7376/1051/2303/56034/63976/9572/7030/4851/6778/4883/2697/216/3397/857/3',"10252/631/1969/7431/4094/161742/4088/7477/10253/468/399473/2247/5309/3299/81029"
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l, list=19%, signal=50%","3133/567/6891/8546/3135/3134/563/912"
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, "3356/26471/5027/54541/351/8671/51341/3479/4609/402/51085/5465/2203/3091/89/3458/677
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1%, list=36%, signal=45%", "80324/55644/54931/64172/51654/8270/112858/3028/54802/55006/51
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i, signal=39%", "5327/3624/1906/4851/1909/1545/2730/2492/2627/7849"
686/5360/4837/6615/6591/6515/5641/1593/4790/157506/5467/8644/9446/1583/113278/27010/8
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%, signal=40%", "162514/5621/493/773/779/59341/7226/799/51393/123041/56302/775/5023/9187
6, list=18%, signal=31%", "3487/367/3488/51232/3489/2690/4824/9451/3479/23236/650/3486/3484
5/5321/1906/5322/5027/624/5025/4828/9536/3553/3552/553/6850/6754/729330/10257/4843/53
;nal=27%", "3399/79365/5187/8553/196/9572/9099/3398/3400/5371/3397/1958/4862/8204/10135
'", "284612/966/3107/3133/567/79953/3105/89866/6856/3106/80863/5066/26056/3708/374/34135
;nal=32%", "8314/131474/64112/26517/9131/10425/207/9927/808/3301/158234/637/7332/10469/
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s=22%, list=10%, signal=20%", "1793/4739/2316/6281/91663/23189/1601/80005/6239/4070/55679/
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list=14%, signal=53%", "3280/4851/4488/3204/9573/28514/8626/130120"
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, "1593/8578/348/4504/51302/6718/1581"
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, "2091/5394/118460/56915/131870/51574/9221/1736/51010/345630/23404"
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%, signal=47%", "50485/51750/7517/84464/7014/7520/9156/1763/641"
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9%", "22925/5321/1906/5027/5025/9536/3553/3552/553/6850/6754"
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, "706/5360/388121/10577/19/57605/54762/51228/348/80765/114879/7274/57655/9619/335/153
360/388121/10577/19/57605/54762/51228/348/80765/114879/7274/57655/9619/335/153768/336

ags=67%, list=27%, signal=49%","1024/51755/23097/23476/8621/1019/1021/983"
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=69%, list=30%, signal=49%","22981/1639/636/11127/80323/90060/5108/2932/84984"
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signal=45%","8531/26471/857/329/4504/57162/9181/8737/8326/8996"
%, signal=32%","4054/2296/7042/4070/221662/6662/3214"
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gnal=21%","3913/57381/4124/1745/7070/1746/5159/10461/7042/4915/6662/5176/196740/5797/4
%","3280/6662/30812/7484/55366"
gnal=34%","7057/7040/4921/59/3688"
al=20%","64285/8742/51429/27185/54209/2316/257364/83547/152503/29116/2308/25976/9709/
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%, signal=36%","2022/2297/3280/4853/4851/4488/4487/23213/8200/53918/2719/1003/94/652/22
=56%, list=30%, signal=39%","4208/4534/1499/28514/6469/89/56203/4618/10211/4654"
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.5/5045/4804/5046/9001"
il=50%", "5887/2071/7507/2072/1161/7515/5424"
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", "9531/824/183/26471/1906/3592/23493/4780/80149/3162/5468/8837/817/3479/468/93649/421
