

Supplement table 1

Supplement table 1 Results of linear relationship of 5 compounds in AT.

Compound	Calibration curve	R^2	Range ($\mu\text{g}\cdot\text{mL}^{-1}$)
Chlorogenic acid	$Y=7396.1X-14999$	0.999 9	5.10~510.00
Isochlorogenic acid B	$Y=9131.7X+4634.7$	0.999 2	2.13~213.00
Isochlorogenic acid A	$Y=9665X+22071$	1.000 0	7.56~756.00
Isochlorogenic acid C	$Y=9571.6X-12753$	0.999 8	3.27~327.00
Scabertopin	$Y=742.33X-303.18$	0.999 9	4.82~482.00

Supplement table 2

Supplement table 2 The methodological examination results of 5 compounds in AT (%).

Compound	Stability RSD	Precision RSD	Repeatability RSD	Recovery rate	Recovery RSD
Chlorogenic acid	0.76	0.89	1.20	100.50	0.09
Isochlorogenic acid B	0.68	0.58	1.60	100.40	0.23
Isochlorogenic acid A	0.79	0.55	1.50	100.10	0.22
Isochlorogenic acid C	1.20	0.12	2.00	100.10	0.25
Scabertopin	0.57	0.50	1.30	99.57	0.35

Supplement table 3

Supplementary Tables 3 520 overlapping targets

NO.	Target	NO.	Target	NO.	Target	NO.	Target
1	AKR1B1	131	ERBB2	261	CYP1A2	391	BCHE
2	CYP1B1	132	FABP1	262	CYP3A4	392	HTR2C
3	ABCC1	133	FAP	263	DCAF5	393	PDGFRB
4	XDH	134	FNTA	264	DIO1	394	FLT4
5	CA2	135	GABRA1	265	DUOX2	395	PLK4
6	CA7	136	GABRA2	266	E2F1	396	TEK
7	CA12	137	GABRA3	267	E2F2	397	MAP3K8
8	CA4	138	GABRA5	268	EGF	398	BRAF
9	PLG	139	GABRA6	269	EIF6	399	EPHB4
10	OPRD1	140	GABRB3	270	ELK1	400	HSPA1A
11	APP	141	GABRG2	271	ERBB3	401	FGR
12	PLA2G2A	142	GCK	272	F3	402	LYN
13	NOX4	143	GPR55	273	F7	403	SQLE
14	ABCB1	144	GRM1	274	GJA1	404	GSR
15	ABCG2	145	GRM2	275	GSTM2	405	DAO
16	ESR2	146	GRM5	276	GSTP1	406	CA5B
17	HSD17B1	147	GSTM1	277	HAS2	407	AURKA
18	CDK5R1	148	GYS1	278	HIF1A	408	HSD17B3
19	CCNB3	149	HCRTR1	279	HK2	409	SRD5A1
20	ARG1	150	HTR2A	280	HMOX1	410	TNNC1
21	CYP19A1	151	HTR2B	281	HSF1	411	MIF
22	KIT	152	HTR6	282	HSPB1	412	ALDH2
23	MAOA	153	HTR7	283	ICAM1	413	SNCA
24	BACE1	154	IDO1	284	IFNG	414	STS
25	PTPRS	155	JUN	285	IGF2	415	COMT
26	FLT3	156	KCNA5	286	IGFBP3	416	NFKB1
27	ALOX5	157	KCNH2	287	IL10	417	QDPR
28	ADORA1	158	KIF11	288	IL1A	418	MB
29	GLO1	159	LRRK2	289	IL1B	419	RNASEH1
30	GSK3B	160	MAOB	290	IL2	420	RPS6KA3
31	MMP9	161	MAPK10	291	IL6	421	KCNMA1
32	MMP2	162	MAPK14	292	IRF1	422	GRIA2
33	SYK	163	MAPK8	293	MAPK1	423	NQO1
34	ADORA2A	164	MAPK9	294	MYC	424	CLK1
35	PARP1	165	MGLL	295	NCF1	425	TYMS
36	TTR	166	MME	296	NCOA2	426	NAT1
37	MMP12	167	MMP1	297	NFE2L2	427	GPR84
38	CD38	168	MMP8	298	NFKBIA	428	CNR1
39	AKR1B10	169	MTNR1A	299	NKX3-1	429	CNR2
40	TNKS2	170	MTNR1B	300	NPEPPS	430	DYRK1B
41	TNKS	171	MYLK	301	NR1I2	431	ALDH5A1

42	TOP1	172	NAAA	302	NR1I3	432	ABAT
43	ESR1	173	NOS1	303	ODC1	433	UPP1
44	TERT	174	NOS2	304	PCOLCE	434	CCNA1
45	CBR1	175	NOS3	305	PLAT	435	TNNT2
46	HSD17B2	176	NR1H2	306	PON1	436	CCNA2
47	PIM1	177	OPRK1	307	POR	437	TNNI3
48	F2	178	P2RX7	308	PPARA	438	EGLN1
49	ST6GAL1	179	PANK3	309	PPARD	439	ACLY
50	OPRM1	180	PCSK7	310	PPARG	440	FDFT1
51	ACHE	181	PDE11A	311	PRKCB	441	HDAC3
52	CDK6	182	PDE1A	312	PSMD3	442	HMGCR
53	IGF1R	183	PDE1C	313	PTGER3	443	SLC1A1
54	EGFR	184	PDE2A	314	RAF1	444	SLC1A2
55	CSNK2A1	185	PDE3A	315	RASA1	445	HAO1
56	PIK3CG	186	PDE3B	316	RASSF1	446	KDM2A
57	NAE1	187	PDE4A	317	RB1	447	PHF8
58	AR	188	PDE4B	318	RELA	448	KDM5C
59	ALOX15	189	PDE4D	319	RUNX1T1	449	PTGER2
60	ALOX12	190	PDE7A	320	RUNX2	450	PTGFR
61	MCL1	191	PGGT1B	321	RXRA	451	NPC1L1
62	CA1	192	PGR	322	SCN5A	452	UGT2B7
63	CA9	193	PIP4K2C	323	SELE	453	SLC6A1
64	AVPR2	194	PLAU	324	SERPINE1	454	GABBR2
65	AURKB	195	POLA1	325	SLC2A4	455	GABRR1
66	DRD4	196	POLB	326	SPP1	456	SLC6A11
67	MPO	197	PRKCA	327	STAT1	457	SLC22A6
68	PIK3R1	198	PRKCD	328	THBD	458	SLC6A13
69	DAPK1	199	PRKCE	329	TNF	459	CPT1A
70	PYGL	200	PSEN2	330	TP53	460	G6PD
71	SRC	201	PTGS1	331	VCAM1	461	FABP4
72	PTK2	202	PTGS2	332	PRKCH	462	FABP3
73	KDR	203	PTK2B	333	PRKCQ	463	FABP5
74	MMP13	204	PTPN1	334	KCNA3	464	FFAR1
75	MMP3	205	RPS6KA2	335	PRKCG	465	FABP2
76	CA3	206	SCN9A	336	VAV1	466	GABBR1
77	PLK1	207	SLC18A3	337	TRPV4	467	INMT
78	CA6	208	SLC6A9	338	PDCD4	468	BBOX1
79	CDK1	209	TBXAS1	339	F2RL1	469	FUT7
80	PKN1	210	TGFBR1	340	CFTR	470	ERN1
81	CA14	211	THRB	341	AMY1A	471	CDC25B
82	MET	212	TLR9	342	GRK6	472	DUSP1
83	NEK2	213	TRPC3	343	PFKFB3	473	DYRK1A
84	CXCR1	214	TRPC6	344	ADCY2	474	ALB
85	CAMK2B	215	TSPO	345	IL4	475	HDAC1

86	ALK	216	TTL	346	MDM2	476	LDHA
87	AKT1	217	CCNH	347	NUF2	477	LDHB
88	NEK6	218	CDK2	348	PCNA	478	FASN
89	PLA2G1B	219	FNTB	349	PTGES	479	HDAC6
90	AXL	220	GABRB2	350	BDKRB2	480	HDAC2
91	NUAK1	221	PSENEN	351	CCND3	481	PTPRC
92	AKR1C2	222	CCNE1	352	CYP2A6	482	ALPG
93	AKR1C1	223	APH1A	353	NQO2	483	PLAA
94	AKR1C3	224	PSEN1	354	TRPA1	484	PSMB5
95	AKR1C4	225	NCSTN	355	PKM	485	DBH
96	AKR1A1	226	APH1B	356	PIK3CD	486	SRD5A2
97	MAPT	227	GPR35	357	SLC6A2	487	KCNA1
98	CCNB2	228	TOP2A	358	SLC6A3	488	KCNA4
99	CCNB1	229	INSR	359	JAK3	489	CRHR1
100	CDK5	230	APEX1	360	CDK4	490	TPMT
101	ADORA2B	231	MPG	361	CCND2	491	PTPN22
102	ADORA3	232	SLC22A12	362	HSD11B1	492	DRD5
103	ADRA2A	233	TYR	363	HTR1B	493	DRD2
104	ADRA2B	234	AHR	364	TAAR1	494	TDP1
105	ADRA2C	235	ESRRA	365	PPOX	495	PIK3CA
106	ADRB3	236	ACACA	366	SIGMAR1	496	EP300
107	ALDH3A1	237	ACP3	367	METAP2	497	GAA
108	ATP2A1	238	ADRB2	368	HRH3	498	FYN
109	CACNA1B	239	AHSA1	369	HCAR2	499	PTPRB
110	CASP3	240	BAX	370	CCKBR	500	LAP3
111	CASP7	241	BCL2	371	CTSC	501	ADRB1
112	CCNE2	242	BCL2L1	372	CTSF	502	ADRA1A
113	CDK7	243	BIRC5	373	DUSP3	503	RARG
114	CHRNA7	244	CASP8	374	PABPC1	504	RARB
115	CMA1	245	CASP9	375	PDE8B	505	OGA
116	CTSB	246	CAV1	376	NTRK1	506	TUBB1
117	CTSK	247	CCL2	377	SLC1A3	507	CTBP2
118	CTSL	248	CCND1	378	TLR4	508	PLA2G4B
119	CTSS	249	CD40LG	379	ALPL	509	ADRA1D
120	CTSV	250	CDKN1A	380	BRD4	510	PIN1
121	CXCR2	251	CHEK2	381	BRD2	511	ENPEP
122	CYP11B1	252	CHUK	382	MCHR1	512	CDA
123	CYP11B2	253	CLDN4	383	HRH4	513	HTR3A
124	CYP2C9	254	CRP	384	GLI1	514	RXRB
125	CYP2D6	255	CTSD	385	PTAFR	515	RXRG
126	DHFR	256	CXCL10	386	EDNRA	516	RARA
127	DRD1	257	CXCL11	387	EPHX1	517	HSP90AA1
128	DRD3	258	CXCL2	388	PRKDC	518	PNMT
129	ECE1	259	CXCL8	389	AOC3	519	HDAC8

130	ELANE	260	CYP1A1	390	LCK	520	TDO2
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Supplement table 4

Supplementary Table 4 166 molecular function (MF) terms

GroupID	Category	Term	Description	LogP	Log(q-value)
1_Summary	GO Molecular Functions	GO:0016773	phosphotransferase activity, alcohol group as acceptor	-52.528	-48.829
1_Member	GO Molecular Functions	GO:0016773	phosphotransferase activity, alcohol group as acceptor	-52.528	-48.829
1_Member	GO Molecular Functions	GO:0004672	protein kinase activity	-51.6337	-48.236
1_Member	GO Molecular Functions	GO:0016301	kinase activity	-50.562	-47.340
1_Member	GO Molecular Functions	GO:0004674	protein serine/threonine kinase activity	-32.808	-29.887
1_Member	GO Molecular Functions	GO:0106310	protein serine kinase activity	-25.6006	-22.856
2_Summary	GO Molecular Functions	GO:0016491	oxidoreductase activity	-37.0873	-33.990
2_Member	GO Molecular Functions	GO:0016491	oxidoreductase activity	-37.0873	-33.990
2_Member	GO Molecular Functions	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	-19.221	-16.801
2_Member	GO Molecular Functions	GO:0004497	monooxygenase activity	-17.3096	-14.991
2_Member	GO Molecular Functions	GO:0020037	heme binding	-16.4438	-14.143
2_Member	GO Molecular Functions	GO:0046906	tetrapyrrole binding	-15.7411	-13.505
2_Member	GO Molecular Functions	GO:0016709	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	-11.9822	-10.047
2_Member	GO Molecular Functions	GO:0005506	iron ion binding	-10.6872	-8.880
3_Summary	GO Molecular Functions	GO:0019900	kinase binding	-33.226	-30.226
3_Member	GO Molecular Functions	GO:0019900	kinase binding	-33.226	-30.226
3_Member	GO Molecular Functions	GO:0019901	protein kinase binding	-31.2753	-28.421

4_Summary	GO Molecular Functions	GO:0030594	neurotransmitter receptor activity	-30.077	-27.281
4_Member	GO Molecular Functions	GO:0030594	neurotransmitter receptor activity	-30.077	-27.281
4_Member	GO Molecular Functions	GO:0098960	postsynaptic neurotransmitter receptor activity	-19.0252	-16.627
4_Member	GO Molecular Functions	GO:0016917	GABA receptor activity	-13.6899	-11.593
4_Member	GO Molecular Functions	GO:0022851	GABA-gated chloride ion channel activity	-11.0691	-9.215
4_Member	GO Molecular Functions	GO:0004890	GABA-A receptor activity	-11.0186	-9.183
4_Member	GO Molecular Functions	GO:0099095	ligand-gated monoatomic anion channel activity	-11.0186	-9.183
4_Member	GO Molecular Functions	GO:0015103	inorganic anion transmembrane transporter activity	-10.7379	-8.926
4_Member	GO Molecular Functions	GO:0005230	extracellular ligand- gated monoatomic ion channel activity	-10.6245	-8.834
4_Member	GO Molecular Functions	GO:0015108	chloride transmembrane transporter activity	-10.6112	-8.826
4_Member	GO Molecular Functions	GO:0008509	monoatomic anion transmembrane transporter activity	-10.413	-8.633
4_Member	GO Molecular Functions	GO:0015276	ligand-gated monoatomic ion channel activity	-9.97149	-8.227
4_Member	GO Molecular Functions	GO:0022834	ligand-gated channel activity	-9.92656	-8.187
4_Member	GO Molecular Functions	GO:0008503	benzodiazepine receptor activity	-9.8821	-8.152
4_Member	GO Molecular Functions	GO:0022824	transmitter-gated monoatomic ion channel activity	-9.59971	-7.888
4_Member	GO Molecular Functions	GO:0022835	transmitter-gated channel activity	-9.59971	-7.888
4_Member	GO Molecular Functions	GO:0099529	neurotransmitter receptor activity involved in regulation	-8.95916	-7.277

			of postsynaptic membrane potential		
4_Member	GO Molecular Functions	GO:0005253	monoatomic anion channel activity	-7.11388	-5.529
4_Member	GO Molecular Functions	GO:0005254	chloride channel activity	-6.8512	-5.295
			transmitter-gated monoatomic ion channel activity		
4_Member	GO Molecular Functions	GO:1904315	involved in regulation of postsynaptic membrane potential	-6.79065	-5.241
			ligand-gated monoatomic ion channel activity		
4_Member	GO Molecular Functions	GO:0099507	involved in regulation of presynaptic membrane potential	-3.87752	-2.674
5_Summary	GO Molecular Functions	GO:0004713	protein tyrosine kinase activity	-22.5494	-19.851
5_Member	GO Molecular Functions	GO:0004713	protein tyrosine kinase activity	-22.5494	-19.851
			transmembrane		
5_Member	GO Molecular Functions	GO:0004714	receptor protein tyrosine kinase activity	-13.149	-11.113
			transmembrane		
5_Member	GO Molecular Functions	GO:0019199	receptor protein kinase activity	-12.4429	-10.484
5_Member	GO Molecular Functions	GO:0019838	growth factor binding	-7.89873	-6.283
6_Summary	GO Molecular Functions	GO:0004879	nuclear receptor activity	-21.5847	-18.927
6_Member	GO Molecular Functions	GO:0004879	nuclear receptor activity	-21.5847	-18.927
			ligand-activated		
6_Member	GO Molecular Functions	GO:0098531	transcription factor activity	-21.3859	-18.770
			transcription factor		
6_Member	GO Molecular Functions	GO:0008134	binding	-21.0237	-18.501
			DNA-binding		
6_Member	GO Molecular Functions	GO:0140297	transcription factor binding	-20.4555	-17.987
			RNA polymerase II-specific DNA-binding		
6_Member	GO Molecular Functions	GO:0061629		-18.1738	-15.817

