

Supplementary Material

Exploring the anti-glioma mechanisms of luteolin based on network pharmacology and experimental verification

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Table S1. Prediction targets of luteolin.

Uniport id	Gene Symbols
P33527	ABCC1
Q92887	ABCC2
Q9UNQ0	ABCG2
P22303	ACHE
P09917	ALOX5
P08243	ASNS
Q07812	BAX
Q07817	BCL2L1
Q13490	BIRC2
P29466	CASP1
P42574	CASP3
P55210	CASP7
P55211	CASP9
P04040	CAT
P13500	CCL2
O76076	CCN5
P20248	CCNA2
P14635	CCNB1
P24385	CCND1
P29965	CD40LG
P04233	CD74
P19022	CDH2
P33151	CDH5
P46527	CDKN1B
P42773	CDKN2C
O15111	CHUK
P04141	CSF2

P48061	CXCL12
Q07325	CXCL9
P05177	CYP1A2
Q16678	CYP1B1
P33261	CYP2C19
P11712	CYP2C9
P05181	CYP2E1
P08684	CYP3A4
P20815	CYP3A5
P35638	DDIT3
P01133	EGF
P18146	EGR1
P05198	EIF2S1
O75460	ERN1
Q9Y624	F11R
P49327	FASN
P09467	FBP1
P01100	FOS
P53539	FOSB
O43524	FOXO3
O75293	GADD45B
P48507	GCLM
P14136	GFAP
Q9HC97	GPR35
P07203	GPX1
Q99075	HBEGF
Q16665	HIF1A
P09601	HMOX1
P11021	HSPA5
P05362	ICAM1
P01574	IFNB1
P01579	IFNG
P22301	IL10
P29460	IL12B
P35225	IL13
Q16552	IL17A
P01584	IL1B
Q8NEV9	IL27
P08700	IL3
P05113	IL5
P06213	INSR
Q14653	IRF3
P05412	JUN

P17275	JUNB
P17535	JUND
P21397	MAOA
P28482	MAPK1
P27361	MAPK3
P45984	MAPK9
P45452	MMP13
P14780	MMP9
P05164	MPO
O94916	NFAT5
Q16236	NFE2L2
P25963	NFKBIA
P35228	NOS2
P29474	NOS3
Q99571	P2RX4
P01127	PDGFB
P14618	PKM
P53350	PLK1
P17252	PRKCA
P35354	PTGS2
Q05397	PTK2
Q9ULZ3	PYCARD
Q04206	RELA
P16581	SELE
P58004	SESN2
P31947	SFN
Q4U2R8	SLC22A6
P11169	SLC2A3
P14672	SLC2A4
P13866	SLC5A1
P00441	SOD1
P04179	SOD2
P36956	SREBF1
P40763	STAT3
Q9UHD2	TBK1
P01137	TGFB1
P01375	TNF
P21580	TNFAIP3
P50591	TNFSF10
P11387	TOP1
Q53FA7	TP53I3
Q9H3D4	TP63
O15350	TP73

Q16881	TXNRD1
P22309	UGT1A1
P35503	UGT1A3
Q9UKW4	VAV3
P19320	VCAM1
P04275	VWF
P56703	WNT3
P17861	XBP1
P47989	XDH
P98170	XIAP
Q9NPH5	NOX4
P15121	AKR1B1
Q15078	CDK5R1
Q00535	CDK5
P36888	FLT3
P00918	CA2
Q8WWL7	CCNB3
P06493	CDK1
O95067	CCNB2
P30542	ADORA1
P43166	CA7
Q04760	GLO1
P05067	APP
P43405	SYK
P49841	GSK3B
P09874	PARP1
P02766	TTR
O43570	CA12
P08253	MMP2
P22748	CA4
P39900	MMP12
P28907	CD38
O60218	AKR1B10
Q9H2K2	TNKS2
O95271	TNKS
P05089	ARG1
Q13332	PTPRS
P14061	HSD17B1
Q00534	CDK6
P08183	ABCB1
P37059	HSD17B2
P16050	ALOX15
P18054	ALOX12

Q92731	ESR2
P11511	CYP19A1
P29274	ADORA2A
P68400	CSNK2A1
P03372	ESR1
P13569	CFTR
P04745	AMY1B
P43250	GRK6
P24941	CDK2
O14746	TERT
P00915	CA1
Q16790	CA9
P14679	TYR
P35869	AHR
P11474	ESRRA
P53355	DAPK1
P30518	AVPR2
P08069	IGF1R
P00533	EGFR
P00734	F2
P11309	PIM1
Q96GD4	AURKB
P21917	DRD4
P27986	PIK3R1
P06737	PYGL
P12931	SRC
P35968	KDR
P08254	MMP3
P07451	CA3
P23280	CA6
Q16512	PKN1
Q9ULX7	CA14
P08581	MET
P51955	NEK2
P25024	CXCR1
Q13554	CAMK2B
Q9UM73	ALK
P31749	AKT1
Q9HC98	NEK6
P04054	PLA2G1B
P35218	CA5A
P56817	BACE1
P30530	AXL

O60285	NUAK1
P52895	AKR1C2
Q04828	AKR1C1
P42330	AKR1C3
P17516	AKR1C4
Q8N1Q1	CA13
P14550	AKR1A1
Q16875	PFKFB3
B2RXH2	KDM4E
P00747	PLG
P10275	AR
P01834	IGKC
P01857	IGHG1
P0CG47	UBB
P62987	UBA52
P62979	RPS27A
P0CG48	UBC
P42684	ABL2
P55263	ADK
P02768	ALB
Q9NZN5	ARHGEF12
P18440	NAT1
O14815	CAPN9
Q9UKF6	CPSF3
O15075	DCLK1
O00338	SULT1C2
P06746	POLB
Q01094	E2F1
P48449	LSS
O95718	ESRRB
Q02790	FKBP4
Q01543	FLI1
P51570	GALK1
P10144	GZMB
P08631	HCK
Q92826	HOXB13
Q9HCP0	CSNK1G1
O94966	USP19
Q9NWW6	NMRK1
Q9H3U1	UNC45A
Q86UL8	MAGI2
Q9BYC5	FUT8
Q9BZI7	UPF3B

Q14449	GRB14
O00151	PDLIM1
Q53H47	SETMAR
Q96C23	GALM
Q96SI9	STRBP
O14936	CASK
Q9BZL6	PRKD2
Q9Y5X1	SNX9
Q9BZC1	CELF4
Q9H2C0	GAN
P49765	VEGFB
Q9UPY3	DICER1
Q9Y265	RUVBL1
Q9Y696	CLIC4
Q9Y6I3	EPN1
P14091	CTSE
P28329	CHAT
Q96QZ7	MAGI1
Q6PML9	SLC30A9
Q9BV79	MECR
Q6NVY1	HIBCH
Q93034	CUL5
O76064	RNF8
P12694	BCKDHA
O75351	VPS4B
P32455	GBP1
P52564	MAP2K6
Q96H20	SNF8
Q9HCB6	SPON1
Q13705	ACVR2B
P19623	SRM
Q9BY41	HDAC8
P10586	PTPRF

Table S2. Prediction targets of glioma.

Uniport id	Gene Symbols
Q9NQ94	A1CF
O95477	ABCA1
P78363	ABCA4
P08183	ABCB1
P21439	ABCB4
Q9NP58	ABCB6

P33527	ABCC1
O15438	ABCC3
O15439	ABCC4
O15440	ABCC5
O95255	ABCC6
P61221	ABCE1
Q9UNQ0	ABCG2
P24752	ACAT1
P12821	ACE
P25106	ACKR3
A6NK06	ACOD1
Q8WXI4	ACOT11
O00154	ACOT7
P15309	ACP3
Q8NEB7	ACRBP
Q96GR2	ACSBG1
P33121	ACSL1
O95573	ACSL3
O60488	ACSL4
Q9ULC5	ACSL5
Q9NR19	ACSS2
P60709	ACTB
Q562R1	ACTBL2
P68032	ACTC1
P63261	ACTG1
P63267	ACTG2
O96019	ACTL6A
O43707	ACTN4
P61160	ACTR2
Q04771	ACVR1
P36896	ACVR1B
P14621	ACYP2
P00813	ADA
Q9NZK5	ADA2
O14672	ADAM10
P78536	ADAM17
Q9P0K1	ADAM22
O75077	ADAM23
Q9UKQ2	ADAM28
Q13443	ADAM9
Q9UHI8	ADAMTS1
Q9UNA0	ADAMTS5
Q9UP79	ADAMTS8

P55265	ADAR
P78563	ADARB1
Q9NS39	ADARB2
Q96PN6	ADCY10
Q08462	ADCY2
P40145	ADCY8
P18509	ADCYAP1
P41586	ADCYAP1R1
Q8N7X0	ADGB
O14514	ADGRB1
Q9UHX3	ADGRE2
Q9BY15	ADGRE3
P48960	ADGRE5
Q5T601	ADGRF1
Q9Y653	ADGRG1
Q9HBW9	ADGRL4
Q15848	ADIPOQ
Q96A54	ADIPOR1
P55263	ADK
P35318	ADM
P30542	ADORA1
P29274	ADORA2A
P25100	ADRA1D
P35348	ADRA1A
P18089	ADRA2B
P07550	ADRB2
P30566	ADSL
Q8IUX7	AEBP1
Q99490	AGAP2
Q15109	AGER
P52594	AGFG1
Q8N302	AGGF1
Q53H12	AGK
Q9UKV8	AGO2
O00116	AGPS
Q09666	AHNAK
P35869	AHR
O95433	AHSA1
Q9GZX7	AICDA
P55008	AIF1
O95831	AIFM1
O14862	AIM2
Q12904	AIMP1

Q13155	AIMP2
Q9UKB5	AJAP1
Q96IF1	AJUBA
Q02952	AKAP12
Q13023	AKAP6
P15121	AKR1B1
P31749	AKT1
Q96B36	AKT1S1
P31751	AKT2
Q9Y243	AKT3
P13716	ALAD
P02768	ALB
Q8TES7	FBF1
P00352	ALDH1A1
P47895	ALDH1A3
Q9UM73	ALK
Q9UHK6	AMACR
P02760	AMBP
P23109	AMPD1
P03950	ANG
Q15389	ANGPT1
O15123	ANGPT2
Q9Y264	ANGPT4
O95841	ANGPTL1
Q9UKU9	ANGPTL2
Q8N2N9	ANKRD36B
Q8WVL7	ANKRD49
Q5XXA6	ANO1
Q4KMQ2	ANO6
P39687	ANP32A
P15144	ANPEP
P58335	ANTXR2
P04083	ANXA1
P07355	ANXA2
P08758	ANXA5
P08133	ANXA6
P20073	ANXA7
O95782	AP2A1
O14727	APAF1
P25054	APC
O95996	APC2
Q9UJX6	ANAPC2
Q9ULZ1	APLN

P35414	APLNR
Q9UH17	APOBEC3B
P02655	APOC2
P05090	APOD
P02649	APOE
P05067	APP
Q06481	APLP2
Q8NEU8	APPL2
P07741	APRT
P29972	AQP1
P55087	AQP4
O14520	AQP7
O43315	AQP9
P10275	AR
P10398	ARAF
O60936	NOL3
Q7LC44	ARC
P48444	ARCN1
P15514	AREG
P62330	ARF6
Q53QZ3	ARHGAP15
Q8N264	ARHGAP24
Q9NRY4	ARHGAP35
Q9BRR9	ARHGAP9
P52565	ARHGDIA
O15085	ARHGEF11
Q92974	ARHGEF2
Q96DR7	ARHGEF26
Q8N1W1	ARHGEF28
Q15052	ARHGEF6
Q14155	ARHGEF7
P36404	ARL2
P36405	ARL3
P40617	ARL4A
P49703	ARL4D
O00327	ARNTL
P52961	ART1
Q8N9N2	ASCC1
P50553	ASCL1
Q16515	ASIC2
Q9UHC3	ASIC3
Q96FT7	ASIC4
P04424	ASL

P45381	ASPA
Q86U10	ASPG
Q8IZT6	ASPM
P15336	ATF2
P18848	ATF4
Q9Y2D1	ATF5
P18850	ATF6
Q8WYN0	ATG4A
Q96DT6	ATG4C
Q86TL0	ATG4D
O95352	ATG7
P31939	ATIC
Q13315	ATM
P54259	ATN1
P05023	ATP1A1
P13637	ATP1A3
P14415	ATP1B2
Q9Y6H3	ATP23
O75787	ATP6AP2
Q04656	ATP7A
P20848	SERPINA2
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Q9H6X2	ANTXR1
O75882	ATRN
O14965	AURKA
Q96GD4	AURKB
Q9Y2T1	AXIN2
P30530	AXL
Q96A70	AZIN2
O43286	B4GALT5
Q9NXR7	BABAM2
Q92934	BAD
Q99933	BAG1
O95817	BAG3
Q13145	BAMBI
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Q96QZ7	MAGI1
Q9NR55	BATF3
Q07812	BAX
Q96GW7	BCAN
P51572	BCAP31
P56945	BCAR1
P54687	BCAT1

O95999	BCL10
Q9C0K0	BCL11B
P10415	BCL2
Q07817	BCL2L1
Q9HB09	BCL2L12
Q92843	BCL2L2
P20749	BCL3
P41182	BCL6
Q6W2J9	BCOR
Q02338	BDH1
P30411	BDKRB2
P23560	BDNF
Q14457	BECN1
Q9BXY8	BEX2
P21810	BGN
Q8NFJ8	BHLHE22
O14503	BHLHE40
Q9C0J9	BHLHE41
Q9NZM4	BICRA
Q13489	BIRC3
O15392	BIRC5
P35226	BMI1
P12644	BMP4
P18075	BMP7
Q13873	BMPR2
Q12983	BNIP3
Q12830	BPTF
P15056	BRAF
Q6UWU4	C6orf89
Q7Z569	BRAP
P38398	BRCA1
P51587	BRCA2
P46736	BRCC3
O60885	BRD4
Q9NPI1	BRD7
Q9H0E9	BRD8
Q9HCU9	BRMS1
Q5PSV4	BRMS1L
P32247	BRS3
P35613	BSG
Q9BSF8	BTBD10
O00478	BTN3A3
P20290	BTF3

P78410	BTN3A2
P62324	BTG1
P78543	BTG2
Q06187	BTK
Q9Y297	BTRC
O43683	BUB1
Q9H8K7	PAAT
Q13901	C1D
Q07021	C1QBP
Q0P641	C2orf80
Q9NS85	CA10
O75493	CA11
Q9NS71	GKN1
P00918	CA2
Q16790	CA9
Q9Y376	CAB39
Q8IZS8	CACNA2D3
Q9HB71	CACYBP
Q9BY67	CADM1
Q8N3J6	CADM2
Q8N126	CADM3
Q8NFZ8	CADM4
P01258	CALCA
P06881	CALCA
P30988	CALCR
Q05682	CALD1
P0DP23	CALM1
P0DP24	CALM2
P0DP25	CALM3
P27482	CALML3
P27797	CALR
Q13554	CAMK2B
Q13555	CAMK2G
Q96RR4	CAMKK2
Q7Z624	CAMKMT
P49913	CAMP
Q96JM3	CHAMP1
P40121	CAPG
P04632	CAPNS1
Q9BWT7	CARD10
Q9BXL7	CARD11
Q6XLA1	CASC2
Q8IU53	CASC2

O14936	CASK
P07498	CSN3
P29466	CASP1
P42575	CASP2
P42574	CASP3
P55212	CASP6
Q14790	CASP8
P55211	CASP9
Q86V15	CASZ1
P04040	CAT
Q03135	CAV1
P51636	CAV2
Q6NZI2	CAVIN1
O95810	CAVIN2
P22681	CBL
Q13185	CBX3
P45973	CBX5
O95931	CBX7
Q8TAB7	CCDC26
P06307	CCK
P55774	CCL18
P13500	CCL2
P78556	CCL20
O00626	CCL22
P13501	CCL5
P80075	CCL8
O00622	CCN1
P29279	CCN2
P78396	CCNA1
P14635	CCNB1
O95067	CCNB2
P24385	CCND1
P30279	CCND2
P30281	CCND3
P24864	CCNE1
P41002	CCNF
Q16589	CCNG2
P51946	CCNH
P22674	CCNO
Q8ND76	CCNY
P46092	CCR10
P51679	CCR4
Q9UK39	NOCT

Q9ULM6	CNOT6
P51681	CCR5
P51684	CCR6
P32248	CCR7
P50991	CCT4
P50990	CCT8
Q6YHK3	CD109
P48509	CD151
Q86VB7	CD163
Q04900	CD164
P06729	CD2
P41217	CD200
P25063	CD24
P20963	CD247
P26842	CD27
Q9NZQ7	CD274
Q5ZPR3	CD276
P10747	CD28
P28906	CD34
P25942	CD40
P29965	CD40LG
P16070	CD44
P15529	CD46
Q08722	CD47
P09326	CD48
P34810	CD68
P32970	CD70
P04233	CD74
P33681	CD80
P27701	CD82
P42081	CD86
Q9NPY3	CD93
P14209	CD99
Q12834	CDC20
P30304	CDC25A
P30305	CDC25B
P30307	CDC25C
P60953	CDC42
O75419	CDC45
Q96GN5	CDCA7L
P12830	CDH1
Q9UM11	FZR1
P55287	CDH11

P55290	CDH13
Q13634	CDH18
P19022	CDH2
Q9UJ99	CDH22
P55283	CDH4
P33151	CDH5
P06493	CDK1
Q15131	CDK10
O94921	CDK14
Q96Q40	CDK15
Q00536	CDK16
P24941	CDK2
O14519	CDK2AP1
O75956	CDK2AP2
P11802	CDK4
Q00535	CDK5
Q00534	CDK6
P50613	CDK7
P49336	CDK8
P38936	CDKN1A
P46527	CDKN1B
P49918	CDKN1C
P42771	CDKN2A
Q8N726	CDKN2A
P42772	CDKN2B
P42773	CDKN2C
P55273	CDKN2D
Q16667	CDKN3
Q99626	CDX2
P13688	CEACAM1
P06731	CEACAM5
P49715	CEBPA
P17676	CEBPB
P49716	CEBPD
Q03701	CEBPZ
Q92879	CELF1
O95319	CELF2
Q9HC77	CENPJ
Q71F23	CENPU
Q6ZU80	CEP128
Q53EZ4	CEP55
P27544	CERS1
O00748	CES2

Q9P2B7	CFAP97
P08603	CFH
P23528	CFL1
O15519	CFLAR
Q9BUX1	CHAC1
Q13111	CHAF1A
O14646	CHD1
Q14839	CHD4
O00258	GET1
Q8TDI0	CHD5
Q9P2D1	CHD7
O14757	CHEK1
O96017	CHEK2
P36222	CHI3L1
P35790	CHKA
O00533	CHL1
Q96FC9	DDX11
Q8IZ52	CHPF
Q8WUD6	CHPT1
Q70JA7	CHSY3
Q9P2E5	CHPF2
Q99828	CIB1
Q96RK0	CIC
P33076	CIITA
Q9UPZ9	CILK1
Q8N5K1	CISD2
Q9NSE2	CISH
Q96RK1	CITED4
Q8WWK9	CKAP2
Q07065	CKAP4
Q14008	CKAP5
Q05315	CLC
Q9UBD9	CLCF1
P51788	CLCN2
P51790	CLCN3
P51793	CLCN4
P51795	CLCN5
P51798	CLCN7
O00501	CLDN5
Q9NY25	CLEC5A
O00299	CLIC1
Q9Y696	CLIC4
P49759	CLK1

O15516	CLOCK
Q96KA5	CLPTM1L
Q8IY22	CMIP
P30085	CMPK1
Q5EBM0	CMPK2
Q9NX76	CMTM6
P21554	CNR1
P26441	CNTF
P26992	CNTFR
Q12860	CNTN1
Q02246	CNTN2
Q9UHC6	CNTNAP2
P13942	COL11A2
P39060	COL18A1
P02461	COL3A1
P02462	COL4A1
Q01955	COL4A3
P20849	COL9A1
Q14055	COL9A2
Q14050	COL9A3
P49747	COMP
Q8NHY2	COP1
Q9Y678	COPG1
Q92905	COPS5
Q14019	COTL1
P00403	MT-CO2
P13073	COX4I1
P20674	COX5A
P10606	COX5B
P14406	COX7A2
P10176	COX8A
P00450	CP
Q9UI42	CPA4
P16870	CPE
Q9BZB8	CPEB1
Q8NE35	CPEB3
Q17RY0	CPEB4
P36551	CPOX
Q9Y646	CPQ
P16220	CREB1
Q96BA8	CREB3L1
P06850	CRH
P34998	CRHR1

P16562	CRISP2
P46108	CRK
Q8IUI8	CRLF3
Q14194	CRMP1
P02741	CRP
Q16526	CRY1
Q49AN0	CRY2
P02511	CRYAB
P09603	CSF1
P07333	CSF1R
P04141	CSF2
P09919	CSF3
P41240	CSK
Q6UVK1	CSPG4
P50461	CSRP3
P01034	CST3
Q15828	CST6
P78358	CTAG1A
Q13363	CTBP1
P56545	CTBP2
Q2NKJ3	CTC1
P16410	CTLA4
P35222	CTNNB1
Q9NSA3	CTNNBIP1
O60716	CTNND1
Q9UQB3	CTNND2
P07858	CTSB
P07339	CTSD
P43235	CTSK
P07711	CTSL
Q14247	CTTN
Q9H467	CUEDC2
Q13616	CUL1
P39880	CUX1
Q13948	CUX1
P49238	CX3CR1
P09341	CXCL1
P02778	CXCL10
O14625	CXCL11
P48061	CXCL12
O95715	CXCL14
Q9H2A7	CXCL16
Q6UXB2	CXCL17

P10145	CXCL8
Q07325	CXCL9
P25025	CXCR2
P49682	CXCR3
P61073	CXCR4
O00574	CXCR6
P08574	CYC1
Q8WWM9	CYGB
Q9NQC7	CYLD
P05093	CYP17A1
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Q8N4C6	NIN
P62875	POLR2L
Q9BQE3	TUBA1C
Q9C035	TRIM5
P05162	LGALS2
Q92806	KCNJ9
P52306	RAP1GDS1
Q8NF91	SYNE1

P16519	PCSK2
Q8TDD2	SP7
O96004	HAND1
P04259	KRT6B
O95405	ZFYVE9
P35900	KRT20
Q92585	MAML1
O75891	ALDH1L1
O00219	HAS3
Q13421	MSLN
P55073	DIO3
Q02083	NAAA
O75461	E2F6
Q9H8S9	MOB1A
O15372	EIF3H
O15492	RGS16
Q15406	NR6A1
Q8N0W4	NLGN4X
Q96DU3	SLAMF6
Q9Y6M0	PRSS21
Q9H0F6	SHARPIN
Q92886	NEUROG1
Q12800	TFCP2
Q01085	TIAL1
P24588	AKAP5
Q9UJ14	GGT7
Q9Y6D6	ARFGEF1
Q76L83	ASXL2
Q6PL18	ATAD2
Q9H2G9	BLZF1
O94911	ABCA8
Q9UJA2	CRLS1
P13378	HOXD8
P52951	GBX2
Q13319	CDK5R2
Q07092	COL16A1
P14866	HNRNPL
Q92839	HAS1
Q01658	DR1
P26378	ELAVL4
O14931	NCR3
Q96EB1	ELP4
O76081	RGS20

O75398	DEAF1
P16150	SPN
Q9NPD7	NRN1
P05000	IFNW1
Q9UG01	IFT172
Q9BST9	RTKN
Q9NYR9	NKIRAS2
Q99969	RARRES2
Q86U70	LDB1
Q9BXJ9	NAA15
Q8IXF0	NPAS3
P49685	GPR15
Q9NR30	DDX21
Q9NY93	DDX56
P55884	EIF3B
P60228	EIF3E
Q7Z6J0	SH3RF1
P56470	LGALS4
Q9Y4X4	KLF12
Q8NHU6	TDRD7
O60675	MAFK
O43513	MED7
Q16570	ACKR1
O00590	ACKR2
Q9BPY8	HOPX
Q9BZE4	GTPBP4
Q01850	CDR2
P15822	HIVEP1
Q9Y4C5	CHST2
Q9C005	DPY30
O15541	RNF113A
Q96JQ0	DCHS1
Q9H159	CDH19
P53618	COPB1
P01569	IFNA5
Q86UN2	RTN4RL1
Q9BV35	SLC25A23
Q96CW5	TUBGCP3
Q96Q89	KIF20B
Q99805	TM9SF2
O43692	PI15
Q9C075	KRT23
Q147X3	NAA30

O15457	MSH4
Q86UP3	ZFHX4
Q96KR1	ZFR
Q13503	MED21
Q8TF66	LRRC15
Q9H0B8	CRISPLD2
O43248	HOXC11
Q9Y222	DMTF1
Q8WXI7	MUC16
Q9Y3A3	MOB4
Q8TAT5	NEIL3
Q8TEC5	SH3RF2
P05013	IFNA6
Q86YD1	PTOV1
P50458	LHX2
Q9NYW7	TAS2R1
Q6UXB8	PI16
Q8IZJ0	IFNL2
Q9UF56	FBXL17
Q9C0F0	ASXL3
Q13686	ALKBH1
Q9NPB9	ACKR4
Q9Y5Q8	GTF3C5
Q58WW2	DCAF6
Q6ZMN7	PDZRN4
P01568	IFNA21
Q9HBI0	PARVG
Q86UN3	RTN4RL2
Q8IZD6	SLC22A15
Q07444	KLRC3
Q9BXU1	STK31
P17152	TMEM11
Q8IZI9	IFNL3
Q8IU57	IFNLR1
Q8WTV1	THAP3
Q9BRH9	ZNF251
Q96DT7	ZBTB10
Q7L311	ARMCX2
Q9H336	CRISPLD1
Q969V6	MRTFA
O60519	CREBL2
Q5M775	SPECC1
P05014	IFNA4