%, signal=33%", "117854/10413/182/3280/4851/144165/4780/5978"
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%, signal=40%", "558/2621/6387/4067/3965"
s=73%, list=29%, signal=51%", "3430/4814/2150/57162/353376/3929/57590/4057"
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8%, list=17%, signal=24%", "2040/54210/2335/9367/858/5806/8542/8091/80149/5978/3429/6355/
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ignal=41%", "824/126969/23682/80736/57153/376497/56994/23446/3931/84879/335/5130/336/25
%", "301/7376/11343/5321/1906/27306/5742/5743/5166/84532/53632/54988/8560/4023/2948/69
nal=35%", "2771/4883/1910/84876/140/1909/796/10886/55366/2492/59350/6786/153/122042/10
27%", "182/4124/2295/7070/1295/1969/4853/2737/4915/8412/10370/6662/2195/5797/220/30812,
683/374378/30815/4124/117248/84752/79623/8985/727936/11227/4245/84002/55568/4121/641
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", "1639/9859/80323/11064/90060/4957/3796/145508"
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3%, signal=36%", "5350/3270/845/477/9446/817/5144/1756/6348/1193/6588/10345/775/1234/626
7043/477/6548/5348/8291/493/7779/779/825/59283/3759/5962"
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524/3625/1066/54762/6608/1605/23209/1581/57655"
58/100507436/2621/639/2214/3133/10461/3592/148022/3916/4783/7305/2000/3601/3134/8486
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3/7015/54386/100134934/80169/65057/2547/25913/7014/7520"
%", "7013/7015/54386/100134934/80169/65057/2547/25913/7014/7520"
%, list=28%, signal=38%", "975/8934/3783/5970/100/25865/8915/8517"
"9696/1639/54875/11127/23177/11190/25914/80817/9662/4957/4751"
,, signal=58%", "55621/24140/60487/54931/6894/158234/80745/10785/25917/81627/93587/57570
=45%", "29081/91893/29063/51106/115939/196074/10436/2091/4839/117246/27292/79066/55006
%", "7376/4929/10865/6867/5468/5916/8204"

125/5321/1906/5322/5027/624/5025/6578/4828/9536/3553/3552/553/6850/6754/729330/10257/4
t=14%, signal=28%", "2303/2022/7040/2296/7042/4851/57493/23493/7049/4092/4061/1909/54567
, "5468/5467/241/6809/165140/6279/6280/2169/2170/2167/5306"
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=11%, signal=36%", "26020/23166/58191/4973/53353/4035"
%, signal=47%", "4023/348/3990/3931/344/335/336"
%, signal=47%", "4023/348/3990/3931/344/335/336"
%, list=17%, signal=48%", "147912/284/5467/2047/8837/6495/2247"
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5, "tags=41%, list=24%, signal=31%", "7376/23645/90993/9709/29761/120892/2907/3309/7466/3303
1/6556/3077/567/392/2512/64116/79689/55640/57348/57192/57817/286133/6536/23479/3458/3
ist=21%, signal=30%", "1843/4681/23143/347/23236/6347/11240/653"
;", "6788/117854/8767/4803/3673/6281/9314/7040/3280/23129/2296/3077/302/567/148022/5329
39%", "6223/3921/6169/27341/29777/51081/26284/7520/64963/5591"
35/2193/2618/79731/3980/790/8883/23395/23438/55278/440/158135/284716/7317/57470/2730.
", "4038/116039/2737/4851/4488/2697/8323/4487/1499/130497/1889/7474/652/6469/341640/10
%", "5715/11047/9861/5701/5719/5706/5708/5718/5717/5704/5707/5700/5705/5710/10213/5702,
=17%, signal=37%", "4926/51529/81620/8697/51434/8452/9787/9700"
;=31%, list=11%, signal=27%", "54209/3133/10769/5045/975/79651/4067/64127/3123/3586/2213/2
365/1975/2332/50485/6594/84083/9401/641/8438"
"1410/631/3316/126393/1414/7431"
1/1910/3162/6781/134/185/6869/525/6865/4867/4881/3758/8645/10699/10686/5002/3778/148/!