6_Member	GO Molecular Functions	GO:0001221	transcription factor binding	-16.4036	-14.120
6_Member	GO Molecular Functions	GO:0001223	transcription coregulator binding	-12.5095	-10.535
6_Member	GO Molecular Functions	GO:0016922	nuclear receptor binding	-11.6087	-9.695
6_Member	GO Molecular Functions	GO:0003707	nuclear steroid receptor activity	-11.2766	-9.404
6_Member	GO Molecular Functions	GO:0003682	chromatin binding	-9.42484	-7.735
6_Member	GO Molecular Functions	GO:0001216	DNA-binding transcription activator activity	-4.89264	-3.563
6_Member	GO Molecular Functions	GO:0001228	DNA-binding transcription activator activity, RNA polymerase II-specific	-4.49639	-3.222
6_Member	GO Molecular Functions	GO:0001217	DNA-binding transcription repressor activity	-2.15623	-1.101
7_Summary	GO Molecular Functions	GO:0042803	protein homodimerization activity	-21.3548	-18.770
7_Member	GO Molecular Functions	GO:0042803	protein homodimerization activity	-21.3548	-18.770
8_Summary	GO Molecular Functions	GO:0008227	G protein-coupled amine receptor activity	-21.2526	-18.700
8_Member	GO Molecular Functions	GO:0008227	G protein-coupled amine receptor activity	-21.2526	-18.700
8_Member	GO Molecular Functions	GO:0004993	G protein-coupled serotonin receptor activity	-10.3074	-8.538
8_Member	GO Molecular Functions	GO:0043176	amine binding	-9.50837	-7.809
8_Member	GO Molecular Functions	GO:0051378	serotonin binding	-7.97155	-6.352
8_Member	GO Molecular Functions	GO:0001587	Gq/11-coupled serotonin receptor activity	-5.29848	-3.916
9_Summary	GO Molecular Functions	GO:0019904	protein domain specific binding	-20.9429	-18.448
9_Member	GO Molecular Functions	GO:0019904	protein domain specific binding	-20.9429	-18.448

10_Summary	GO Molecular Functions	GO:0019207	kinase regulator activity	-19.9175	-17.474
10_Member	GO Molecular Functions	GO:0019207	kinase regulator activity	-19.9175	-17.474
10_Member	GO Molecular Functions	GO:0019887	protein kinase regulator activity	-16.2246	-13.957
10_Member	GO Molecular Functions	GO:0008047	enzyme activator activity	-15.3696	-13.162
10_Member	GO Molecular Functions	GO:0016538	cyclin-dependent protein serine/threonine kinase regulator activity	-14.4542	-12.299
10_Member	GO Molecular Functions	GO:0019209	kinase activator activity	-9.72498	-7.999
10_Member	GO Molecular Functions	GO:0030295	protein kinase activator activity	-8.31293	-6.663
10_Member	GO Molecular Functions	GO:0061575	cyclin-dependent protein serine/threonine kinase activator activity	-5.26269	-3.890
10_Member	GO Molecular Functions	GO:0043539	protein serine/threonine kinase activator activity	-3.99267	-2.779
11_Summary	GO Molecular Functions	GO:0031406	carboxylic acid binding	-18.2257	-15.849
11_Member	GO Molecular Functions	GO:0031406	carboxylic acid binding	-18.2257	-15.849
11_Member	GO Molecular Functions	GO:0043177	organic acid binding	-17.4938	-15.157
11_Member	GO Molecular Functions	GO:0033293	monocarboxylic acid binding	-14.7788	-12.598
11_Member	GO Molecular Functions	GO:0005504	fatty acid binding	-8.03661	-6.410
11_Member	GO Molecular Functions	GO:0036041	long-chain fatty acid binding	-6.58171	-5.060
11_Member	GO Molecular Functions	GO:0005324	long-chain fatty acid transporter activity	-3.87752	-2.674
11_Member	GO Molecular Functions	GO:0005319	lipid transporter activity	-2.50362	-1.413
12_Summary	GO Molecular Functions	GO:0033218	amide binding	-15.825	-13.573
12_Member	GO Molecular Functions	GO:0033218	amide binding	-15.825	-13.573
12_Member	GO Molecular Functions	GO:0042277	peptide binding	-11.4607	-9.568
12_Member	GO Molecular Functions	GO:0001540	amyloid-beta binding	-4.80565	-3.485
13_Summary	GO Molecular Functions	GO:0004175	endopeptidase activity	-15.4826	-13.261
13_Member	GO Molecular Functions	GO:0004175	endopeptidase activity	-15.4826	-13.261
13_Member	GO Molecular Functions	GO:0008233	peptidase activity	-12.4279	-10.477

13_Member	GO Molecular Functions	GO:0004252	serine-type endopeptidase activity	-11.5032	-9.597
13_Member	GO Molecular Functions	GO:0017171	serine hydrolase activity	-11.381	-9.502
13_Member	GO Molecular Functions	GO:0008236	serine-type peptidase activity	-10.6761	-8.875
13_Member	GO Molecular Functions	GO:0008237	metallopeptidase activity	-4.73683	-3.422
13_Member	GO Molecular Functions	GO:0004222	metalloendopeptidase activity	-3.91746	-2.709
14_Summary	GO Molecular Functions	GO:1901338	catecholamine binding	-15.2543	-13.061
14_Member	GO Molecular Functions	GO:1901338	catecholamine binding	-15.2543	-13.061
14_Member	GO Molecular Functions	GO:0004952	dopamine neurotransmitter receptor activity	-8.83493	-7.161
14_Member	GO Molecular Functions	GO:0035240	dopamine binding	-7.5251	-5.920
14_Member	GO Molecular Functions	GO:0032795	heterotrimeric G-protein binding	-5.90212	-4.446
14_Member	GO Molecular Functions	GO:0001591	dopamine neurotransmitter receptor activity, coupled via Gi/Go	-5.29848	-3.916
14_Member	GO Molecular Functions	GO:0001965	G-protein alpha-subunit binding	-5.07359	-3.723
15_Summary	GO Molecular Functions	GO:1901702	salt transmembrane transporter activity	-14.7008	-12.533
15_Member	GO Molecular Functions	GO:1901702	salt transmembrane transporter activity	-14.7008	-12.533
15_Member	GO Molecular Functions	GO:0015267	channel activity	-12.9387	-10.923
15_Member	GO Molecular Functions	GO:0022803	passive transmembrane transporter activity	-12.9121	-10.912
15_Member	GO Molecular Functions	GO:0015318	inorganic molecular entity transmembrane transporter activity	-12.4868	-10.520
15_Member	GO Molecular Functions	GO:0015075	monoatomic ion transmembrane transporter activity	-12.3678	-10.425
15_Member	GO Molecular Functions	GO:0005216	monoatomic ion channel activity	-11.7845	-9.864
15_Member	GO Molecular Functions	GO:0022836	gated channel activity	-11.4814	-9.582
15_Member	GO Molecular Functions	GO:0046873	metal ion transmembrane transporter activity	-7.88102	-6.269

15_Member	GO Molecular Functions	GO:0022890	inorganic cation transmembrane transporter activity	-7.29236	-5.701
15_Member	GO Molecular Functions	GO:0008324	monoatomic cation transmembrane transporter activity	-6.69219	-5.155
15_Member	GO Molecular Functions	GO:0005261	channel activity calcium ion	-5.3191	-3.917
15_Member	GO Molecular Functions	GO:0015085	transmembrane transporter activity	-4.00819	-2.788
15_Member	GO Molecular Functions	GO:0005251	delayed rectifier potassium channel activity	-3.98439	-2.773
15_Member	GO Molecular Functions	GO:0005262	calcium channel activity	-3.79878	-2.598
15_Member	GO Molecular Functions	GO:0005244	voltage-gated monoatomic ion channel activity	-3.08598	-1.943
15_Member	GO Molecular Functions	GO:0022843	voltage-gated monoatomic cation channel activity	-3.07302	-1.932
15_Member	GO Molecular Functions	GO:0022832	voltage-gated channel activity	-3.06669	-1.927
15_Member	GO Molecular Functions	GO:0005249	voltage-gated potassium channel activity	-2.13838	-1.084
16_Summary	GO Molecular Functions	GO:0004089	carbonate dehydratase activity	-14.2465	-12.104
16_Member	GO Molecular Functions	GO:0004089	carbonate dehydratase activity	-14.2465	-12.104
16_Member	GO Molecular Functions	GO:0016836	hydro-lyase activity	-13.0333	-11.006
16_Member	GO Molecular Functions	GO:0016835	carbon-oxygen lyase activity	-12.6272	-10.644
16_Member	GO Molecular Functions	GO:0016829	lyase activity	-9.61286	-7.892
17_Summary	GO Molecular Functions	GO:0044389	ubiquitin-like protein ligase binding	-13.8591	-11.728
17_Member	GO Molecular Functions	GO:0044389	ubiquitin-like protein ligase binding	-13.8591	-11.728
17_Member	GO Molecular Functions	GO:0031625	ubiquitin protein ligase binding	-12.9313	-10.923
18_Summary	GO Molecular Functions	GO:0016614	oxidoreductase activity, acting on CH- OH group of donors	-13.7159	-11.597

18_Member	GO Molecular Functions	GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	-13.7159	-11.597
18_Member	GO Molecular Functions	GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	-13.3328	-11.257
18_Member	GO Molecular Functions	GO:0032052	bile acid binding	-10.315	-8.540
18_Member	GO Molecular Functions	GO:0008106	alcohol dehydrogenase (NADP+) activity	-10.0984	-8.339
18_Member	GO Molecular Functions	GO:0030283	testosterone dehydrogenase [NAD(P)] activity	-9.8821	-8.152
18_Member	GO Molecular Functions	GO:0016229	steroid dehydrogenase activity	-9.59404	-7.886
18_Member	GO Molecular Functions	GO:0004032	alditol:NADP+ 1-oxidoreductase activity	-9.50837	-7.809
18_Member	GO Molecular Functions	GO:0004033	aldo-keto reductase (NADP) activity	-8.9016	-7.224
18_Member	GO Molecular Functions	GO:0033764	steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	-8.62249	-6.957
18_Member	GO Molecular Functions	GO:0004303	estradiol 17-beta-dehydrogenase [NAD(P)] activity	-7.75008	-6.141
18_Member	GO Molecular Functions	GO:0035410	dihydrotestosterone 17-beta-dehydrogenase activity	-7.06629	-5.495
18_Member	GO Molecular Functions	GO:0047045	testosterone 17-beta-dehydrogenase (NADP+) activity	-6.75933	-5.216
18_Member	GO Molecular Functions	GO:0016651	oxidoreductase activity, acting on NAD(P)H	-6.57982	-5.060
18_Member	GO Molecular Functions	GO:0047086	ketosteroid monooxygenase activity	-6.37328	-4.873
18_Member	GO Molecular Functions	GO:0016628	oxidoreductase activity, acting on the CH-CH group of	-6.00929	-4.543

			donors, NAD or NADP as acceptor		
18_Member	GO Molecular Functions	GO:0018636	phenanthrene 9,10-monooxygenase activity	-5.29848	-3.916
18_Member	GO Molecular Functions	GO:0047718	indanol dehydrogenase activity	-5.29848	-3.916
18_Member	GO Molecular Functions	GO:0047023	androsterone dehydrogenase activity	-5.24501	-3.879
18_Member	GO Molecular Functions	GO:0047035	testosterone dehydrogenase (NAD+) activity	-5.24501	-3.879
18_Member	GO Molecular Functions	GO:0016627	oxidoreductase activity, acting on the CH-CH group of donors	-5.13389	-3.775
18_Member	GO Molecular Functions	GO:0047044	androstan-3-alpha,17-beta-diol dehydrogenase activity	-4.99569	-3.657
18_Member	GO Molecular Functions	GO:0035671	enone reductase activity	-4.30967	-3.055
18_Member	GO Molecular Functions	GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	-4.27493	-3.023
18_Member	GO Molecular Functions	GO:0047024	5alpha-androstane-3beta,17beta-diol dehydrogenase activity	-4.01423	-2.792
19_Summary	GO Molecular Functions	GO:0004115	3',5'-cyclic-AMP phosphodiesterase activity	-13.6899	-11.593
19_Member	GO Molecular Functions	GO:0004115	3',5'-cyclic-AMP phosphodiesterase activity	-13.6899	-11.593
19_Member	GO Molecular Functions	GO:0047555	3',5'-cyclic-GMP phosphodiesterase activity	-13.4141	-11.328
19_Member	GO Molecular Functions	GO:0004114	3',5'-cyclic-nucleotide phosphodiesterase activity	-13.1545	-11.113
19_Member	GO Molecular Functions	GO:0004112	cyclic-nucleotide phosphodiesterase activity	-12.6773	-10.686

19_Member	GO Molecular Functions	GO:0008081	phosphoric diester hydrolase activity	-10.639	-8.843
19_Member	GO Molecular Functions	GO:0030551	cyclic nucleotide binding	-3.39265	-2.227
19_Member	GO Molecular Functions	GO:0030552	cAMP binding	-3.23176	-2.084
20_Summary	GO Molecular Functions	GO:0097110	scaffold protein binding	-13.3205	-11.255
20_Member	GO Molecular Functions	GO:0097110	scaffold protein binding	-13.3205	-11.255
20_Member	GO Molecular Functions	GO:0044325	transmembrane transporter binding	-4.70574	-3.406

Supplement table 5

Supplementary Table 5 1033 biological process (BP) terms

GroupID	Category	Term	Description	LogP	Log(q-value)
1_Summary	GO Biological Processes	GO:0007172	signal complex assembly	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0007172	signal complex assembly	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0007197	adenylate cyclase-inhibiting G protein-coupled acetylcholine receptor signaling pathway	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0009448	gamma-aminobutyric acid metabolic process	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0010359	regulation of anion channel activity	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0010742	macrophage derived foam cell differentiation	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0010757	negative regulation of plasminogen activation	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0015874	norepinephrine transport	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0032222	regulation of synaptic transmission, cholinergic	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0032847	regulation of cellular pH reduction	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0034141	positive regulation of toll-like receptor 3 signaling pathway	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0038089	positive regulation of cell migration by vascular endothelial growth factor signaling pathway	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0038134	ERBB2-EGFR signaling pathway	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0043550	regulation of lipid kinase activity	-3.57823	-2.705
1_Member	GO Biological Processes	GO:0045760	positive regulation of action potential	-3.57823	-2.705

1_Member	GO Biological Processes	GO:0030326	embryonic limb morphogenesis	-3.57654	-2.704
1_Member	GO Biological Processes	GO:0035113	embryonic appendage morphogenesis	-3.57654	-2.704
1_Member	GO Biological Processes	GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	-3.56922	-2.698
1_Member	GO Biological Processes	GO:0002828	regulation of type 2 immune response	-3.56922	-2.698
1_Member	GO Biological Processes	GO:0006691	leukotriene metabolic process	-3.56922	-2.698
1_Member	GO Biological Processes	GO:0010661	positive regulation of muscle cell apoptotic process	-3.56922	-2.698
1_Member	GO Biological Processes	GO:0036230	granulocyte activation	-3.56922	-2.698
1_Member	GO Biological Processes	GO:0090313	regulation of protein targeting to membrane	-3.56922	-2.698
1_Member	GO Biological Processes	GO:1901797	negative regulation of signal transduction by p53 class mediator	-3.56922	-2.698
1_Member	GO Biological Processes	GO:1903725	regulation of phospholipid metabolic process	-3.56922	-2.698
1_Member	GO Biological Processes	GO:0002281	macrophage activation involved in immune response	-3.56695	-2.698
1_Member	GO Biological Processes	GO:0003417	growth plate cartilage development	-3.56695	-2.698
1_Member	GO Biological Processes	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	-3.56695	-2.698
1_Member	GO Biological Processes	GO:0010744	positive regulation of macrophage derived foam cell differentiation	-3.56695	-2.698
1_Member	GO Biological Processes	GO:0010885	regulation of cholesterol storage	-3.56695	-2.698
1_Member	GO Biological Processes	GO:0033194	response to hydroperoxide	-3.56695	-2.698