P32881	IFNA8
P01566	IFNA10
Q96JJ6	JPH4
Q05215	EGR4
O95389	CCN6
Q9Y692	GMEB1
Q9UH62	ARMCX3
P0C7T5	ATXN1L
Q96LK0	CEP19
Q8WUJ3	CEMIP
Q9Y5L2	HILPDA
Q15369	ELOC
P01567	IFNA7
Q0D2I5	IFFO1
Q96FV3	TSPAN17
Q693B1	KCTD11
P01571	IFNA17
Q96GA3	LTV1
Q8N1E6	FBXL14
Q8N865	C7orf31
Q15370	ELOB
P01570	IFNA14
P05015	IFNA16
Q96FX7	TRMT61A
Q9UKQ9	KLK9
P16619	CCL3L1
O76076	CCN5
Q4G1C9	GLIPR1L2
Q9P291	ARMCX1
Q8NDZ0	BEND2
Q9BY89	KIAA1671
Q08117	TLE5
P13762	HLA-DRB4
Q92599	SEPTIN8
O15446	POLR1G
Q8TF63	DCANP1
A6NI86	GOLGA6L10
Q13072	BAGE

Table S3. Signaling pathways in KEGG enrichment analysis of glioma-related targets

ID	Description	pvalue
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hsa04151	PI3K-Akt signaling pathway	9.99E-61
hsa04015	Rap1 signaling pathway	1.02E-39
hsa04010	MAPK signaling pathway	1.84E-36
hsa04933	AGE-RAGE signaling pathway in diabetic complications	3.44E-33
hsa04014	Ras signaling pathway	1.67E-30
hsa04620	Toll-like receptor signaling pathway	1.23E-29
hsa04012	ErbB signaling pathway	1.71E-28
hsa04722	Neurotrophin signaling pathway	1.09E-27
hsa04630	JAK-STAT signaling pathway	1.62E-27
hsa04062	Chemokine signaling pathway	2.76E-27
hsa04668	TNF signaling pathway	3.88E-25
hsa04625	C-type lectin receptor signaling pathway	3.25E-23
hsa04068	FoxO signaling pathway	7.31E-23
hsa04912	GnRH signaling pathway	3.58E-22
hsa04066	HIF-1 signaling pathway	2.64E-21
hsa04660	T cell receptor signaling pathway	1.87E-20
hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	9.66E-20
hsa04024	cAMP signaling pathway	1.29E-19
hsa04926	Relaxin signaling pathway	4.04E-19
hsa04917	Prolactin signaling pathway	7.38E-19
hsa04657	IL-17 signaling pathway	9.33E-19
hsa04020	Calcium signaling pathway	2.30E-18
hsa04915	Estrogen signaling pathway	2.32E-18
hsa04071	Sphingolipid signaling pathway	3.58E-18
hsa04621	NOD-like receptor signaling pathway	3.87E-18
hsa04211	Longevity regulating pathway	4.85E-17
hsa04213	Longevity regulating pathway - multiple species	6.25E-17
hsa04664	Fc epsilon RI signaling pathway	4.85E-16
hsa04064	NF-kappa B signaling pathway	1.19E-15
hsa04390	Hippo signaling pathway	1.20E-15
hsa04072	Phospholipase D signaling pathway	1.60E-15
hsa04371	Apelin signaling pathway	1.83E-15
hsa04350	TGF-beta signaling pathway	1.83E-15
hsa04115	p53 signaling pathway	5.07E-15
hsa04550	Signaling pathways regulating pluripotency of stem cells	9.84E-15
hsa04310	Wnt signaling pathway	1.08E-14
hsa04910	Insulin signaling pathway	1.11E-13
hsa04370	VEGF signaling pathway	7.82E-13
hsa04919	Thyroid hormone signaling pathway	8.41E-13
hsa04022	cGMP-PKG signaling pathway	6.71E-12
hsa04622	RIG-I-like receptor signaling pathway	1.44E-11
hsa04921	Oxytocin signaling pathway	1.01E-10

hsa04150	mTOR signaling pathway	1.33E-09
hsa05022	Pathways of neurodegeneration - multiple diseases	6.67E-09
hsa04920	Adipocytokine signaling pathway	1.57E-08
hsa04662	B cell receptor signaling pathway	5.09E-08
hsa04152	AMPK signaling pathway	6.17E-08
hsa05130	Pathogenic Escherichia coli infection	9.98E-07
hsa05414	Dilated cardiomyopathy	1.57E-06
hsa04623	Cytosolic DNA-sensing pathway	8.21E-06
hsa05410	Hypertrophic cardiomyopathy	0.000168
hsa05412	Arrhythmogenic right ventricular cardiomyopathy	0.000359
hsa05415	Diabetic cardiomyopathy	0.000384
hsa04330	Notch signaling pathway	0.000546
hsa04340	Hedgehog signaling pathway	0.000919
hsa04922	Glucagon signaling pathway	0.002313

Table S4. Result of GO enrichment analysis

Biological process

ID	Description	LogP
GO:0010035	response to inorganic substance	-51.4694
GO:0006979	response to oxidative stress	-41.7269
GO:0097190	apoptotic signaling pathway	-40.6086
GO:0009636	response to toxic substance	-40.318
GO:0034599	cellular response to oxidative stress	-38.5367
GO:0000302	response to reactive oxygen species	-36.1625
GO:0010942	positive regulation of cell death	-34.9653
GO:0071407	cellular response to organic cyclic compound	-34.4405
GO:0010038	response to metal ion	-34.3255
GO:1901699	cellular response to nitrogen compound	-34.0321
GO:1901652	response to peptide	-33.4979

GO:00513 47	positive regulation of transferase activity	-33.1327
GO:00713 96	cellular response to lipid	-32.9785
GO:00346 14	cellular response to reactive oxygen species	-32.0839
GO:00096 11	response to wounding	-31.6759
GO:00725 93	reactive oxygen species metabolic process	-31.5893
GO:00712 41	cellular response to inorganic substance	-31.351
GO:00336 74	positive regulation of kinase activity	-31.0399
GO:00709 97	neuron death	-30.7141
GO:00714 17	cellular response to organonitrogen compound	-30.2748
GO:00430 65	positive regulation of apoptotic process	-30.0645
GO:00430 68	positive regulation of programmed cell death	-29.8179
GO:00466 77	response to antibiotic	-29.6909
GO:00324 96	response to lipopolysaccharide	-29.3228
GO:00303 35	positive regulation of cell migration	-29.1178
GO:00719 00	regulation of protein serine/threonine kinase activity	-29.0829
GO:00712 48	cellular response to metal ion	-28.8839
GO:00356 90	cellular response to drug	-28.7306
GO:20012 33	regulation of apoptotic signaling pathway	-28.5335
GO:00022 37	response to molecule of bacterial origin	-28.3591
GO:20001 47	positive regulation of cell motility	-28.3352
GO:00182 09	peptidyl-serine modification	-28.0928
GO:00181 05	peptidyl-serine phosphorylation	-27.854

GO:0051272	positive regulation of cellular component movement	-27.8157	
GO:0040017	positive regulation of locomotion	-27.5346	
GO:0048732	gland development	-27.3986	
GO:0045860	positive regulation of protein kinase activity	-26.5444	
GO:0071902	positive regulation of protein serine/threonine kinase activity	-26.21	
GO:0007568	aging	-26.1821	
GO:0043410	positive regulation of MAPK cascade	-26.1028	
GO:1901214	regulation of neuron death	-26.096	
GO:0071216	cellular response to biotic stimulus	-25.7531	
GO:0030155	regulation of cell adhesion	-25.5956	
GO:0048608	reproductive structure development	-25.0777	
GO:0042060	wound healing	-25.0686	
GO:0071363	cellular response to growth factor stimulus	-25.0242	
GO:0061458	reproductive system development	-24.9463	
GO:0070848	response to growth factor	-24.333	
GO:0001568	blood vessel development	-24.3322	
GO:0097237	cellular response to toxic substance	-24.2388	
GO:0009617	response to bacterium	-24.2209	
GO:2000377	regulation of reactive oxygen species metabolic process	-24.2169	
GO:0009991	response to extracellular stimulus	-24.1556	
GO:2001234	negative regulation of apoptotic signaling pathway	-23.777	
GO:0080135	regulation of cellular response to stress	-23.6944	

GO:00466 86	response to cadmium ion	-23.3374
GO:00025 21	leukocyte differentiation	-23.3315
GO:00506 73	epithelial cell proliferation	-23.2873
GO:00330 02	muscle cell proliferation	-23.2338
GO:00514 02	neuron apoptotic process	-23.1858
GO:00434 08	regulation of MAPK cascade	-23.1449
GO:00328 70	cellular response to hormone stimulus	-22.901
GO:00181 08	peptidyl-tyrosine phosphorylation	-22.8069
GO:00182 12	peptidyl-tyrosine modification	-22.7031
GO:00011 01	response to acid chemical	-22.6362
GO:00971 93	intrinsic apoptotic signaling pathway	-22.4439
GO:00712 22	cellular response to lipopolysaccharide	-22.4267
GO:00071 69	transmembrane receptor protein tyrosine kinase signaling pathway	-22.2768
GO:00434 06	positive regulation of MAP kinase activity	-22.1815
GO:00316 67	response to nutrient levels	-21.8571
GO:00506 78	regulation of epithelial cell proliferation	-21.8083
GO:00224 07	regulation of cell-cell adhesion	-21.8053
GO:00712 19	cellular response to molecule of bacterial origin	-21.7146
GO:00434 34	response to peptide hormone	-21.5675
GO:00485 45	response to steroid hormone	-21.4317
GO:00971 91	extrinsic apoptotic signaling pathway	-21.3299
GO:00714 96	cellular response to external stimulus	-21.2578

GO:0001819	positive regulation of cytokine production	-21.1626
GO:2000379	positive regulation of reactive oxygen species metabolic process	-20.5312
GO:0009314	response to radiation	-20.5137
GO:0043491	protein kinase B signaling	-20.4953
GO:0003006	developmental process involved in reproduction	-20.4133
GO:0048514	blood vessel morphogenesis	-20.3509
GO:0043405	regulation of MAP kinase activity	-20.3159
GO:0048660	regulation of smooth muscle cell proliferation	-20.3123
GO:0009410	response to xenobiotic stimulus	-20.2201
GO:0048659	smooth muscle cell proliferation	-20.2008
GO:0001666	response to hypoxia	-19.9181
GO:0070482	response to oxygen levels	-19.868
GO:0010638	positive regulation of organelle organization	-19.8457
GO:0032147	activation of protein kinase activity	-19.7168
GO:0050900	leukocyte migration	-19.6967
GO:0051098	regulation of binding	-19.6294
GO:0036293	response to decreased oxygen levels	-19.5349
GO:0032103	positive regulation of response to external stimulus	-19.4469
GO:0048511	rhythmic process	-19.438
GO:0042063	gliogenesis	-19.4023
GO:0051090	regulation of DNA-binding transcription factor activity	-19.2575
GO:0050727	regulation of inflammatory response	-19.1593

GO:0045785	positive regulation of cell adhesion	-18.9401
GO:1901654	response to ketone	-18.9156
GO:1903409	reactive oxygen species biosynthetic process	-18.9006
GO:1904645	response to amyloid-beta	-18.7771
GO:0008285	negative regulation of cell proliferation	-18.7755
GO:0050865	regulation of cell activation	-18.6105
GO:0062012	regulation of small molecule metabolic process	-18.5795
GO:0002573	myeloid leukocyte differentiation	-18.4061
GO:0062013	positive regulation of small molecule metabolic process	-18.3457
GO:0043523	regulation of neuron apoptotic process	-18.2722
GO:0071276	cellular response to cadmium ion	-18.2623
GO:1901216	positive regulation of neuron death	-18.2383
GO:1902895	positive regulation of pri-miRNA transcription by RNA polymerase II	-17.9211
GO:0070201	regulation of establishment of protein localization	-17.7775
GO:0002064	epithelial cell development	-17.7572
GO:0030099	myeloid cell differentiation	-17.756
GO:0051046	regulation of secretion	-17.6083
GO:0001525	angiogenesis	-17.5829
GO:1901653	cellular response to peptide	-17.5441
GO:1904951	positive regulation of establishment of protein localization	-17.5167
GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	-17.4777
GO:0032787	monocarboxylic acid metabolic process	-17.4545

GO:00973 05	response to alcohol	-17.3906
GO:00467 77	protein autophosphorylation	-17.3112
GO:00455 96	negative regulation of cell differentiation	-17.2708
GO:00488 71	multicellular organismal homeostasis	-17.2534
GO:00098 96	positive regulation of catabolic process	-17.2433
GO:00001 87	activation of MAPK activity	-17.1779
GO:00900 87	regulation of peptide transport	-17.1662
GO:19038 27	regulation of cellular protein localization	-17.0097
GO:00316 68	cellular response to extracellular stimulus	-16.8279
GO:00323 55	response to estradiol	-16.7191
GO:00518 96	regulation of protein kinase B signaling	-16.7024
GO:19040 19	epithelial cell apoptotic process	-16.6008
GO:00071 59	leukocyte cell-cell adhesion	-16.4877
GO:00466 49	lymphocyte activation	-16.4781
GO:19030 37	regulation of leukocyte cell-cell adhesion	-16.4334
GO:00106 31	epithelial cell migration	-16.4316
GO:00100 01	glial cell differentiation	-16.3926
GO:00901 32	epithelium migration	-16.3481
GO:00486 61	positive regulation of smooth muscle cell proliferation	-16.3138
GO:19028 93	regulation of pri-miRNA transcription by RNA polymerase II	-16.232
GO:00106 34	positive regulation of epithelial cell migration	-16.1859
GO:00901 30	tissue migration	-16.1834

GO:19038 29	positive regulation of cellular protein localization	-16.1665
GO:19037 06	regulation of hemopoiesis	-16.134
GO:00457 86	negative regulation of cell cycle	-16.1204
GO:00616 14	pri-miRNA transcription by RNA polymerase II	-16.1126
GO:00019 35	endothelial cell proliferation	-16.1117
GO:00506 79	positive regulation of epithelial cell proliferation	-15.9484
GO:00105 06	regulation of autophagy	-15.8791
GO:00224 09	positive regulation of cell-cell adhesion	-15.8
GO:00706 61	leukocyte proliferation	-15.7998
GO:00313 31	positive regulation of cellular catabolic process	-15.7844
GO:00508 78	regulation of body fluid levels	-15.7836
GO:00463 94	carboxylic acid biosynthetic process	-15.7013
GO:00160 53	organic acid biosynthetic process	-15.6787
GO:00319 60	response to corticosteroid	-15.5298
GO:00181 07	peptidyl-threonine phosphorylation	-15.4001
GO:00507 31	positive regulation of peptidyl-tyrosine phosphorylation	-15.3949
GO:19030 34	regulation of response to wounding	-15.3121
GO:00464 25	regulation of JAK-STAT cascade	-15.2833
GO:19040 35	regulation of epithelial cell apoptotic process	-15.2244
GO:00507 30	regulation of peptidyl-tyrosine phosphorylation	-15.2078
GO:19035 30	regulation of secretion by cell	-15.1454
GO:00425 42	response to hydrogen peroxide	-15.1291

GO:00458 62	positive regulation of proteolysis	-15.0448
GO:00305 22	intracellular receptor signaling pathway	-15.043
GO:00512 23	regulation of protein transport	-15.0388
GO:19040 18	positive regulation of vasculature development	-15.0364
GO:00712 36	cellular response to antibiotic	-14.9785
GO:00518 97	positive regulation of protein kinase B signaling	-14.8939
GO:00182 10	peptidyl-threonine modification	-14.8753
GO:00512 49	regulation of lymphocyte activation	-14.8583
GO:20003 51	regulation of endothelial cell apoptotic process	-14.8555
GO:00096 12	response to mechanical stimulus	-14.8343
GO:19048 92	regulation of STAT cascade	-14.8312
GO:00603 26	cell chemotaxis	-14.7824
GO:00027 91	regulation of peptide secretion	-14.7082
GO:00723 30	monocarboxylic acid biosynthetic process	-14.6966
GO:00073 46	regulation of mitotic cell cycle	-14.6358
GO:00313 49	positive regulation of defense response	-14.5936
GO:00016 67	ameboidal-type cell migration	-14.5867
GO:00602 49	anatomical structure homeostasis	-14.5712
GO:00094 16	response to light stimulus	-14.554
GO:00432 81	regulation of cysteine-type endopeptidase activity involved in apoptotic process	-14.4957
GO:00316 69	cellular response to nutrient levels	-14.4847
GO:19013 42	regulation of vasculature development	-14.4364

GO:00725 77	endothelial cell apoptotic process	-14.4084	
GO:00026 83	negative regulation of immune system process	-14.3971	
GO:00512 22	positive regulation of protein transport	-14.3848	
GO:20012 36	regulation of extrinsic apoptotic signaling pathway	-14.3626	
GO:00019 36	regulation of endothelial cell proliferation	-14.3517	
GO:00400 08	regulation of growth	-14.3317	
GO:00313 34	positive regulation of protein complex assembly	-14.327	
GO:19021 05	regulation of leukocyte differentiation	-14.2974	
GO:00610 41	regulation of wound healing	-14.2284	
GO:00094 11	response to UV	-14.0876	
GO:00511 86	cofactor metabolic process	-14.0763	
GO:00069 35	chemotaxis	-14.0258	
GO:00432 69	regulation of ion transport	-14.0207	
GO:00511 00	negative regulation of binding	-14.0105	
GO:00106 32	regulation of epithelial cell migration	-14.0069	
GO:00030 13	circulatory system process	-13.9921	
GO:00423 30	taxis		-13.992
GO:00026 94	regulation of leukocyte activation	-13.9871	
GO:00070 50	cell cycle arrest	-13.8969	
GO:00510 91	positive regulation of DNA-binding transcription factor activity	-13.8789	
GO:00316 63	lipopolysaccharide-mediated signaling pathway	-13.8466	
GO:00066 90	icosanoid metabolic process	-13.7635	

GO:19037 08	positive regulation of hemopoiesis	-13.7385
GO:00706 63	regulation of leukocyte proliferation	-13.7301
GO:00713 83	cellular response to steroid hormone stimulus	-13.702
GO:00345 04	protein localization to nucleus	-13.6678
GO:20001 16	regulation of cysteine-type endopeptidase activity	-13.6644
GO:00435 36	positive regulation of blood vessel endothelial cell migration	-13.614
GO:19001 82	positive regulation of protein localization to nucleus	-13.614
GO:00705 55	response to interleukin-1	-13.5935
GO:00000 79	regulation of cyclin-dependent protein serine/threonine kinase activity	-13.5602
GO:00456 39	positive regulation of myeloid cell differentiation	-13.5602
GO:19028 82	regulation of response to oxidative stress	-13.5602
GO:19012 15	negative regulation of neuron death	-13.5578
GO:00714 66	cellular response to xenobiotic stimulus	-13.5556
GO:00346 12	response to tumor necrosis factor	-13.5107
GO:19001 80	regulation of protein localization to nucleus	-13.4997
GO:00069 14	autophagy	-13.4688
GO:00619 19	process utilizing autophagic mechanism	-13.4688
GO:00328 68	response to insulin	-13.4338
GO:00507 08	regulation of protein secretion	-13.4247
GO:00432 54	regulation of protein complex assembly	-13.3688
GO:00018 90	placenta development	-13.3445
GO:19040 29	regulation of cyclin-dependent protein kinase activity	-13.3214

GO:00080 15	blood circulation	-13.3018
GO:00108 17	regulation of hormone levels	-13.2652
GO:00421 36	neurotransmitter biosynthetic process	-13.2058
GO:00082 02	steroid metabolic process	-13.1972
GO:00703 71	ERK1 and ERK2 cascade	-13.1972
GO:00510 47	positive regulation of secretion	-13.1651
GO:00420 35	regulation of cytokine biosynthetic process	-13.1398
GO:00072 59	JAK-STAT cascade	-13.1296
GO:00075 65	female pregnancy	-12.9828
GO:00421 08	positive regulation of cytokine biosynthetic process	-12.9818
GO:00456 37	regulation of myeloid cell differentiation	-12.9803
GO:20012 42	regulation of intrinsic apoptotic signaling pathway	-12.9629
GO:00432 00	response to amino acid	-12.8727
GO:00464 27	positive regulation of JAK-STAT cascade	-12.8604
GO:00192 16	regulation of lipid metabolic process	-12.8575
GO:00310 99	regeneration	-12.8027
GO:19051 14	cell surface receptor signaling pathway involved in cell-cell signaling	-12.8
GO:19004 07	regulation of cellular response to oxidative stress	-12.797
GO:19030 39	positive regulation of leukocyte cell-cell adhesion	-12.7838
GO:00308 79	mammary gland development	-12.7732
GO:00420 89	cytokine biosynthetic process	-12.7451
GO:00976 96	STAT cascade	-12.7212

GO:19025 32	negative regulation of intracellular signal transduction	-12.7162
GO:00421 10	T cell activation	-12.7115
GO:19048 94	positive regulation of STAT cascade	-12.6725
GO:00421 07	cytokine metabolic process	-12.6699
GO:00457 87	positive regulation of cell cycle	-12.664
GO:00466 60	female sex differentiation	-12.6098
GO:00030 18	vascular process in circulatory system	-12.6038
GO:19015 68	fatty acid derivative metabolic process	-12.6038
GO:00165 72	histone phosphorylation	-12.6038
GO:00068 01	superoxide metabolic process	-12.5959
GO:00987 71	inorganic ion homeostasis	-12.5727
GO:00457 66	positive regulation of angiogenesis	-12.5589
GO:00513 84	response to glucocorticoid	-12.5499
GO:00510 54	positive regulation of DNA metabolic process	-12.5345
GO:00075 48	sex differentiation	-12.4945
GO:00712 29	cellular response to acid chemical	-12.4909
GO:00424 45	hormone metabolic process	-12.4736
GO:00433 93	regulation of protein binding	-12.4237
GO:00140 74	response to purine-containing compound	-12.42
GO:00466 51	lymphocyte proliferation	-12.4123
GO:00027 61	regulation of myeloid leukocyte differentiation	-12.4082
GO:00015 05	regulation of neurotransmitter levels	-12.3979

GO:00606 27	regulation of vesicle-mediated transport	-12.3871
GO:00027 63	positive regulation of myeloid leukocyte differentiation	-12.3789
GO:00193 69	arachidonic acid metabolic process	-12.3789
GO:00487 71	tissue remodeling	-12.3385
GO:00329 43	mononuclear cell proliferation	-12.331
GO:00435 42	endothelial cell migration	-12.331
GO:00086 37	apoptotic mitochondrial changes	-12.3102
GO:00458 34	positive regulation of lipid metabolic process	-12.293
GO:00459 81	positive regulation of nucleotide metabolic process	-12.292
GO:19005 44	positive regulation of purine nucleotide metabolic process	-12.292
GO:00027 90	peptide secretion	-12.2831
GO:19016 15	organic hydroxy compound metabolic process	-12.2831
GO:00140 65	phosphatidylinositol 3-kinase signaling	-12.2512
GO:00068 09	nitric oxide biosynthetic process	-12.2417
GO:00140 66	regulation of phosphatidylinositol 3-kinase signaling	-12.2138
GO:00713 75	cellular response to peptide hormone stimulus	-12.1948
GO:00075 84	response to nutrient	-12.1939
GO:00712 14	cellular response to abiotic stimulus	-12.1706
GO:01040 04	cellular response to environmental stimulus	-12.1706
GO:00421 33	neurotransmitter metabolic process	-12.1687
GO:00725 94	establishment of protein localization to organelle	-12.1633
GO:00488 72	homeostasis of number of cells	-12.1197

GO:0045080	positive regulation of chemokine biosynthetic process	-12.1066
GO:0043534	blood vessel endothelial cell migration	-12.0491
GO:0030168	platelet activation	-12.047
GO:0008610	lipid biosynthetic process	-12.0045
GO:0044706	multi-multicellular organism process	-11.9722
GO:1902107	positive regulation of leukocyte differentiation	-11.9674
GO:0031098	stress-activated protein kinase signaling cascade	-11.9387
GO:0010595	positive regulation of endothelial cell migration	-11.9347
GO:0098754	detoxification	-11.9347
GO:0046209	nitric oxide metabolic process	-11.9118
GO:0007596	blood coagulation	-11.9104
GO:1905475	regulation of protein localization to membrane	-11.875
GO:0046683	response to organophosphorus	-11.8448
GO:0007599	hemostasis	-11.7953
GO:0050817	coagulation	-11.7725
GO:0009615	response to virus	-11.7498
GO:1904646	cellular response to amyloid-beta	-11.7385
GO:0009743	response to carbohydrate	-11.7282
GO:2001057	reactive nitrogen species metabolic process	-11.7243
GO:0070372	regulation of ERK1 and ERK2 cascade	-11.6893
GO:0032102	negative regulation of response to external stimulus	-11.6779
GO:0001938	positive regulation of endothelial cell proliferation	-11.6199