=32%, signal=52%", "1107/2074/1106/84181/6594/8467/56916/55636/57680/1108"
5%", "57662/114791/4926/10844/10426/157922/27229"
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2/9319/5901/6790/11073/9985"
4209/10417/5027/671/6403/23643/929/4814/7097/7099/6037/5724/84659/3929/254240/245932/
list=20%, signal=23%", "6556/183/477/6548/23682/1203/55647/10312/440400/6337/482/6507/120
ist=23%, signal=47%", "8013/4780/3082/120892/3586/5151/55074/79772/9283/65018/4233"
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348775646,3089, "tags=50%, list=17%, signal=41%", "347/5739/4035/93649/5782/5795"
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;", "858/5339/2876/6608/58/55909/6495/131377/89/6261/1827/9456/56203/4618/7480"
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18%, list=21%, signal=38%", "27185/2737/4851/2735/2771/7424/1950/6376/4067/1499/1638/54567
31/55062/7107/117854/8767/5587/5768/54209/706/2308/1611/81603/10769/5476/26471/4170/!
57085/5743/4780/857/4790/1281/5580/185/1535/4609"
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6324/23704/2316/5592/3779/6446/6236/5348/3708/857/2669/28954/126755/493/6330/5349/308
%", "2564/3775/309/53373/22821/5027/3708/358/54795/3710/2892/9424/6337/2555/1134/5025/.
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al=43%", "55214/8974/283208/5033/64175/54583"
signal=51%", "5592/114897/10019/5580/170692/928/84959/2266"
"183/3356/477/2668/7432/5027/151/3688/6529/8501/6387/140/5028/341359/134/8973/91683/6!
il=46%", "861/3635/714/10221/3059/51176/54997/8451/2124"
l=27%", "100507436/2214/3133/3592/135250/3105/3106/3916/5817/3135/3965/3134/84868/1468

4%, list=21%, signal=27%", "4038/6810/54209/3958/2040/1969/7130/10519/8878/975/1956/3688/32934/1906/6548/2353/4790/1499/3725/4792/1756/5970"
:=44%, list=23%, signal=34%", "10252/7042/161742/1942/4092/114990/10253/3169/399473/753/641232842822835,3262,"tags=55%, list=18%, signal=45%", "3270/857/79191/817/5144/10345"
4/7040/7048/3625/1066/54762/6608/1605/23209/6348/1581/57655/1234"
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, "162514/5621/493/773/779/59341/7226/799/51393/123041/56302/775/5023"
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32006660587868,3135,"tags=46%, list=17%, signal=38%", "8767/51296/64127/4792/329/7128/3304/
48/3625/1066/54762/6608/1605/23209/6348/1581/57655"
%, list=22%, signal=36%", "64114/7040/5525/1601/116372/2633/8301/3753/51225/23433/9270/832
, signal=24%", "25937/26524/10252/9052/1843/7070/4616/183/7538/5525/11221/7026/57493/946
%, signal=28%", "6324/23704/2316/9948/2697/6330/3784/3762/3752/3753/2702/3759"
%", "631/7431/5339/4534/7062/3861/3881/3885/6469/1674/4747/3883/3856/1832/144501/3892/3
"6915/5468/5739/5734/5729/3248"
0111,2156,"tags=36%, list=12%, signal=32%", "3487/367/3488/3479"
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, signal=24%", "7376/1051/467/64764/7057/57333/23645/90993/9709/8406/29761/26471/837/478
, "tags=60%, list=22%, signal=47%", "6470/51247/56853/400961/6472/163255/10658/1719/7298"
t=24%, signal=41%", "8767/7098/84282/148022/9636/81844/23586/3659/64135/7097/7099/79132,
978/27122/1583/650/1609/653/1585"
nal=42%", "8531/80303/5743/624/59341/23209/9181"
177/2668/7432/5027/151/3688/6529/8501/6387/140/5028/341359/134/8973/91683/6865/2865/8:
514/53373/1513/1508/5580/1520/1175/160/6609/51284/3949/255738/51311"
gnal=38%", "9646/10914/6626/56254/9810/11052/4686/11051/22916/79882/123169/79869"
'80789/25836/55174/55656/57508/26173/25896"