1_Member	GO Biological Processes	GO:0048266	behavioral response to pain	-3.56695	-2.698
1_Member	GO Biological Processes	GO:1902514	regulation of calcium ion transmembrane transport via high voltage-gated calcium channel	-3.56695	-2.698
1_Member	GO Biological Processes	GO:1903376	regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway	-3.56695	-2.698
1_Member	GO Biological Processes	GO:1904044	response to aldosterone	-3.56695	-2.698
1_Member	GO Biological Processes	GO:0000723	telomere maintenance	-3.56657	-2.698
1_Member	GO Biological Processes	GO:0002790	peptide secretion	-3.55076	-2.682
1_Member	GO Biological Processes	GO:0060415	muscle tissue morphogenesis	-3.55076	-2.682
1_Member	GO Biological Processes	GO:0002639	positive regulation of immunoglobulin production	-3.54054	-2.673
1_Member	GO Biological Processes	GO:0046622	positive regulation of organ growth	-3.54054	-2.673
1_Member	GO Biological Processes	GO:0050850	positive regulation of calcium-mediated signaling	-3.54054	-2.673
1_Member	GO Biological Processes	GO:0071385	cellular response to glucocorticoid stimulus	-3.54054	-2.673
1_Member	GO Biological Processes	GO:0051651	maintenance of location in cell	-3.53605	-2.669
1_Member	GO Biological Processes	GO:0010811	positive regulation of cell-substrate adhesion	-3.52388	-2.657
1_Member	GO Biological Processes	GO:0046632	alpha-beta T cell differentiation	-3.5146	-2.648
1_Member	GO Biological Processes	GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	-3.5146	-2.648
1_Member	GO Biological Processes	GO:0001935	endothelial cell proliferation	-3.5084	-2.643
1_Member	GO Biological Processes	GO:0002021	response to dietary excess	-3.5084	-2.643
1_Member	GO Biological Processes	GO:0002719	negative regulation of cytokine production	-3.5084	-2.643

			involved in immune response		
1_Member	GO Biological Processes	GO:0048147	negative regulation of fibroblast proliferation	-3.5084	-2.643
			positive regulation of myeloid leukocyte cytokine production		
1_Member	GO Biological Processes	GO:0061081	involved in immune response	-3.5084	-2.643
			intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress		
1_Member	GO Biological Processes	GO:0070059	stress	-3.5084	-2.643
			negative regulation of angiogenesis		
1_Member	GO Biological Processes	GO:0016525	angiogenesis	-3.50695	-2.642
			regulation of T cell mediated immunity		
1_Member	GO Biological Processes	GO:0002709	mediated immunity	-3.50592	-2.641
			regulation of fatty acid biosynthetic process		
1_Member	GO Biological Processes	GO:0042304	biosynthetic process	-3.49566	-2.631
			positive regulation of biomineral tissue development		
1_Member	GO Biological Processes	GO:0070169	development	-3.49566	-2.631
			regulation of cellular senescence		
1_Member	GO Biological Processes	GO:2000772	senescence	-3.49566	-2.631
			actin-mediated cell contraction		
1_Member	GO Biological Processes	GO:0070252	contraction	-3.47901	-2.615
			negative regulation of chromosome organization		
1_Member	GO Biological Processes	GO:2001251	organization	-3.47901	-2.615
			regulation of phagocytosis		
1_Member	GO Biological Processes	GO:0050764	phagocytosis	-3.47617	-2.613
			regulation of protein kinase A signaling		
1_Member	GO Biological Processes	GO:0010738	kinase A signaling	-3.47595	-2.613
			regulation of cell adhesion molecule production		
1_Member	GO Biological Processes	GO:0060353	production	-3.47595	-2.613
			response to nitric oxide		
1_Member	GO Biological Processes	GO:0071731	oxide	-3.47595	-2.613
			negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway		
1_Member	GO Biological Processes	GO:1902236	signaling pathway	-3.47595	-2.613

			regulation of chemokine (C-X-C motif) ligand 2		
1_Member	GO Biological Processes	GO:2000341	production	-3.47595	-2.613
1_Member	GO Biological Processes	GO:0043588	skin development	-3.46373	-2.601
			negative regulation of blood vessel		
1_Member	GO Biological Processes	GO:2000181	morphogenesis	-3.4616	-2.599
			tetrapyrrole metabolic process		
1_Member	GO Biological Processes	GO:0033013	process	-3.45177	-2.590
			positive regulation of microtubule		
			polymerization or depolymerization		
1_Member	GO Biological Processes	GO:0031112	cellular modified amino acid metabolic process	-3.44958	-2.588
1_Member	GO Biological Processes	GO:0006575	process	-3.44691	-2.585
1_Member	GO Biological Processes	GO:0031589	cell-substrate adhesion	-3.44183	-2.580
			muscle organ		
1_Member	GO Biological Processes	GO:0007517	development	-3.43909	-2.578
			mesenchyme		
1_Member	GO Biological Processes	GO:0060485	development	-3.42308	-2.562
			negative regulation of vasculature		
1_Member	GO Biological Processes	GO:1901343	development	-3.41702	-2.556
			ovulation from ovarian		
1_Member	GO Biological Processes	GO:0001542	follicle	-3.40771	-2.550
			respiratory burst		
			involved in defense		
1_Member	GO Biological Processes	GO:0002679	response	-3.40771	-2.550
			androgen biosynthetic process		
1_Member	GO Biological Processes	GO:0006702	process	-3.40771	-2.550
			adenylate cyclase-inhibiting G protein-coupled glutamate receptor signaling		
1_Member	GO Biological Processes	GO:0007196	pathway	-3.40771	-2.550
			artery smooth muscle		
1_Member	GO Biological Processes	GO:0014824	contraction	-3.40771	-2.550
			peroxisome		
			proliferator activated receptor signaling		
1_Member	GO Biological Processes	GO:0035357	pathway	-3.40771	-2.550

1_Member	GO Biological Processes	GO:0042416	dopamine biosynthetic process	-3.40771	-2.550
1_Member	GO Biological Processes	GO:0060385	axonogenesis involved in innervation	-3.40771	-2.550
1_Member	GO Biological Processes	GO:0070255	regulation of mucus secretion	-3.40771	-2.550
1_Member	GO Biological Processes	GO:0070472	regulation of uterine smooth muscle contraction	-3.40771	-2.550
1_Member	GO Biological Processes	GO:0090077	foam cell differentiation	-3.40771	-2.550
1_Member	GO Biological Processes	GO:1903959	regulation of monoatomic anion transmembrane transport	-3.40771	-2.550
1_Member	GO Biological Processes	GO:2000669	negative regulation of dendritic cell apoptotic process	-3.40771	-2.550
1_Member	GO Biological Processes	GO:0050821	protein stabilization	-3.3943	-2.536
1_Member	GO Biological Processes	GO:0038061	non-canonical NF-kappaB signal transduction	-3.39265	-2.536
1_Member	GO Biological Processes	GO:0070873	regulation of glycogen metabolic process	-3.39265	-2.536
1_Member	GO Biological Processes	GO:0010288	response to lead ion	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0010829	negative regulation of glucose transmembrane transport	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0014821	phasic smooth muscle contraction	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0030220	platelet formation	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0032495	response to muramyl dipeptide	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0033033	negative regulation of myeloid cell apoptotic process	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0034104	negative regulation of tissue remodeling	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0043586	tongue development	-3.39009	-2.536

1_Member	GO Biological Processes	GO:0051988	regulation of attachment of spindle microtubules to kinetochore	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0060444	branching involved in mammary gland duct morphogenesis	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0071637	regulation of monocyte chemotactic protein-1 production	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0090043	regulation of tubulin deacetylation	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0090266	regulation of mitotic cell cycle spindle assembly checkpoint	-3.39009	-2.536
1_Member	GO Biological Processes	GO:1903504	regulation of mitotic spindle checkpoint	-3.39009	-2.536
1_Member	GO Biological Processes	GO:0045685	regulation of glial cell differentiation	-3.37562	-2.522
1_Member	GO Biological Processes	GO:0072676	lymphocyte migration	-3.37562	-2.522
1_Member	GO Biological Processes	GO:1903533	regulation of protein targeting	-3.37562	-2.522
1_Member	GO Biological Processes	GO:0043433	negative regulation of DNA-binding transcription factor activity	-3.3732	-2.520
1_Member	GO Biological Processes	GO:0000280	nuclear division	-3.35258	-2.499
1_Member	GO Biological Processes	GO:0016051	carbohydrate biosynthetic process	-3.34787	-2.495
1_Member	GO Biological Processes	GO:0045621	positive regulation of lymphocyte differentiation	-3.34787	-2.495
1_Member	GO Biological Processes	GO:0045740	positive regulation of DNA replication	-3.3375	-2.485
1_Member	GO Biological Processes	GO:0045823	positive regulation of heart contraction	-3.3375	-2.485
1_Member	GO Biological Processes	GO:0070507	regulation of microtubule cytoskeleton organization	-3.33011	-2.478
1_Member	GO Biological Processes	GO:0048168	regulation of neuronal synaptic plasticity	-3.32562	-2.473
1_Member	GO Biological Processes	GO:1902115	regulation of organelle assembly	-3.32326	-2.471

1_Member	GO Biological Processes	GO:0008344	adult locomotory behavior	-3.30935	-2.459
1_Member	GO Biological Processes	GO:0048644	muscle organ morphogenesis	-3.30935	-2.459
1_Member	GO Biological Processes	GO:0021756	striatum development	-3.30884	-2.459
1_Member	GO Biological Processes	GO:0032094	response to food activation of protein	-3.30884	-2.459
1_Member	GO Biological Processes	GO:0032148	kinase B activity thyroid hormone	-3.30884	-2.459
1_Member	GO Biological Processes	GO:0042403	metabolic process	-3.30884	-2.459
1_Member	GO Biological Processes	GO:0060004	reflex regulation of spindle	-3.30884	-2.459
1_Member	GO Biological Processes	GO:0090231	checkpoint	-3.30884	-2.459
1_Member	GO Biological Processes	GO:0051321	meiotic cell cycle regulation of Ras	-3.3082	-2.458
1_Member	GO Biological Processes	GO:0046578	protein signal transduction	-3.30485	-2.455
1_Member	GO Biological Processes	GO:0010921	regulation of phosphatase activity	-3.28531	-2.436
1_Member	GO Biological Processes	GO:0006953	acute-phase response female meiotic nuclear	-3.28403	-2.436
1_Member	GO Biological Processes	GO:0007143	division	-3.28403	-2.436
1_Member	GO Biological Processes	GO:0032350	regulation of hormone metabolic process	-3.28403	-2.436
1_Member	GO Biological Processes	GO:0035025	positive regulation of Rho protein signal	-3.28403	-2.436
1_Member	GO Biological Processes	GO:0043388	transduction positive regulation of	-3.28403	-2.436
1_Member	GO Biological Processes	GO:0043388	DNA binding	-3.28403	-2.436
1_Member	GO Biological Processes	GO:0055078	sodium ion homeostasis	-3.28403	-2.436
1_Member	GO Biological Processes	GO:0060306	regulation of membrane repolarization	-3.28403	-2.436
1_Member	GO Biological Processes	GO:1903524	positive regulation of blood circulation	-3.28403	-2.436
1_Member	GO Biological Processes	GO:0006650	glycerophospholipid metabolic process	-3.26553	-2.418
1_Member	GO Biological Processes	GO:0007191	adenylate cyclase- activating dopamine receptor signaling	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0014047	pathway glutamate secretion	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0032025	response to cobalt ion	-3.25837	-2.414

1_Member	GO Biological Processes	GO:0032070	regulation of deoxyribonuclease activity	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0035022	positive regulation of Rac protein signal transduction	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0042711	maternal behavior	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0048304	positive regulation of isotype switching to IgG isotypes	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0060068	vagina development	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0060397	growth hormone receptor signaling pathway via JAK-STAT	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0070391	response to lipoteichoic acid	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0070431	nucleotide-binding oligomerization domain containing 2 signaling pathway	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0070432	regulation of nucleotide-binding oligomerization domain containing 2 signaling pathway	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0071223	cellular response to lipoteichoic acid	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0071803	positive regulation of podosome assembly	-3.25837	-2.414
1_Member	GO Biological Processes	GO:1901984	negative regulation of protein acetylation	-3.25837	-2.414
1_Member	GO Biological Processes	GO:1903943	regulation of hepatocyte apoptotic process	-3.25837	-2.414
1_Member	GO Biological Processes	GO:1903980	positive regulation of microglial cell activation	-3.25837	-2.414
1_Member	GO Biological Processes	GO:1904760	regulation of myofibroblast differentiation	-3.25837	-2.414
1_Member	GO Biological Processes	GO:0140115	export across plasma membrane	-3.24581	-2.402

1_Member	GO Biological Processes	GO:0032886	regulation of microtubule-based process	-3.24457	-2.401
1_Member	GO Biological Processes	GO:0001953	negative regulation of cell-matrix adhesion	-3.23215	-2.391
1_Member	GO Biological Processes	GO:0046676	negative regulation of insulin secretion	-3.23215	-2.391
1_Member	GO Biological Processes	GO:0062098	regulation of programmed necrotic cell death	-3.23215	-2.391
1_Member	GO Biological Processes	GO:0086091	regulation of heart rate by cardiac conduction	-3.23215	-2.391
1_Member	GO Biological Processes	GO:1901532	regulation of hematopoietic progenitor cell differentiation	-3.23215	-2.391
1_Member	GO Biological Processes	GO:0033365	protein localization to organelle	-3.23191	-2.391
1_Member	GO Biological Processes	GO:0002446	neutrophil mediated immunity	-3.23176	-2.391
1_Member	GO Biological Processes	GO:0002689	negative regulation of leukocyte chemotaxis	-3.23176	-2.391
1_Member	GO Biological Processes	GO:0010893	positive regulation of steroid biosynthetic process	-3.23176	-2.391
1_Member	GO Biological Processes	GO:0036344	platelet morphogenesis	-3.23176	-2.391
1_Member	GO Biological Processes	GO:0043171	peptide catabolic process	-3.23176	-2.391
1_Member	GO Biological Processes	GO:0090075	relaxation of muscle	-3.23176	-2.391
1_Member	GO Biological Processes	GO:1902254	negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator	-3.23176	-2.391
1_Member	GO Biological Processes	GO:2001252	positive regulation of chromosome organization	-3.22433	-2.383
1_Member	GO Biological Processes	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	-3.21117	-2.370
1_Member	GO Biological Processes	GO:0002040	sprouting angiogenesis	-3.20711	-2.367

			regulation of microtubule		
1_Member	GO Biological Processes	GO:0031113	polymerization	-3.20711	-2.367
1_Member	GO Biological Processes	GO:0035904	aorta development	-3.20711	-2.367
			negative regulation of canonical NF-kappaB		
1_Member	GO Biological Processes	GO:0043124	signal transduction	-3.20711	-2.367
			cardiac muscle tissue		
1_Member	GO Biological Processes	GO:0055008	morphogenesis	-3.20711	-2.367
			chromatin		
1_Member	GO Biological Processes	GO:0006325	organization	-3.19801	-2.358
			cellular response to		
1_Member	GO Biological Processes	GO:0071230	amino acid stimulus	-3.1827	-2.343
			antigen processing and presentation of		
			exogenous peptide		
1_Member	GO Biological Processes	GO:0002478	antigen	-3.18177	-2.343
			fat-soluble vitamin		
1_Member	GO Biological Processes	GO:0006775	metabolic process	-3.18177	-2.343
			DNA damage		
			response, signal		
			transduction by p53		
1_Member	GO Biological Processes	GO:0030330	class mediator	-3.18177	-2.343
			semaphorin-plexin		
1_Member	GO Biological Processes	GO:0071526	signaling pathway	-3.18177	-2.343
1_Member	GO Biological Processes	GO:0006260	DNA replication	-3.17461	-2.336
			positive regulation of		
			plasma membrane		
			bounded cell		
1_Member	GO Biological Processes	GO:0120034	projection assembly	-3.17195	-2.334
			positive regulation of		
			myeloid leukocyte		
1_Member	GO Biological Processes	GO:0002763	differentiation	-3.16916	-2.332
			negative regulation of		
			adaptive immune		
1_Member	GO Biological Processes	GO:0002820	response	-3.16916	-2.332
			L-alpha-amino acid		
			transmembrane		
1_Member	GO Biological Processes	GO:1902475	transport	-3.16916	-2.332
			regulation of cell		
1_Member	GO Biological Processes	GO:0008360	shape	-3.16115	-2.324
			regulation of platelet-		
1_Member	GO Biological Processes	GO:0010640	derived growth factor	-3.15848	-2.324

			receptor signaling pathway		
1_Member	GO Biological Processes	GO:0030539	male genitalia development	-3.15848	-2.324
1_Member	GO Biological Processes	GO:0031103	axon regeneration	-3.15848	-2.324
			regulation of heterotypic cell-cell		
1_Member	GO Biological Processes	GO:0034114	adhesion	-3.15848	-2.324
			response to		
1_Member	GO Biological Processes	GO:0034695	prostaglandin E	-3.15848	-2.324
			ionotropic glutamate		
1_Member	GO Biological Processes	GO:0035235	receptor signaling pathway	-3.15848	-2.324
			dendritic cell		
1_Member	GO Biological Processes	GO:0036336	migration	-3.15848	-2.324
			superoxide anion		
1_Member	GO Biological Processes	GO:0042554	generation	-3.15848	-2.324
			negative regulation of		
1_Member	GO Biological Processes	GO:0045822	heart contraction	-3.15848	-2.324
			positive regulation of		
1_Member	GO Biological Processes	GO:0046628	insulin receptor signaling pathway	-3.15848	-2.324
			regulation of hormone		
1_Member	GO Biological Processes	GO:0046885	biosynthetic process	-3.15848	-2.324
			regulation of B cell		
1_Member	GO Biological Processes	GO:0050855	receptor signaling pathway	-3.15848	-2.324
			regulation of cellular		
1_Member	GO Biological Processes	GO:1900407	response to oxidative stress	-3.15848	-2.324
			multicellular organism		
1_Member	GO Biological Processes	GO:0035264	growth	-3.15219	-2.318
			negative regulation of		
1_Member	GO Biological Processes	GO:0045824	innate immune response	-3.15219	-2.318
			membrane		
1_Member	GO Biological Processes	GO:0061024	organization	-3.13923	-2.305
			regulation of cellular		
1_Member	GO Biological Processes	GO:0002691	extravasation	-3.13283	-2.299
			hexose catabolic		
1_Member	GO Biological Processes	GO:0019320	process	-3.13283	-2.299
			positive regulation of		
1_Member	GO Biological Processes	GO:0035307	protein dephosphorylation	-3.13283	-2.299