GO:00086 25	extrinsic apoptotic signaling pathway via death domain receptors	-11.6033
GO:19907 48	cellular detoxification	-11.5701
GO:00457 65	regulation of angiogenesis	-11.5545
GO:00425 94	response to starvation	-11.5092
GO:00481 46	positive regulation of fibroblast proliferation	-11.4559
GO:00714 56	cellular response to hypoxia	-11.445
GO:00432 70	positive regulation of ion transport	-11.3879
GO:00335 59	unsaturated fatty acid metabolic process	-11.3756
GO:00381 27	ERBB signaling pathway	-11.3755
GO:00015 03	ossification	-11.3733
GO:00070 05	mitochondrion organization	-11.3647
GO:00485 89	developmental growth	-11.3162
GO:00026 85	regulation of leukocyte migration	-11.2876
GO:00514 03	stress-activated MAPK cascade	-11.2862
GO:00440 89	positive regulation of cellular component biogenesis	-11.2838
GO:00093 06	protein secretion	-11.2323
GO:00508 63	regulation of T cell activation	-11.217
GO:00525 47	regulation of peptidase activity	-11.2074
GO:00450 73	regulation of chemokine biosynthetic process	-11.2048
GO:00519 24	regulation of calcium ion transport	-11.1846
GO:00019 59	regulation of cytokine-mediated signaling pathway	-11.158
GO:20012 35	positive regulation of apoptotic signaling pathway	-11.158

GO:19016 55	cellular response to ketone	-11.1479
GO:00454 71	response to ethanol	-11.1427
GO:00550 80	cation homeostasis	-11.1394
GO:00362 94	cellular response to decreased oxygen levels	-11.1344
GO:00703 74	positive regulation of ERK1 and ERK2 cascade	-11.1042
GO:00364 73	cell death in response to oxidative stress	-11.094
GO:20012 43	negative regulation of intrinsic apoptotic signaling pathway	-11.094
GO:00311 00	animal organ regeneration	-11.0932
GO:00380 34	signal transduction in absence of ligand	-11.0932
GO:00971 92	extrinsic apoptotic signaling pathway in absence of ligand	-11.0932
GO:00713 56	cellular response to tumor necrosis factor	-11.0633
GO:00226 12	gland morphogenesis	-11.0524
GO:00459 30	negative regulation of mitotic cell cycle	-11.0151
GO:00725 11	divalent inorganic cation transport	-10.9935
GO:00085 85	female gonad development	-10.9879
GO:00084 06	gonad development	-10.9851
GO:00071 62	negative regulation of cell adhesion	-10.9667
GO:01500 76	neuroinflammatory response	-10.9639
GO:19032 01	regulation of oxidative stress-induced cell death	-10.9639
GO:00420 33	chemokine biosynthetic process	-10.9577
GO:00507 55	chemokine metabolic process	-10.9577
GO:00975 29	myeloid leukocyte migration	-10.9557

GO:00900 68	positive regulation of cell cycle process	-10.9428
GO:00525 48	regulation of endopeptidase activity	-10.9117
GO:00480 15	phosphatidylinositol-mediated signaling	-10.8579
GO:00027 93	positive regulation of peptide secretion	-10.8395
GO:00086 30	intrinsic apoptotic signaling pathway in response to DNA damage	-10.8331
GO:00988 69	cellular oxidant detoxification	-10.8331
GO:00510 92	positive regulation of NF-kappaB transcription factor activity	-10.8325
GO:00451 37	development of primary sexual characteristics	-10.8108
GO:00109 59	regulation of metal ion transport	-10.7987
GO:00723 31	signal transduction by p53 class mediator	-10.7873
GO:00435 25	positive regulation of neuron apoptotic process	-10.7863
GO:00421 76	regulation of protein catabolic process	-10.779
GO:00465 45	development of primary female sexual characteristics	-10.7327
GO:00480 17	inositol lipid-mediated signaling	-10.7296
GO:00607 59	regulation of response to cytokine stimulus	-10.7296
GO:00092 67	cellular response to starvation	-10.723
GO:00305 95	leukocyte chemotaxis	-10.6975
GO:00459 36	negative regulation of phosphate metabolic process	-10.6809
GO:00092 66	response to temperature stimulus	-10.6695
GO:00105 63	negative regulation of phosphorus metabolic process	-10.6661
GO:00435 35	regulation of blood vessel endothelial cell migration	-10.6513
GO:19013 61	organic cyclic compound catabolic process	-10.6446

GO:00714 53	cellular response to oxygen levels	-10.6417
GO:00327 22	positive regulation of chemokine production	-10.6348
GO:19034 26	regulation of reactive oxygen species biosynthetic process	-10.6344
GO:00508 04	modulation of chemical synaptic transmission	-10.6025
GO:00481 45	regulation of fibroblast proliferation	-10.5974
GO:00487 08	astrocyte differentiation	-10.5974
GO:00718 87	leukocyte apoptotic process	-10.586
GO:00991 77	regulation of trans-synaptic signaling	-10.5847
GO:00513 45	positive regulation of hydrolase activity	-10.5692
GO:00459 31	positive regulation of mitotic cell cycle	-10.5456
GO:00481 44	fibroblast proliferation	-10.5392
GO:00105 94	regulation of endothelial cell migration	-10.5316
GO:00105 64	regulation of cell cycle process	-10.4698
GO:00300 98	lymphocyte differentiation	-10.4444
GO:00068 73	cellular ion homeostasis	-10.433
GO:00031 58	endothelium development	-10.4232
GO:00507 14	positive regulation of protein secretion	-10.3914
GO:00018 89	liver development	-10.384
GO:00450 55	regulated exocytosis	-10.3839
GO:19047 05	regulation of vascular smooth muscle cell proliferation	-10.3692
GO:19908 74	vascular smooth muscle cell proliferation	-10.3692
GO:00342 84	response to monosaccharide	-10.3617

GO:0001676	long-chain fatty acid metabolic process	-10.3514
GO:0042113	B cell activation	-10.3511
GO:0007249	I-kappaB kinase/NF-kappaB signaling	-10.3429
GO:0002697	regulation of immune effector process	-10.3237
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	-10.314
GO:0032642	regulation of chemokine production	-10.314
GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	-10.3078
GO:0035296	regulation of tube diameter	-10.3064
GO:0050880	regulation of blood vessel size	-10.3064
GO:0097746	regulation of blood vessel diameter	-10.3064
GO:0006109	regulation of carbohydrate metabolic process	-10.3027
GO:0034764	positive regulation of transmembrane transport	-10.3027
GO:0035150	regulation of tube size	-10.2681
GO:0061008	hepaticobiliary system development	-10.2681
GO:0043620	regulation of DNA-templated transcription in response to stress	-10.2608
GO:0002764	immune response-regulating signaling pathway	-10.2584
GO:0070838	divalent metal ion transport	-10.2389
GO:0002700	regulation of production of molecular mediator of immune response	-10.2301
GO:0030810	positive regulation of nucleotide biosynthetic process	-10.1771
GO:1900373	positive regulation of purine nucleotide biosynthetic process	-10.1771
GO:1903580	positive regulation of ATP metabolic process	-10.1771
GO:0034976	response to endoplasmic reticulum stress	-10.1555

GO:19005 42	regulation of purine nucleotide metabolic process	-10.1178
GO:00435 24	negative regulation of neuron apoptotic process	-10.0809
GO:00076 23	circadian rhythm	-10.073
GO:19035 32	positive regulation of secretion by cell	-10.0546
GO:00713 47	cellular response to interleukin-1	-10.0469
GO:00506 70	regulation of lymphocyte proliferation	-10.045
GO:00426 98	ovulation cycle	-10.0163
GO:19040 36	negative regulation of epithelial cell apoptotic process	-10.0082
GO:00329 44	regulation of mononuclear cell proliferation	-9.98935
GO:00061 40	regulation of nucleotide metabolic process	-9.97194
GO:00427 59	long-chain fatty acid biosynthetic process	-9.95392
GO:00326 02	chemokine production	-9.94602
GO:00511 29	negative regulation of cellular component organization	-9.92985
GO:00069 84	ER-nucleus signaling pathway	-9.92664
GO:00447 72	mitotic cell cycle phase transition	-9.91465
GO:00066 31	fatty acid metabolic process	-9.90209
GO:00067 21	terpenoid metabolic process	-9.87372
GO:00511 01	regulation of DNA binding	-9.87372
GO:00421 00	B cell proliferation	-9.84643
GO:00022 63	cell activation involved in immune response	-9.84526
GO:19040 31	positive regulation of cyclin-dependent protein kinase activity	-9.84394
GO:00300 03	cellular cation homeostasis	-9.84001

GO:00448 43	cell cycle G1/S phase transition	-9.79793
GO:00303 16	osteoclast differentiation	-9.79748
GO:00510 52	regulation of DNA metabolic process	-9.79481
GO:00487 29	tissue morphogenesis	-9.78729
GO:00020 09	morphogenesis of an epithelium	-9.77194
GO:00518 81	regulation of mitochondrial membrane potential	-9.7694
GO:00344 05	response to fluid shear stress	-9.73751
GO:20003 52	negative regulation of endothelial cell apoptotic process	-9.73751
GO:00140 13	regulation of gliogenesis	-9.71165
GO:00985 42	defense response to other organism	-9.70553
GO:00703 01	cellular response to hydrogen peroxide	-9.70125
GO:00108 21	regulation of mitochondrion organization	-9.68013
GO:00430 62	extracellular structure organization	-9.67751
GO:00704 23	nucleotide-binding oligomerization domain containing signaling pathway	-9.63443
GO:00434 67	regulation of generation of precursor metabolites and energy	-9.62543
GO:00995 36	synaptic signaling	-9.61058
GO:00431 12	receptor metabolic process	-9.53477
GO:00358 72	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	-9.53449
GO:00224 11	cellular component disassembly	-9.52608
GO:00160 55	Wnt signaling pathway	-9.52053
GO:00432 79	response to alkaloid	-9.51508
GO:00060 91	generation of precursor metabolites and energy	-9.49035

GO:01987 38	cell-cell signaling by wnt	-9.49035
GO:00347 54	cellular hormone metabolic process	-9.47888
GO:00094 08	response to heat	-9.46109
GO:00508 67	positive regulation of cell activation	-9.45468
GO:00097 46	response to hexose	-9.44952
GO:00192 33	sensory perception of pain	-9.42496
GO:00068 16	calcium ion transport	-9.36897
GO:00016 55	urogenital system development	-9.35976
GO:00000 82	G1/S transition of mitotic cell cycle	-9.35515
GO:00508 66	negative regulation of cell activation	-9.33805
GO:00301 00	regulation of endocytosis	-9.3331
GO:00464 56	icosanoid biosynthetic process	-9.3326
GO:00447 70	cell cycle phase transition	-9.3054
GO:00436 18	regulation of transcription from RNA polymerase II promoter in response to stress	-9.29329
GO:00066 33	fatty acid biosynthetic process	-9.27105
GO:00977 55	positive regulation of blood vessel diameter	-9.26476
GO:19034 28	positive regulation of reactive oxygen species biosynthetic process	-9.26476
GO:00423 26	negative regulation of phosphorylation	-9.25986
GO:00380 83	peptidyl-tyrosine autophosphorylation	-9.25177
GO:19020 42	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	-9.25177
GO:00016 59	temperature homeostasis	-9.2401
GO:00459 13	positive regulation of carbohydrate metabolic process	-9.21225

GO:0055065	metal ion homeostasis	-9.17708
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	-9.16065
GO:0002366	leukocyte activation involved in immune response	-9.15952
GO:0007254	JNK cascade	-9.14875
GO:0071384	cellular response to corticosteroid stimulus	-9.1328
GO:0051301	cell division	-9.12652
GO:0006720	isoprenoid metabolic process	-9.11577
GO:0050921	positive regulation of chemotaxis	-9.11577
GO:0001776	leukocyte homeostasis	-9.10972
GO:0042446	hormone biosynthetic process	-9.10972
GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	-9.09729
GO:0007268	chemical synaptic transmission	-9.08786
GO:0098916	anterograde trans-synaptic signaling	-9.08786
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	-9.07605
GO:0032386	regulation of intracellular transport	-9.07006
GO:0044270	cellular nitrogen compound catabolic process	-9.0405
GO:0030198	extracellular matrix organization	-9.01353
GO:0051493	regulation of cytoskeleton organization	-9.01178
GO:0060135	maternal process involved in female pregnancy	-9.00552
GO:0099537	trans-synaptic signaling	-8.99347
GO:0001892	embryonic placenta development	-8.91241
GO:20000	regulation of G1/S transition of mitotic cell cycle	-8.9124

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GO:0070665	positive regulation of leukocyte proliferation	-8.91125
GO:0045429	positive regulation of nitric oxide biosynthetic process	-8.90933
GO:0002253	activation of immune response	-8.90036
GO:0072521	purine-containing compound metabolic process	-8.87733
GO:0051251	positive regulation of lymphocyte activation	-8.86021
GO:0002696	positive regulation of leukocyte activation	-8.85943
GO:0038061	NIK/NF-kappaB signaling	-8.85519
GO:0061061	muscle structure development	-8.85451
GO:0016999	antibiotic metabolic process	-8.84512
GO:1900371	regulation of purine nucleotide biosynthetic process	-8.84299
GO:0045732	positive regulation of protein catabolic process	-8.84013
GO:0045088	regulation of innate immune response	-8.83183
GO:1904407	positive regulation of nitric oxide metabolic process	-8.82908
GO:0044057	regulation of system process	-8.82607
GO:0030808	regulation of nucleotide biosynthetic process	-8.80436
GO:0032869	cellular response to insulin stimulus	-8.79052
GO:2000117	negative regulation of cysteine-type endopeptidase activity	-8.77074
GO:0021782	glial cell development	-8.76609
GO:0045446	endothelial cell differentiation	-8.76609
GO:0050920	regulation of chemotaxis	-8.7659
GO:0045428	regulation of nitric oxide biosynthetic process	-8.76378

GO:19043 75	regulation of protein localization to cell periphery	-8.72817
GO:00018 94	tissue homeostasis	-8.71702
GO:00347 62	regulation of transmembrane transport	-8.71162
GO:00900 66	regulation of anatomical structure size	-8.70997
GO:00018 85	endothelial cell development	-8.70583
GO:00027 53	cytoplasmic pattern recognition receptor signaling pathway	-8.70583
GO:20005 73	positive regulation of DNA biosynthetic process	-8.70583
GO:00904 07	organophosphate biosynthetic process	-8.69892
GO:00071 73	epidermal growth factor receptor signaling pathway	-8.69059
GO:00515 91	response to cAMP	-8.6791
GO:00309 68	endoplasmic reticulum unfolded protein response	-8.65335
GO:19035 78	regulation of ATP metabolic process	-8.65335
GO:00314 00	negative regulation of protein modification process	-8.63739
GO:00018 18	negative regulation of cytokine production	-8.62623
GO:00611 80	mammary gland epithelium development	-8.59267
GO:19054 77	positive regulation of protein localization to membrane	-8.57986
GO:00097 49	response to glucose	-8.55248
GO:00480 10	vascular endothelial growth factor receptor signaling pathway	-8.54559
GO:00082 10	estrogen metabolic process	-8.53209
GO:00381 28	ERBB2 signaling pathway	-8.53209
GO:00717 15	icosanoid transport	-8.52661
GO:19015 71	fatty acid derivative transport	-8.52661

GO:19047 07	positive regulation of vascular smooth muscle cell proliferation	-8.52661
GO:00603 59	response to ammonium ion	-8.50766
GO:00328 72	regulation of stress-activated MAPK cascade	-8.50296
GO:00973 27	response to antineoplastic agent	-8.5021
GO:00718 97	DNA biosynthetic process	-8.4995
GO:00726 57	protein localization to membrane	-8.47826
GO:00060 66	alcohol metabolic process	-8.46988
GO:00091 17	nucleotide metabolic process	-8.45515
GO:00027 57	immune response-activating signal transduction	-8.4421
GO:00703 02	regulation of stress-activated protein kinase signaling cascade	-8.43364
GO:00069 09	phagocytosis	-8.41873
GO:00326 37	interleukin-8 production	-8.41657
GO:00359 24	cellular response to vascular endothelial growth factor stimulus	-8.37666
GO:00067 53	nucleoside phosphate metabolic process	-8.37589
GO:19030 76	regulation of protein localization to plasma membrane	-8.37451
GO:00017 01	in utero embryonic development	-8.36807
GO:00427 70	signal transduction in response to DNA damage	-8.36695
GO:19028 06	regulation of cell cycle G1/S phase transition	-8.34412
GO:00425 93	glucose homeostasis	-8.34275
GO:00467 00	heterocycle catabolic process	-8.34221
GO:00091 65	nucleotide biosynthetic process	-8.33455
GO:19015 70	fatty acid derivative biosynthetic process	-8.33291

GO:0033500	carbohydrate homeostasis	-8.32029	
GO:0046890	regulation of lipid biosynthetic process	-8.31873	
GO:0045089	positive regulation of innate immune response	-8.31787	
GO:0061756	leukocyte adhesion to vascular endothelial cell	-8.31706	
GO:0007610	behavior		-8.29932
GO:0010042	response to manganese ion	-8.29246	
GO:0032635	interleukin-6 production	-8.29075	
GO:1901293	nucleoside phosphate biosynthetic process	-8.28466	
GO:0044070	regulation of anion transport	-8.25105	
GO:0001933	negative regulation of protein phosphorylation	-8.25102	
GO:0032757	positive regulation of interleukin-8 production	-8.25014	
GO:0051194	positive regulation of cofactor metabolic process	-8.2396	
GO:0030856	regulation of epithelial cell differentiation	-8.23328	
GO:0050806	positive regulation of synaptic transmission	-8.23328	
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	-8.23149	
GO:0071156	regulation of cell cycle arrest	-8.21077	
GO:0019439	aromatic compound catabolic process	-8.19831	
GO:0009145	purine nucleoside triphosphate biosynthetic process	-8.17657	
GO:0051099	positive regulation of binding	-8.17657	
GO:0032091	negative regulation of protein binding	-8.17091	
GO:0036499	PERK-mediated unfolded protein response	-8.14898	
GO:00105	regulation of platelet activation	-8.14838	

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GO:0010332	response to gamma radiation	-8.12037
GO:0033138	positive regulation of peptidyl-serine phosphorylation	-8.09243
GO:0061045	negative regulation of wound healing	-8.07562
GO:0019932	second-messenger-mediated signaling	-8.0718
GO:0002687	positive regulation of leukocyte migration	-8.06702
GO:0048638	regulation of developmental growth	-8.06507
GO:0006164	purine nucleotide biosynthetic process	-8.065
GO:0090218	positive regulation of lipid kinase activity	-8.06
GO:1904994	regulation of leukocyte adhesion to vascular endothelial cell	-8.06
GO:2001171	positive regulation of ATP biosynthetic process	-8.06
GO:0051607	defense response to virus	-8.05868
GO:0042743	hydrogen peroxide metabolic process	-8.05741
GO:0010720	positive regulation of cell development	-8.05095
GO:0046886	positive regulation of hormone biosynthetic process	-8.04866
GO:0005975	carbohydrate metabolic process	-8.03118
GO:0030193	regulation of blood coagulation	-8.02787
GO:0002440	production of molecular mediator of immune response	-8.00806
GO:1901617	organic hydroxy compound biosynthetic process	-7.99547
GO:0071277	cellular response to calcium ion	-7.98076
GO:1900046	regulation of hemostasis	-7.98076
GO:0032885	regulation of polysaccharide biosynthetic process	-7.97427

GO:00102 12	response to ionizing radiation	-7.97177
GO:00331 35	regulation of peptidyl-serine phosphorylation	-7.97177
GO:00713 46	cellular response to interferon-gamma	-7.9569
GO:00346 20	cellular response to unfolded protein	-7.94051
GO:00713 85	cellular response to glucocorticoid stimulus	-7.93511
GO:19049 96	positive regulation of leukocyte adhesion to vascular endothelial cell	-7.8847
GO:00515 92	response to calcium ion	-7.87872
GO:00091 68	purine ribonucleoside monophosphate biosynthetic process	-7.87734
GO:00018 36	release of cytochrome c from mitochondria	-7.87568
GO:00619 00	glial cell activation	-7.87568
GO:00313 48	negative regulation of defense response	-7.87151
GO:00725 22	purine-containing compound biosynthetic process	-7.85937
GO:00068 75	cellular metal ion homeostasis	-7.85077
GO:00069 70	response to osmotic stress	-7.84315
GO:00061 63	purine nucleotide metabolic process	-7.82623
GO:00091 27	purine nucleoside monophosphate biosynthetic process	-7.82511
GO:00066 06	protein import into nucleus	-7.81786
GO:00336 19	membrane protein proteolysis	-7.81734
GO:19020 41	regulation of extrinsic apoptotic signaling pathway via death domain receptors	-7.81734
GO:00070 77	mitotic nuclear envelope disassembly	-7.81717
GO:00718 03	positive regulation of podosome assembly	-7.81717
GO:00431 23	positive regulation of I-kappaB kinase/NF-kappaB signaling	-7.79923

GO:0051341	regulation of oxidoreductase activity	-7.79387
GO:0097530	granulocyte migration	-7.78778
GO:0051188	cofactor biosynthetic process	-7.76868
GO:0002719	negative regulation of cytokine production involved in immune response	-7.76242
GO:0045821	positive regulation of glycolytic process	-7.76242
GO:1902993	positive regulation of amyloid precursor protein catabolic process	-7.76242
GO:0002260	lymphocyte homeostasis	-7.76007
GO:0030888	regulation of B cell proliferation	-7.76007
GO:0032755	positive regulation of interleukin-6 production	-7.75435
GO:0050818	regulation of coagulation	-7.75435
GO:0090559	regulation of membrane permeability	-7.75435
GO:0009142	nucleoside triphosphate biosynthetic process	-7.74795
GO:0022408	negative regulation of cell-cell adhesion	-7.72254
GO:0045807	positive regulation of endocytosis	-7.69885
GO:0009895	negative regulation of catabolic process	-7.69731
GO:0010822	positive regulation of mitochondrion organization	-7.68776
GO:0030111	regulation of Wnt signaling pathway	-7.68106
GO:0043900	regulation of multi-organism process	-7.67514
GO:0070542	response to fatty acid	-7.66777
GO:0051193	regulation of cofactor metabolic process	-7.65305
GO:0070920	regulation of production of small RNA involved in gene silencing by RNA	-7.64588
GO:0050864	regulation of B cell activation	-7.6224

GO:00326 12	interleukin-1 production	-7.61866
GO:00519 28	positive regulation of calcium ion transport	-7.61866
GO:00507 28	negative regulation of inflammatory response	-7.59773
GO:00327 68	regulation of monooxygenase activity	-7.59421
GO:00341 03	regulation of tissue remodeling	-7.58331
GO:19058 97	regulation of response to endoplasmic reticulum stress	-7.58331
GO:00466 88	response to copper ion	-7.58061
GO:00516 03	proteolysis involved in cellular protein catabolic process	-7.55875
GO:00326 75	regulation of interleukin-6 production	-7.55492
GO:00507 77	negative regulation of immune response	-7.55492
GO:00066 94	steroid biosynthetic process	-7.54882
GO:00326 77	regulation of interleukin-8 production	-7.54184
GO:00468 24	positive regulation of nucleocytoplasmic transport	-7.54081
GO:00194 30	removal of superoxide radicals	-7.53459
GO:00308 13	positive regulation of nucleotide catabolic process	-7.53459
GO:00511 97	positive regulation of coenzyme metabolic process	-7.53459
GO:00091 56	ribonucleoside monophosphate biosynthetic process	-7.52458
GO:00328 81	regulation of polysaccharide metabolic process	-7.50804
GO:00328 90	regulation of organic acid transport	-7.48831
GO:00435 50	regulation of lipid kinase activity	-7.48831
GO:00456 70	regulation of osteoclast differentiation	-7.48831
GO:20001 34	negative regulation of G1/S transition of mitotic cell cycle	-7.4842

GO:00423 91	regulation of membrane potential	-7.47247
GO:00067 54	ATP biosynthetic process	-7.471
GO:00343 41	response to interferon-gamma	-7.45268
GO:00716 21	granulocyte chemotaxis	-7.45134
GO:00140 02	astrocyte development	-7.43731
GO:00309 00	forebrain development	-7.43013
GO:00456 72	positive regulation of osteoclast differentiation	-7.42809
GO:00468 85	regulation of hormone biosynthetic process	-7.42809
GO:00481 43	astrocyte activation	-7.42809
GO:19030 35	negative regulation of response to wounding	-7.42037
GO:00105 08	positive regulation of autophagy	-7.41876
GO:00109 52	positive regulation of peptidase activity	-7.40543
GO:19019 90	regulation of mitotic cell cycle phase transition	-7.40197
GO:00107 21	negative regulation of cell development	-7.38858
GO:00025 76	platelet degranulation	-7.38647
GO:00026 37	regulation of immunoglobulin production	-7.38587
GO:00486 62	negative regulation of smooth muscle cell proliferation	-7.38587
GO:00009 04	cell morphogenesis involved in differentiation	-7.38444
GO:00160 98	monoterpenoid metabolic process	-7.38285
GO:00022 21	pattern recognition receptor signaling pathway	-7.382
GO:00157 11	organic anion transport	-7.36957
GO:00507 68	negative regulation of neurogenesis	-7.36935