s=71%, list=22%, signal=55%", "6830/9972/29072/55051/7175/11052/22916/55677/1660/10657"
47%", "8528/2752/443/122970/137872/2571/197322/2747/2746/23475/10840"
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5247,"tags=57%, list=29%, signal=40%", "5028/9934/2857/5029/64805/5724/5031/286530"
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6, list=24%, signal=38%", "1903/8877/1901/5291/5294/53637/7430"
12/63874/857/9249/1896/157506/8605/5010/1066/91543/196410/84883/80270/57104/195814/25
8%, signal=33%", "857/4790/493/2717"
3, list=22%, signal=31%", "161291/89866/975/55741/27248/10134/123264/9695/337867/56681"
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signal=58%", "1051/3106/10288/55365/3135/2213/28959/3965"
", "23409/790/2673/440/5198/56474/8833/5471/92292/89839/1503"
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, "84193/55870/56950/11105/55209/6419/23476/29072/64324/55677/22976/54880"
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9/3678/3688/958/79155/942/7128/10758"
5%, signal=44%", "57662/25876/146057/57551/324/55201/23122/79929/10013/23332/2258/11075,
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%, signal=21%", "23368/666/10210/55367/9100/10419/51616/546/22938/7874/3094/11200/23246,
%, signal=34%", "5327/1843/6615/7076/27306/4627/2697/5176/4824/23213/3976/7474/3479/652/:
%, signal=34%", "2274/9454/29995/6548/10519/5621/493/64581/3479/58529/2065/5336/89/11261
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gnal=22%","56937/367/26524/25959/10413/5187/26508/8013/5241/1601/2690/9572/4306/6751/2
L94056773674098,406,"tags=36%, list=2%, signal=35%","6788/467/7057/7078/8682"
90/4853/7042/23493/7481/7474/6608/2702"
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9,"tags=42%, list=9%, signal=38%","3356/56925/6387/55107/796/134/94233/2047"
%","90/3280/1906/7042/51804/3199/4824/1909/1889/652"
l=38%","11343/1906/2149/6548/7432/1910/55273/134/3586/3552/6348/5724/10879/4986"
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i%, signal=20%","1051/79365/467/7050/90993/2308/9580/8553/26508/3280/4286/2004/639/6397
208/604/602/4791/7128/100/10673/10563"
"83933/23411/54531/10014/8841/51548/51547/10013/3065/3066/64426/9219/55869"
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st=13%, signal=28%","10856/57609/26053/6598/84656/6871/4089/2625/22976/29117/3670/672"
ist=19%, signal=35%","6908/10629/2958/55729/6882/6878/55832/6873/1810/3146/6874/6877"
t=14%, signal=52%","1847/1843/11221/1848/1844/1846"
:17%, signal=58%","677/1435/2242/146433/3123/972/81501"
6%, signal=36%","26471/84875/79577/10437/4609/6422/11314/6648/26272/2495/2950/11285/58
:80%, list=24%, signal=61%","55011/54700/6872/9014/11176/6598/6597/7343"
3513/8851/429/1386/8941/401"
st=28%, signal=39%","64210/122961/10539/51218/9391/64110"
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16/8531/54587/117583/54532/5872/5912/79778/51421/7408/90952/57125/23562/1366/5010/584
24%, list=13%, signal=21%","4038/2316/10501/29116/3280/23189/7070/10512/1601/567/7431/105
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21%, signal=42%","4929/8321/7484/1499/7474/22943/6423/6422/6259"
%, signal=34%","477/6548/5348/482/8671/483"
%","4055/4853/7048/29108/6688/3586/84868/5971/55509/81501/1794/3696/1437/116071"
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list=17%, signal=31%","10142/4926/4137/8851/23332/1027/122060/22919/55755/403/84722/979
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4%","2297/5159/51804/6943/130497/5311/652/6469/4609/6495"