1_Member	GO Biological Processes	GO:0002090	regulation of receptor internalization	-3.13195	-2.299
1_Member	GO Biological Processes	GO:0006112	energy reserve metabolic process	-3.13195	-2.299
1_Member	GO Biological Processes	GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	-3.13195	-2.299
1_Member	GO Biological Processes	GO:0016079	synaptic vesicle exocytosis	-3.13195	-2.299
1_Member	GO Biological Processes	GO:0032663	regulation of interleukin-2 production	-3.13195	-2.299
1_Member	GO Biological Processes	GO:0006703	estrogen biosynthetic process	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0014049	positive regulation of glutamate secretion	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0018342	protein prenylation	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0019372	lipoygenase pathway	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0032000	positive regulation of fatty acid beta-oxidation	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0051987	positive regulation of attachment of spindle microtubules to kinetochore	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0060736	prostate gland growth	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0060746	parental behavior	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0062100	positive regulation of programmed necrotic cell death	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0070213	protein auto-ADP-ribosylation	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0070242	thymocyte apoptotic process	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0070778	L-aspartate transmembrane transport	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0071476	cellular hypotonic response	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0071872	cellular response to epinephrine stimulus	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0072577	endothelial cell apoptotic process	-3.12563	-2.297

1_Member	GO Biological Processes	GO:0097062	dendritic spine maintenance	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0097354	prenylation	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0140353	lipid export from cell	-3.12563	-2.297
1_Member	GO Biological Processes	GO:1900222	negative regulation of amyloid-beta clearance	-3.12563	-2.297
1_Member	GO Biological Processes	GO:1902510	regulation of apoptotic DNA fragmentation	-3.12563	-2.297
1_Member	GO Biological Processes	GO:2000343	positive regulation of chemokine (C-X-C motif) ligand 2 production	-3.12563	-2.297
1_Member	GO Biological Processes	GO:2000833	positive regulation of steroid hormone secretion	-3.12563	-2.297
1_Member	GO Biological Processes	GO:0007269	neurotransmitter secretion	-3.12212	-2.294
1_Member	GO Biological Processes	GO:0050829	defense response to Gram-negative bacterium	-3.12212	-2.294
1_Member	GO Biological Processes	GO:0099643	signal release from synapse	-3.12212	-2.294
1_Member	GO Biological Processes	GO:0048812	neuron projection morphogenesis	-3.09666	-2.269
1_Member	GO Biological Processes	GO:0042440	pigment metabolic process	-3.09545	-2.268
1_Member	GO Biological Processes	GO:0015833	peptide transport	-3.09249	-2.266
1_Member	GO Biological Processes	GO:0034440	lipid oxidation	-3.09249	-2.266
1_Member	GO Biological Processes	GO:0035023	regulation of Rho protein signal transduction	-3.09249	-2.266
1_Member	GO Biological Processes	GO:0045185	maintenance of protein location	-3.09249	-2.266
1_Member	GO Biological Processes	GO:0090287	regulation of cellular response to growth factor stimulus	-3.09155	-2.265
1_Member	GO Biological Processes	GO:0001919	regulation of receptor recycling	-3.08865	-2.264
1_Member	GO Biological Processes	GO:0006007	glucose catabolic process	-3.08865	-2.264
1_Member	GO Biological Processes	GO:0045730	respiratory burst	-3.08865	-2.264
1_Member	GO Biological Processes	GO:0046716	muscle cell cellular homeostasis	-3.08865	-2.264

1_Member	GO Biological Processes	GO:0048520	positive regulation of behavior	-3.08865	-2.264
1_Member	GO Biological Processes	GO:0090335	regulation of brown fat cell differentiation	-3.08865	-2.264
1_Member	GO Biological Processes	GO:1901863	positive regulation of muscle tissue development	-3.08865	-2.264
1_Member	GO Biological Processes	GO:1903523	negative regulation of blood circulation	-3.08865	-2.264
1_Member	GO Biological Processes	GO:2000353	positive regulation of endothelial cell apoptotic process	-3.08865	-2.264
1_Member	GO Biological Processes	GO:0031638	zymogen activation	-3.08525	-2.261
1_Member	GO Biological Processes	GO:0046640	regulation of alpha-beta T cell proliferation	-3.08525	-2.261
1_Member	GO Biological Processes	GO:0051216	cartilage development	-3.06669	-2.243
1_Member	GO Biological Processes	GO:0010812	negative regulation of cell-substrate adhesion	-3.05964	-2.236
1_Member	GO Biological Processes	GO:0048762	mesenchymal cell differentiation	-3.04754	-2.224
1_Member	GO Biological Processes	GO:0141091	transforming growth factor beta receptor superfamily signaling pathway	-3.04754	-2.224
1_Member	GO Biological Processes	GO:0048259	regulation of receptor-mediated endocytosis	-3.04615	-2.223
1_Member	GO Biological Processes	GO:0120039	plasma membrane bounded cell projection	-3.04419	-2.221
1_Member	GO Biological Processes	GO:0002224	morphogenesis	-3.04419	-2.221
1_Member	GO Biological Processes	GO:0002224	toll-like receptor signaling pathway	-3.03897	-2.217
1_Member	GO Biological Processes	GO:0030501	positive regulation of bone mineralization	-3.03897	-2.217
1_Member	GO Biological Processes	GO:0043268	positive regulation of potassium ion transport	-3.03897	-2.217
1_Member	GO Biological Processes	GO:0090199	regulation of release of cytochrome c from mitochondria	-3.03897	-2.217
1_Member	GO Biological Processes	GO:2000300	regulation of synaptic vesicle exocytosis	-3.03897	-2.217

1_Member	GO Biological Processes	GO:0051607	defense response to virus	-3.03272	-2.211
1_Member	GO Biological Processes	GO:0001556	oocyte maturation	-3.02199	-2.202
1_Member	GO Biological Processes	GO:0010460	positive regulation of heart rate	-3.02199	-2.202
1_Member	GO Biological Processes	GO:0018904	ether metabolic process	-3.02199	-2.202
1_Member	GO Biological Processes	GO:0022038	corpus callosum development	-3.02199	-2.202
1_Member	GO Biological Processes	GO:0035902	response to immobilization stress	-3.02199	-2.202
1_Member	GO Biological Processes	GO:0045649	regulation of macrophage differentiation	-3.02199	-2.202
1_Member	GO Biological Processes	GO:0046717	acid secretion	-3.02199	-2.202
1_Member	GO Biological Processes	GO:0060575	intestinal epithelial cell differentiation	-3.02199	-2.202
1_Member	GO Biological Processes	GO:0071549	cellular response to dexamethasone stimulus	-3.02199	-2.202
1_Member	GO Biological Processes	GO:1900078	positive regulation of cellular response to insulin stimulus	-3.02199	-2.202
1_Member	GO Biological Processes	GO:1903421	regulation of synaptic vesicle recycling	-3.02199	-2.202
1_Member	GO Biological Processes	GO:0002832	negative regulation of response to biotic stimulus	-3.02183	-2.202
1_Member	GO Biological Processes	GO:0140546	defense response to symbiont	-3.0182	-2.199
1_Member	GO Biological Processes	GO:0055088	lipid homeostasis	-3.0097	-2.190
1_Member	GO Biological Processes	GO:0001783	B cell apoptotic process	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0002544	chronic inflammatory response	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0003084	positive regulation of systemic arterial blood pressure	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0006978	DNA damage response, signal transduction by p53 class mediator resulting in	-3.00625	-2.190

			transcription of p21 class mediator		
1_Member	GO Biological Processes	GO:0010659	cardiac muscle cell apoptotic process	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0031392	regulation of prostaglandin biosynthetic process	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0032351	negative regulation of hormone metabolic process	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0033083	regulation of immature T cell proliferation	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0033084	regulation of immature T cell proliferation in thymus	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0033629	negative regulation of cell adhesion mediated by integrin	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0040015	negative regulation of multicellular organism growth	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0043276	anoikis	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0043353	enucleate erythrocyte differentiation	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0048548	regulation of pinocytosis	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0050847	progesterone receptor signaling pathway	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0071493	cellular response to UV-B	-3.00625	-2.190
1_Member	GO Biological Processes	GO:1990535	neuron projection maintenance	-3.00625	-2.190
1_Member	GO Biological Processes	GO:0048285	organelle fission	-3.00434	-2.188
1_Member	GO Biological Processes	GO:0050830	defense response to Gram-positive bacterium	-2.99778	-2.182
1_Member	GO Biological Processes	GO:0006096	glycolytic process	-2.99391	-2.179
1_Member	GO Biological Processes	GO:0014014	negative regulation of gliogenesis	-2.99391	-2.179
1_Member	GO Biological Processes	GO:0015695	organic cation transport	-2.99391	-2.179

1_Member	GO Biological Processes	GO:0086002	cardiac muscle cell action potential involved in contraction	-2.99391	-2.179
1_Member	GO Biological Processes	GO:0090278	negative regulation of peptide hormone secretion	-2.99391	-2.179
1_Member	GO Biological Processes	GO:1903426	regulation of reactive oxygen species biosynthetic process	-2.99391	-2.179
1_Member	GO Biological Processes	GO:0048858	cell projection morphogenesis	-2.9926	-2.178
1_Member	GO Biological Processes	GO:0060760	positive regulation of response to cytokine stimulus	-2.98999	-2.176
1_Member	GO Biological Processes	GO:0061337	cardiac conduction	-2.98999	-2.176
1_Member	GO Biological Processes	GO:0007098	centrosome cycle	-2.97804	-2.164
1_Member	GO Biological Processes	GO:0014812	muscle cell migration	-2.95823	-2.146
1_Member	GO Biological Processes	GO:0032753	positive regulation of interleukin-4 production	-2.95823	-2.146
1_Member	GO Biological Processes	GO:0045940	positive regulation of steroid metabolic process	-2.95823	-2.146
1_Member	GO Biological Processes	GO:0051984	positive regulation of chromosome segregation	-2.95823	-2.146
1_Member	GO Biological Processes	GO:0097300	programmed necrotic cell death	-2.95823	-2.146
1_Member	GO Biological Processes	GO:1900543	negative regulation of purine nucleotide metabolic process	-2.95823	-2.146
1_Member	GO Biological Processes	GO:1904357	negative regulation of telomere maintenance via telomere lengthening	-2.95823	-2.146
1_Member	GO Biological Processes	GO:2000272	negative regulation of signaling receptor activity	-2.95823	-2.146
1_Member	GO Biological Processes	GO:0140029	exocytic process	-2.95612	-2.144
1_Member	GO Biological Processes	GO:0150116	regulation of cell- substrate junction organization	-2.95612	-2.144

1_Member	GO Biological Processes	GO:0071897	DNA biosynthetic process	-2.95041	-2.139
1_Member	GO Biological Processes	GO:0002792	negative regulation of peptide secretion	-2.95003	-2.139
1_Member	GO Biological Processes	GO:0006303	double-strand break repair via nonhomologous end joining	-2.95003	-2.139
1_Member	GO Biological Processes	GO:0008347	glial cell migration	-2.95003	-2.139
1_Member	GO Biological Processes	GO:0034446	substrate adhesion-dependent cell spreading	-2.95003	-2.139
1_Member	GO Biological Processes	GO:0070849	response to epidermal growth factor appendage	-2.95003	-2.139
1_Member	GO Biological Processes	GO:0035107	morphogenesis	-2.94681	-2.136
1_Member	GO Biological Processes	GO:0035108	limb morphogenesis	-2.94681	-2.136
1_Member	GO Biological Processes	GO:0007229	integrin-mediated signaling pathway	-2.92315	-2.113
1_Member	GO Biological Processes	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	-2.92285	-2.113
1_Member	GO Biological Processes	GO:0005976	polysaccharide metabolic process	-2.92285	-2.113
1_Member	GO Biological Processes	GO:0006839	mitochondrial transport	-2.91763	-2.108
1_Member	GO Biological Processes	GO:0045580	regulation of T cell differentiation	-2.91763	-2.108
1_Member	GO Biological Processes	GO:0098609	cell-cell adhesion	-2.9129	-2.104
1_Member	GO Biological Processes	GO:0002701	negative regulation of production of molecular mediator of immune response	-2.90728	-2.099
1_Member	GO Biological Processes	GO:0043666	regulation of phosphoprotein	-2.90728	-2.099
1_Member	GO Biological Processes	GO:0046032	phosphatase activity	-2.90728	-2.099
1_Member	GO Biological Processes	GO:0055010	ADP catabolic process	-2.90728	-2.099
1_Member	GO Biological Processes	GO:0002698	ventricular cardiac muscle tissue morphogenesis	-2.90728	-2.099
1_Member	GO Biological Processes	GO:0006971	negative regulation of immune effector process	-2.90417	-2.096
1_Member	GO Biological Processes	GO:0006971	hypotonic response	-2.89786	-2.094

1_Member	GO Biological Processes	GO:0007144	female meiosis I striated muscle cell	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0010658	apoptotic process removal of superoxide	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0019430	radicals	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0030728	ovulation	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0035810	positive regulation of urine volume	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0035865	cellular response to potassium ion DNA damage response, signal transduction resulting	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0042772	in transcription negative regulation of	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0043508	JUN kinase activity	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0051231	spindle elongation	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0060402	calcium ion transport into cytosol	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0061029	eyelid development in camera-type eye	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0070234	positive regulation of T cell apoptotic process	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0070243	regulation of thymocyte apoptotic process	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0071801	regulation of podosome assembly	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0090235	regulation of metaphase plate congression	-2.89786	-2.094
1_Member	GO Biological Processes	GO:1903624	regulation of DNA catabolic process	-2.89786	-2.094
1_Member	GO Biological Processes	GO:2000551	regulation of T-helper 2 cell cytokine production	-2.89786	-2.094
1_Member	GO Biological Processes	GO:0003416	endochondral bone growth	-2.89717	-2.094
1_Member	GO Biological Processes	GO:0010800	positive regulation of peptidyl-threonine phosphorylation	-2.89717	-2.094
1_Member	GO Biological Processes	GO:0021544	subpallium development	-2.89717	-2.094