GO:0007093	mitotic cell cycle checkpoint	-7.36181
GO:0035967	cellular response to topologically incorrect protein	-7.36181
GO:2001169	regulation of ATP biosynthetic process	-7.34172
GO:0071695	anatomical structure maturation	-7.33498
GO:0051348	negative regulation of transferase activity	-7.33289
GO:0032770	positive regulation of monooxygenase activity	-7.32601
GO:0071450	cellular response to oxygen radical	-7.32601
GO:0071451	cellular response to superoxide	-7.32601
GO:0019218	regulation of steroid metabolic process	-7.32273
GO:0051271	negative regulation of cellular component movement	-7.30925
GO:0002819	regulation of adaptive immune response	-7.30834
GO:0009167	purine ribonucleoside monophosphate metabolic process	-7.30622
GO:0043255	regulation of carbohydrate biosynthetic process	-7.30306
GO:0050810	regulation of steroid biosynthetic process	-7.30306
GO:0022602	ovulation cycle process	-7.30095
GO:0030225	macrophage differentiation	-7.30095
GO:0042572	retinol metabolic process	-7.30095
GO:1902807	negative regulation of cell cycle G1/S phase transition	-7.29126
GO:0009124	nucleoside monophosphate biosynthetic process	-7.28959
GO:0042982	amyloid precursor protein metabolic process	-7.28668
GO:0030336	negative regulation of cell migration	-7.27368
GO:0009126	purine nucleoside monophosphate metabolic process	-7.25749

GO:0016125	sterol metabolic process	-7.25558
GO:0034349	glial cell apoptotic process	-7.24611
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	-7.23825
GO:0034248	regulation of cellular amide metabolic process	-7.22947
GO:0051170	import into nucleus	-7.22947
GO:0001782	B cell homeostasis	-7.22798
GO:0042116	macrophage activation	-7.22705
GO:0071560	cellular response to transforming growth factor beta stimulus	-7.22265
GO:0006511	ubiquitin-dependent protein catabolic process	-7.22263
GO:0051966	regulation of synaptic transmission, glutamatergic	-7.19055
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	-7.17776
GO:0032680	regulation of tumor necrosis factor production	-7.17776
GO:0050870	positive regulation of T cell activation	-7.1769
GO:0002758	innate immune response-activating signal transduction	-7.17234
GO:0030850	prostate gland development	-7.17093
GO:0042149	cellular response to glucose starvation	-7.17093
GO:0019941	modification-dependent protein catabolic process	-7.15699
GO:0000303	response to superoxide	-7.13372
GO:0035666	TRIF-dependent toll-like receptor signaling pathway	-7.13372
GO:0060055	angiogenesis involved in wound healing	-7.13372
GO:0040013	negative regulation of locomotion	-7.1333
GO:0031589	cell-substrate adhesion	-7.11422

GO:0001961	positive regulation of cytokine-mediated signaling pathway	-7.10812
GO:0042987	amyloid precursor protein catabolic process	-7.10812
GO:0071559	response to transforming growth factor beta	-7.10536
GO:0016241	regulation of macroautophagy	-7.10146
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	-7.10146
GO:0046323	glucose import	-7.09731
GO:0019372	lipxygenase pathway	-7.08597
GO:0030397	membrane disassembly	-7.08597
GO:0032352	positive regulation of hormone metabolic process	-7.08597
GO:0051081	nuclear envelope disassembly	-7.08597
GO:0071801	regulation of podosome assembly	-7.08597
GO:0009161	ribonucleoside monophosphate metabolic process	-7.08297
GO:0002367	cytokine production involved in immune response	-7.07994
GO:0009135	purine nucleoside diphosphate metabolic process	-7.07829
GO:0009179	purine ribonucleoside diphosphate metabolic process	-7.07829
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	-7.05192
GO:0010469	regulation of signaling receptor activity	-7.05141
GO:0032640	tumor necrosis factor production	-7.05141
GO:0050435	amyloid-beta metabolic process	-7.04669
GO:0000305	response to oxygen radical	-7.04295
GO:0043632	modification-dependent macromolecule catabolic process	-7.03865
GO:2000146	negative regulation of cell motility	-7.03648

GO:0009201	ribonucleoside triphosphate biosynthetic process	-7.02663
GO:0023061	signal release	-7.02422
GO:0030330	DNA damage response, signal transduction by p53 class mediator	-7.00872
GO:0032611	interleukin-1 beta production	-7.00872
GO:0014015	positive regulation of gliogenesis	-7.0068
GO:0046902	regulation of mitochondrial membrane permeability	-7.0068
GO:0009185	ribonucleoside diphosphate metabolic process	-6.9907
GO:0050999	regulation of nitric-oxide synthase activity	-6.98658
GO:0002699	positive regulation of immune effector process	-6.98153
GO:0044257	cellular protein catabolic process	-6.97486
GO:0051961	negative regulation of nervous system development	-6.96676
GO:0002274	myeloid leukocyte activation	-6.96466
GO:0051385	response to mineralocorticoid	-6.95542
GO:0009792	embryo development ending in birth or egg hatching	-6.95417
GO:0015732	prostaglandin transport	-6.93729
GO:0030540	female genitalia development	-6.93729
GO:1904355	positive regulation of telomere capping	-6.93729
GO:0042737	drug catabolic process	-6.93346
GO:0006986	response to unfolded protein	-6.92906
GO:0071706	tumor necrosis factor superfamily cytokine production	-6.92906
GO:0032731	positive regulation of interleukin-1 beta production	-6.92775
GO:0043392	negative regulation of DNA binding	-6.92775

GO:00973 66	response to bronchodilator	-6.92775
GO:00712 60	cellular response to mechanical stimulus	-6.91887
GO:00507 69	positive regulation of neurogenesis	-6.90858
GO:00082 86	insulin receptor signaling pathway	-6.90518
GO:00323 88	positive regulation of intracellular transport	-6.8976
GO:19019 87	regulation of cell cycle phase transition	-6.89589
GO:00463 28	regulation of JNK cascade	-6.88119
GO:00061 10	regulation of glycolytic process	-6.87583
GO:00435 52	positive regulation of phosphatidylinositol 3-kinase activity	-6.87092
GO:19020 03	regulation of amyloid-beta formation	-6.87092
GO:19046 59	glucose transmembrane transport	-6.87066
GO:00308 57	negative regulation of epithelial cell differentiation	-6.87015
GO:00310 50	dsRNA processing	-6.87015
GO:00709 18	production of small RNA involved in gene silencing by RNA	-6.87015
GO:00346 55	nucleobase-containing compound catabolic process	-6.86068
GO:00091 66	nucleotide catabolic process	-6.85748
GO:00344 04	nucleobase-containing small molecule biosynthetic process	-6.85628
GO:00028 31	regulation of response to biotic stimulus	-6.84927
GO:00193 59	nicotinamide nucleotide biosynthetic process	-6.84927
GO:00193 63	pyridine nucleotide biosynthetic process	-6.84927
GO:00326 52	regulation of interleukin-1 production	-6.83702
GO:00468 22	regulation of nucleocytoplasmic transport	-6.83702

GO:0008217	regulation of blood pressure	-6.83391
GO:0061138	morphogenesis of a branching epithelium	-6.83391
GO:0010833	telomere maintenance via telomere lengthening	-6.83338
GO:0071158	positive regulation of cell cycle arrest	-6.83338
GO:0051962	positive regulation of nervous system development	-6.81885
GO:0051353	positive regulation of oxidoreductase activity	-6.81371
GO:0002285	lymphocyte activation involved in immune response	-6.81048
GO:0016049	cell growth	-6.808
GO:0032963	collagen metabolic process	-6.80371
GO:2000278	regulation of DNA biosynthetic process	-6.80371
GO:0002756	MyD88-independent toll-like receptor signaling pathway	-6.78925
GO:0042311	vasodilation	-6.78925
GO:0071478	cellular response to radiation	-6.7872
GO:0002218	activation of innate immune response	-6.78627
GO:0009123	nucleoside monophosphate metabolic process	-6.78144
GO:0008645	hexose transmembrane transport	-6.77073
GO:0016101	diterpenoid metabolic process	-6.77073
GO:0072525	pyridine-containing compound biosynthetic process	-6.767
GO:0009152	purine ribonucleotide biosynthetic process	-6.75377
GO:0002718	regulation of cytokine production involved in immune response	-6.75021
GO:0030811	regulation of nucleotide catabolic process	-6.75021
GO:0035265	organ growth	-6.74106

GO:0006096	glycolytic process	-6.73807
GO:0009914	hormone transport	-6.72241
GO:1901292	nucleoside phosphate catabolic process	-6.7182
GO:1901030	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	-6.71022
GO:0006757	ATP generation from ADP	-6.70573
GO:0015749	monosaccharide transmembrane transport	-6.70573
GO:0001541	ovarian follicle development	-6.70419
GO:0060760	positive regulation of response to cytokine stimulus	-6.70419
GO:0019362	pyridine nucleotide metabolic process	-6.69548
GO:0046496	nicotinamide nucleotide metabolic process	-6.69548
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	-6.68658
GO:0043500	muscle adaptation	-6.67371
GO:0060749	mammary gland alveolus development	-6.66852
GO:0061377	mammary gland lobule development	-6.66852
GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	-6.66852
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	-6.65102
GO:1900408	negative regulation of cellular response to oxidative stress	-6.65102
GO:1903202	negative regulation of oxidative stress-induced cell death	-6.65102
GO:0007219	Notch signaling pathway	-6.65043
GO:0021700	developmental maturation	-6.64853
GO:0034219	carbohydrate transmembrane transport	-6.64199

GO:0006090	pyruvate metabolic process	-6.63396
GO:0002701	negative regulation of production of molecular mediator of immune response	-6.63369
GO:0042554	superoxide anion generation	-6.63369
GO:1901099	negative regulation of signal transduction in absence of ligand	-6.63369
GO:2001240	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	-6.63369
GO:0038093	Fc receptor signaling pathway	-6.61688
GO:0042866	pyruvate biosynthetic process	-6.61057
GO:0006636	unsaturated fatty acid biosynthetic process	-6.59886
GO:0045454	cell redox homeostasis	-6.59886
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	-6.59039
GO:0072507	divalent inorganic cation homeostasis	-6.57705
GO:0048568	embryonic organ development	-6.57629
GO:0090322	regulation of superoxide metabolic process	-6.5595
GO:0009132	nucleoside diphosphate metabolic process	-6.55646
GO:0050729	positive regulation of inflammatory response	-6.55646
GO:0002065	columnar/cuboidal epithelial cell differentiation	-6.54861
GO:0032732	positive regulation of interleukin-1 production	-6.54767
GO:1902883	negative regulation of response to oxidative stress	-6.54767
GO:0071800	podosome assembly	-6.54617
GO:1902004	positive regulation of amyloid-beta formation	-6.54617
GO:0072524	pyridine-containing compound metabolic process	-6.54011
GO:0090316	positive regulation of intracellular protein transport	-6.531

GO:00092 60	ribonucleotide biosynthetic process	-6.529
GO:00064 69	negative regulation of protein kinase activity	-6.52121
GO:00017 63	morphogenesis of a branching structure	-6.51843
GO:19012 22	regulation of NIK/NF-kappaB signaling	-6.51807
GO:00091 44	purine nucleoside triphosphate metabolic process	-6.50597
GO:19043 56	regulation of telomere maintenance via telomere lengthening	-6.49742
GO:00059 96	monosaccharide metabolic process	-6.49547
GO:00713 92	cellular response to estradiol stimulus	-6.48751
GO:19058 98	positive regulation of response to endoplasmic reticulum stress	-6.48751
GO:00072 60	tyrosine phosphorylation of STAT protein	-6.4758
GO:00434 70	regulation of carbohydrate catabolic process	-6.4758
GO:00430 09	chordate embryonic development	-6.47247
GO:00468 49	bone remodeling	-6.43856
GO:00518 99	membrane depolarization	-6.43856
GO:00359 66	response to topologically incorrect protein	-6.43293
GO:00610 42	vascular wound healing	-6.43066
GO:19019 91	negative regulation of mitotic cell cycle phase transition	-6.42778
GO:00140 37	Schwann cell differentiation	-6.41761
GO:00342 05	amyloid-beta formation	-6.41761
GO:00605 57	positive regulation of vitamin D biosynthetic process	-6.41227
GO:00605 59	positive regulation of calcidiol 1-monooxygenase activity	-6.41227
GO:00071 79	transforming growth factor beta receptor signaling pathway	-6.41186

GO:00466 61	male sex differentiation	-6.40638
GO:00069 13	nucleocytoplasmic transport	-6.40166
GO:00315 71	mitotic G1 DNA damage checkpoint	-6.39961
GO:00068 05	xenobiotic metabolic process	-6.39865
GO:00463 90	ribose phosphate biosynthetic process	-6.39647
GO:00075 07	heart development	-6.39606
GO:00302 17	T cell differentiation	-6.39103
GO:00170 38	protein import	-6.3909
GO:00070 88	regulation of mitotic nuclear division	-6.38198
GO:00068 20	anion transport	-6.38186
GO:00000 86	G2/M transition of mitotic cell cycle	-6.37278
GO:00460 31	ADP metabolic process	-6.36946
GO:00511 69	nuclear transport	-6.35771
GO:00447 83	G1 DNA damage checkpoint	-6.35199
GO:00448 19	mitotic G1/S transition checkpoint	-6.35199
GO:00454 53	bone resorption	-6.35199
GO:00323 50	regulation of hormone metabolic process	-6.34967
GO:00423 07	positive regulation of protein import into nucleus	-6.34967
GO:19029 91	regulation of amyloid precursor protein catabolic process	-6.34967
GO:00109 48	negative regulation of cell cycle process	-6.32867
GO:00519 00	regulation of mitochondrial depolarization	-6.32127
GO:00467 17	acid secretion	-6.31186

GO:0031341	regulation of cell killing	-6.29401
GO:0097194	execution phase of apoptosis	-6.29401
GO:0030278	regulation of ossification	-6.28786
GO:0038095	Fc-epsilon receptor signaling pathway	-6.28603
GO:0042533	tumor necrosis factor biosynthetic process	-6.2836
GO:0042534	regulation of tumor necrosis factor biosynthetic process	-6.2836
GO:0071548	response to dexamethasone	-6.2836
GO:0006733	oxidoreduction coenzyme metabolic process	-6.2676
GO:0035249	synaptic transmission, glutamatergic	-6.25893
GO:0051196	regulation of coenzyme metabolic process	-6.25893
GO:0046034	ATP metabolic process	-6.25229
GO:0002676	regulation of chronic inflammatory response	-6.24672
GO:0051302	regulation of cell division	-6.23903
GO:0009141	nucleoside triphosphate metabolic process	-6.22853
GO:2001023	regulation of response to drug	-6.22426
GO:0001558	regulation of cell growth	-6.21934
GO:1904591	positive regulation of protein import	-6.2193
GO:0051043	regulation of membrane protein ectodomain proteolysis	-6.2174
GO:0060149	negative regulation of posttranscriptional gene silencing	-6.2174
GO:0060967	negative regulation of gene silencing by RNA	-6.2174
GO:1901522	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	-6.2174
GO:19037	regulation of production of miRNAs involved in	-6.2174

98	gene silencing by miRNA		
GO:0010498	proteasomal protein catabolic process	-6.20677	
GO:0006165	nucleoside diphosphate phosphorylation	-6.19962	
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	-6.19365	
GO:0033209	tumor necrosis factor-mediated signaling pathway	-6.19266	
GO:0032651	regulation of interleukin-1 beta production	-6.18999	
GO:0045833	negative regulation of lipid metabolic process	-6.18999	
GO:0071674	mononuclear cell migration	-6.18999	
GO:0016236	macroautophagy	-6.18981	
GO:0010810	regulation of cell-substrate adhesion	-6.18762	
GO:0045123	cellular extravasation	-6.16946	
GO:0045124	regulation of bone resorption	-6.15668	
GO:0000075	cell cycle checkpoint	-6.14827	
GO:0046939	nucleotide phosphorylation	-6.14493	
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	-6.14453	
GO:1902903	regulation of supramolecular fiber organization	-6.14453	
GO:0033673	negative regulation of kinase activity	-6.12583	
GO:0007004	telomere maintenance via telomerase	-6.12568	
GO:0019748	secondary metabolic process	-6.12568	
GO:0071230	cellular response to amino acid stimulus	-6.12568	
GO:0001906	cell killing		-6.12424
GO:00215	pallium development	-6.12424	

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GO:0036003	positive regulation of transcription from RNA polymerase II promoter in response to stress	-6.11853
GO:0051882	mitochondrial depolarization	-6.11853
GO:0050671	positive regulation of lymphocyte proliferation	-6.11793
GO:0045861	negative regulation of proteolysis	-6.10315
GO:0050680	negative regulation of epithelial cell proliferation	-6.10173
GO:1901031	regulation of response to reactive oxygen species	-6.09565
GO:1901988	negative regulation of cell cycle phase transition	-6.0918
GO:0030183	B cell differentiation	-6.09116
GO:0032946	positive regulation of mononuclear cell proliferation	-6.09116
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	-6.09116
GO:0019722	calcium-mediated signaling	-6.09002
GO:0072503	cellular divalent inorganic cation homeostasis	-6.08993
GO:0015908	fatty acid transport	-6.08949
GO:0050715	positive regulation of cytokine secretion	-6.08261
GO:0090303	positive regulation of wound healing	-6.08261
GO:0043619	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	-6.05293
GO:0051712	positive regulation of killing of cells of other organism	-6.05293
GO:0051235	maintenance of location	-6.05264
GO:0044839	cell cycle G2/M phase transition	-6.04131
GO:0006509	membrane protein ectodomain proteolysis	-6.03615
GO:00341	positive regulation of tissue remodeling	-6.03615

05		
GO:0035094	response to nicotine	-6.03615
GO:1901028	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	-6.03615
GO:1901796	regulation of signal transduction by p53 class mediator	-6.03507
GO:0046883	regulation of hormone secretion	-6.02463
GO:0070498	interleukin-1-mediated signaling pathway	-6.02433
GO:0042535	positive regulation of tumor necrosis factor biosynthetic process	-6.02421
GO:0045619	regulation of lymphocyte differentiation	-6.01314
GO:0008584	male gonad development	-5.98623
GO:0043401	steroid hormone mediated signaling pathway	-5.98623
GO:0032309	icosanoid secretion	-5.9781
GO:0032570	response to progesterone	-5.9781
GO:0046546	development of primary male sexual characteristics	-5.96052
GO:0070227	lymphocyte apoptotic process	-5.95739
GO:0072401	signal transduction involved in DNA integrity checkpoint	-5.95739
GO:0072422	signal transduction involved in DNA damage checkpoint	-5.95739
GO:0051051	negative regulation of transport	-5.9536
GO:0060562	epithelial tube morphogenesis	-5.9491
GO:0002695	negative regulation of leukocyte activation	-5.94817
GO:0010950	positive regulation of endopeptidase activity	-5.94817
GO:0001783	B cell apoptotic process	-5.93404
GO:0002092	positive regulation of receptor internalization	-5.93404

GO:00706 33	transepithelial transport	-5.93404
GO:19043 53	regulation of telomere capping	-5.93404
GO:00069 53	acute-phase response	-5.92143
GO:00140 75	response to amine	-5.92143
GO:00488 06	genitalia development	-5.92143
GO:00723 95	signal transduction involved in cell cycle checkpoint	-5.91692
GO:00329 90	cell part morphogenesis	-5.91553
GO:19907 78	protein localization to cell periphery	-5.90553
GO:00016 49	osteoblast differentiation	-5.90234
GO:00423 68	vitamin D biosynthetic process	-5.87933
GO:00726 59	protein localization to plasma membrane	-5.87768
GO:00436 27	response to estrogen	-5.87705
GO:00015 23	retinoid metabolic process	-5.86746
GO:00085 93	regulation of Notch signaling pathway	-5.86746
GO:20012 39	regulation of extrinsic apoptotic signaling pathway in absence of ligand	-5.86608
GO:00713 22	cellular response to carbohydrate stimulus	-5.85973
GO:00062 78	RNA-dependent DNA biosynthetic process	-5.83777
GO:00454 44	fat cell differentiation	-5.82991
GO:00517 83	regulation of nuclear division	-5.82182
GO:00092 05	purine ribonucleoside triphosphate metabolic process	-5.8198
GO:00140 38	regulation of Schwann cell differentiation	-5.81257
GO:00026 86	negative regulation of leukocyte migration	-5.812

GO:0035196	production of miRNAs involved in gene silencing by miRNA	-5.812
GO:0090199	regulation of release of cytochrome c from mitochondria	-5.812
GO:1990090	cellular response to nerve growth factor stimulus	-5.812
GO:0006874	cellular calcium ion homeostasis	-5.80195
GO:0033157	regulation of intracellular protein transport	-5.77653
GO:0003012	muscle system process	-5.767
GO:0010575	positive regulation of vascular endothelial growth factor production	-5.76484
GO:0033598	mammary gland epithelial cell proliferation	-5.76484
GO:1900101	regulation of endoplasmic reticulum unfolded protein response	-5.76484
GO:1990776	response to angiotensin	-5.76484
GO:2000191	regulation of fatty acid transport	-5.76484
GO:0045580	regulation of T cell differentiation	-5.76204
GO:0046850	regulation of bone remodeling	-5.75912
GO:1903727	positive regulation of phospholipid metabolic process	-5.75912
GO:0099565	chemical synaptic transmission, postsynaptic	-5.74774
GO:0008643	carbohydrate transport	-5.73809
GO:0009199	ribonucleoside triphosphate metabolic process	-5.7359
GO:0000271	polysaccharide biosynthetic process	-5.72329
GO:0010827	regulation of glucose transmembrane transport	-5.72329
GO:0030656	regulation of vitamin metabolic process	-5.72213
GO:0061043	regulation of vascular wound healing	-5.72213
GO:0071287	cellular response to manganese ion	-5.72213

GO:19001 03	positive regulation of endoplasmic reticulum unfolded protein response	-5.72213
GO:00352 72	exocrine system development	-5.70741
GO:00380 84	vascular endothelial growth factor signaling pathway	-5.70741
GO:00519 72	regulation of telomerase activity	-5.70741
GO:00610 28	establishment of endothelial barrier	-5.70741
GO:00420 98	T cell proliferation	-5.70002
GO:00986 93	regulation of synaptic vesicle cycle	-5.68967
GO:00322 04	regulation of telomere maintenance	-5.68621
GO:00486 78	response to axon injury	-5.68621
GO:19012 24	positive regulation of NIK/NF-kappaB signaling	-5.68621
GO:00328 00	receptor biosynthetic process	-5.68524
GO:00615 64	axon development	-5.68237
GO:00016 78	cellular glucose homeostasis	-5.66729
GO:00082 03	cholesterol metabolic process	-5.66729
GO:00512 50	negative regulation of lymphocyte activation	-5.66729
GO:20010 56	positive regulation of cysteine-type endopeptidase activity	-5.66729
GO:00550 74	calcium ion homeostasis	-5.66383
GO:00001 86	activation of MAPKK activity	-5.65681
GO:00512 05	protein insertion into membrane	-5.65681
GO:19900 89	response to nerve growth factor	-5.65681
GO:00022 24	toll-like receptor signaling pathway	-5.64405
GO:00022 62	myeloid cell homeostasis	-5.64405

GO:00469 42	carboxylic acid transport	-5.64023	
GO:00316 23	receptor internalization	-5.63275	
GO:00158 49	organic acid transport	-5.62675	
GO:00346 44	cellular response to UV	-5.61357	
GO:00018 44	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	-5.60864	
GO:00108 00	positive regulation of peptidyl-threonine phosphorylation	-5.60864	
GO:00434 57	regulation of cellular respiration	-5.60864	
GO:00322 10	regulation of telomere maintenance via telomerase	-5.60727	
GO:00063 52	DNA-templated transcription, initiation	-5.60416	
GO:19026 52	secondary alcohol metabolic process	-5.59806	
GO:00508 90	cognition		- 5.5850 3
GO:00302 13	hyaluronan biosynthetic process	-5.5785	
GO:00323 10	prostaglandin secretion	-5.5785	
GO:00517 09	regulation of killing of cells of other organism	-5.5785	
GO:19037 99	negative regulation of production of miRNAs involved in gene silencing by miRNA	-5.5785	
GO:00226 17	extracellular matrix disassembly	-5.57799	
GO:00311 45	anaphase-promoting complex-dependent catabolic process	-5.57799	
GO:19029 30	regulation of alcohol biosynthetic process	-5.57799	
GO:19030 36	positive regulation of response to wounding	-5.57799	
GO:00075 69	cell aging		- 5.5769 2
GO:00456 64	regulation of neuron differentiation	-5.5657	

GO:00106 39	negative regulation of organelle organization	-5.55138
GO:00715 49	cellular response to dexamethasone stimulus	-5.53484
GO:00108 76	lipid localization	-5.52744
GO:00193 18	hexose metabolic process	-5.52102
GO:00459 26	negative regulation of growth	-5.52102
GO:00326 55	regulation of interleukin-12 production	-5.51124
GO:00973 45	mitochondrial outer membrane permeabilization	-5.51124
GO:00347 67	positive regulation of ion transmembrane transport	-5.50808
GO:00091 50	purine ribonucleotide metabolic process	-5.50712
GO:20001 06	regulation of leukocyte apoptotic process	-5.47405
GO:00069 77	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	-5.46466
GO:00109 51	negative regulation of endopeptidase activity	-5.4559
GO:00902 87	regulation of cellular response to growth factor stimulus	-5.45406
GO:00423 62	fat-soluble vitamin biosynthetic process	-5.4463
GO:00510 44	positive regulation of membrane protein ectodomain proteolysis	-5.4463
GO:00905 94	inflammatory response to wounding	-5.4463
GO:20010 28	positive regulation of endothelial cell chemotaxis	-5.4463
GO:00017 64	neuron migration	-5.44227
GO:00461 65	alcohol biosynthetic process	-5.44227
GO:00091 08	coenzyme biosynthetic process	-5.43981
GO:00074 20	brain development	-5.43254
GO:00027 03	regulation of leukocyte mediated immunity	-5.43197