19/3799/27067/3800/6421/8936/3192"
ial=53%","55781/84946/27340/8780/117246/55720/83732/8568/705/79050/161424/23076"
, signal=25%","27242/58494/3586/9451/1075"
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2697/857/1495/79191/2702/3553/2706/2705/125111/59272"
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170/54749/5660/6403/4067/1200/51228/4099/3306/5538/2215/3558"
2%, signal=29%","8528/89874/8985/10157/23743/445/443/10993/123688/23464/55256/4482/535
5360/10577/19/54762/348/80765/57655/9619/335/336"

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gs=46%, list=30%, signal=33%", "56548/9469/55034/10090/8459/79783/4166/166012/9956/9957/68
077/64116/79689/6536/23479/3458/261729"
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' , "6742/4331/4437/25913/26097/4171/2956/4436"
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0%, signal=37%", "2033/6659/60560/80018/10988/79612/23173/80155/1387/79929/5494/122830/4
, "27185/4313/84676/3164/6548/1728/5027/5978/7832/929/6869/6865/199/23191/6121/6648/95:
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, signal=32%", "301/7376/5743/5166/972/3553/51085/344/1581/9104/37/335/215/10613/11160/3:
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43%", "10289/3646/27335/728689/8668/8667/10480/51386/8663/8661/8665/8669/8662/1965/545
al=27%", "2239/3556/8321/10082/351/145581/26280/11141/22943/139065/84631"
:27%", "2239/3556/8321/10082/351/145581/26280/11141/22943/139065/84631"
:0%", "4052/2934/2316/706/4681/11015/6672/2200/4188/85477/5552/5371/23345/857/152404/479
ist=35%, signal=36%", "3984/8945/6135/55208/6201/9529/648/6125/7332/55294/11315/23142/54:
7%", "6324/23704/2316/9096/477/2697/857/54795/6330/3784/817/3762/3752/3753/2702/6327/37
6, signal=63%", "10975/7386/7384/29796/7388/440567/27089/7385/1537/617"
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%, list=23%, signal=36%", "4124/3556/7098/3554/141/683/148022/8808/9173/26280/7097/7096/11
tags=57%, list=30%, signal=40%", "3269/5028/2852/553/5724/5031/5745/6622"
' , "4208/1514/80301/64127/3665/1234/3661"
, list=28%, signal=53%", "3357/23213/55959/6865/5724/3815/3352/80763"
al=51%", "3569/3570/6774/30009/3594/51561/10538/84695/3662/4063"
t=16%, signal=33%", "2296/4851/6424/5583/6820/652/7421/8643/2118"
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3698165, 5363, "tags=59%, list=30%, signal=41%", "148022/3569/64127/64581/7099/23765/63940/30
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325,1904, "tags=46%, list=11%, signal=41%", "1839/1950/2069/374/134/685"
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3%", "538/5629/79809/23017/8861/85442/8925/91137/23287/2624/8929"
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21%, signal=35%", "2274/9454/29995/6548/10519/5621/493/64581/3479/58529/2065/5336/89/11:
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signal=36%", "2737/3398/348093/5156/3142/6943/6469"
gnal=55%", "7015/54386/100134934/80169/65057/2547/25913/55183/7014/7520"
58/1051/2621/8013/4837/2737/4851/2735/7049/7048/3082/3162/3569/6387/133/10076/3586/30
%", "301/308/307/302/306"
56/8322"
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967,5014, "tags=70%, list=28%, signal=50%", "3162/3965/5169/11314/2294/3598/8832"
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%, list=35%, signal=46%", "6857/22999/6861/127833/8447/6812/488/9699/23025/10497/9066/9783
1906/5027/5025/9536/3553/3552"
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