1_Member	GO Biological Processes	GO:0030325	adrenal gland development	-2.89717	-2.094
1_Member	GO Biological Processes	GO:0038179	neurotrophin signaling pathway	-2.89717	-2.094
1_Member	GO Biological Processes	GO:0043304	regulation of mast cell degranulation	-2.89717	-2.094
1_Member	GO Biological Processes	GO:0090025	regulation of monocyte chemotaxis	-2.89717	-2.094
1_Member	GO Biological Processes	GO:0090314	positive regulation of protein targeting to membrane	-2.89717	-2.094
1_Member	GO Biological Processes	GO:0006090	pyruvate metabolic process	-2.89018	-2.087
1_Member	GO Biological Processes	GO:0032206	positive regulation of telomere maintenance	-2.89018	-2.087
1_Member	GO Biological Processes	GO:1903053	regulation of extracellular matrix organization	-2.89018	-2.087
1_Member	GO Biological Processes	GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	-2.88139	-2.078
1_Member	GO Biological Processes	GO:0007281	germ cell development	-2.88098	-2.078
1_Member	GO Biological Processes	GO:0001910	regulation of leukocyte mediated cytotoxicity	-2.86972	-2.067
1_Member	GO Biological Processes	GO:0021795	cerebral cortex cell migration	-2.8656	-2.064
1_Member	GO Biological Processes	GO:0032369	negative regulation of lipid transport	-2.8656	-2.064
1_Member	GO Biological Processes	GO:0032660	regulation of interleukin-17 production	-2.8656	-2.064
1_Member	GO Biological Processes	GO:0060043	regulation of cardiac muscle cell proliferation	-2.8656	-2.064
1_Member	GO Biological Processes	GO:1990090	cellular response to nerve growth factor stimulus	-2.8656	-2.064

1_Member	GO Biological Processes	GO:0043244	regulation of protein-containing complex	-2.85886	-2.057
1_Member	GO Biological Processes	GO:0003208	disassembly	-2.85807	-2.057
1_Member	GO Biological Processes	GO:0009064	cardiac ventricle	-2.85807	-2.057
1_Member	GO Biological Processes	GO:0045670	morphogenesis	-2.85807	-2.057
1_Member	GO Biological Processes	GO:0072089	glutamine family amino acid metabolic process	-2.85807	-2.057
1_Member	GO Biological Processes	GO:0048736	regulation of osteoclast	-2.85807	-2.057
1_Member	GO Biological Processes	GO:0060173	differentiation	-2.85807	-2.057
1_Member	GO Biological Processes	GO:0007435	stem cell proliferation	-2.84648	-2.046
1_Member	GO Biological Processes	GO:0099623	appendage development	-2.84648	-2.046
1_Member	GO Biological Processes	GO:0007127	limb development	-2.83859	-2.039
1_Member	GO Biological Processes	GO:0007127	salivary gland morphogenesis	-2.83859	-2.039
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1_Member	GO Biological Processes	GO:0007127	regulation of androgen receptor signaling	-2.83859	-2.039
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1_Member	GO Biological Processes	GO:0007127	regulation of cardiac muscle cell membrane	-2.83859	-2.039
1_Member	GO Biological Processes	GO:0007127	repolarization	-2.83656	-2.037
1_Member	GO Biological Processes	GO:0007127	meiosis I	-2.82854	-2.029
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1_Member	GO Biological Processes	GO:0007127	vasculogenesis	-2.82652	-2.028
1_Member	GO Biological Processes	GO:0007127	regulation of cartilage development	-2.82494	-2.027
1_Member	GO Biological Processes	GO:0007127	negative regulation of muscle cell apoptotic process	-2.82494	-2.027
1_Member	GO Biological Processes	GO:0007127	pyridine nucleotide	-2.82494	-2.027
1_Member	GO Biological Processes	GO:0007127	catabolic process	-2.82494	-2.027
1_Member	GO Biological Processes	GO:0007127	mitotic spindle	-2.82494	-2.027
1_Member	GO Biological Processes	GO:0007127	assembly	-2.82494	-2.027
1_Member	GO Biological Processes	GO:0007127	modulation of excitatory postsynaptic potential	-2.82494	-2.027

1_Member	GO Biological Processes	GO:0001921	positive regulation of receptor recycling	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0001977	renal system process involved in regulation	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0006287	base-excision repair, gap-filling	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0007216	G protein-coupled glutamate receptor signaling pathway	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0007625	grooming behavior regulation of interleukin-18	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0032661	production mammary gland epithelial cell	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0033598	proliferation positive regulation of mast cell	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0043306	degranulation	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0045472	response to ether regulation of isotype switching to IgG	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0048302	isotypes ventricular cardiac muscle cell	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0055012	differentiation regulation of response	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0060330	to type II interferon regulation of type II interferon-mediated	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0060334	signaling pathway response to	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0071871	epinephrine atrial cardiac muscle	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0086014	cell action potential atrial cardiac muscle cell to AV node cell	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0086026	signaling hepatocyte apoptotic	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0097284	process intestinal lipid	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0098856	absorption	-2.79867	-2.004
1_Member	GO Biological Processes	GO:1904321	response to forskolin	-2.79867	-2.004

1_Member	GO Biological Processes	GO:1904322	cellular response to forskolin	-2.79867	-2.004
1_Member	GO Biological Processes	GO:2001279	regulation of unsaturated fatty acid biosynthetic process	-2.79867	-2.004
1_Member	GO Biological Processes	GO:0042130	negative regulation of T cell proliferation	-2.7955	-2.001
1_Member	GO Biological Processes	GO:0005977	glycogen metabolic process	-2.78527	-1.993
1_Member	GO Biological Processes	GO:0009137	purine nucleoside diphosphate catabolic process	-2.78527	-1.993
1_Member	GO Biological Processes	GO:0009181	purine ribonucleoside diphosphate catabolic process	-2.78527	-1.993
1_Member	GO Biological Processes	GO:0019884	antigen processing and presentation of exogenous antigen	-2.78527	-1.993
1_Member	GO Biological Processes	GO:0046365	monosaccharide catabolic process	-2.78527	-1.993
1_Member	GO Biological Processes	GO:0048247	lymphocyte chemotaxis	-2.78527	-1.993
1_Member	GO Biological Processes	GO:0051646	mitochondrion localization	-2.78527	-1.993
1_Member	GO Biological Processes	GO:1990089	response to nerve growth factor	-2.78527	-1.993
1_Member	GO Biological Processes	GO:0033137	negative regulation of peptidyl-serine phosphorylation	-2.78231	-1.990
1_Member	GO Biological Processes	GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	-2.78231	-1.990
1_Member	GO Biological Processes	GO:0060037	pharyngeal system development	-2.78231	-1.990
1_Member	GO Biological Processes	GO:1900101	regulation of endoplasmic reticulum unfolded protein response	-2.78231	-1.990
1_Member	GO Biological Processes	GO:0002708	positive regulation of lymphocyte mediated immunity	-2.77106	-1.980

1_Member	GO Biological Processes	GO:0061982	meiosis I cell cycle process	-2.77106	-1.980
1_Member	GO Biological Processes	GO:0030218	erythrocyte differentiation	-2.76702	-1.976
1_Member	GO Biological Processes	GO:0048667	cell morphogenesis involved in neuron differentiation	-2.75714	-1.966
1_Member	GO Biological Processes	GO:0002821	positive regulation of adaptive immune response	-2.74968	-1.959
1_Member	GO Biological Processes	GO:0006968	cellular defense response	-2.74654	-1.956
1_Member	GO Biological Processes	GO:0071622	regulation of granulocyte chemotaxis	-2.74654	-1.956
1_Member	GO Biological Processes	GO:0007179	transforming growth factor beta receptor signaling pathway	-2.74216	-1.952
1_Member	GO Biological Processes	GO:0030048	actin filament-based movement	-2.74216	-1.952
1_Member	GO Biological Processes	GO:0042632	cholesterol homeostasis	-2.74216	-1.952
1_Member	GO Biological Processes	GO:0060840	artery development	-2.74216	-1.952
1_Member	GO Biological Processes	GO:0016239	positive regulation of macroautophagy	-2.73502	-1.945
1_Member	GO Biological Processes	GO:0032200	telomere organization	-2.72852	-1.941
1_Member	GO Biological Processes	GO:0009072	aromatic amino acid metabolic process	-2.72819	-1.941
1_Member	GO Biological Processes	GO:0010765	positive regulation of sodium ion transport	-2.72819	-1.941
1_Member	GO Biological Processes	GO:0031102	neuron projection regeneration	-2.72819	-1.941
1_Member	GO Biological Processes	GO:0034391	regulation of smooth muscle cell apoptotic process	-2.72819	-1.941
1_Member	GO Biological Processes	GO:0040018	positive regulation of multicellular organism growth	-2.72819	-1.941
1_Member	GO Biological Processes	GO:0043392	negative regulation of DNA binding	-2.72819	-1.941
1_Member	GO Biological Processes	GO:0048679	regulation of axon regeneration	-2.72819	-1.941

			positive regulation of cardiac muscle cell		
1_Member	GO Biological Processes	GO:0060045	proliferation	-2.72819	-1.941
			cellular response to		
1_Member	GO Biological Processes	GO:0071353	interleukin-4	-2.72819	-1.941
1_Member	GO Biological Processes	GO:0098868	bone growth	-2.72819	-1.941
			positive regulation of cell-substrate junction		
1_Member	GO Biological Processes	GO:0150117	organization	-2.72819	-1.941
			positive regulation of		
1_Member	GO Biological Processes	GO:1900745	p38MAPK cascade	-2.72819	-1.941
			meiotic cell cycle		
1_Member	GO Biological Processes	GO:1903046	process	-2.72701	-1.940
1_Member	GO Biological Processes	GO:0048477	oogenesis	-2.71762	-1.931
1_Member	GO Biological Processes	GO:0055092	sterol homeostasis	-2.71762	-1.931
			protein		
1_Member	GO Biological Processes	GO:0051260	homooligomerization	-2.71044	-1.925
			glucan metabolic		
1_Member	GO Biological Processes	GO:0044042	process	-2.70871	-1.925
			pyridine-containing compound catabolic		
1_Member	GO Biological Processes	GO:0072526	process	-2.70871	-1.925
			positive regulation of		
1_Member	GO Biological Processes	GO:1904263	TORC1 signaling	-2.70871	-1.925
			glucocorticoid		
1_Member	GO Biological Processes	GO:0008211	metabolic process	-2.7073	-1.925
			pyrimidine nucleoside monophosphate		
1_Member	GO Biological Processes	GO:0009130	biosynthetic process	-2.7073	-1.925
			positive regulation of		
1_Member	GO Biological Processes	GO:0010763	fibroblast migration	-2.7073	-1.925
1_Member	GO Biological Processes	GO:0031000	response to caffeine	-2.7073	-1.925
			positive regulation of granulocyte		
			macrophage colony-stimulating factor		
1_Member	GO Biological Processes	GO:0032725	production	-2.7073	-1.925
1_Member	GO Biological Processes	GO:0033189	response to vitamin A	-2.7073	-1.925
			norepinephrine		
1_Member	GO Biological Processes	GO:0042415	metabolic process	-2.7073	-1.925
			negative regulation of DNA damage		
1_Member	GO Biological Processes	GO:0043518	response, signal	-2.7073	-1.925

			transduction by p53 class mediator		
1_Member	GO Biological Processes	GO:0046321	positive regulation of fatty acid oxidation	-2.7073	-1.925
1_Member	GO Biological Processes	GO:0060033	anatomical structure regression	-2.7073	-1.925
1_Member	GO Biological Processes	GO:0061043	regulation of vascular wound healing	-2.7073	-1.925
1_Member	GO Biological Processes	GO:0070207	protein homotrimerization	-2.7073	-1.925
			regulation of nucleotide-binding oligomerization domain containing		
1_Member	GO Biological Processes	GO:0070424	signaling pathway	-2.7073	-1.925
1_Member	GO Biological Processes	GO:0071450	cellular response to oxygen radical	-2.7073	-1.925
1_Member	GO Biological Processes	GO:0071451	cellular response to superoxide	-2.7073	-1.925
			positive regulation of monocyte chemotactic		
1_Member	GO Biological Processes	GO:0071639	protein-1 production	-2.7073	-1.925
1_Member	GO Biological Processes	GO:0071732	cellular response to nitric oxide	-2.7073	-1.925
			atrial cardiac muscle cell to AV node cell		
1_Member	GO Biological Processes	GO:0086066	communication	-2.7073	-1.925
			response to		
1_Member	GO Biological Processes	GO:0097396	interleukin-17	-2.7073	-1.925
			cellular response to		
1_Member	GO Biological Processes	GO:0097398	interleukin-17	-2.7073	-1.925
			regulation of presynaptic cytosolic calcium ion		
1_Member	GO Biological Processes	GO:0099509	concentration	-2.7073	-1.925
			regulation of motor neuron apoptotic		
1_Member	GO Biological Processes	GO:2000671	process	-2.7073	-1.925
			positive regulation of endothelial cell		
1_Member	GO Biological Processes	GO:2001028	chemotaxis	-2.7073	-1.925
			cellular anatomical		
1_Member	GO Biological Processes	GO:0032989	entity morphogenesis	-2.69703	-1.915

1_Member	GO Biological Processes	GO:0001508	action potential	-2.69339	-1.912
1_Member	GO Biological Processes	GO:0015807	L-amino acid transport	-2.67653	-1.896
1_Member	GO Biological Processes	GO:0061515	myeloid cell development	-2.67653	-1.896
1_Member	GO Biological Processes	GO:0001958	endochondral ossification	-2.67606	-1.896
1_Member	GO Biological Processes	GO:0007431	salivary gland development	-2.67606	-1.896
1_Member	GO Biological Processes	GO:0031116	positive regulation of microtubule polymerization	-2.67606	-1.896
1_Member	GO Biological Processes	GO:0036075	replacement	-2.67606	-1.896
1_Member	GO Biological Processes	GO:0070293	ossification	-2.67606	-1.896
1_Member	GO Biological Processes	GO:0070293	renal absorption	-2.67606	-1.896
1_Member	GO Biological Processes	GO:1902235	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	-2.67606	-1.896
1_Member	GO Biological Processes	GO:0009191	ribonucleoside diphosphate catabolic process	-2.67176	-1.892
1_Member	GO Biological Processes	GO:0045778	positive regulation of ossification	-2.67176	-1.892
1_Member	GO Biological Processes	GO:0046031	ADP metabolic process	-2.67176	-1.892
1_Member	GO Biological Processes	GO:0048599	process	-2.67176	-1.892
1_Member	GO Biological Processes	GO:0051899	oocyte development membrane	-2.67176	-1.892
1_Member	GO Biological Processes	GO:0051899	depolarization	-2.67176	-1.892
1_Member	GO Biological Processes	GO:0097194	execution phase of apoptosis	-2.67176	-1.892
1_Member	GO Biological Processes	GO:0140014	mitotic nuclear division	-2.6593	-1.880
1_Member	GO Biological Processes	GO:0140014	lymphocyte activation involved in immune response	-2.64599	-1.867
1_Member	GO Biological Processes	GO:0002285	regulation of pH	-2.64583	-1.867
1_Member	GO Biological Processes	GO:0006885	regulation of muscle	-2.64583	-1.867
1_Member	GO Biological Processes	GO:0051147	cell differentiation	-2.64142	-1.863
1_Member	GO Biological Processes	GO:0051147	sulfur compound	-2.64142	-1.863
1_Member	GO Biological Processes	GO:0072348	transport	-2.63563	-1.857
1_Member	GO Biological Processes	GO:0072348	sodium ion	-2.63563	-1.857
1_Member	GO Biological Processes	GO:0035725	transmembrane transport	-2.62587	-1.849
1_Member	GO Biological Processes	GO:0035725	transport	-2.62587	-1.849