GO:0030520	intracellular estrogen receptor signaling pathway	-5.419
GO:0032615	interleukin-12 production	-5.419
GO:0071398	cellular response to fatty acid	-5.419
GO:0072431	signal transduction involved in mitotic G1 DNA damage checkpoint	-5.419
GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	-5.419
GO:1905517	macrophage migration	-5.419
GO:0002677	negative regulation of chronic inflammatory response	-5.41698
GO:0014805	smooth muscle adaptation	-5.41698
GO:0032747	positive regulation of interleukin-23 production	-5.41698
GO:0046136	positive regulation of vitamin metabolic process	-5.41698
GO:1990962	drug transport across blood-brain barrier	-5.41698
GO:0002688	regulation of leukocyte chemotaxis	-5.41566
GO:0046889	positive regulation of lipid biosynthetic process	-5.40698
GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	-5.39487
GO:0046434	organophosphate catabolic process	-5.39198
GO:0001952	regulation of cell-matrix adhesion	-5.38964
GO:0006869	lipid transport	-5.37924
GO:0042129	regulation of T cell proliferation	-5.37784
GO:0021537	telencephalon development	-5.37618
GO:0002090	regulation of receptor internalization	-5.37421
GO:0007566	embryo implantation	-5.37421
GO:0035306	positive regulation of dephosphorylation	-5.37421

GO:0034605	cellular response to heat	-5.36386
GO:0016051	carbohydrate biosynthetic process	-5.35921
GO:0009259	ribonucleotide metabolic process	-5.35823
GO:0034250	positive regulation of cellular amide metabolic process	-5.35665
GO:0042058	regulation of epidermal growth factor receptor signaling pathway	-5.3416
GO:0042306	regulation of protein import into nucleus	-5.33028
GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	-5.33028
GO:1902402	signal transduction involved in mitotic DNA damage checkpoint	-5.33028
GO:1902403	signal transduction involved in mitotic DNA integrity checkpoint	-5.33028
GO:0032212	positive regulation of telomere maintenance via telomerase	-5.32837
GO:0051204	protein insertion into mitochondrial membrane	-5.32837
GO:1904030	negative regulation of cyclin-dependent protein kinase activity	-5.32837
GO:0002070	epithelial cell maturation	-5.32385
GO:0034116	positive regulation of heterotypic cell-cell adhesion	-5.32385
GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	-5.32385
GO:1901550	regulation of endothelial cell development	-5.32385
GO:1903140	regulation of establishment of endothelial barrier	-5.32385
GO:0051701	interaction with host	-5.32343
GO:0002250	adaptive immune response	-5.32183
GO:0032874	positive regulation of stress-activated MAPK cascade	-5.31472
GO:1905952	regulation of lipid localization	-5.31472
GO:0046879	hormone secretion	-5.31383

GO:0033273	response to vitamin	-5.30952
GO:0060333	interferon-gamma-mediated signaling pathway	-5.30952
GO:0061098	positive regulation of protein tyrosine kinase activity	-5.28716
GO:0032760	positive regulation of tumor necrosis factor production	-5.27783
GO:0106027	neuron projection organization	-5.27783
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	-5.27336
GO:0006691	leukotriene metabolic process	-5.264
GO:0032735	positive regulation of interleukin-12 production	-5.264
GO:0060251	regulation of glial cell proliferation	-5.264
GO:0071312	cellular response to alkaloid	-5.264
GO:0015718	monocarboxylic acid transport	-5.25289
GO:0032088	negative regulation of NF-kappaB transcription factor activity	-5.24653
GO:0061097	regulation of protein tyrosine kinase activity	-5.24653
GO:0046324	regulation of glucose import	-5.24483
GO:1902110	positive regulation of mitochondrial membrane permeability involved in apoptotic process	-5.24483
GO:0010466	negative regulation of peptidase activity	-5.23716
GO:0034308	primary alcohol metabolic process	-5.2156
GO:1901992	positive regulation of mitotic cell cycle phase transition	-5.2156
GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	-5.2156
GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	-5.20327
GO:1904589	regulation of protein import	-5.20327
GO:0001893	maternal placenta development	-5.20165

GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	-5.20165
GO:0051973	positive regulation of telomerase activity	-5.20165
GO:0097435	supramolecular fiber organization	-5.18825
GO:1903725	regulation of phospholipid metabolic process	-5.18504
GO:0002768	immune response-regulating cell surface receptor signaling pathway	-5.18329
GO:0030324	lung development	-5.17235
GO:0019693	ribose phosphate metabolic process	-5.16759
GO:0032368	regulation of lipid transport	-5.16567
GO:0120035	regulation of plasma membrane bounded cell projection organization	-5.16365
GO:1902686	mitochondrial outer membrane permeabilization involved in programmed cell death	-5.16244
GO:0002532	production of molecular mediator involved in inflammatory response	-5.15484
GO:0010975	regulation of neuron projection development	-5.15319
GO:0015980	energy derivation by oxidation of organic compounds	-5.14751
GO:0042692	muscle cell differentiation	-5.14687
GO:0071333	cellular response to glucose stimulus	-5.14184
GO:0030212	hyaluronan metabolic process	-5.14118
GO:1904358	positive regulation of telomere maintenance via telomere lengthening	-5.14118
GO:1901184	regulation of ERBB signaling pathway	-5.12499
GO:0002066	columnar/cuboidal epithelial cell development	-5.12233
GO:0070141	response to UV-A	-5.11831
GO:0140014	mitotic nuclear division	-5.10356
GO:00359	response to muscle stretch	-5.1032

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GO:00507 64	regulation of phagocytosis	-5.09548
GO:00713 31	cellular response to hexose stimulus	-5.0948
GO:19030 38	negative regulation of leukocyte cell-cell adhesion	-5.0948
GO:00303 23	respiratory tube development	-5.0939
GO:00105 73	vascular endothelial growth factor production	-5.08291
GO:00357 94	positive regulation of mitochondrial membrane permeability	-5.08291
GO:00313 44	regulation of cell projection organization	-5.08265
GO:00302 24	monocyte differentiation	-5.08249
GO:00327 33	positive regulation of interleukin-10 production	-5.08249
GO:19011 86	positive regulation of ERBB signaling pathway	-5.08249
GO:19031 31	mononuclear cell differentiation	-5.08249
GO:20012 52	positive regulation of chromosome organization	-5.0746
GO:00463 30	positive regulation of JNK cascade	-5.07157
GO:00713 26	cellular response to monosaccharide stimulus	-5.07157
GO:00071 60	cell-matrix adhesion	-5.06697
GO:00165 79	protein deubiquitination	-5.06017
GO:00301 77	positive regulation of Wnt signaling pathway	-5.05543
GO:00434 33	negative regulation of DNA-binding transcription factor activity	-5.05543
GO:19021 08	regulation of mitochondrial membrane permeability involved in apoptotic process	-5.04416
GO:00516 40	organelle localization	-5.03477
GO:00488 12	neuron projection morphogenesis	-5.02804

GO:00726 55	establishment of protein localization to mitochondrion	-5.02569
GO:00074 31	salivary gland development	-5.02548
GO:00331 46	regulation of intracellular estrogen receptor signaling pathway	-5.02548
GO:00463 26	positive regulation of glucose import	-5.02548
GO:00447 73	mitotic DNA damage checkpoint	-5.00896
GO:19000 15	regulation of cytokine production involved in inflammatory response	-5.00605
GO:19057 10	positive regulation of membrane permeability	-5.00605
GO:00105 44	negative regulation of platelet activation	-5.00303
GO:00329 30	positive regulation of superoxide anion generation	-5.00303
GO:00457 80	positive regulation of bone resorption	-5.00303
GO:00468 52	positive regulation of bone remodeling	-5.00303
GO:00510 23	regulation of immunoglobulin secretion	-5.00303
GO:00709 89	oxidative demethylation	-5.00303
GO:00435 02	regulation of muscle adaptation	-4.98076
GO:00070 06	mitochondrial membrane organization	-4.98055
GO:00457 40	positive regulation of DNA replication	-4.97007
GO:00506 91	regulation of defense response to virus by host	-4.97007
GO:20002 73	positive regulation of signaling receptor activity	-4.97007
GO:00108 12	negative regulation of cell-substrate adhesion	-4.96857
GO:00162 39	positive regulation of macroautophagy	-4.96857
GO:00067 32	coenzyme metabolic process	-4.96186
GO:00455 98	regulation of fat cell differentiation	-4.95825

GO:00305 93	neutrophil chemotaxis	-4.95287
GO:00600 79	excitatory postsynaptic potential	-4.95287
GO:00063 67	transcription initiation from RNA polymerase II promoter	-4.9429
GO:00600 78	regulation of postsynaptic membrane potential	-4.93614
GO:00705 85	protein localization to mitochondrion	-4.93614
GO:00326 49	regulation of interferon-gamma production	-4.92529
GO:20000 60	positive regulation of ubiquitin-dependent protein catabolic process	-4.92529
GO:00513 46	negative regulation of hydrolase activity	-4.9207
GO:01200 39	plasma membrane bounded cell projection morphogenesis	-4.91175
GO:00025 44	chronic inflammatory response	-4.90861
GO:00029 02	regulation of B cell apoptotic process	-4.90861
GO:00193 73	epoxygenase P450 pathway	-4.90861
GO:00323 03	regulation of icosanoid secretion	-4.90861
GO:00514 12	response to corticosterone	-4.90861
GO:00517 67	nitric-oxide synthase biosynthetic process	-4.90861
GO:00517 69	regulation of nitric-oxide synthase biosynthetic process	-4.90861
GO:00609 65	negative regulation of gene silencing by miRNA	-4.90861
GO:19004 09	positive regulation of cellular response to oxidative stress	-4.90861
GO:00030 15	heart process	-4.90571
GO:00608 28	regulation of canonical Wnt signaling pathway	-4.90571
GO:00456 21	positive regulation of lymphocyte differentiation	-4.898
GO:00002 26	microtubule cytoskeleton organization	-4.89725

GO:00025 34	cytokine production involved in inflammatory response	-4.89542
GO:00712 42	cellular response to ammonium ion	-4.89542
GO:00723 47	response to anesthetic	-4.89542
GO:19033 20	regulation of protein modification by small protein conjugation or removal	-4.89115
GO:00439 02	positive regulation of multi-organism process	-4.88819
GO:00488 58	cell projection morphogenesis	-4.87912
GO:00511 46	striated muscle cell differentiation	-4.87839
GO:00029 33	lipid hydroxylation	-4.87762
GO:00098 20	alkaloid metabolic process	-4.87762
GO:00313 94	positive regulation of prostaglandin biosynthetic process	-4.87762
GO:00316 22	positive regulation of fever generation	-4.87762
GO:00326 27	interleukin-23 production	-4.87762
GO:00326 67	regulation of interleukin-23 production	-4.87762
GO:00605 58	regulation of calcidiol 1-monooxygenase activity	-4.87762
GO:01200 41	positive regulation of macrophage proliferation	-4.87762
GO:20013 00	lipoxin metabolic process	-4.87762
GO:20013 01	lipoxin biosynthetic process	-4.87762
GO:00551 23	digestive system development	-4.87083
GO:19040 64	positive regulation of cation transmembrane transport	-4.87083
GO:00482 46	macrophage chemotaxis	-4.86371
GO:00609 69	negative regulation of gene silencing	-4.86371
GO:00902 79	regulation of calcium ion import	-4.86371

GO:19040 37	positive regulation of epithelial cell apoptotic process	-4.86371
GO:00106 75	regulation of cellular carbohydrate metabolic process	-4.8494
GO:00302 60	entry into host cell	-4.8494
GO:00444 09	entry into host	-4.8494
GO:00518 06	entry into cell of other organism involved in symbiotic interaction	-4.8494
GO:00518 28	entry into other organism involved in symbiotic interaction	-4.82814
GO:00706 46	protein modification by small protein removal	-4.8244
GO:00091 10	vitamin biosynthetic process	-4.81934
GO:00108 93	positive regulation of steroid biosynthetic process	-4.81934
GO:00607 16	labyrinthine layer blood vessel development	-4.81934
GO:00714 98	cellular response to fluid shear stress	-4.81934
GO:00902 80	positive regulation of calcium ion import	-4.81934
GO:00903 30	regulation of platelet aggregation	-4.81934
GO:00447 74	mitotic DNA integrity checkpoint	-4.81788
GO:00330 44	regulation of chromosome organization	-4.81414
GO:01500 77	regulation of neuroinflammatory response	-4.8126
GO:19033 64	positive regulation of cellular protein catabolic process	-4.80704
GO:00022 86	T cell activation involved in immune response	-4.79173
GO:00217 61	limbic system development	-4.79173
GO:00000 77	DNA damage checkpoint	-4.78611
GO:00347 65	regulation of ion transmembrane transport	-4.78049
GO:19019 89	positive regulation of cell cycle phase transition	-4.76585

GO:00020 40	sprouting angiogenesis	-4.76436
GO:19055 21	regulation of macrophage migration	-4.76279
GO:00316 70	cellular response to nutrient	-4.75586
GO:00163 11	dephosphorylation	-4.75112
GO:00160 52	carbohydrate catabolic process	-4.74709
GO:00482 59	regulation of receptor-mediated endocytosis	-4.74024
GO:00329 28	regulation of superoxide anion generation	-4.73468
GO:00423 59	vitamin D metabolic process	-4.73468
GO:00483 05	immunoglobulin secretion	-4.73468
GO:00510 00	positive regulation of nitric-oxide synthase activity	-4.73468
GO:19028 84	positive regulation of response to oxidative stress	-4.73468
GO:19011 37	carbohydrate derivative biosynthetic process	-4.72868
GO:00456 85	regulation of glial cell differentiation	-4.72229
GO:00108 28	positive regulation of glucose transmembrane transport	-4.71422
GO:00604 43	mammary gland morphogenesis	-4.71422
GO:00097 55	hormone-mediated signaling pathway	-4.71285
GO:00487 54	branching morphogenesis of an epithelial tube	-4.70394
GO:00508 08	synapse organization	-4.69043
GO:00059 76	polysaccharide metabolic process	-4.68979
GO:00620 14	negative regulation of small molecule metabolic process	-4.68979
GO:00226 04	regulation of cell morphogenesis	-4.68349
GO:00902 57	regulation of muscle system process	-4.68076

GO:00605 41	respiratory system development	-4.67901
GO:00019 55	blood vessel maturation	-4.67586
GO:00022 46	wound healing involved in inflammatory response	-4.67586
GO:00316 20	regulation of fever generation	-4.67586
GO:00331 29	positive regulation of histone phosphorylation	-4.67586
GO:00356 55	interleukin-18-mediated signaling pathway	-4.67586
GO:00713 51	cellular response to interleukin-18	-4.67586
GO:01200 40	regulation of macrophage proliferation	-4.67586
GO:19001 25	regulation of hyaluronan biosynthetic process	-4.67586
GO:00433 30	response to exogenous dsRNA	-4.66682
GO:00485 38	thymus development	-4.66682
GO:00074 22	peripheral nervous system development	-4.65661
GO:00614 18	regulation of transcription from RNA polymerase II promoter in response to hypoxia	-4.65661
GO:00102 88	response to lead ion	-4.6542
GO:00357 43	CD4-positive, alpha-beta T cell cytokine production	-4.6542
GO:00326 09	interferon-gamma production	-4.64034
GO:00506 88	regulation of defense response to virus	-4.62449
GO:00076 11	learning or memory	-4.62318
GO:00421 80	cellular ketone metabolic process	-4.62318
GO:19033 62	regulation of cellular protein catabolic process	-4.62318
GO:00305 74	collagen catabolic process	-4.62055
GO:00357 22	interleukin-12-mediated signaling pathway	-4.62055

GO:00466 20	regulation of organ growth	-4.61599
GO:19029 05	positive regulation of supramolecular fiber organization	-4.6125
GO:00353 03	regulation of dephosphorylation	-4.59611
GO:00310 16	pancreas development	-4.59282
GO:00996 01	regulation of neurotransmitter receptor activity	-4.59282
GO:00507 07	regulation of cytokine secretion	-4.59187
GO:00007 23	telomere maintenance	-4.58519
GO:00315 70	DNA integrity checkpoint	-4.58519
GO:20000 58	regulation of ubiquitin-dependent protein catabolic process	-4.58519
GO:00427 38	exogenous drug catabolic process	-4.57751
GO:00509 95	negative regulation of lipid catabolic process	-4.57751
GO:00107 99	regulation of peptidyl-threonine phosphorylation	-4.57536
GO:00305 18	intracellular steroid hormone receptor signaling pathway	-4.56799
GO:00358 21	modification of morphology or physiology of other organism	-4.5659
GO:00023 77	immunoglobulin production	-4.5636
GO:00488 63	stem cell differentiation	-4.55271
GO:00902 76	regulation of peptide hormone secretion	-4.53146
GO:00020 67	glandular epithelial cell differentiation	-4.53119
GO:00032 54	regulation of membrane depolarization	-4.53119
GO:00456 01	regulation of endothelial cell differentiation	-4.53119
GO:00607 11	labyrinthine layer development	-4.53119
GO:00713 49	cellular response to interleukin-12	-4.53119

GO:2000107	negative regulation of leukocyte apoptotic process	-4.53119
GO:0021766	hippocampus development	-4.5308
GO:0006006	glucose metabolic process	-4.51553
GO:1903305	regulation of regulated secretory pathway	-4.50885
GO:0032647	regulation of interferon-alpha production	-4.50428
GO:0046697	decidualization	-4.50428
GO:0060571	morphogenesis of an epithelial fold	-4.50428
GO:1904385	cellular response to angiotensin	-4.50428
GO:2001026	regulation of endothelial cell chemotaxis	-4.50428
GO:0051121	hepoxilin metabolic process	-4.50212
GO:0051122	hepoxilin biosynthetic process	-4.50212
GO:0060556	regulation of vitamin D biosynthetic process	-4.50212
GO:0097011	cellular response to granulocyte macrophage colony-stimulating factor stimulus	-4.50212
GO:0097012	response to granulocyte macrophage colony-stimulating factor	-4.50212
GO:1901857	positive regulation of cellular respiration	-4.50212
GO:2001280	positive regulation of unsaturated fatty acid biosynthetic process	-4.50212
GO:0010906	regulation of glucose metabolic process	-4.4977
GO:0021987	cerebral cortex development	-4.4977
GO:0001774	microglial cell activation	-4.48801
GO:0002269	leukocyte activation involved in inflammatory response	-4.48801
GO:0002833	positive regulation of response to biotic stimulus	-4.48801
GO:0014009	glial cell proliferation	-4.48801

GO:00301 95	negative regulation of blood coagulation	-4.48801
GO:00706 71	response to interleukin-12	-4.48801
GO:00427 52	regulation of circadian rhythm	-4.47471
GO:19902 66	neutrophil migration	-4.45193
GO:00311 13	regulation of microtubule polymerization	-4.44578
GO:00322 06	positive regulation of telomere maintenance	-4.44578
GO:00713 54	cellular response to interleukin-6	-4.44578
GO:00716 75	regulation of mononuclear cell migration	-4.44578
GO:19000 47	negative regulation of hemostasis	-4.44578
GO:00345 02	protein localization to chromosome	-4.44093
GO:00607 40	prostate gland epithelium morphogenesis	-4.43422
GO:19007 39	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	-4.43422
GO:19007 40	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	-4.43422
GO:19055 23	positive regulation of macrophage migration	-4.43422
GO:00459 27	positive regulation of growth	-4.42984
GO:00320 92	positive regulation of protein binding	-4.41178
GO:00705 09	calcium ion import	-4.41178
GO:00324 79	regulation of type I interferon production	-4.40702
GO:00069 98	nuclear envelope organization	-4.40445
GO:00068 98	receptor-mediated endocytosis	-4.39848
GO:00486 67	cell morphogenesis involved in neuron differentiation	-4.36864

GO:0001963	synaptic transmission, dopaminergic	-4.36707
GO:0010971	positive regulation of G2/M transition of mitotic cell cycle	-4.36707
GO:0032607	interferon-alpha production	-4.36707
GO:0034114	regulation of heterotypic cell-cell adhesion	-4.36707
GO:0034698	response to gonadotropin	-4.36707
GO:0042501	serine phosphorylation of STAT protein	-4.36707
GO:2000353	positive regulation of endothelial cell apoptotic process	-4.36707
GO:0043331	response to dsRNA	-4.36399
GO:0048260	positive regulation of receptor-mediated endocytosis	-4.36399
GO:0032606	type I interferon production	-4.36292
GO:0050954	sensory perception of mechanical stimulus	-4.36246
GO:0010507	negative regulation of autophagy	-4.3546
GO:0034637	cellular carbohydrate biosynthetic process	-4.3546
GO:0048013	ephrin receptor signaling pathway	-4.3546
GO:0051781	positive regulation of cell division	-4.3546
GO:0060070	canonical Wnt signaling pathway	-4.35192
GO:0001660	fever generation	-4.34957
GO:0032308	positive regulation of prostaglandin secretion	-4.34957
GO:0034350	regulation of glial cell apoptotic process	-4.34957
GO:0036500	ATF6-mediated unfolded protein response	-4.34957
GO:0045348	positive regulation of MHC class II biosynthetic process	-4.34957
GO:0051541	elastin metabolic process	-4.34957

GO:0051901	positive regulation of mitochondrial depolarization	-4.34957
GO:0060068	vagina development	-4.34957
GO:0070424	regulation of nucleotide-binding oligomerization domain containing signaling pathway	-4.34957
GO:0097267	omega-hydroxylase P450 pathway	-4.34957
GO:0032200	telomere organization	-4.34472
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	-4.34116
GO:0017157	regulation of exocytosis	-4.33097
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	-4.33097
GO:0006749	glutathione metabolic process	-4.32437
GO:0010524	positive regulation of calcium ion transport into cytosol	-4.32437
GO:0019058	viral life cycle	-4.31745
GO:0032970	regulation of actin filament-based process	-4.30526
GO:0030194	positive regulation of blood coagulation	-4.30262
GO:0060512	prostate gland morphogenesis	-4.30262
GO:0071280	cellular response to copper ion	-4.30262
GO:1900048	positive regulation of hemostasis	-4.30262
GO:1902932	positive regulation of alcohol biosynthetic process	-4.30262
GO:0001822	kidney development	-4.29898
GO:0007411	axon guidance	-4.29898
GO:0034101	erythrocyte homeostasis	-4.29824
GO:0071482	cellular response to light stimulus	-4.29824
GO:0090150	establishment of protein localization to membrane	-4.29468

GO:00974 85	neuron projection guidance	-4.2862
GO:00162 33	telomere capping	-4.28555
GO:00508 19	negative regulation of coagulation	-4.28555
GO:00707 41	response to interleukin-6	-4.28555
GO:00069 19	activation of cysteine-type endopeptidase activity involved in apoptotic process	-4.27155
GO:00484 69	cell maturation	-4.25778
GO:00158 93	drug transport	-4.25751
GO:00506 63	cytokine secretion	-4.25607
GO:00702 28	regulation of lymphocyte apoptotic process	-4.24751
GO:00508 20	positive regulation of coagulation	-4.24065
GO:00509 01	leukocyte tethering or rolling	-4.24065
GO:19040 62	regulation of cation transmembrane transport	-4.23848
GO:00507 96	regulation of insulin secretion	-4.22381
GO:00455 82	positive regulation of T cell differentiation	-4.2179
GO:00022 75	myeloid cell activation involved in immune response	-4.21734
GO:00065 27	arginine catabolic process	-4.21362
GO:00316 52	positive regulation of heat generation	-4.21362
GO:00323 06	regulation of prostaglandin secretion	-4.21362
GO:00331 97	response to vitamin E	-4.21362
GO:00605 25	prostate glandular acinus development	-4.21362
GO:00706 73	response to interleukin-18	-4.21362
GO:00074 09	axonogenesis	-4.21266

GO:0045840	positive regulation of mitotic nuclear division	-4.21021
GO:0002705	positive regulation of leukocyte mediated immunity	-4.19418
GO:0072001	renal system development	-4.18596
GO:0001516	prostaglandin biosynthetic process	-4.18099
GO:0005979	regulation of glycogen biosynthetic process	-4.18099
GO:0007176	regulation of epidermal growth factor-activated receptor activity	-4.18099
GO:0010758	regulation of macrophage chemotaxis	-4.18099
GO:0010962	regulation of glucan biosynthetic process	-4.18099
GO:0034110	regulation of homotypic cell-cell adhesion	-4.18099
GO:0046457	prostanoid biosynthetic process	-4.18099
GO:0071480	cellular response to gamma radiation	-4.18099
GO:1902751	positive regulation of cell cycle G2/M phase transition	-4.18099
GO:1903205	regulation of hydrogen peroxide-induced cell death	-4.18099
GO:2001025	positive regulation of response to drug	-4.18099
GO:0006766	vitamin metabolic process	-4.1739
GO:0055076	transition metal ion homeostasis	-4.1739
GO:0022900	electron transport chain	-4.17367
GO:1903793	positive regulation of anion transport	-4.17363
GO:0002444	myeloid leukocyte mediated immunity	-4.16733
GO:0044262	cellular carbohydrate metabolic process	-4.16143
GO:1901888	regulation of cell junction assembly	-4.13985
GO:0051480	regulation of cytosolic calcium ion concentration	-4.13984