1_Member	GO Biological Processes	GO:0006734	NADH metabolic process	-2.62581	-1.849
1_Member	GO Biological Processes	GO:0033198	response to ATP regulation of toll-like receptor 4 signaling pathway	-2.62581	-1.849
1_Member	GO Biological Processes	GO:0034143	exploration behavior	-2.62581	-1.849
1_Member	GO Biological Processes	GO:0035640	negative regulation of osteoclast differentiation	-2.62581	-1.849
1_Member	GO Biological Processes	GO:0045671	establishment of skin barrier	-2.62581	-1.849
1_Member	GO Biological Processes	GO:0061436	regulation of neuron projection regeneration	-2.62581	-1.849
1_Member	GO Biological Processes	GO:0070570	response to interleukin-6	-2.62581	-1.849
1_Member	GO Biological Processes	GO:0070741	regulation of response to oxidative stress	-2.62581	-1.849
1_Member	GO Biological Processes	GO:1902882	regulation of aerobic respiration	-2.62581	-1.849
1_Member	GO Biological Processes	GO:1903715	natural killer cell differentiation	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0001779	pyrimidine nucleobase metabolic process	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0006206	aromatic amino acid family catabolic process	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0009074	muscle cell apoptotic process	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0010657	vascular associated smooth muscle contraction	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0014829	positive regulation of smooth muscle cell apoptotic process	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0034393	angiotensin-activated signaling pathway	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0038166	positive regulation of B cell differentiation	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0045579	negative regulation of bone resorption	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0045779	response to corticosterone	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0051412			

1_Member	GO Biological Processes	GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway positive regulation of brown fat cell	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0090336	differentiation regulation of adipose	-2.62266	-1.848
1_Member	GO Biological Processes	GO:1904177	tissue development microtubule organizing center	-2.62266	-1.848
1_Member	GO Biological Processes	GO:0031023	organization diencephalon	-2.62248	-1.848
1_Member	GO Biological Processes	GO:0021536	development	-2.59226	-1.818
1_Member	GO Biological Processes	GO:0030258	lipid modification negative regulation of	-2.58867	-1.815
1_Member	GO Biological Processes	GO:0050869	B cell activation potassium ion	-2.57731	-1.804
1_Member	GO Biological Processes	GO:0055075	homeostasis response to	-2.57731	-1.804
1_Member	GO Biological Processes	GO:0070670	interleukin-4 positive regulation of	-2.57731	-1.804
1_Member	GO Biological Processes	GO:1902624	neutrophil migration positive regulation of	-2.57731	-1.804
1_Member	GO Biological Processes	GO:0031398	protein ubiquitination mitotic sister	-2.57665	-1.804
1_Member	GO Biological Processes	GO:0000070	chromatid segregation regulation of actin cytoskeleton	-2.56671	-1.794
1_Member	GO Biological Processes	GO:0032956	organization positive regulation of	-2.56653	-1.794
1_Member	GO Biological Processes	GO:0001954	cell-matrix adhesion osteoclast	-2.56576	-1.794
1_Member	GO Biological Processes	GO:0030316	differentiation negative regulation of carbohydrate	-2.56576	-1.794
1_Member	GO Biological Processes	GO:0045912	metabolic process regulation of insulin secretion involved in cellular response to	-2.56576	-1.794
1_Member	GO Biological Processes	GO:0061178	glucose stimulus cardiac muscle cell	-2.56576	-1.794
1_Member	GO Biological Processes	GO:0086001	action potential	-2.56576	-1.794

1_Member	GO Biological Processes	GO:0061387	regulation of extent of cell growth	-2.55415	-1.783
1_Member	GO Biological Processes	GO:0001956	positive regulation of neurotransmitter secretion	-2.54388	-1.775
1_Member	GO Biological Processes	GO:0002407	dendritic cell chemotaxis	-2.54388	-1.775
1_Member	GO Biological Processes	GO:0019896	axonal transport of mitochondrion	-2.54388	-1.775
1_Member	GO Biological Processes	GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	-2.54388	-1.775
1_Member	GO Biological Processes	GO:0045019	negative regulation of nitric oxide biosynthetic process	-2.54388	-1.775
1_Member	GO Biological Processes	GO:0050872	white fat cell differentiation	-2.54388	-1.775
1_Member	GO Biological Processes	GO:0060253	negative regulation of glial cell proliferation	-2.54388	-1.775
1_Member	GO Biological Processes	GO:0070198	protein localization to chromosome, telomeric region	-2.54388	-1.775
1_Member	GO Biological Processes	GO:0070206	protein trimerization	-2.54388	-1.775
1_Member	GO Biological Processes	GO:0110096	cellular response to aldehyde	-2.54388	-1.775
1_Member	GO Biological Processes	GO:1902036	regulation of hematopoietic stem cell differentiation	-2.54388	-1.775
1_Member	GO Biological Processes	GO:1902170	cellular response to reactive nitrogen species	-2.54388	-1.775
1_Member	GO Biological Processes	GO:1904406	negative regulation of nitric oxide metabolic process	-2.54388	-1.775
1_Member	GO Biological Processes	GO:1905906	regulation of amyloid fibril formation	-2.54388	-1.775
1_Member	GO Biological Processes	GO:0090596	sensory organ morphogenesis	-2.54138	-1.772
1_Member	GO Biological Processes	GO:0019395	fatty acid oxidation	-2.53827	-1.769
1_Member	GO Biological Processes	GO:0140013	meiotic nuclear division	-2.53722	-1.768

1_Member	GO Biological Processes	GO:0002823	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	-2.53196	-1.764
1_Member	GO Biological Processes	GO:0009134	nucleoside diphosphate catabolic process	-2.53196	-1.764
1_Member	GO Biological Processes	GO:0009994	oocyte differentiation	-2.53196	-1.764
1_Member	GO Biological Processes	GO:0032835	glomerulus development	-2.53196	-1.764
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1_Member	GO Biological Processes	GO:0009119	ribonucleoside metabolic process	-2.53046	-1.764
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1_Member	GO Biological Processes	GO:0030947	regulation of vascular endothelial growth factor receptor signaling pathway	-2.53046	-1.764
1_Member	GO Biological Processes	GO:0032205	negative regulation of telomere maintenance	-2.53046	-1.764
1_Member	GO Biological Processes	GO:0032673	regulation of interleukin-4 production	-2.53046	-1.764
1_Member	GO Biological Processes	GO:0045577	regulation of B cell differentiation	-2.53046	-1.764
1_Member	GO Biological Processes	GO:0046164	alcohol catabolic process	-2.53046	-1.764
1_Member	GO Biological Processes	GO:0046825	regulation of protein export from nucleus	-2.53046	-1.764
1_Member	GO Biological Processes	GO:0048873	homeostasis of number of cells within a tissue	-2.53046	-1.764
1_Member	GO Biological Processes	GO:0006914	autophagy	-2.51973	-1.754
1_Member	GO Biological Processes	GO:0061919	process utilizing autophagic mechanism	-2.51973	-1.754
1_Member	GO Biological Processes	GO:0090407	organophosphate biosynthetic process	-2.51304	-1.747

1_Member	GO Biological Processes	GO:2000736	regulation of stem cell differentiation	-2.51189	-1.746
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1_Member	GO Biological Processes	GO:0060998	regulation of dendritic spine development	-2.49887	-1.734
1_Member	GO Biological Processes	GO:0048864	stem cell development	-2.48591	-1.721
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1_Member	GO Biological Processes	GO:1902745	positive regulation of lamellipodium organization	-2.48516	-1.721
1_Member	GO Biological Processes	GO:1905332	positive regulation of morphogenesis of an epithelium	-2.48516	-1.721
1_Member	GO Biological Processes	GO:0006281	DNA repair	-2.48243	-1.718
1_Member	GO Biological Processes	GO:0000303	response to superoxide	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0006735	NADH regeneration	-2.47022	-1.709
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1_Member	GO Biological Processes	GO:0010755	regulation of plasminogen activation	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0010759	positive regulation of macrophage chemotaxis	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0030949	positive regulation of vascular endothelial growth factor receptor signaling pathway	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0032645	regulation of granulocyte macrophage colony-stimulating factor production	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0033003	regulation of mast cell activation	-2.47022	-1.709

1_Member	GO Biological Processes	GO:0035864	response to potassium ion	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0042574	retinal metabolic process	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0043116	negative regulation of vascular permeability	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0046851	negative regulation of bone remodeling	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0060571	morphogenesis of an epithelial fold	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0061621	canonical glycolysis	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0061718	glucose catabolic process to pyruvate	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0071371	cellular response to gonadotropin stimulus	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0071371	positive regulation of mitotic sister chromatid separation	-2.47022	-1.709
1_Member	GO Biological Processes	GO:1901970	developmental cell growth	-2.47022	-1.709
1_Member	GO Biological Processes	GO:0048588	ventricular cardiac muscle tissue	-2.46677	-1.706
1_Member	GO Biological Processes	GO:0003229	development	-2.46647	-1.706
1_Member	GO Biological Processes	GO:0003229	positive regulation of epithelial to mesenchymal transition	-2.46647	-1.706
1_Member	GO Biological Processes	GO:0010718	regulation of interferon-beta production	-2.46647	-1.706
1_Member	GO Biological Processes	GO:0032648	potassium ion transport	-2.46647	-1.706
1_Member	GO Biological Processes	GO:0006813	platelet-derived growth factor receptor signaling pathway	-2.45423	-1.694
1_Member	GO Biological Processes	GO:0048008	positive regulation of cardiac muscle tissue growth	-2.44132	-1.681
1_Member	GO Biological Processes	GO:0055023	Wnt signaling pathway	-2.44132	-1.681
1_Member	GO Biological Processes	GO:0016055	cell-cell signaling by wnt	-2.44062	-1.681
1_Member	GO Biological Processes	GO:0198738	wnt	-2.44062	-1.681

1_Member	GO Biological Processes	GO:0001961	positive regulation of cytokine-mediated signaling pathway	-2.43474	-1.675
1_Member	GO Biological Processes	GO:0140888	interferon-mediated signaling pathway	-2.43474	-1.675
1_Member	GO Biological Processes	GO:0016049	cell growth	-2.4246	-1.665
1_Member	GO Biological Processes	GO:0001837	epithelial to mesenchymal transition	-2.41029	-1.651
1_Member	GO Biological Processes	GO:0007422	peripheral nervous system development	-2.41029	-1.651
1_Member	GO Biological Processes	GO:0001756	somitogenesis	-2.40365	-1.645
1_Member	GO Biological Processes	GO:0043954	cellular component maintenance	-2.40365	-1.645
1_Member	GO Biological Processes	GO:0045599	negative regulation of fat cell differentiation	-2.40365	-1.645
1_Member	GO Biological Processes	GO:0000305	response to oxygen radical	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0002363	alpha-beta T cell lineage commitment	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0006144	purine nucleobase metabolic process	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0009110	vitamin biosynthetic process	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0015936	coenzyme A metabolic process	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0030038	contractile actin filament bundle assembly	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0032026	response to magnesium ion	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0032695	negative regulation of interleukin-12 production	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0043149	stress fiber assembly	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0046827	positive regulation of protein export from nucleus	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0060438	trachea development	-2.40111	-1.645
1_Member	GO Biological Processes	GO:0061298	retina vasculature development in camera-type eye	-2.40111	-1.645
1_Member	GO Biological Processes	GO:2001169	regulation of ATP biosynthetic process	-2.40111	-1.645

1_Member	GO Biological Processes	GO:0002724	regulation of T cell cytokine production	-2.39886	-1.644
1_Member	GO Biological Processes	GO:0035633	maintenance of blood-brain barrier	-2.39886	-1.644
1_Member	GO Biological Processes	GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator	-2.39886	-1.644
1_Member	GO Biological Processes	GO:0045191	regulation of isotype switching	-2.39886	-1.644
1_Member	GO Biological Processes	GO:0048144	fibroblast proliferation	-2.39886	-1.644
1_Member	GO Biological Processes	GO:0055094	response to lipoprotein particle	-2.39886	-1.644
1_Member	GO Biological Processes	GO:0071404	cellular response to low-density lipoprotein particle stimulus	-2.39886	-1.644
1_Member	GO Biological Processes	GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	-2.3902	-1.635
1_Member	GO Biological Processes	GO:0051702	biological process involved in interaction with symbiont	-2.3834	-1.629
1_Member	GO Biological Processes	GO:0006814	sodium ion transport	-2.37451	-1.620
1_Member	GO Biological Processes	GO:0045132	meiotic chromosome segregation	-2.36171	-1.607
1_Member	GO Biological Processes	GO:0006302	double-strand break repair	-2.36043	-1.606
1_Member	GO Biological Processes	GO:0016311	dephosphorylation	-2.34645	-1.592
1_Member	GO Biological Processes	GO:0002712	regulation of B cell mediated immunity	-2.34332	-1.590
1_Member	GO Biological Processes	GO:0002889	regulation of immunoglobulin mediated immune response	-2.34332	-1.590
1_Member	GO Biological Processes	GO:0051893	regulation of focal adhesion assembly	-2.34332	-1.590
1_Member	GO Biological Processes	GO:0090109	regulation of cell-substrate junction assembly	-2.34332	-1.590
1_Member	GO Biological Processes	GO:0007413	axonal fasciculation	-2.33605	-1.585

1_Member	GO Biological Processes	GO:0015810	aspartate transmembrane transport	-2.33605	-1.585
1_Member	GO Biological Processes	GO:0022616	DNA strand elongation	-2.33605	-1.585
1_Member	GO Biological Processes	GO:0042454	ribonucleoside catabolic process	-2.33605	-1.585
1_Member	GO Biological Processes	GO:0046323	glucose import	-2.33605	-1.585
1_Member	GO Biological Processes	GO:0050901	leukocyte tethering or rolling	-2.33605	-1.585
1_Member	GO Biological Processes	GO:0060716	labyrinthine layer blood vessel development	-2.33605	-1.585
1_Member	GO Biological Processes	GO:0061615	glycolytic process through fructose-6- phosphate	-2.33605	-1.585
1_Member	GO Biological Processes	GO:0061620	glycolytic process through glucose-6- phosphate	-2.33605	-1.585
1_Member	GO Biological Processes	GO:0070266	necroptotic process	-2.33605	-1.585
1_Member	GO Biological Processes	GO:0106030	neuron projection fasciculation	-2.33605	-1.585
1_Member	GO Biological Processes	GO:1900227	positive regulation of NLRP3 inflammasome complex assembly	-2.33605	-1.585
1_Member	GO Biological Processes	GO:2000269	regulation of fibroblast apoptotic process	-2.33605	-1.585
1_Member	GO Biological Processes	GO:0007409	axonogenesis	-2.32912	-1.578
1_Member	GO Biological Processes	GO:0009595	detection of biotic stimulus	-2.31779	-1.567
1_Member	GO Biological Processes	GO:0032728	positive regulation of interferon-beta production	-2.31779	-1.567
1_Member	GO Biological Processes	GO:0042168	heme metabolic process	-2.31779	-1.567
1_Member	GO Biological Processes	GO:1903146	regulation of autophagy of mitochondrion	-2.31779	-1.567
1_Member	GO Biological Processes	GO:0021545	cranial nerve development	-2.31404	-1.564
1_Member	GO Biological Processes	GO:0030101	natural killer cell activation	-2.31404	-1.564