GO:0017001	antibiotic catabolic process	-4.13775
GO:0014044	Schwann cell development	-4.12348
GO:0045940	positive regulation of steroid metabolic process	-4.12348
GO:0002690	positive regulation of leukocyte chemotaxis	-4.11445
GO:0010660	regulation of muscle cell apoptotic process	-4.11445
GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	-4.11409
GO:0035304	regulation of protein dephosphorylation	-4.11409
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	-4.11409
GO:0032956	regulation of actin cytoskeleton organization	-4.10765
GO:0032653	regulation of interleukin-10 production	-4.10253
GO:0043388	positive regulation of DNA binding	-4.10253
GO:0006983	ER overload response	-4.09103
GO:0031392	regulation of prostaglandin biosynthetic process	-4.09103
GO:0043696	dedifferentiation	-4.09103
GO:0043697	cell dedifferentiation	-4.09103
GO:0060736	prostate gland growth	-4.09103
GO:0060742	epithelial cell differentiation involved in prostate gland development	-4.09103
GO:0061517	macrophage proliferation	-4.09103
GO:0072584	caveolin-mediated endocytosis	-4.09103
GO:1904181	positive regulation of membrane depolarization	-4.09103
GO:0030308	negative regulation of cell growth	-4.07623
GO:00705	regulation of microtubule cytoskeleton	-4.07623

07	organization	
GO:0035767	endothelial cell chemotaxis	-4.06797
GO:0050869	negative regulation of B cell activation	-4.06797
GO:0051968	positive regulation of synaptic transmission, glutamatergic	-4.06797
GO:0071353	cellular response to interleukin-4	-4.06797
GO:0097421	liver regeneration	-4.06797
GO:0010574	regulation of vascular endothelial growth factor production	-4.06796
GO:0031343	positive regulation of cell killing	-4.06796
GO:1903078	positive regulation of protein localization to plasma membrane	-4.06796
GO:0048167	regulation of synaptic plasticity	-4.06035
GO:0038094	Fc-gamma receptor signaling pathway	-4.05575
GO:0002449	lymphocyte mediated immunity	-4.04429
GO:0010657	muscle cell apoptotic process	-4.01578
GO:0050848	regulation of calcium-mediated signaling	-4.01578
GO:0001975	response to amphetamine	-4.01434
GO:0002861	regulation of inflammatory response to antigenic stimulus	-4.01434
GO:0010039	response to iron ion	-4.01434
GO:0042573	retinoic acid metabolic process	-4.01434
GO:2001038	regulation of cellular response to drug	-4.01434
GO:0021885	forebrain cell migration	-4.00068
GO:0032613	interleukin-10 production	-4.00068
GO:0034113	heterotypic cell-cell adhesion	-4.00068

GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	-4.00068	
GO:0002431	Fc receptor mediated stimulatory signaling pathway	-3.99883	
GO:0007612	learning		-3.99883
GO:0007423	sensory organ development	-3.99789	
GO:0002702	positive regulation of production of molecular mediator of immune response	-3.99181	
GO:0031650	regulation of heat generation	-3.97944	
GO:0032725	positive regulation of granulocyte macrophage colony-stimulating factor production	-3.97944	
GO:0033127	regulation of histone phosphorylation	-3.97944	
GO:0045741	positive regulation of epidermal growth factor-activated receptor activity	-3.97944	
GO:0051988	regulation of attachment of spindle microtubules to kinetochore	-3.97944	
GO:0060340	positive regulation of type I interferon-mediated signaling pathway	-3.97944	
GO:0072683	T cell extravasation	-3.97944	
GO:0002437	inflammatory response to antigenic stimulus	-3.96792	
GO:0030431	sleep		-3.96247
GO:0032148	activation of protein kinase B activity	-3.96247	
GO:0033198	response to ATP	-3.96247	
GO:0036474	cell death in response to hydrogen peroxide	-3.96247	
GO:0043276	anoikis		-3.96247
GO:0045907	positive regulation of vasoconstriction	-3.96247	
GO:0071901	negative regulation of protein serine/threonine kinase activity	-3.94326	
GO:00075	excretion		-

88			3.9357 3
GO:00316 40	killing of cells of other organism	-3.93573	
GO:00443 64	disruption of cells of other organism	-3.93573	
GO:00103 89	regulation of G2/M transition of mitotic cell cycle	-3.92171	
GO:00074 35	salivary gland morphogenesis	-3.91225	
GO:00606 74	placenta blood vessel development	-3.91225	
GO:00706 70	response to interleukin-4	-3.91225	
GO:19036 70	regulation of sprouting angiogenesis	-3.90694	
GO:00995 04	synaptic vesicle cycle	-3.90677	
GO:00300 72	peptide hormone secretion	-3.90433	
GO:00343 30	cell junction organization	-3.89341	
GO:00508 71	positive regulation of B cell activation	-3.889	
GO:00148 54	response to inactivity	-3.87705	
GO:00704 31	nucleotide-binding oligomerization domain containing 2 signaling pathway	-3.87705	
GO:20012 79	regulation of unsaturated fatty acid biosynthetic process	-3.87705	
GO:00064 17	regulation of translation	-3.8744	
GO:00509 18	positive chemotaxis	-3.87297	
GO:00726 78	T cell migration	-3.87297	
GO:19036 72	positive regulation of sprouting angiogenesis	-3.87297	
GO:00337 62	response to glucagon	-3.86359	
GO:00708 73	regulation of glycogen metabolic process	-3.86359	
GO:20003 10	regulation of NMDA receptor activity	-3.86359	

GO:00519 83	regulation of chromosome segregation	-3.85345
GO:00072 04	positive regulation of cytosolic calcium ion concentration	-3.84928
GO:00507 66	positive regulation of phagocytosis	-3.84238
GO:19043 77	positive regulation of protein localization to cell periphery	-3.84238
GO:00027 06	regulation of lymphocyte mediated immunity	-3.83598
GO:00300 38	contractile actin filament bundle assembly	-3.83126
GO:00431 49	stress fiber assembly	-3.83126
GO:00614 48	connective tissue development	-3.81667
GO:00972 42	amyloid-beta clearance	-3.81638
GO:00323 70	positive regulation of lipid transport	-3.81228
GO:00019 09	leukocyte mediated cytotoxicity	-3.80929
GO:00510 48	negative regulation of secretion	-3.79036
GO:00511 87	cofactor catabolic process	-3.78266
GO:00060 00	fructose metabolic process	-3.78249
GO:00107 63	positive regulation of fibroblast migration	-3.78249
GO:00326 45	regulation of granulocyte macrophage colony-stimulating factor production	-3.78249
GO:00453 46	regulation of MHC class II biosynthetic process	-3.78249
GO:00483 08	organelle inheritance	-3.78249
GO:00483 13	Golgi inheritance	-3.78249
GO:00905 57	establishment of endothelial intestinal barrier	-3.78249
GO:00107 42	macrophage derived foam cell differentiation	-3.77056
GO:00430 29	T cell homeostasis	-3.77056

GO:0048009	insulin-like growth factor receptor signaling pathway	-3.77056
GO:0090077	foam cell differentiation	-3.77056
GO:0006839	mitochondrial transport	-3.76786
GO:0043271	negative regulation of ion transport	-3.76715
GO:0060968	regulation of gene silencing	-3.76715
GO:0042303	molting cycle	-3.76605
GO:0042633	hair cycle	-3.76605
GO:0031396	regulation of protein ubiquitination	-3.76209
GO:0043043	peptide biosynthetic process	-3.7609
GO:0014823	response to activity	-3.75351
GO:0051785	positive regulation of nuclear division	-3.75351
GO:0035051	cardiocyte differentiation	-3.75026
GO:0006275	regulation of DNA replication	-3.74476
GO:0030073	insulin secretion	-3.73415
GO:0030258	lipid modification	-3.73184
GO:0043299	leukocyte degranulation	-3.73165
GO:0032660	regulation of interleukin-17 production	-3.72605
GO:0042092	type 2 immune response	-3.72605
GO:0043114	regulation of vascular permeability	-3.72605
GO:0060416	response to growth hormone	-3.72605
GO:1904706	negative regulation of vascular smooth muscle cell proliferation	-3.72605
GO:19044	positive regulation of calcium ion	-3.72483

27	transmembrane transport	
GO:0051656	establishment of organelle localization	-3.71603
GO:0016485	protein processing	-3.71052
GO:0046916	cellular transition metal ion homeostasis	-3.70284
GO:0016570	histone modification	-3.70064
GO:0048285	organelle fission	-3.70064
GO:1903747	regulation of establishment of protein localization to mitochondrion	-3.69658
GO:0032604	granulocyte macrophage colony-stimulating factor production	-3.69466
GO:0045342	MHC class II biosynthetic process	-3.69466
GO:0045725	positive regulation of glycogen biosynthetic process	-3.69466
GO:0071732	cellular response to nitric oxide	-3.69466
GO:0031214	biomineral tissue development	-3.68394
GO:0006730	one-carbon metabolic process	-3.68278
GO:0007257	activation of JUN kinase activity	-3.68278
GO:0032892	positive regulation of organic acid transport	-3.68278
GO:0045746	negative regulation of Notch signaling pathway	-3.68278
GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	-3.68278
GO:1902749	regulation of cell cycle G2/M phase transition	-3.67921
GO:0032481	positive regulation of type I interferon production	-3.66876
GO:0043507	positive regulation of JUN kinase activity	-3.66876
GO:1902117	positive regulation of organelle assembly	-3.66876
GO:1903828	negative regulation of cellular protein localization	-3.66175

GO:0007517	muscle organ development	-3.65343
GO:0030282	bone mineralization	-3.64151
GO:0072676	lymphocyte migration	-3.64151
GO:0030890	positive regulation of B cell proliferation	-3.64068
GO:0016042	lipid catabolic process	-3.6285
GO:0031330	negative regulation of cellular catabolic process	-3.62668
GO:0050868	negative regulation of T cell activation	-3.62147
GO:0002429	immune response-activating cell surface receptor signaling pathway	-3.61741
GO:0009064	glutamine family amino acid metabolic process	-3.61438
GO:1900076	regulation of cellular response to insulin stimulus	-3.61438
GO:0030889	negative regulation of B cell proliferation	-3.61268
GO:0030949	positive regulation of vascular endothelial growth factor receptor signaling pathway	-3.61268
GO:0031649	heat generation	-3.61268
GO:0032305	positive regulation of eicosanoid secretion	-3.61268
GO:0033599	regulation of mammary gland epithelial cell proliferation	-3.61268
GO:0035729	cellular response to hepatocyte growth factor stimulus	-3.61268
GO:0045986	negative regulation of smooth muscle contraction	-3.61268
GO:0050665	hydrogen peroxide biosynthetic process	-3.61268
GO:0070875	positive regulation of glycogen metabolic process	-3.61268
GO:1903209	positive regulation of oxidative stress-induced cell death	-3.61268
GO:0006836	neurotransmitter transport	-3.60389
GO:0097479	synaptic vesicle localization	-3.6037

GO:00109 07	positive regulation of glucose metabolic process	-3.59969
GO:00330 48	negative regulation of mitotic sister chromatid segregation	-3.59969
GO:00328 86	regulation of microtubule-based process	-3.59906
GO:00165 69	covalent chromatin modification	-3.5929
GO:00025 26	acute inflammatory response	-3.58596
GO:00601 47	regulation of posttranscriptional gene silencing	-3.58197
GO:00609 66	regulation of gene silencing by RNA	-3.58197
GO:00456 65	negative regulation of neuron differentiation	-3.57293
GO:00600 47	heart contraction	-3.57007
GO:00070 52	mitotic spindle organization	-3.56251
GO:00331 43	regulation of intracellular steroid hormone receptor signaling pathway	-3.56158
GO:00467 85	microtubule polymerization	-3.56158
GO:00723 32	intrinsic apoptotic signaling pathway by p53 class mediator	-3.56158
GO:00019 53	negative regulation of cell-matrix adhesion	-3.55977
GO:00023 69	T cell cytokine production	-3.55977
GO:00157 01	bicarbonate transport	-3.55977
GO:00189 04	ether metabolic process	-3.53585
GO:00331 94	response to hydroperoxide	-3.53585
GO:00451 87	regulation of circadian sleep/wake cycle, sleep	-3.53585
GO:00612 98	retina vasculature development in camera-type eye	-3.53585
GO:00713 18	cellular response to ATP	-3.53585
GO:20006 41	regulation of early endosome to late endosome transport	-3.53585

GO:20011 70	negative regulation of ATP biosynthetic process	-3.53585
GO:00422 46	tissue regeneration	-3.53575
GO:00603 95	SMAD protein signal transduction	-3.53575
GO:19000 34	regulation of cellular response to heat	-3.53575
GO:00991 73	postsynapse organization	-3.52624
GO:00508 07	regulation of synapse organization	-3.52151
GO:00326 20	interleukin-17 production	-3.52086
GO:00330 46	negative regulation of sister chromatid segregation	-3.52086
GO:00353 07	positive regulation of protein dephosphorylation	-3.52086
GO:00456 87	positive regulation of glial cell differentiation	-3.52086
GO:00002 80	nuclear division	-3.51087
GO:00023 12	B cell activation involved in immune response	-3.51029
GO:20003 00	regulation of synaptic vesicle exocytosis	-3.51029
GO:00514 95	positive regulation of cytoskeleton organization	-3.50882
GO:00026 98	negative regulation of immune effector process	-3.50521
GO:00322 71	regulation of protein polymerization	-3.49621
GO:00030 14	renal system process	-3.48647
GO:00352 70	endocrine system development	-3.48647
GO:00019 74	blood vessel remodeling	-3.48291
GO:00067 75	fat-soluble vitamin metabolic process	-3.48291
GO:00341 98	cellular response to amino acid starvation	-3.48291
GO:00519 85	negative regulation of chromosome segregation	-3.48291

GO:0002862	negative regulation of inflammatory response to antigenic stimulus	-3.46356
GO:0010759	positive regulation of macrophage chemotaxis	-3.46356
GO:0034393	positive regulation of smooth muscle cell apoptotic process	-3.46356
GO:0035728	response to hepatocyte growth factor	-3.46356
GO:0060252	positive regulation of glial cell proliferation	-3.46356
GO:1902170	cellular response to reactive nitrogen species	-3.46356
GO:0002446	neutrophil mediated immunity	-3.45001
GO:0002639	positive regulation of immunoglobulin production	-3.44588
GO:0005978	glycogen biosynthetic process	-3.44588
GO:0009250	glucan biosynthetic process	-3.44588
GO:0010761	fibroblast migration	-3.44588
GO:0010863	positive regulation of phospholipase C activity	-3.44588
GO:0001570	vasculogenesis	-3.436
GO:0001937	negative regulation of endothelial cell proliferation	-3.436
GO:0014855	striated muscle cell proliferation	-3.436
GO:0060560	developmental growth involved in morphogenesis	-3.43412
GO:0031647	regulation of protein stability	-3.42856
GO:0097061	dendritic spine organization	-3.41191
GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	-3.40973
GO:0032480	negative regulation of type I interferon production	-3.40973
GO:0045776	negative regulation of blood pressure	-3.40973
GO:0070849	response to epidermal growth factor	-3.40973

GO:00065 25	arginine metabolic process	-3.39532
GO:00072 52	I-kappaB phosphorylation	-3.39532
GO:00324 95	response to muramyl dipeptide	-3.39532
GO:00327 27	positive regulation of interferon-alpha production	-3.39532
GO:00717 31	response to nitric oxide	-3.39532
GO:20001 93	positive regulation of fatty acid transport	-3.39532
GO:00902 88	negative regulation of cellular response to growth factor stimulus	-3.39334
GO:20012 57	regulation of cation channel activity	-3.39334
GO:00311 10	regulation of microtubule polymerization or depolymerization	-3.38815
GO:00508 03	regulation of synapse structure or activity	-3.38561
GO:00456 67	regulation of osteoblast differentiation	-3.37757
GO:00149 11	positive regulation of smooth muscle cell migration	-3.37442
GO:00422 20	response to cocaine	-3.37442
GO:19002 71	regulation of long-term synaptic potentiation	-3.37442
GO:19909 28	response to amino acid starvation	-3.37442
GO:19035 22	regulation of blood circulation	-3.36586
GO:00149 10	regulation of smooth muscle cell migration	-3.3647
GO:00454 45	myoblast differentiation	-3.3647
GO:00706 64	negative regulation of leukocyte proliferation	-3.3647
GO:00977 56	negative regulation of blood vessel diameter	-3.3647
GO:19028 03	regulation of synaptic vesicle transport	-3.3647
GO:00602 91	long-term synaptic potentiation	-3.34155

GO:00066 92	prostanoid metabolic process	-3.33992	
GO:00066 93	prostaglandin metabolic process	-3.33992	
GO:00075 95	lactation		- 3.3399 2
GO:00326 63	regulation of interleukin-2 production	-3.33992	
GO:00450 58	T cell selection	-3.33992	
GO:00485 12	circadian behavior	-3.33992	
GO:19000 87	positive regulation of G1/S transition of mitotic cell cycle	-3.33992	
GO:19002 74	regulation of phospholipase C activity	-3.33992	
GO:00165 40	protein autoprocessing	-3.33072	
GO:00170 00	antibiotic biosynthetic process	-3.33072	
GO:00307 28	ovulation		- 3.3307 2
GO:00308 09	negative regulation of nucleotide biosynthetic process	-3.33072	
GO:00436 51	linoleic acid metabolic process	-3.33072	
GO:00467 16	muscle cell cellular homeostasis	-3.33072	
GO:00600 65	uterus development	-3.33072	
GO:00902 01	negative regulation of release of cytochrome c from mitochondria	-3.33072	
GO:00903 12	positive regulation of protein deacetylation	-3.33072	
GO:19003 72	negative regulation of purine nucleotide biosynthetic process	-3.33072	
GO:19024 14	protein localization to cell junction	-3.33072	
GO:20007 37	negative regulation of stem cell differentiation	-3.33072	
GO:00705 88	calcium ion transmembrane transport	-3.32493	

GO:004533	cellular respiration	-3.32287
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	-3.31871
GO:0070098	chemokine-mediated signaling pathway	-3.31871
GO:0046718	viral entry into host cell	-3.30815
GO:0048565	digestive tract development	-3.30815
GO:0007622	rhythmic behavior	-3.30618
GO:0097300	programmed necrotic cell death	-3.30618
GO:0043506	regulation of JUN kinase activity	-3.29616
GO:0010565	regulation of cellular ketone metabolic process	-3.29532
GO:0048598	embryonic morphogenesis	-3.27485
GO:0032273	positive regulation of protein polymerization	-3.27434
GO:0045540	regulation of cholesterol biosynthetic process	-3.27319
GO:0045646	regulation of erythrocyte differentiation	-3.27319
GO:0045912	negative regulation of carbohydrate metabolic process	-3.27319
GO:0106118	regulation of sterol biosynthetic process	-3.27319
GO:1903573	negative regulation of response to endoplasmic reticulum stress	-3.27319
GO:0000717	nucleotide-excision repair, DNA duplex unwinding	-3.26939
GO:0032700	negative regulation of interleukin-17 production	-3.26939
GO:0042749	regulation of circadian sleep/wake cycle	-3.26939
GO:0045655	regulation of monocyte differentiation	-3.26939
GO:0050802	circadian sleep/wake cycle, sleep	-3.26939
GO:0097306	cellular response to alcohol	-3.25192

GO:0045839	negative regulation of mitotic nuclear division	-3.2409
GO:0071622	regulation of granulocyte chemotaxis	-3.2409
GO:2000677	regulation of transcription regulatory region DNA binding	-3.2409
GO:0006644	phospholipid metabolic process	-3.23833
GO:0031058	positive regulation of histone modification	-3.23021
GO:0000715	nucleotide-excision repair, DNA damage recognition	-3.21104
GO:0031281	positive regulation of cyclase activity	-3.21104
GO:0035162	embryonic hemopoiesis	-3.21104
GO:0045723	positive regulation of fatty acid biosynthetic process	-3.21104
GO:1900017	positive regulation of cytokine production involved in inflammatory response	-3.21104
GO:1901032	negative regulation of response to reactive oxygen species	-3.21104
GO:1903077	negative regulation of protein localization to plasma membrane	-3.21104
GO:1903206	negative regulation of hydrogen peroxide-induced cell death	-3.21104
GO:2001039	negative regulation of cellular response to drug	-3.21104
GO:0045599	negative regulation of fat cell differentiation	-3.2093
GO:0045661	regulation of myoblast differentiation	-3.2093
GO:0014909	smooth muscle cell migration	-3.20877
GO:0045185	maintenance of protein location	-3.20877
GO:0051702	interaction with symbiont	-3.20877
GO:0051952	regulation of amine transport	-3.20877
GO:1905954	positive regulation of lipid localization	-3.20877
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	-3.20115

GO:20000 27	regulation of animal organ morphogenesis	-3.20115
GO:00072 92	female gamete generation	-3.1923
GO:00147 06	striated muscle tissue development	-3.19206
GO:00343 29	cell junction assembly	-3.1791
GO:00096 20	response to fungus	-3.17835
GO:00100 43	response to zinc ion	-3.17835
GO:00326 23	interleukin-2 production	-3.17835
GO:00713 20	cellular response to cAMP	-3.17835
GO:00030 73	regulation of systemic arterial blood pressure	-3.16667
GO:00603 37	type I interferon signaling pathway	-3.16667
GO:00713 57	cellular response to type I interferon	-3.16667
GO:00076 26	locomotory behavior	-3.16267
GO:00102 56	endomembrane system organization	-3.16095
GO:01061 06	cold-induced thermogenesis	-3.16043
GO:01201 61	regulation of cold-induced thermogenesis	-3.16043
GO:00508 51	antigen receptor-mediated signaling pathway	-3.15829
GO:00062 97	nucleotide-excision repair, DNA gap filling	-3.15539
GO:00443 21	response to leptin	-3.15539
GO:00511 95	negative regulation of cofactor metabolic process	-3.15539
GO:00603 96	growth hormone receptor signaling pathway	-3.15539
GO:00604 44	branching involved in mammary gland duct morphogenesis	-3.15539
GO:19018 89	negative regulation of cell junction assembly	-3.15539

GO:20006 37	positive regulation of gene silencing by miRNA	-3.15539
GO:00029 31	response to ischemia	-3.14803
GO:00083 47	glial cell migration	-3.14803
GO:00466 31	alpha-beta T cell activation	-3.12908
GO:00075 89	body fluid secretion	-3.12557
GO:00466 34	regulation of alpha-beta T cell activation	-3.12557
GO:19908 68	response to chemokine	-3.12557
GO:19908 69	cellular response to chemokine	-3.12557
GO:00164 47	somatic recombination of immunoglobulin gene segments	-3.11832
GO:00312 95	T cell costimulation	-3.11832
GO:00515 88	regulation of neurotransmitter transport	-3.1136
GO:19028 50	microtubule cytoskeleton organization involved in mitosis	-3.1136
GO:00300 36	actin cytoskeleton organization	-3.1115
GO:00324 12	regulation of ion transmembrane transporter activity	-3.10362
GO:00094 04	toxin metabolic process	-3.10221
GO:00224 10	circadian sleep/wake cycle process	-3.10221
GO:00456 62	negative regulation of myoblast differentiation	-3.10221
GO:00509 27	positive regulation of positive chemotaxis	-3.10221
GO:00601 48	positive regulation of posttranscriptional gene silencing	-3.10221
GO:00614 36	establishment of skin barrier	-3.10221
GO:00713 78	cellular response to growth hormone stimulus	-3.10221
GO:19043 76	negative regulation of protein localization to cell periphery	-3.10221

GO:20006 79	positive regulation of transcription regulatory region DNA binding	-3.10221
GO:00316 44	regulation of neurological system process	-3.09824
GO:20012 51	negative regulation of chromosome organization	-3.09824
GO:00457 47	positive regulation of Notch signaling pathway	-3.08919
GO:00480 16	inositol phosphate-mediated signaling	-3.08919
GO:00343 40	response to type I interferon	-3.08543
GO:00158 50	organic hydroxy compound transport	-3.07204
GO:00902 63	positive regulation of canonical Wnt signaling pathway	-3.06789
GO:00312 94	lymphocyte costimulation	-3.06063
GO:19037 49	positive regulation of establishment of protein localization to mitochondrion	-3.06063
GO:00516 04	protein maturation	-3.05903
GO:00072 76	gamete generation	-3.05887
GO:00313 33	negative regulation of protein complex assembly	-3.05289
GO:19031 69	regulation of calcium ion transmembrane transport	-3.05289
GO:00020 68	glandular epithelial cell development	-3.0513
GO:00063 09	apoptotic DNA fragmentation	-3.0513
GO:00067 06	steroid catabolic process	-3.0513
GO:00359 02	response to immobilization stress	-3.0513
GO:00428 32	defense response to protozoan	-3.0513
GO:00509 26	regulation of positive chemotaxis	-3.0513
GO:00709 11	global genome nucleotide-excision repair	-3.0513
GO:19036 49	regulation of cytoplasmic transport	-3.0513