1_Member	GO Biological Processes	GO:0030029	actin filament-based process	-2.30521	-1.555
1_Member	GO Biological Processes	GO:0060041	retina development in camera-type eye	-2.29519	-1.545
1_Member	GO Biological Processes	GO:0030516	regulation of axon extension	-2.29141	-1.542
1_Member	GO Biological Processes	GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	-2.28532	-1.536
1_Member	GO Biological Processes	GO:0009135	purine nucleoside diphosphate metabolic process	-2.28532	-1.536
1_Member	GO Biological Processes	GO:0009179	purine ribonucleoside diphosphate metabolic process	-2.28532	-1.536
1_Member	GO Biological Processes	GO:0043903	regulation of biological process involved in symbiotic interaction	-2.28532	-1.536
1_Member	GO Biological Processes	GO:0019730	antimicrobial humoral response	-2.28438	-1.536
1_Member	GO Biological Processes	GO:0010762	regulation of fibroblast migration	-2.27904	-1.531
1_Member	GO Biological Processes	GO:0060421	positive regulation of heart growth	-2.27904	-1.531
1_Member	GO Biological Processes	GO:0071402	cellular response to lipoprotein particle stimulus	-2.27904	-1.531
1_Member	GO Biological Processes	GO:0002042	cell migration involved in sprouting angiogenesis	-2.27461	-1.528
1_Member	GO Biological Processes	GO:0002888	positive regulation of myeloid leukocyte mediated immunity	-2.27461	-1.528
1_Member	GO Biological Processes	GO:0003081	regulation of systemic arterial blood pressure by renin-angiotensin	-2.27461	-1.528
1_Member	GO Biological Processes	GO:0007263	nitric oxide mediated signal transduction	-2.27461	-1.528
1_Member	GO Biological Processes	GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	-2.27461	-1.528

			pyrimidine nucleoside monophosphate		
1_Member	GO Biological Processes	GO:0009129	metabolic process	-2.27461	-1.528
			leukotriene		
1_Member	GO Biological Processes	GO:0019370	biosynthetic process	-2.27461	-1.528
			NAD catabolic		
1_Member	GO Biological Processes	GO:0019677	process	-2.27461	-1.528
1_Member	GO Biological Processes	GO:0044321	response to leptin	-2.27461	-1.528
1_Member	GO Biological Processes	GO:0045056	transcytosis	-2.27461	-1.528
			hematopoietic stem		
1_Member	GO Biological Processes	GO:0060218	cell differentiation	-2.27461	-1.528
			membrane		
			repolarization during		
1_Member	GO Biological Processes	GO:0086011	action potential	-2.27461	-1.528
			positive regulation of		
			inflammasome-		
			mediated signaling		
1_Member	GO Biological Processes	GO:0141087	pathway	-2.27461	-1.528
			regulation of DNA		
1_Member	GO Biological Processes	GO:0006275	replication	-2.26523	-1.519
			negative regulation of		
			G2/M transition of		
1_Member	GO Biological Processes	GO:0010972	mitotic cell cycle	-2.25715	-1.512
			maintenance of protein		
1_Member	GO Biological Processes	GO:0032507	location in cell	-2.25715	-1.512
			phosphatidylinositol		
			phosphate biosynthetic		
1_Member	GO Biological Processes	GO:0046854	process	-2.25715	-1.512
			negative regulation of		
1_Member	GO Biological Processes	GO:0050771	axonogenesis	-2.25715	-1.512
			regulation of		
1_Member	GO Biological Processes	GO:0050770	axonogenesis	-2.24528	-1.500
			positive regulation of		
			B cell mediated		
1_Member	GO Biological Processes	GO:0002714	immunity	-2.24141	-1.498
			positive regulation of		
			immunoglobulin		
			mediated immune		
1_Member	GO Biological Processes	GO:0002891	response	-2.24141	-1.498
1_Member	GO Biological Processes	GO:0006284	base-excision repair	-2.24141	-1.498
			pituitary gland		
1_Member	GO Biological Processes	GO:0021983	development	-2.24141	-1.498

1_Member	GO Biological Processes	GO:0050691	regulation of defense response to virus by host	-2.24141	-1.498
1_Member	GO Biological Processes	GO:0060612	adipose tissue development	-2.24141	-1.498
1_Member	GO Biological Processes	GO:0071364	cellular response to epidermal growth factor stimulus	-2.24141	-1.498
1_Member	GO Biological Processes	GO:0072595	maintenance of protein localization in organelle	-2.24141	-1.498
1_Member	GO Biological Processes	GO:1904659	glucose transmembrane transport	-2.24141	-1.498
1_Member	GO Biological Processes	GO:1904706	negative regulation of vascular associated smooth muscle cell proliferation	-2.24141	-1.498
1_Member	GO Biological Processes	GO:0007411	axon guidance	-2.23797	-1.495
1_Member	GO Biological Processes	GO:0097485	neuron projection guidance	-2.23797	-1.495
1_Member	GO Biological Processes	GO:0035710	CD4-positive, alpha-beta T cell activation	-2.2295	-1.486
1_Member	GO Biological Processes	GO:0045667	regulation of osteoblast differentiation	-2.22895	-1.486
1_Member	GO Biological Processes	GO:0007265	Ras protein signal transduction	-2.22416	-1.482
1_Member	GO Biological Processes	GO:0030641	regulation of cellular pH	-2.22402	-1.482
1_Member	GO Biological Processes	GO:0042303	molting cycle	-2.22402	-1.482
1_Member	GO Biological Processes	GO:0042633	hair cycle	-2.22402	-1.482
1_Member	GO Biological Processes	GO:0055007	cardiac muscle cell differentiation	-2.22402	-1.482
1_Member	GO Biological Processes	GO:0007530	sex determination	-2.21645	-1.475
1_Member	GO Biological Processes	GO:0030520	intracellular estrogen receptor signaling pathway	-2.21645	-1.475
1_Member	GO Biological Processes	GO:0036092	phosphatidylinositol-3-phosphate biosynthetic process	-2.21645	-1.475
1_Member	GO Biological Processes	GO:0072012	glomerulus vasculature development	-2.21645	-1.475

1_Member	GO Biological Processes	GO:0098801	regulation of renal system process	-2.21645	-1.475
1_Member	GO Biological Processes	GO:0048592	eye morphogenesis	-2.21276	-1.471
			negative regulation of transforming growth factor beta receptor signaling pathway		
1_Member	GO Biological Processes	GO:0030512	inflammatory response	-2.20902	-1.468
1_Member	GO Biological Processes	GO:0002437	to antigenic stimulus	-2.20483	-1.464
1_Member	GO Biological Processes	GO:0010712	regulation of collagen	-2.20483	-1.464
1_Member	GO Biological Processes	GO:0042551	metabolic process	-2.20483	-1.464
			neuron maturation	-2.20483	-1.464
			developmental		
1_Member	GO Biological Processes	GO:0048066	pigmentation	-2.20483	-1.464
			regulation of dendritic spine morphogenesis	-2.20483	-1.464
1_Member	GO Biological Processes	GO:0061001	regulation of small GTPase mediated signal transduction	-2.18519	-1.445
			positive regulation of T cell mediated immunity	-2.17573	-1.436
1_Member	GO Biological Processes	GO:0002711	phosphatidylcholine	-2.17573	-1.436
1_Member	GO Biological Processes	GO:0046470	metabolic process	-2.17573	-1.436
			regulation of meiotic cell cycle	-2.17573	-1.436
1_Member	GO Biological Processes	GO:0051445	negative regulation of cell cycle G2/M phase	-2.17573	-1.436
1_Member	GO Biological Processes	GO:1902750	transition	-2.17573	-1.436
			ensheathment of neurons	-2.17254	-1.433
1_Member	GO Biological Processes	GO:0007272	axon ensheathment	-2.17254	-1.433
1_Member	GO Biological Processes	GO:0008366	regulation of peptidyl-threonine phosphorylation	-2.16926	-1.431
			negative regulation of type II interferon production	-2.16926	-1.431
1_Member	GO Biological Processes	GO:0032689	regulation of activated T cell proliferation	-2.16926	-1.431
1_Member	GO Biological Processes	GO:0046006	trabecula	-2.16926	-1.431
1_Member	GO Biological Processes	GO:0061383	morphogenesis	-2.16926	-1.431
			renal system process	-2.16126	-1.425
1_Member	GO Biological Processes	GO:0003071	involved in regulation	-2.16126	-1.425

			of systemic arterial blood pressure		
1_Member	GO Biological Processes	GO:0003091	renal water homeostasis	-2.16126	-1.425
1_Member	GO Biological Processes	GO:0006972	hyperosmotic response	-2.16126	-1.425
			deoxyribonucleoside monophosphate		
1_Member	GO Biological Processes	GO:0009162	metabolic process	-2.16126	-1.425
			regulation of heterochromatin		
1_Member	GO Biological Processes	GO:0031445	formation	-2.16126	-1.425
			embryonic		
1_Member	GO Biological Processes	GO:0035162	hemopoiesis	-2.16126	-1.425
			indole-containing compound metabolic		
1_Member	GO Biological Processes	GO:0042430	process	-2.16126	-1.425
			positive regulation of fatty acid biosynthetic		
1_Member	GO Biological Processes	GO:0045723	process	-2.16126	-1.425
			carbohydrate		
1_Member	GO Biological Processes	GO:0046835	phosphorylation	-2.16126	-1.425
			glucose 6-phosphate		
1_Member	GO Biological Processes	GO:0051156	metabolic process	-2.16126	-1.425
			leukocyte adhesion to vascular endothelial		
1_Member	GO Biological Processes	GO:0061756	cell	-2.16126	-1.425
			interleukin-1-mediated		
1_Member	GO Biological Processes	GO:0070498	signaling pathway	-2.16126	-1.425
			cellular response to		
1_Member	GO Biological Processes	GO:0071359	dsRNA	-2.16126	-1.425
			amyloid-beta		
1_Member	GO Biological Processes	GO:0097242	clearance	-2.16126	-1.425
			regulation of heterochromatin		
1_Member	GO Biological Processes	GO:0120261	organization	-2.16126	-1.425
			regulation of cell		
1_Member	GO Biological Processes	GO:1903429	maturation	-2.16126	-1.425
			regulation of neuron		
1_Member	GO Biological Processes	GO:0045664	differentiation	-2.1532	-1.417
1_Member	GO Biological Processes	GO:0031016	pancreas development	-2.14957	-1.414
			positive regulation of		
			alpha-beta T cell		
1_Member	GO Biological Processes	GO:0046635	activation	-2.14957	-1.414

1_Member	GO Biological Processes	GO:0048002	antigen processing and presentation of peptide antigen	-2.14957	-1.414
1_Member	GO Biological Processes	GO:2000401	regulation of lymphocyte migration	-2.14957	-1.414
1_Member	GO Biological Processes	GO:1903322	positive regulation of protein modification by small protein conjugation or removal	-2.13684	-1.402
1_Member	GO Biological Processes	GO:0008038	neuron recognition	-2.13465	-1.400
1_Member	GO Biological Processes	GO:0008645	hexose transmembrane transport	-2.13465	-1.400
1_Member	GO Biological Processes	GO:0035249	synaptic transmission, glutamatergic	-2.13465	-1.400
1_Member	GO Biological Processes	GO:0042149	cellular response to glucose starvation	-2.13465	-1.400
1_Member	GO Biological Processes	GO:0071763	nuclear membrane organization	-2.13465	-1.400
1_Member	GO Biological Processes	GO:0071677	positive regulation of mononuclear cell migration	-2.12388	-1.390
1_Member	GO Biological Processes	GO:0072594	establishment of protein localization to organelle	-2.11831	-1.384
1_Member	GO Biological Processes	GO:0002922	positive regulation of humoral immune response	-2.10877	-1.377
1_Member	GO Biological Processes	GO:0030521	androgen receptor signaling pathway	-2.10877	-1.377
1_Member	GO Biological Processes	GO:0046641	positive regulation of alpha-beta T cell proliferation	-2.10877	-1.377
1_Member	GO Biological Processes	GO:0048015	phosphatidylinositol-mediated signaling	-2.10877	-1.377
1_Member	GO Biological Processes	GO:0060307	regulation of ventricular cardiac muscle cell membrane repolarization	-2.10877	-1.377
1_Member	GO Biological Processes	GO:0060343	trabecula formation	-2.10877	-1.377
1_Member	GO Biological Processes	GO:0060706	cell differentiation involved in embryonic placenta development	-2.10877	-1.377

1_Member	GO Biological Processes	GO:0061437	renal system vasculature development	-2.10877	-1.377
1_Member	GO Biological Processes	GO:0061440	kidney vasculature development	-2.10877	-1.377
1_Member	GO Biological Processes	GO:0090200	positive regulation of release of cytochrome c from mitochondria	-2.10877	-1.377
1_Member	GO Biological Processes	GO:1903579	negative regulation of ATP metabolic process	-2.10877	-1.377
1_Member	GO Biological Processes	GO:2001026	regulation of endothelial cell chemotaxis	-2.10877	-1.377
1_Member	GO Biological Processes	GO:0046173	polyol biosynthetic process	-2.10096	-1.369
1_Member	GO Biological Processes	GO:0050856	regulation of T cell receptor signaling pathway	-2.10096	-1.369
1_Member	GO Biological Processes	GO:1902622	regulation of neutrophil migration	-2.10096	-1.369
1_Member	GO Biological Processes	GO:0110053	regulation of actin filament organization	-2.09893	-1.368
1_Member	GO Biological Processes	GO:0008088	axo-dendritic transport regulation of alpha- beta T cell	-2.09865	-1.368
1_Member	GO Biological Processes	GO:0046637	differentiation negative regulation of muscle cell	-2.09865	-1.368
1_Member	GO Biological Processes	GO:0051148	differentiation cardiac septum	-2.09865	-1.368
1_Member	GO Biological Processes	GO:0060411	morphogenesis proteolysis involved in protein catabolic	-2.09865	-1.368
1_Member	GO Biological Processes	GO:0051603	process regulation of neural precursor cell	-2.09274	-1.362
1_Member	GO Biological Processes	GO:2000177	proliferation regulation of myoblast	-2.07709	-1.346
1_Member	GO Biological Processes	GO:0045661	differentiation neuromuscular	-2.07386	-1.343
1_Member	GO Biological Processes	GO:0007528	junction development regulation of muscle	-2.06814	-1.338
1_Member	GO Biological Processes	GO:1901861	tissue development	-2.06814	-1.338

1_Member	GO Biological Processes	GO:1901976	regulation of cell cycle checkpoint	-2.06814	-1.338
1_Member	GO Biological Processes	GO:0003016	respiratory system process	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0007271	synaptic transmission, cholinergic	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0009164	nucleoside catabolic process	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0032331	negative regulation of chondrocyte differentiation	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0034643	establishment of mitochondrion localization, microtubule-mediated	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0035020	regulation of Rac protein signal transduction	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0042026	protein refolding	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0042659	regulation of cell fate specification	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0043567	regulation of insulin-like growth factor receptor signaling pathway	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0045662	negative regulation of myoblast differentiation	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0047497	mitochondrion transport along microtubule	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0060065	uterus development	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0071676	negative regulation of mononuclear cell migration	-2.05874	-1.331
1_Member	GO Biological Processes	GO:1905523	positive regulation of macrophage migration	-2.05874	-1.331
1_Member	GO Biological Processes	GO:2000773	negative regulation of cellular senescence	-2.05874	-1.331
1_Member	GO Biological Processes	GO:0050792	regulation of viral process	-2.05848	-1.331
1_Member	GO Biological Processes	GO:0061351	neural precursor cell proliferation	-2.05719	-1.330

1_Member	GO Biological Processes	GO:0003281	ventricular septum development	-2.04949	-1.322
1_Member	GO Biological Processes	GO:0019882	antigen processing and presentation	-2.03755	-1.310
1_Member	GO Biological Processes	GO:0015749	monosaccharide transmembrane transport	-2.03616	-1.310
1_Member	GO Biological Processes	GO:0030073	insulin secretion	-2.03616	-1.310
1_Member	GO Biological Processes	GO:2001222	regulation of neuron migration	-2.03616	-1.310
1_Member	GO Biological Processes	GO:0009141	nucleoside triphosphate metabolic process	-2.03198	-1.306
1_Member	GO Biological Processes	GO:0009185	ribonucleoside diphosphate metabolic process	-2.02554	-1.299
1_Member	GO Biological Processes	GO:0060560	developmental growth involved in morphogenesis	-2.01762	-1.291
1_Member	GO Biological Processes	GO:0002053	positive regulation of mesenchymal cell proliferation	-2.01098	-1.286
1_Member	GO Biological Processes	GO:0002726	positive regulation of T cell cytokine production	-2.01098	-1.286
1_Member	GO Biological Processes	GO:0015740	C4-dicarboxylate transport	-2.01098	-1.286
1_Member	GO Biological Processes	GO:0021895	cerebral cortex neuron differentiation	-2.01098	-1.286
1_Member	GO Biological Processes	GO:0086009	membrane repolarization	-2.01098	-1.286
1_Member	GO Biological Processes	GO:1901623	regulation of lymphocyte chemotaxis	-2.01098	-1.286
1_Member	GO Biological Processes	GO:0002250	adaptive immune response	-2.01036	-1.285
1_Member	GO Biological Processes	GO:0007259	receptor signaling pathway via JAK-STAT	-2.00498	-1.281
1_Member	GO Biological Processes	GO:0019915	lipid storage	-2.00498	-1.281
1_Member	GO Biological Processes	GO:0045581	negative regulation of T cell differentiation	-2.00498	-1.281
1_Member	GO Biological Processes	GO:0048546	digestive tract morphogenesis	-2.00498	-1.281