GO:0007215	glutamate receptor signaling pathway	-3.04622
GO:0010522	regulation of calcium ion transport into cytosol	-3.04622
GO:0015837	amine transport	-3.04622
GO:0019217	regulation of fatty acid metabolic process	-3.04622
GO:0042102	positive regulation of T cell proliferation	-3.04622
GO:0002886	regulation of myeloid leukocyte mediated immunity	-3.03261
GO:0060043	regulation of cardiac muscle cell proliferation	-3.03261
GO:0055024	regulation of cardiac muscle tissue development	-3.02695
GO:0060537	muscle tissue development	-3.02687
GO:0019229	regulation of vasoconstriction	-3.00512
GO:0022029	telencephalon cell migration	-3.00512
GO:0050994	regulation of lipid catabolic process	-3.00512
GO:0051784	negative regulation of nuclear division	-3.00512
GO:0061077	chaperone-mediated protein folding	-3.00512
GO:1902808	positive regulation of cell cycle G1/S phase transition	-3.00512
GO:0001562	response to protozoan	-3.00249
GO:0002825	regulation of T-helper 1 type immune response	-3.00249
GO:0009065	glutamine family amino acid catabolic process	-3.00249
GO:0009651	response to salt stress	-3.00249
GO:1900120	regulation of receptor binding	-3.00249
GO:1903203	regulation of oxidative stress-induced neuron death	-3.00249
GO:1904357	negative regulation of telomere maintenance via telomere lengthening	-3.00249

GO:0006260	DNA replication	-3.00006
GO:0043312	neutrophil degranulation	-2.99846
GO:1990845	adaptive thermogenesis	-2.99407
GO:0022898	regulation of transmembrane transporter activity	-2.98997
GO:0008360	regulation of cell shape	-2.97965
GO:0033013	tetrapyrrole metabolic process	-2.97814
GO:0002283	neutrophil activation involved in immune response	-2.97709
GO:0110053	regulation of actin filament organization	-2.96992
GO:0022011	myelination in peripheral nervous system	-2.95561
GO:0032292	peripheral nervous system axon ensheathment	-2.95561
GO:0033561	regulation of water loss via skin	-2.95561
GO:0042745	circadian sleep/wake cycle	-2.95561
GO:0044331	cell-cell adhesion mediated by cadherin	-2.95561
GO:0045932	negative regulation of muscle contraction	-2.95561
GO:0090200	positive regulation of release of cytochrome c from mitochondria	-2.95561
GO:1903579	negative regulation of ATP metabolic process	-2.95561
GO:0002456	T cell mediated immunity	-2.95199
GO:0014812	muscle cell migration	-2.95199
GO:0032414	positive regulation of ion transmembrane transporter activity	-2.95199
GO:0034446	substrate adhesion-dependent cell spreading	-2.95199
GO:0046632	alpha-beta T cell differentiation	-2.95199
GO:0046928	regulation of neurotransmitter secretion	-2.95199

GO:19052 69	positive regulation of chromatin organization	-2.95199	
GO:00022 94	CD4-positive, alpha-beta T cell differentiation involved in immune response	-2.95165	
GO:00105 18	positive regulation of phospholipase activity	-2.95165	
GO:00106 76	positive regulation of cellular carbohydrate metabolic process	-2.95165	
GO:00486 45	animal organ formation	-2.95165	
GO:00550 25	positive regulation of cardiac muscle tissue development	-2.95165	
GO:00550 81	anion homeostasis	-2.95165	
GO:20012 44	positive regulation of intrinsic apoptotic signaling pathway	-2.95165	
GO:00550 67	monovalent inorganic cation homeostasis	-2.95114	
GO:00604 02	calcium ion transport into cytosol	-2.95114	
GO:19037 07	negative regulation of hemopoiesis	-2.95114	
GO:00064 12	translation	-2.93426	
GO:00971 64	ammonium ion metabolic process	-2.93177	
GO:00022 87	alpha-beta T cell activation involved in immune response	-2.92563	
GO:00022 93	alpha-beta T cell differentiation involved in immune response	-2.92563	
GO:00466 22	positive regulation of organ growth	-2.92563	
GO:00705 27	platelet aggregation	-2.92563	
GO:00510 17	actin filament bundle assembly	-2.92305	
GO:00062 94	nucleotide-excision repair, preincision complex assembly	-2.91052	
GO:00072 63	nitric oxide mediated signal transduction	-2.91052	
GO:00082 09	androgen metabolic process	-2.91052	
GO:00198 35	cytolysis		- 2.9105

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GO:0046637	regulation of alpha-beta T cell differentiation	-2.90007	
GO:0051898	negative regulation of protein kinase B signaling	-2.90007	
GO:1900449	regulation of glutamate receptor signaling pathway	-2.90007	
GO:2000401	regulation of lymphocyte migration	-2.90007	
GO:0018958	phenol-containing compound metabolic process	-2.89788	
GO:0042119	neutrophil activation	-2.89339	
GO:0007229	integrin-mediated signaling pathway	-2.88023	
GO:0015696	ammonium transport	-2.88023	
GO:1901800	positive regulation of proteasomal protein catabolic process	-2.88023	
GO:0032729	positive regulation of interferon-gamma production	-2.87495	
GO:0051926	negative regulation of calcium ion transport	-2.87495	
GO:0070265	necrotic cell death	-2.87495	
GO:1905953	negative regulation of lipid localization	-2.87495	
GO:0061572	actin filament bundle organization	-2.86813	
GO:0031116	positive regulation of microtubule polymerization	-2.8671	
GO:0036475	neuron death in response to oxidative stress	-2.8671	
GO:0070168	negative regulation of biomineral tissue development	-2.8671	
GO:0034440	lipid oxidation	-2.86277	
GO:1901605	alpha-amino acid metabolic process	-2.85291	
GO:0036230	granulocyte activation	-2.85258	
GO:0016445	somatic diversification of immunoglobulins	-2.85027	

GO:00901 81	regulation of cholesterol metabolic process	-2.85027
GO:00985 86	cellular response to virus	-2.85027
GO:19058 18	regulation of chromosome separation	-2.85027
GO:20003 78	negative regulation of reactive oxygen species metabolic process	-2.85027
GO:00072 64	small GTPase mediated signal transduction	-2.84585
GO:00062 89	nucleotide-excision repair	-2.84548
GO:00324 09	regulation of transporter activity	-2.84399
GO:00464 86	glycerolipid metabolic process	-2.84245
GO:00171 58	regulation of calcium ion-dependent exocytosis	-2.82838
GO:19035 10	mucopolysaccharide metabolic process	-2.82838
GO:00070 15	actin filament organization	-2.82771
GO:00068 79	cellular iron ion homeostasis	-2.826
GO:00364 98	IRE1-mediated unfolded protein response	-2.826
GO:00466 26	regulation of insulin receptor signaling pathway	-2.826
GO:00026 75	positive regulation of acute inflammatory response	-2.82523
GO:00028 28	regulation of type 2 immune response	-2.82523
GO:00109 54	positive regulation of protein processing	-2.82523
GO:00610 82	myeloid leukocyte cytokine production	-2.82523
GO:00702 29	negative regulation of lymphocyte apoptotic process	-2.82523
GO:00900 75	relaxation of muscle	-2.82523
GO:19005 43	negative regulation of purine nucleotide metabolic process	-2.82523
GO:19007 45	positive regulation of p38MAPK cascade	-2.82523

GO:19022 30	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	-2.82523
GO:19054 76	negative regulation of protein localization to membrane	-2.82523
GO:00324 11	positive regulation of transporter activity	-2.81145
GO:00025 62	somatic diversification of immune receptors via germline recombination within a single locus	-2.80214
GO:00066 25	protein targeting to peroxisome	-2.80214
GO:00164 44	somatic cell DNA recombination	-2.80214
GO:00714 79	cellular response to ionizing radiation	-2.80214
GO:00726 62	protein localization to peroxisome	-2.80214
GO:00726 63	establishment of protein localization to peroxisome	-2.80214
GO:00903 07	mitotic spindle assembly	-2.80214
GO:00486 40	negative regulation of developmental growth	-2.7947
GO:00027 24	regulation of T cell cytokine production	-2.78481
GO:00028 88	positive regulation of myeloid leukocyte mediated immunity	-2.78481
GO:00107 43	regulation of macrophage derived foam cell differentiation	-2.78481
GO:00326 73	regulation of interleukin-4 production	-2.78481
GO:00427 44	hydrogen peroxide catabolic process	-2.78481
GO:00459 80	negative regulation of nucleotide metabolic process	-2.78481
GO:00606 03	mammary gland duct morphogenesis	-2.78481
GO:19022 35	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	-2.78481
GO:00435 74	peroxisomal transport	-2.77867
GO:00600 38	cardiac muscle cell proliferation	-2.77867
GO:00609 64	regulation of gene silencing by miRNA	-2.77811

GO:0030307	positive regulation of cell growth	-2.77581
GO:0002244	hematopoietic progenitor cell differentiation	-2.76299
GO:0051258	protein polymerization	-2.75197
GO:0060401	cytosolic calcium ion transport	-2.75027
GO:0035587	purinergic receptor signaling pathway	-2.74576
GO:1903319	positive regulation of protein maturation	-2.74576
GO:0051209	release of sequestered calcium ion into cytosol	-2.74544
GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	-2.74544
GO:0002292	T cell differentiation involved in immune response	-2.73287
GO:0033627	cell adhesion mediated by integrin	-2.73287
GO:0050795	regulation of behavior	-2.73287
GO:0050891	multicellular organismal water homeostasis	-2.73287
GO:0031109	microtubule polymerization or depolymerization	-2.72935
GO:0051283	negative regulation of sequestering of calcium ion	-2.72935
GO:0007269	neurotransmitter secretion	-2.72509
GO:0045216	cell-cell junction organization	-2.72509
GO:0099643	signal release from synapse	-2.72509
GO:2000736	regulation of stem cell differentiation	-2.71341
GO:0033047	regulation of mitotic sister chromatid segregation	-2.71051
GO:0033692	cellular polysaccharide biosynthetic process	-2.71051
GO:0070988	demethylation	-2.71051
GO:0000737	DNA catabolic process, endonucleolytic	-2.70797

GO:0002691	regulation of cellular extravasation	-2.70797
GO:0007094	mitotic spindle assembly checkpoint	-2.70797
GO:0008608	attachment of spindle microtubules to kinetochore	-2.70797
GO:0010762	regulation of fibroblast migration	-2.70797
GO:0030851	granulocyte differentiation	-2.70797
GO:0031112	positive regulation of microtubule polymerization or depolymerization	-2.70797
GO:0031577	spindle checkpoint	-2.70797
GO:0035633	maintenance of permeability of blood-brain barrier	-2.70797
GO:0071173	spindle assembly checkpoint	-2.70797
GO:0071174	mitotic spindle checkpoint	-2.70797
GO:2001024	negative regulation of response to drug	-2.70797
GO:0002792	negative regulation of peptide secretion	-2.69763
GO:0016079	synaptic vesicle exocytosis	-2.69763
GO:0031398	positive regulation of protein ubiquitination	-2.69763
GO:0051282	regulation of sequestering of calcium ion	-2.69763
GO:0002709	regulation of T cell mediated immunity	-2.6885
GO:0005977	glycogen metabolic process	-2.6885
GO:0010611	regulation of cardiac muscle hypertrophy	-2.6885
GO:0030218	erythrocyte differentiation	-2.682
GO:0010769	regulation of cell morphogenesis involved in differentiation	-2.6725
GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	-2.67138
GO:0030262	apoptotic nuclear changes	-2.67138

GO:00309 47	regulation of vascular endothelial growth factor receptor signaling pathway	-2.67138
GO:00322 28	regulation of synaptic transmission, GABAergic	-2.67138
GO:00326 33	interleukin-4 production	-2.67138
GO:00343 90	smooth muscle cell apoptotic process	-2.67138
GO:00343 91	regulation of smooth muscle cell apoptotic process	-2.67138
GO:00433 04	regulation of mast cell degranulation	-2.67138
GO:00456 48	positive regulation of erythrocyte differentiation	-2.67138
GO:00603 38	regulation of type I interferon-mediated signaling pathway	-2.67138
GO:00708 84	regulation of calcineurin-NFAT signaling cascade	-2.67138
GO:00718 68	cellular response to monoamine stimulus	-2.67138
GO:00718 70	cellular response to catecholamine stimulus	-2.67138
GO:00988 01	regulation of renal system process	-2.67138
GO:00060 73	cellular glucan metabolic process	-2.66683
GO:00105 17	regulation of phospholipase activity	-2.66683
GO:00440 42	glucan metabolic process	-2.66683
GO:00486 75	axon extension	-2.66653
GO:00325 35	regulation of cellular component size	-2.66582
GO:00016 54	eye development	-2.65822
GO:00512 08	sequestering of calcium ion	-2.6512
GO:00019 10	regulation of leukocyte mediated cytotoxicity	-2.64549
GO:00508 05	negative regulation of synaptic transmission	-2.64549
GO:00083 61	regulation of cell size	-2.63965

GO:00706 13	regulation of protein processing	-2.63965
GO:00033 82	epithelial cell morphogenesis	-2.63593
GO:00322 05	negative regulation of telomere maintenance	-2.63593
GO:00330 06	regulation of mast cell activation involved in immune response	-2.63593
GO:00433 68	positive T cell selection	-2.63593
GO:00458 41	negative regulation of mitotic metaphase/anaphase transition	-2.63593
GO:00716 34	regulation of transforming growth factor beta production	-2.63593
GO:01060 56	regulation of calcineurin-mediated signaling	-2.63593
GO:01500 63	visual system development	-2.62807
GO:00066 95	cholesterol biosynthetic process	-2.62447
GO:00083 06	associative learning	-2.62447
GO:00147 43	regulation of muscle hypertrophy	-2.62447
GO:00330 77	T cell differentiation in thymus	-2.62447
GO:00601 93	positive regulation of lipase activity	-2.62447
GO:19026 53	secondary alcohol biosynthetic process	-2.62447
GO:19035 24	positive regulation of blood circulation	-2.62447
GO:00163 58	dendrite development	-2.62385
GO:00074 16	synapse assembly	-2.61598
GO:19033 17	regulation of protein maturation	-2.61598
GO:19035 31	negative regulation of secretion by cell	-2.61598
GO:00060 81	cellular aldehyde metabolic process	-2.60376
GO:00327 20	negative regulation of tumor necrosis factor production	-2.60376

GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	-2.60153
GO:0006471	protein ADP-ribosylation	-2.60153
GO:0006921	cellular component disassembly involved in execution phase of apoptosis	-2.60153
GO:0043243	positive regulation of protein complex disassembly	-2.60153
GO:0090050	positive regulation of cell migration involved in sprouting angiogenesis	-2.60153
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	-2.60153
GO:0050770	regulation of axonogenesis	-2.59263
GO:0048880	sensory system development	-2.58365
GO:0042310	vasoconstriction	-2.58336
GO:0043367	CD4-positive, alpha-beta T cell differentiation	-2.58336
GO:0048639	positive regulation of developmental growth	-2.58106
GO:0034763	negative regulation of transmembrane transport	-2.57669
GO:0051147	regulation of muscle cell differentiation	-2.56958
GO:0010661	positive regulation of muscle cell apoptotic process	-2.56815
GO:0032094	response to food	-2.56815
GO:0032689	negative regulation of interferon-gamma production	-2.56815
GO:0042769	DNA damage response, detection of DNA damage	-2.56815
GO:0045923	positive regulation of fatty acid metabolic process	-2.56815
GO:0051954	positive regulation of amine transport	-2.56815
GO:0051955	regulation of amino acid transport	-2.56815
GO:0060045	positive regulation of cardiac muscle cell proliferation	-2.56815
GO:0071604	transforming growth factor beta production	-2.56815

GO:0002200	somatic diversification of immune receptors	-2.56326
GO:0030104	water homeostasis	-2.56326
GO:0050672	negative regulation of lymphocyte proliferation	-2.56326
GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	-2.56326
GO:0006470	protein dephosphorylation	-2.56292
GO:0008544	epidermis development	-2.54487
GO:0032945	negative regulation of mononuclear cell proliferation	-2.54344
GO:0055021	regulation of cardiac muscle tissue growth	-2.54344
GO:0006656	phosphatidylcholine biosynthetic process	-2.53572
GO:0006778	porphyrin-containing compound metabolic process	-2.53572
GO:0033683	nucleotide-excision repair, DNA incision	-2.53572
GO:0038179	neurotrophin signaling pathway	-2.53572
GO:0045022	early endosome to late endosome transport	-2.53572
GO:0055090	acylglycerol homeostasis	-2.53572
GO:0070328	triglyceride homeostasis	-2.53572
GO:0071867	response to monoamine	-2.53572
GO:0071869	response to catecholamine	-2.53572
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	-2.53572
GO:2000249	regulation of actin cytoskeleton reorganization	-2.53572
GO:2000816	negative regulation of mitotic sister chromatid separation	-2.53572
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	-2.53362
GO:0043010	camera-type eye development	-2.53037

GO:0051279	regulation of release of sequestered calcium ion into cytosol	-2.52391
GO:0042177	negative regulation of protein catabolic process	-2.51952
GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	-2.51952
GO:0061136	regulation of proteasomal protein catabolic process	-2.51326
GO:0045995	regulation of embryonic development	-2.50555
GO:0016126	sterol biosynthetic process	-2.50465
GO:0008207	C21-steroid hormone metabolic process	-2.50418
GO:0010613	positive regulation of cardiac muscle hypertrophy	-2.50418
GO:1905819	negative regulation of chromosome separation	-2.50418
GO:0007031	peroxisome organization	-2.48565
GO:0006997	nucleus organization	-2.47797
GO:0051225	spindle assembly	-2.47797
GO:0007212	dopamine receptor signaling pathway	-2.47351
GO:0009112	nucleobase metabolic process	-2.47351
GO:0014742	positive regulation of muscle hypertrophy	-2.47351
GO:0033574	response to testosterone	-2.47351
GO:0046825	regulation of protein export from nucleus	-2.47351
GO:0050832	defense response to fungus	-2.47351
GO:2000008	regulation of protein localization to cell surface	-2.47351
GO:0051216	cartilage development	-2.4695
GO:0015844	monoamine transport	-2.46692
GO:00330	regulation of sister chromatid segregation	-2.46692

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GO:0051651	maintenance of location in cell	-2.46692
GO:0055072	iron ion homeostasis	-2.46692
GO:0030534	adult behavior	-2.46436
GO:0045844	positive regulation of striated muscle tissue development	-2.44844
GO:0048636	positive regulation of muscle organ development	-2.44844
GO:0110110	positive regulation of animal organ morphogenesis	-2.44844
GO:0051590	positive regulation of neurotransmitter transport	-2.44365
GO:0072595	maintenance of protein localization in organelle	-2.44365
GO:0098927	vesicle-mediated transport between endosomal compartments	-2.44365
GO:0006112	energy reserve metabolic process	-2.43022
GO:1901863	positive regulation of muscle tissue development	-2.43022
GO:0031032	actomyosin structure organization	-2.42684
GO:0097553	calcium ion transmembrane import into cytosol	-2.42425
GO:0006308	DNA catabolic process	-2.41457
GO:0046006	regulation of activated T cell proliferation	-2.41457
GO:0050850	positive regulation of calcium-mediated signaling	-2.41457
GO:0050856	regulation of T cell receptor signaling pathway	-2.41457
GO:0071470	cellular response to osmotic stress	-2.41457
GO:0001942	hair follicle development	-2.41223
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	-2.41223
GO:0034109	homotypic cell-cell adhesion	-2.41223

GO:00604 20	regulation of heart growth	-2.41223
GO:00070 43	cell-cell junction assembly	-2.41111
GO:19033 22	positive regulation of protein modification by small protein conjugation or removal	-2.41111
GO:00450 17	glycerolipid biosynthetic process	-2.41069
GO:00070 51	spindle organization	-2.39554
GO:00020 28	regulation of sodium ion transport	-2.39448
GO:00331 73	calcineurin-NFAT signaling cascade	-2.38623
GO:00420 88	T-helper 1 type immune response	-2.38623
GO:00421 81	ketone biosynthetic process	-2.38623
GO:00224 04	molting cycle process	-2.37697
GO:00224 05	hair cycle process	-2.37697
GO:19038 45	negative regulation of cellular response to transforming growth factor beta stimulus	-2.37697
GO:00072 65	Ras protein signal transduction	-2.37532
GO:00508 52	T cell receptor signaling pathway	-2.37499
GO:00600 41	retina development in camera-type eye	-2.37235
GO:00435 88	skin development	-2.36817
GO:00987 73	skin epidermis development	-2.35968
GO:00106 77	negative regulation of cellular carbohydrate metabolic process	-2.35859
GO:00217 95	cerebral cortex cell migration	-2.35859
GO:00310 18	endocrine pancreas development	-2.35859
GO:00427 71	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	-2.35859
GO:00903	regulation of protein deacetylation	-2.35859

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GO:01401 15	export across plasma membrane	-2.35859
GO:00443 44	cellular response to fibroblast growth factor stimulus	-2.34705
GO:00488 13	dendrite morphogenesis	-2.34705
GO:00459 21	positive regulation of exocytosis	-2.34261
GO:00514 92	regulation of stress fiber assembly	-2.34261
GO:20001 77	regulation of neural precursor cell proliferation	-2.34261
GO:00427 42	defense response to bacterium	-2.33844
GO:00987 42	cell-cell adhesion via plasma-membrane adhesion molecules	-2.33362
GO:00140 14	negative regulation of gliogenesis	-2.33162
GO:00970 28	dendritic cell differentiation	-2.33162
GO:19033 21	negative regulation of protein modification by small protein conjugation or removal	-2.32576
GO:00343 32	adherens junction organization	-2.30988
GO:00085 42	visual learning	-2.3053
GO:00330 03	regulation of mast cell activation	-2.3053
GO:00358 50	epithelial cell differentiation involved in kidney development	-2.3053
GO:00466 38	positive regulation of alpha-beta T cell differentiation	-2.3053
GO:19047 38	vascular associated smooth muscle cell migration	-2.3053
GO:19047 52	regulation of vascular associated smooth muscle cell migration	-2.3053
GO:00015 01	skeletal system development	-2.30036
GO:00352 64	multicellular organism growth	-2.29769
GO:00306 41	regulation of cellular pH	-2.29268

GO:0045778	positive regulation of ossification	-2.29268
GO:0051304	chromosome separation	-2.29268
GO:0016331	morphogenesis of embryonic epithelium	-2.2856
GO:0002820	negative regulation of adaptive immune response	-2.27959
GO:0031952	regulation of protein autophosphorylation	-2.27959
GO:0033628	regulation of cell adhesion mediated by integrin	-2.27959
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	-2.27959
GO:0050798	activated T cell proliferation	-2.27959
GO:0051932	synaptic transmission, GABAergic	-2.27959
GO:0055023	positive regulation of cardiac muscle tissue growth	-2.27959
GO:0060324	face development	-2.27959
GO:0061001	regulation of dendritic spine morphogenesis	-2.27959
GO:1900744	regulation of p38MAPK cascade	-2.27959
GO:0048814	regulation of dendrite morphogenesis	-2.27645
GO:0070167	regulation of biomineral tissue development	-2.27645
GO:0099003	vesicle-mediated transport in synapse	-2.2759
GO:0007605	sensory perception of sound	-2.27361
GO:0016202	regulation of striated muscle tissue development	-2.26171
GO:0031056	regulation of histone modification	-2.26171
GO:0071774	response to fibroblast growth factor	-2.26171
GO:0031279	regulation of cyclase activity	-2.25447
GO:0042059	negative regulation of epidermal growth factor receptor signaling pathway	-2.25447

GO:0043277	apoptotic cell clearance	-2.25447
GO:0070231	T cell apoptotic process	-2.25447
GO:0097720	calcineurin-mediated signaling	-2.25447
GO:0017156	calcium ion regulated exocytosis	-2.24991
GO:0006605	protein targeting	-2.24671
GO:0030516	regulation of axon extension	-2.24458
GO:0035710	CD4-positive, alpha-beta T cell activation	-2.24458
GO:0120162	positive regulation of cold-induced thermogenesis	-2.24458
GO:0010976	positive regulation of neuron projection development	-2.24376
GO:0060485	mesenchyme development	-2.24376
GO:0030509	BMP signaling pathway	-2.2382
GO:0050773	regulation of dendrite development	-2.2382
GO:1902115	regulation of organelle assembly	-2.23789
GO:0008038	neuron recognition	-2.22992
GO:0031648	protein destabilization	-2.22992
GO:0043300	regulation of leukocyte degranulation	-2.22992
GO:0043303	mast cell degranulation	-2.22992
GO:0048546	digestive tract morphogenesis	-2.22992
GO:0010771	negative regulation of cell morphogenesis involved in differentiation	-2.22893
GO:0008277	regulation of G protein-coupled receptor signaling pathway	-2.22659
GO:1901861	regulation of muscle tissue development	-2.22659
GO:0007163	establishment or maintenance of cell polarity	-2.21922

GO:0048489	synaptic vesicle transport	-2.21506
GO:0048634	regulation of muscle organ development	-2.21506
GO:0097480	establishment of synaptic vesicle localization	-2.21506
GO:0002204	somatic recombination of immunoglobulin genes involved in immune response	-2.20591
GO:0002208	somatic diversification of immunoglobulins involved in immune response	-2.20591
GO:0002279	mast cell activation involved in immune response	-2.20591
GO:0045190	isotype switching	-2.20591
GO:0006790	sulfur compound metabolic process	-2.2046
GO:0007519	skeletal muscle tissue development	-2.20363
GO:0030203	glycosaminoglycan metabolic process	-2.20363
GO:2000241	regulation of reproductive process	-2.20363
GO:0043583	ear development	-2.20076
GO:2001020	regulation of response to DNA damage stimulus	-2.18251
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	-2.18242
GO:0002448	mast cell mediated immunity	-2.18242
GO:0002704	negative regulation of leukocyte mediated immunity	-2.18242
GO:0046580	negative regulation of Ras protein signal transduction	-2.18242
GO:0060421	positive regulation of heart growth	-2.18242
GO:0060425	lung morphogenesis	-2.18242
GO:0044264	cellular polysaccharide metabolic process	-2.16816
GO:0060191	regulation of lipase activity	-2.16816
GO:0110020	regulation of actomyosin structure organization	-2.16816

GO:0007632	visual behavior	-2.15943
GO:0032964	collagen biosynthetic process	-2.15943
GO:0038066	p38MAPK cascade	-2.15943
GO:2000772	regulation of cellular senescence	-2.15943
GO:0019827	stem cell population maintenance	-2.15877
GO:0002042	cell migration involved in sprouting angiogenesis	-2.1534
GO:0006885	regulation of pH	-2.1534
GO:0006959	humoral immune response	-2.15105
GO:0002673	regulation of acute inflammatory response	-2.14776
GO:0051494	negative regulation of cytoskeleton organization	-2.14776
GO:0046474	glycerophospholipid biosynthetic process	-2.14663
GO:0048762	mesenchymal cell differentiation	-2.14663
GO:0003300	cardiac muscle hypertrophy	-2.13881
GO:0032231	regulation of actin filament bundle assembly	-2.13881
GO:0006584	catecholamine metabolic process	-2.13692
GO:0006968	cellular defense response	-2.13692
GO:0009712	catechol-containing compound metabolic process	-2.13692
GO:0044764	multi-organism cellular process	-2.13692
GO:1901185	negative regulation of ERBB signaling pathway	-2.13692
GO:0000070	mitotic sister chromatid segregation	-2.13685
GO:0098727	maintenance of cell number	-2.13685
GO:0048738	cardiac muscle tissue development	-2.12899

GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	-2.12439
GO:1902106	negative regulation of leukocyte differentiation	-2.12439
GO:0001954	positive regulation of cell-matrix adhesion	-2.11488
GO:0042304	regulation of fatty acid biosynthetic process	-2.11488
GO:0002708	positive regulation of lymphocyte mediated immunity	-2.11013
GO:0007631	feeding behavior	-2.11013
GO:0019395	fatty acid oxidation	-2.11013
GO:0014897	striated muscle hypertrophy	-2.09603
GO:0055017	cardiac muscle tissue growth	-2.09603
GO:0099175	regulation of postsynapse organization	-2.09603
GO:0060538	skeletal muscle organ development	-2.09398
GO:0071772	response to BMP	-2.09398
GO:0071773	cellular response to BMP stimulus	-2.09398
GO:0002712	regulation of B cell mediated immunity	-2.09328
GO:0002889	regulation of immunoglobulin mediated immune response	-2.09328
GO:0030071	regulation of mitotic metaphase/anaphase transition	-2.09328
GO:0043113	receptor clustering	-2.09328
GO:0060688	regulation of morphogenesis of a branching structure	-2.09328
GO:0071825	protein-lipid complex subunit organization	-2.09328
GO:0090183	regulation of kidney development	-2.09328
GO:1903307	positive regulation of regulated secretory pathway	-2.09328

GO:0048588	developmental cell growth	-2.08574
GO:0006024	glycosaminoglycan biosynthetic process	-2.08208
GO:0061005	cell differentiation involved in kidney development	-2.07211
GO:0014896	muscle hypertrophy	-2.06828
GO:0051224	negative regulation of protein transport	-2.06266
GO:0090305	nucleic acid phosphodiester bond hydrolysis	-2.06266
GO:0031346	positive regulation of cell projection organization	-2.05481
GO:0002821	positive regulation of adaptive immune response	-2.05464
GO:0006641	triglyceride metabolic process	-2.05464
GO:0006022	aminoglycan metabolic process	-2.05238
GO:1990138	neuron projection extension	-2.05238
GO:0034249	negative regulation of cellular amide metabolic process	-2.052
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	-2.05136
GO:0010656	negative regulation of muscle cell apoptotic process	-2.05136
GO:0051055	negative regulation of lipid biosynthetic process	-2.05136
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	-2.05136
GO:0051149	positive regulation of muscle cell differentiation	-2.04114
GO:0061387	regulation of extent of cell growth	-2.04114
GO:0043030	regulation of macrophage activation	-2.03101
GO:0051058	negative regulation of small GTPase mediated signal transduction	-2.03101
GO:0043087	regulation of GTPase activity	-2.03038
GO:0006941	striated muscle contraction	-2.02196

GO:0010921	regulation of phosphatase activity	-2.02196
GO:1904950	negative regulation of establishment of protein localization	-2.02196
GO:0002223	stimulatory C-type lectin receptor signaling pathway	-2.01458
GO:0030004	cellular monovalent inorganic cation homeostasis	-2.01458
GO:0042093	T-helper cell differentiation	-2.01104
GO:0044784	metaphase/anaphase transition of cell cycle	-2.01104

Cellular component

GO	Description	LogP
GO:1902911	protein kinase complex	-13.4395
GO:1902554	serine/threonine protein kinase complex	-11.6033
GO:0061695	transferase complex, transferring phosphorus-containing groups	-11.1846
GO:0098552	side of membrane	-10.3754
GO:0045121	membrane raft	-10.2864
GO:0098857	membrane microdomain	-10.2649
GO:0098589	membrane region	-9.9929
GO:0031983	vesicle lumen	-9.18179
GO:0035976	transcription factor AP-1 complex	-8.55394
GO:0060205	cytoplasmic vesicle lumen	-8.31367
GO:0009897	external side of plasma membrane	-7.85534
GO:0034774	secretory granule lumen	-7.75074
GO:0000307	cyclin-dependent protein kinase holoenzyme complex	-7.58061

GO:003109 3	platelet alpha granule lumen	- 7.48831
GO:000566 7	transcription factor complex	- 7.33899
GO:004485 3	plasma membrane raft	- 6.77073
GO:000590 1	caveola	- 6.75021
GO:003101 2	extracellular matrix	- 6.62528
GO:003109 1	platelet alpha granule	- 6.43856
GO:004847 1	perinuclear region of cytoplasm	- 6.33181
GO:004302 5	neuronal cell body	- 5.76736
GO:000563 5	nuclear envelope	- 5.61878
GO:000578 8	endoplasmic reticulum lumen	-5.4972
GO:006202 3	collagen-containing extracellular matrix	- 5.43312
GO:199023 4	transferase complex	- 5.35132
GO:004323 5	receptor complex	-5.1432
GO:004429 7	cell body	- 5.07546
GO:0005911	cell-cell junction	- 5.06478
GO:009898 4	neuron to neuron synapse	- 4.71992
GO:000581 5	microtubule organizing center	- 4.68465
GO:009879 4	postsynapse	- 4.65222
GO:000032 3	lytic vacuole	- 4.65007
GO:000576 4	lysosome	- 4.65007
GO:009057 5	RNA polymerase II transcription factor complex	- 4.64391
GO:003042 5	dendrite	- 4.63587

GO:003042 4	axon	- 4.62772
GO:009744 7	dendritic tree	- 4.61959
GO:001989 7	extrinsic component of plasma membrane	- 4.38032
GO:000577 0	late endosome	-4.3768
GO:001406 9	postsynaptic density	-4.37511
GO:004479 8	nuclear transcription factor complex	- 4.34472
GO:003227 9	asymmetric synapse	- 4.30604
GO:000591 2	adherens junction	- 4.19225
GO:000590 2	microvillus	- 4.19157
GO:000592 5	focal adhesion	-4.1845
GO:000592 4	cell-substrate adherens junction	- 4.15501
GO:009957 2	postsynaptic specialization	- 4.10765
GO:003005 5	cell-substrate junction	- 4.10646
GO:007016 1	anchoring junction	- 4.06144
GO:000581 9	spindle	- 4.04429
GO:001632 3	basolateral plasma membrane	- 4.02146
GO:004517 7	apical part of cell	- 4.02091
GO:000581 3	centrosome	- 3.95878
GO:001562 9	actin cytoskeleton	- 3.94216
GO:000587 6	spindle microtubule	- 3.90409
GO:003299 3	protein-DNA complex	- 3.84788
GO:000989 8	cytoplasmic side of plasma membrane	- 3.66766

GO:003196 8	organelle outer membrane	- 3.66566
GO:001986 7	outer membrane	-3.6388
GO:009885 8	actin-based cell projection	-3.6388
GO:003065 9	cytoplasmic vesicle membrane	- 3.63512
GO:003196 5	nuclear membrane	- 3.39701
GO:003049 6	midbody	- 3.39334
GO:001989 8	extrinsic component of membrane	- 3.34531
GO:009856 2	cytoplasmic side of membrane	- 3.30905
GO:003013 9	endocytic vesicle	- 3.27471
GO:000574 1	mitochondrial outer membrane	- 3.25464
GO:003123 4	extrinsic component of cytoplasmic side of plasma membrane	- 3.08543
GO:003326 7	axon part	- 3.05903
GO:004320 4	perikaryon	- 2.97965
GO:003125 2	cell leading edge	- 2.93288
GO:009868 7	chromosomal region	- 2.88179
GO:003066 6	endocytic vesicle membrane	- 2.86813
GO:000078 0	condensed nuclear chromosome, centromeric region	- 2.78481
GO:000574 0	mitochondrial envelope	- 2.76785
GO:003013 5	coated vesicle	- 2.76099
GO:009879 3	presynapse	- 2.74701
GO:009879 7	plasma membrane protein complex	- 2.71795
GO:009738 6	glial cell projection	- 2.70797

GO:000592 3	bicellular tight junction	-2.682
GO:190481 3	ficolin-1-rich granule lumen	-2.6512
GO:005123 3	spindle midzone	- 2.63593
GO:003159 4	neuromuscular junction	- 2.62447
GO:004878 6	presynaptic active zone	- 2.62447
GO:010100 2	ficolin-1-rich granule	- 2.60426
GO:007016 0	tight junction	- 2.57669
GO:000177 2	immunological synapse	- 2.53572
GO:003013 6	clathrin-coated vesicle	- 2.48034
GO:009868 5	Schaffer collateral - CA1 synapse	- 2.46692
GO:004329 6	apical junction complex	- 2.38516
GO:003197 0	organelle envelope lumen	- 2.35968
GO:003557 8	azurophil granule lumen	- 2.34261
GO:009897 8	glutamatergic synapse	- 2.27383
GO:003125 3	cell projection membrane	- 2.26679
GO:001632 4	apical plasma membrane	- 2.25977
GO:000992 5	basal plasma membrane	- 2.20591
GO:000079 3	condensed chromosome	- 2.20076
GO:000079 4	condensed nuclear chromosome	-2.1534
GO:000579 6	Golgi lumen	-2.1534
GO:000078 1	chromosome, telomeric region	- 2.14776
GO:000092 2	spindle pole	- 2.12601

GO:003196 6	mitochondrial membrane	-2.11924
GO:003086 3	cortical cytoskeleton	-2.11013
GO:015003 4	distal axon	- 2.09881
GO:000577 5	vacuolar lumen	- 2.04216
GO:000563 7	nuclear inner membrane	-2.01104

Molecular function

ID	Description	LogP
GO:00167 73	phosphotransferase activity, alcohol group as acceptor	- 30.17 52
GO:00046 72	protein kinase activity	- 29.94 15
GO:00163 01	kinase activity	- 28.43 54
GO:00199 00	kinase binding	- 19.41 27
GO:00046 74	protein serine/threonine kinase activity	- 18.69 32
GO:00199 01	protein kinase binding	- 17.37 69
GO:00051 26	cytokine receptor binding	- 17.21 2
GO:00081 34	transcription factor binding	- 16.04 49
GO:00305 45	receptor regulator activity	- 14.47 4
GO:00199	protein domain specific binding	-

04		13.92 46
GO:00164 91	oxidoreductase activity	- 13.26 29
GO:00508 39	cell adhesion molecule binding	- 13.00 33
GO:00200 37	heme binding	- 12.95 82
GO:00708 51	growth factor receptor binding	- 12.81 89
GO:00051 25	cytokine activity	- 12.78 38
GO:00480 18	receptor ligand activity	- 12.65 37
GO:00469 06	tetrapyrrole binding	- 12.50 63
GO:00310 72	heat shock protein binding	- 12.21 38
GO:00199 02	phosphatase binding	- 11.90 94
GO:00051 78	integrin binding	- 11.45 78
GO:00428 03	protein homodimerization activity	- 11.40 34
GO:00047 13	protein tyrosine kinase activity	- 10.46 28
GO:00012 28	DNA-binding transcription activator activity, RNA polymerase II-specific	- 10.40 42
GO:00480 37	cofactor binding	- 9.689 05

GO:0004497	monooxygenase activity	- 9.60715
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	- 9.59211
GO:0070330	aromatase activity	- 9.35846
GO:0051879	Hsp90 protein binding	- 9.16273
GO:0019903	protein phosphatase binding	- 8.94469
GO:0035173	histone kinase activity	- 8.78031
GO:0008083	growth factor activity	- 8.52853
GO:0016538	cyclin-dependent protein serine/threonine kinase regulator activity	- 8.52661
GO:0004879	nuclear receptor activity	- 8.3854
GO:0098531	transcription factor activity, direct ligand regulated sequence-specific DNA binding	- 8.3854
GO:0016712	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	- 8.2396
GO:0019825	oxygen binding	- 8.14838
GO:0008395	steroid hydroxylase activity	- 7.97427
GO:0016209	antioxidant activity	- 7.84315
GO:00055	iron ion binding	-

06		7.787 78
GO:00047 14	transmembrane receptor protein tyrosine kinase activity	- 7.648 53
GO:00085 59	xenobiotic transmembrane transporting ATPase activity	- 7.382 85
GO:00510 87	chaperone binding	- 7.116 12
GO:00012 21	transcription cofactor binding	- 7.046 69
GO:00443 89	ubiquitin-like protein ligase binding	- 7.000 38
GO:00191 99	transmembrane receptor protein kinase activity	- 6.750 21
GO:00452 96	cadherin binding	- 6.722 41
GO:01010 20	estrogen 16-alpha-hydroxylase activity	- 6.718 84
GO:00512 19	phosphoprotein binding	- 6.669 25
GO:00316 25	ubiquitin protein ligase binding	- 6.478 8
GO:00167 25	oxidoreductase activity, acting on CH or CH2 groups	- 6.246 72
GO:00425 62	hormone binding	- 6.122 61
GO:00047 12	protein serine/threonine/tyrosine kinase activity	- 6.036 15
GO:00167 09	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	- 6.036 15

GO:00054 96	steroid binding	- 6.024 33
GO:00352 57	nuclear hormone receptor binding	- 5.909 73
GO:00010 85	RNA polymerase II transcription factor binding	- 5.884 63
GO:00336 95	oxidoreductase activity, acting on CH or CH2 groups, quinone or similar compound as acceptor	- 5.812 57
GO:00348 75	caffeine oxidase activity	- 5.812 57
GO:00972 00	cysteine-type endopeptidase activity involved in execution phase of apoptosis	- 5.722 13
GO:00012 23	transcription coactivator binding	- 5.685 24
GO:00352 58	steroid hormone receptor binding	- 5.649 64
GO:00971 53	cysteine-type endopeptidase activity involved in apoptotic process	- 5.446 3
GO:00040 89	carbonate dehydratase activity	- 5.323 85
GO:00192 07	kinase regulator activity	- 5.323 43
GO:00041 75	endopeptidase activity	- 5.250 97
GO:00514 27	hormone receptor binding	- 5.172 35
GO:00435 59	insulin binding	- 5.118 31
GO:00020 39	p53 binding	- 5.044

		16
GO:0003682	chromatin binding	- 5.03919
GO:0019887	protein kinase regulator activity	- 5.01744
GO:0005518	collagen binding	- 4.89542
GO:0030235	nitric-oxide synthase regulator activity	- 4.87762
GO:0001784	phosphotyrosine residue binding	- 4.86371
GO:0030544	Hsp70 protein binding	- 4.86371
GO:0046982	protein heterodimerization activity	- 4.56707
GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	- 4.50428
GO:0042910	xenobiotic transmembrane transporter activity	- 4.50428
GO:0003707	steroid hormone receptor activity	- 4.43422
GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	- 4.43422
GO:0008013	beta-catenin binding	-4.383
GO:0045309	protein phosphorylated amino acid binding	- 4.36399
GO:0043560	insulin receptor substrate binding	- 4.34957
GO:0097199	cysteine-type endopeptidase activity involved in apoptotic signaling pathway	- 4.349

		57
GO:0050661	NADP binding	- 4.324 37
GO:0070011	peptidase activity, acting on L-amino acid peptides	- 4.264 39
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	- 4.247 51
GO:0004693	cyclin-dependent protein serine/threonine kinase activity	- 4.240 65
GO:0097472	cyclin-dependent protein kinase activity	- 4.240 65
GO:0030546	receptor activator activity	- 4.213 62
GO:0030332	cyclin binding	- 4.180 99
GO:0043548	phosphatidylinositol 3-kinase binding	- 4.180 99
GO:0002020	protease binding	- 4.153 79
GO:0019838	growth factor binding	- 4.153 79
GO:0016836	hydro-lyase activity	- 4.137 75
GO:0050662	coenzyme binding	- 4.125 02
GO:0008233	peptidase activity	- 4.124 89
GO:0004861	cyclin-dependent protein serine/threonine kinase inhibitor activity	- 4.091 03
GO:00083	RNA polymerase II CTD heptapeptide repeat kinase activity	-

53		4.091 03
GO:00155 62	efflux transmembrane transporter activity	- 3.877 05
GO:00428 05	actinin binding	- 3.863 59
GO:00474 85	protein N-terminus binding	- 3.853 45
GO:00166 51	oxidoreductase activity, acting on NAD(P)H	- 3.809 29
GO:00352 59	glucocorticoid receptor binding	- 3.782 49
GO:00090 55	electron transfer activity	- 3.766 05
GO:00046 97	protein kinase C activity	- 3.694 66
GO:00046 98	calcium-dependent protein kinase C activity	- 3.694 66
GO:00168 35	carbon-oxygen lyase activity	- 3.641 37
GO:00016 18	virus receptor activity	- 3.614 38
GO:01040 05	hijacked molecular function	- 3.614 38
GO:00082 01	heparin binding	- 3.587 99
GO:00047 08	MAP kinase kinase activity	- 3.535 85
GO:00506 60	flavin adenine dinucleotide binding	- 3.485 18

GO:0001091	RNA polymerase II basal transcription factor binding	- 3.46356
GO:0004715	non-membrane spanning protein tyrosine kinase activity	- 3.44588
GO:0004707	MAP kinase activity	- 3.39532
GO:0032813	tumor necrosis factor receptor superfamily binding	- 3.37442
GO:0033218	amide binding	- 3.25256
GO:0016829	lyase activity	- 3.24126
GO:0017171	serine hydrolase activity	- 3.24126
GO:0004601	peroxidase activity	- 3.2409
GO:0042277	peptide binding	- 3.22551
GO:0005158	insulin receptor binding	- 3.21104
GO:0009931	calcium-dependent protein serine/threonine kinase activity	- 3.21104
GO:0070412	R-SMAD binding	- 3.21104
GO:0010857	calcium-dependent protein kinase activity	- 3.15539
GO:0070696	transmembrane receptor protein serine/threonine kinase binding	- 3.15539
GO:0005516	calmodulin binding	- 3.149

		85
GO:0005080	protein kinase C binding	- 3.14803
GO:0008289	lipid binding	- 3.12875
GO:0004190	aspartic-type endopeptidase activity	- 3.10221
GO:0035586	purinergic receptor activity	- 3.10221
GO:0070001	aspartic-type peptidase activity	- 3.0513
GO:0005507	copper ion binding	- 3.00512
GO:0097110	scaffold protein binding	- 3.00512
GO:0046875	ephrin receptor binding	- 3.00249
GO:0051393	alpha-actinin binding	- 3.00249
GO:0004222	metalloendopeptidase activity	- 2.91572
GO:0005520	insulin-like growth factor binding	- 2.91052
GO:0033612	receptor serine/threonine kinase binding	- 2.91052
GO:0031406	carboxylic acid binding	- 2.86399
GO:0005164	tumor necrosis factor receptor binding	- 2.82523
GO:00302	protein serine/threonine kinase inhibitor activity	-

91		2.825 23
GO:00510 59	NF-kappaB binding	- 2.825 23
GO:00428 26	histone deacetylase binding	- 2.794 7
GO:00042 52	serine-type endopeptidase activity	- 2.775 81
GO:00055 39	glycosaminoglycan binding	- 2.755 92
GO:00423 79	chemokine receptor binding	- 2.755 58
GO:00431 77	organic acid binding	-2.735
GO:00010 98	basal transcription machinery binding	- 2.710 51
GO:00010 99	basal RNA polymerase II transcription machinery binding	- 2.710 51
GO:00080 47	enzyme activator activity	- 2.708 59
GO:00051 54	epidermal growth factor receptor binding	- 2.707 97
GO:00463 32	SMAD binding	- 2.563 26
GO:00082 36	serine-type peptidase activity	- 2.558 17
GO:00336 13	activating transcription factor binding	- 2.543 44
GO:00015 40	amyloid-beta binding	- 2.523 91
GO:00421	SH2 domain binding	-

69		2.473 51
GO:19016 81	sulfur compound binding	- 2.463 97
GO:00303 31	estrogen receptor binding	- 2.443 65
GO:00430 28	cysteine-type endopeptidase regulator activity involved in apoptotic process	- 2.414 57
GO:00511 17	ATPase binding	- 2.394 48
GO:00481 56	tau protein binding	- 2.358 59
GO:00512 13	dioxygenase activity	- 2.342 61
GO:00010 46	core promoter sequence-specific DNA binding	- 2.305 3
GO:00010 47	core promoter binding	- 2.305 3
GO:00011 02	RNA polymerase II activating transcription factor binding	- 2.305 3
GO:00080 09	chemokine activity	- 2.254 47
GO:00048 96	cytokine receptor activity	- 2.244 58
GO:00016 64	G protein-coupled receptor binding	- 2.220 04
GO:00170 46	peptide hormone binding	- 2.205 91
GO:00436 21	protein self-association	- 2.072 11

GO:0015238	drug transmembrane transporter activity	-2.01458
GO:0016597	amino acid binding	-2.01104

Table S5. 49 signaling pathways in KEGG pathway enrichment

ID	Description	LogP
hsa05200	Pathways in cancer	-49.811
hsa04668	TNF signaling pathway	-34.1958
hsa04657	IL-17 signaling pathway	-33.2423
hsa04933	AGE-RAGE signaling pathway in diabetic complications	-30.0409
hsa04068	foxo signaling pathway	-25.599
hsa04151	PI3K-Akt signaling pathway	-24.9743
hsa04010	MAPK signaling pathway	-21.2708
hsa04660	T cell receptor signaling pathway	-19.8973
hsa04066	HIF-1 signaling pathway	-19.5263
hsa04064	NF-kappa B signaling pathway	-18.9481
hsa04625	c-type lectin receptor signaling pathway	-18.9481
hsa04620	Toll-like receptor signaling pathway	-18.6471
hsa04012	ErbB signaling pathway	-18.484
hsa04926	relaxin signaling pathway	-18.3847
hsa04115	p53 signaling pathway	-16.7018
hsa04664	Fc epsilon RI signaling pathway	-16.6144
hsa04062	Chemokine signaling pathway	-16.3209
hsa04621	NOD-like receptor signaling pathway	-15.7797
hsa04917	Prolactin signaling pathway	-15.5108
hsa04014	Ras signaling pathway	-15.3423
hsa04015	Rap1 signaling pathway	-14.1374
hsa04630	JAK-STAT signaling pathway	-13.9678
hsa04915	Estrogen signaling pathway	-13.8456
hsa04662	B cell receptor signaling pathway	-12.107
hsa04370	VEGF signaling pathway	-11.8037
hsa04722	Neurotrophin signaling pathway	-11.0973
hsa04912	GnRH signaling pathway	-11.094
hsa04211	Longevity regulating pathway	-10.5382
hsa04024	cAMP signaling pathway	-9.85272
hsa04071	Sphingolipid signaling pathway	-9.71165
hsa04910	Insulin signaling pathway	-8.74773

hsa04919	thyroid hormone signaling pathway	-8.72817
hsa04622	RIG-I-like receptor signaling pathway	-8.53742
hsa04152	AMPK signaling pathway	-8.50766
hsa04072	Phospholipase D signaling pathway	-8.49809
hsa04213	Longevity regulating pathway - multiple species	-7.76007
hsa04623	Cytosolic DNA-sensing pathway	-7.64853
hsa04150	mTOR signaling pathway	-7.58329
hsa04921	Oxytocin signaling pathway	-7.49878
hsa04920	Adipocytokine signaling pathway	-5.99848
hsa04371	Apelin signaling pathway	-4.89243
hsa04550	Signaling pathways regulating pluripotency of stem cells	-4.74471
hsa04310	Wnt signaling pathway	-3.58799
hsa04350	TGF-beta signaling pathway	-3.20877
hsa04020	Calcium signaling pathway	-3.07456
hsa04922	Glucagon signaling pathway	-2.93376
hsa04022	cGMP-PKG signaling pathway	-2.75027
hsa04390	Hippo signaling pathway	-2.73763
hsa04340	Hedgehog signaling pathway	-2.25447