1_Member	GO Biological Processes	GO:2000514	regulation of CD4-positive, alpha-beta T cell activation protein	-2.002	-1.278
1_Member	GO Biological Processes	GO:0006470	dephosphorylation skeletal muscle tissue	-2.00128	-1.277
1_Member	GO Biological Processes	GO:0007519	development	-2.00128	-1.277
1_Member	GO Biological Processes	GO:0072006	nephron development	-2.00128	-1.277
2_Summary	GO Biological Processes	GO:0009725	response to hormone	-76.9027	-72.725
2_Member	GO Biological Processes	GO:0009725	response to hormone	-76.9027	-72.725
			cellular response to organonitrogen		
2_Member	GO Biological Processes	GO:0071417	compound	-65.9574	-62.257
			cellular response to		
2_Member	GO Biological Processes	GO:1901699	nitrogen compound	-65.6145	-62.039
2_Member	GO Biological Processes	GO:1901652	response to peptide	-52.7235	-49.500
			cellular response to		
2_Member	GO Biological Processes	GO:0032870	hormone stimulus	-49.1151	-46.052
			cellular response to		
2_Member	GO Biological Processes	GO:1901653	peptide	-38.2649	-35.731
			response to peptide		
2_Member	GO Biological Processes	GO:0043434	hormone	-32.6676	-30.353
			cellular response to		
			peptide hormone		
2_Member	GO Biological Processes	GO:0071375	stimulus	-26.4014	-24.265
2_Member	GO Biological Processes	GO:0032868	response to insulin	-20.9085	-19.001
			cellular response to		
2_Member	GO Biological Processes	GO:0032869	insulin stimulus	-14.8884	-13.254
			response to xenobiotic		
3_Summary	GO Biological Processes	GO:0009410	stimulus	-74.2136	-70.337
			response to xenobiotic		
3_Member	GO Biological Processes	GO:0009410	stimulus	-74.2136	-70.337
			cellular response to		
3_Member	GO Biological Processes	GO:0071466	xenobiotic stimulus	-33.2403	-30.895
			xenobiotic metabolic		
3_Member	GO Biological Processes	GO:0006805	process	-18.9582	-17.117
			response to inorganic		
4_Summary	GO Biological Processes	GO:0010035	substance	-60.8041	-57.326
			response to inorganic		
4_Member	GO Biological Processes	GO:0010035	substance	-60.8041	-57.326
			response to oxidative		
4_Member	GO Biological Processes	GO:0006979	stress	-39.9955	-37.337
4_Member	GO Biological Processes	GO:0010038	response to metal ion	-39.1057	-36.508

4_Member	GO Biological Processes	GO:0062197	cellular response to chemical stress	-38.9741	-36.388
4_Member	GO Biological Processes	GO:0000302	response to reactive oxygen species	-34.5979	-32.213
4_Member	GO Biological Processes	GO:0034599	cellular response to oxidative stress	-31.7483	-29.463
4_Member	GO Biological Processes	GO:0034614	cellular response to reactive oxygen species	-28.2367	-26.050
4_Member	GO Biological Processes	GO:0071241	cellular response to inorganic substance	-23.2773	-21.264
4_Member	GO Biological Processes	GO:0071248	cellular response to metal ion	-22.0615	-20.099
4_Member	GO Biological Processes	GO:0042542	response to hydrogen peroxide	-21.3988	-19.474
4_Member	GO Biological Processes	GO:0070301	cellular response to hydrogen peroxide	-16.2685	-14.562
4_Member	GO Biological Processes	GO:0046686	response to cadmium ion	-14.4716	-12.855
4_Member	GO Biological Processes	GO:0071276	cellular response to cadmium ion	-12.1402	-10.655
5_Summary	GO Biological Processes	GO:0006468	protein phosphorylation	-56.5517	-53.152
5_Member	GO Biological Processes	GO:0006468	protein phosphorylation	-56.5517	-53.152
5_Member	GO Biological Processes	GO:0016310	phosphorylation	-55.876	-52.544
5_Member	GO Biological Processes	GO:0018193	peptidyl-amino acid modification	-33.1891	-30.850
5_Member	GO Biological Processes	GO:0018105	peptidyl-serine phosphorylation	-26.3342	-24.202
5_Member	GO Biological Processes	GO:0018209	peptidyl-serine modification	-25.1542	-23.074
5_Member	GO Biological Processes	GO:0018107	peptidyl-threonine phosphorylation	-13.8966	-12.309
5_Member	GO Biological Processes	GO:0018210	peptidyl-threonine modification	-12.6994	-11.177
6_Summary	GO Biological Processes	GO:0003013	circulatory system process	-54.1987	-50.924
6_Member	GO Biological Processes	GO:0003013	circulatory system process	-54.1987	-50.924
6_Member	GO Biological Processes	GO:0008015	blood circulation	-46.1106	-43.212
6_Member	GO Biological Processes	GO:0003018	vascular process in circulatory system	-40.0759	-37.404

6_Member	GO Biological Processes	GO:0035296	regulation of tube diameter	-29.8563	-27.628
6_Member	GO Biological Processes	GO:0097746	blood vessel diameter maintenance	-29.8563	-27.628
6_Member	GO Biological Processes	GO:0035150	regulation of tube size	-29.7466	-27.523
6_Member	GO Biological Processes	GO:0090066	regulation of anatomical structure size	-26.6288	-24.477
6_Member	GO Biological Processes	GO:0003012	muscle system process	-17.6807	-15.895
6_Member	GO Biological Processes	GO:0019229	regulation of vasoconstriction	-16.0174	-14.323
6_Member	GO Biological Processes	GO:0042311	vasodilation	-14.7541	-13.124
6_Member	GO Biological Processes	GO:0006936	muscle contraction	-14.0358	-12.435
6_Member	GO Biological Processes	GO:0042310	vasoconstriction smooth muscle	-12.6486	-11.129
6_Member	GO Biological Processes	GO:0006939	contraction	-10.7195	-9.316
6_Member	GO Biological Processes	GO:0045907	positive regulation of vasoconstriction	-9.87807	-8.527
7_Summary	GO Biological Processes	GO:0071396	cellular response to lipid	-52.2956	-49.118
7_Member	GO Biological Processes	GO:0071396	cellular response to lipid	-52.2956	-49.118
7_Member	GO Biological Processes	GO:0032496	response to lipopolysaccharide	-48.2284	-45.227
7_Member	GO Biological Processes	GO:0002237	response to molecule of bacterial origin	-47.6212	-44.648
7_Member	GO Biological Processes	GO:0009617	response to bacterium	-38.9357	-36.371
7_Member	GO Biological Processes	GO:0006954	inflammatory response	-37.4151	-34.919
7_Member	GO Biological Processes	GO:0071216	cellular response to biotic stimulus	-33.0538	-30.721
7_Member	GO Biological Processes	GO:0071219	cellular response to molecule of bacterial origin	-30.5749	-28.322
7_Member	GO Biological Processes	GO:0071222	cellular response to lipopolysaccharide	-30.5218	-28.274
8_Summary	GO Biological Processes	GO:0010562	positive regulation of phosphorus metabolic process	-49.6727	-46.574
8_Member	GO Biological Processes	GO:0010562	positive regulation of phosphorus metabolic process	-49.6727	-46.574
8_Member	GO Biological Processes	GO:0045937	positive regulation of phosphate metabolic process	-49.6727	-46.574

8_Member	GO Biological Processes	GO:0051338	regulation of transferase activity	-48.8854	-45.854
8_Member	GO Biological Processes	GO:0042327	positive regulation of phosphorylation	-46.7928	-43.846
8_Member	GO Biological Processes	GO:0043549	regulation of kinase activity	-44.8168	-42.001
8_Member	GO Biological Processes	GO:0043408	regulation of MAPK cascade	-44.5938	-41.797
8_Member	GO Biological Processes	GO:0043410	positive regulation of MAPK cascade	-41.2702	-38.555
8_Member	GO Biological Processes	GO:0001934	positive regulation of protein phosphorylation	-41.2493	-38.549
8_Member	GO Biological Processes	GO:0051347	positive regulation of transferase activity	-38.9452	-36.371
8_Member	GO Biological Processes	GO:0031401	positive regulation of protein modification process	-37.4061	-34.919
8_Member	GO Biological Processes	GO:0045859	regulation of protein kinase activity	-36.178	-33.749
8_Member	GO Biological Processes	GO:0033674	positive regulation of kinase activity	-34.2278	-31.850
8_Member	GO Biological Processes	GO:0071900	regulation of protein serine/threonine kinase activity	-32.2959	-29.999
8_Member	GO Biological Processes	GO:0070372	regulation of ERK1 and ERK2 cascade	-26.5279	-24.380
8_Member	GO Biological Processes	GO:0045860	positive regulation of protein kinase activity	-24.4686	-22.412
8_Member	GO Biological Processes	GO:0070374	positive regulation of ERK1 and ERK2 cascade	-22.0275	-20.067
8_Member	GO Biological Processes	GO:0071902	positive regulation of protein serine/threonine kinase activity	-20.888	-18.985
8_Member	GO Biological Processes	GO:0043405	regulation of MAP kinase activity	-19.3418	-17.478
8_Member	GO Biological Processes	GO:0043406	positive regulation of MAP kinase activity	-15.8223	-14.139
9_Summary	GO Biological Processes	GO:0099536	synaptic signaling	-46.4214	-43.499
9_Member	GO Biological Processes	GO:0099536	synaptic signaling	-46.4214	-43.499
9_Member	GO Biological Processes	GO:0099537	trans-synaptic signaling	-44.0299	-41.250

9_Member	GO Biological Processes	GO:0007268	chemical synaptic transmission	-39.7728	-37.139
9_Member	GO Biological Processes	GO:0098916	anterograde trans-synaptic signaling	-39.7728	-37.139
9_Member	GO Biological Processes	GO:0099177	regulation of trans-synaptic signaling	-38.1223	-35.608
9_Member	GO Biological Processes	GO:0050804	modulation of chemical synaptic transmission	-37.1785	-34.709
9_Member	GO Biological Processes	GO:0050806	positive regulation of synaptic transmission	-17.608	-15.827
9_Member	GO Biological Processes	GO:0048167	regulation of synaptic plasticity	-16.0059	-14.314
10_Summary	GO Biological Processes	GO:0071407	cellular response to organic cyclic compound	-45.888	-43.012
10_Member	GO Biological Processes	GO:0071407	cellular response to organic cyclic compound	-45.888	-43.012
10_Member	GO Biological Processes	GO:0030522	intracellular receptor signaling pathway	-18.7445	-16.913
10_Member	GO Biological Processes	GO:0009755	hormone-mediated signaling pathway	-13.9173	-12.328
10_Member	GO Biological Processes	GO:0071383	cellular response to steroid hormone stimulus	-13.6085	-12.036
10_Member	GO Biological Processes	GO:0043401	steroid hormone mediated signaling pathway	-10.1384	-8.775
11_Summary	GO Biological Processes	GO:0044057	regulation of system process	-45.4747	-42.636
11_Member	GO Biological Processes	GO:0044057	regulation of system process	-45.4747	-42.636
11_Member	GO Biological Processes	GO:1903522	regulation of blood circulation	-27.7273	-25.550
11_Member	GO Biological Processes	GO:0090257	regulation of muscle system process	-19.2278	-17.373
11_Member	GO Biological Processes	GO:0006937	regulation of muscle contraction	-15.8058	-14.125
11_Member	GO Biological Processes	GO:0008016	regulation of heart contraction	-15.6343	-13.962
11_Member	GO Biological Processes	GO:0055117	regulation of cardiac muscle contraction	-8.11302	-6.877

11_Member	GO Biological Processes	GO:0006942	regulation of striated muscle contraction	-7.86079	-6.640
11_Member	GO Biological Processes	GO:0002027	regulation of heart rate	-7.54416	-6.344
11_Member	GO Biological Processes	GO:1903115	regulation of actin filament-based movement	-5.31741	-4.289
			regulation of cardiac muscle cell contraction	-4.65319	-3.684
11_Member	GO Biological Processes	GO:0086004	contraction	-4.65319	-3.684
12_Summary	GO Biological Processes	GO:1902074	response to salt	-45.4715	-42.636
12_Member	GO Biological Processes	GO:1902074	response to salt	-45.4715	-42.636
12_Member	GO Biological Processes	GO:0043279	response to alkaloid	-38.1824	-35.658
12_Member	GO Biological Processes	GO:0042220	response to cocaine	-26.7124	-24.552
12_Member	GO Biological Processes	GO:1902075	cellular response to salt	-15.2075	-13.556
			cellular response to alkaloid	-11.8292	-10.369
12_Member	GO Biological Processes	GO:0071312	alkaloid	-11.8292	-10.369
13_Summary	GO Biological Processes	GO:0043068	positive regulation of programmed cell death	-43.7795	-41.017
13_Member	GO Biological Processes	GO:0043068	positive regulation of programmed cell death	-43.7795	-41.017
			positive regulation of apoptotic process	-37.0583	-34.597
13_Member	GO Biological Processes	GO:0043065	negative regulation of cell population	-37.0583	-34.597
			proliferation	-27.5149	-25.346
13_Member	GO Biological Processes	GO:0008285	proliferation	-27.5149	-25.346
14_Summary	GO Biological Processes	GO:0010817	regulation of hormone levels	-43.6145	-40.868
14_Member	GO Biological Processes	GO:0010817	regulation of hormone levels	-43.6145	-40.868
			hormone metabolic process	-23.8888	-21.851
14_Member	GO Biological Processes	GO:0042445	process	-23.8888	-21.851
15_Summary	GO Biological Processes	GO:0097305	response to alcohol	-42.9629	-40.233
15_Member	GO Biological Processes	GO:0097305	response to alcohol	-42.9629	-40.233
15_Member	GO Biological Processes	GO:0045471	response to ethanol	-30.8378	-28.574
16_Summary	GO Biological Processes	GO:0070482	response to oxygen	-40.5749	-37.889
			levels	-40.5749	-37.889
16_Member	GO Biological Processes	GO:0070482	response to oxygen levels	-40.5749	-37.889
16_Member	GO Biological Processes	GO:0036293	response to decreased oxygen levels	-39.25	-36.641
			response to hypoxia	-37.9863	-35.481
16_Member	GO Biological Processes	GO:0001666	response to hypoxia	-37.9863	-35.481
16_Member	GO Biological Processes	GO:0071453	cellular response to oxygen levels	-13.0842	-11.539
			oxygen levels	-13.0842	-11.539

16_Member	GO Biological Processes	GO:0036294	cellular response to decreased oxygen levels	-13.0207	-11.483
16_Member	GO Biological Processes	GO:0071456	cellular response to hypoxia	-12.4332	-10.930
17_Summary	GO Biological Processes	GO:0043269	regulation of monoatomic ion transport	-39.4428	-36.822
17_Member	GO Biological Processes	GO:0043269	regulation of monoatomic ion transport	-39.4428	-36.822
17_Member	GO Biological Processes	GO:0034762	regulation of transmembrane transport	-35.3643	-32.958
17_Member	GO Biological Processes	GO:0010959	regulation of metal ion transport	-30.6681	-28.410
17_Member	GO Biological Processes	GO:0051924	regulation of calcium ion transport	-29.6342	-27.416
17_Member	GO Biological Processes	GO:0034765	regulation of monoatomic ion transmembrane transport	-24.3056	-22.258
17_Member	GO Biological Processes	GO:0034764	positive regulation of transmembrane transport	-23.3084	-21.289
17_Member	GO Biological Processes	GO:0043270	positive regulation of monoatomic ion transport	-22.3689	-20.390
17_Member	GO Biological Processes	GO:1903169	regulation of calcium ion transmembrane transport	-21.133	-19.218
17_Member	GO Biological Processes	GO:1904062	regulation of monoatomic cation transmembrane transport	-19.719	-17.843
17_Member	GO Biological Processes	GO:0034767	positive regulation of monoatomic ion transmembrane transport	-16.6696	-14.933
17_Member	GO Biological Processes	GO:0051928	positive regulation of calcium ion transport	-13.9029	-12.314
17_Member	GO Biological Processes	GO:1904064	positive regulation of cation transmembrane transport	-12.4938	-10.985

17_Member	GO Biological Processes	GO:0051282	regulation of sequestering of calcium ion	-12.4332	-10.930
17_Member	GO Biological Processes	GO:1904427	positive regulation of calcium ion transmembrane transport	-8.83322	-7.550
17_Member	GO Biological Processes	GO:0051279	regulation of release of sequestered calcium ion into cytosol	-7.73264	-6.518
17_Member	GO Biological Processes	GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	-5.24254	-4.224
18_Summary	GO Biological Processes	GO:1901615	organic hydroxy compound metabolic process	-38.7444	-36.190
18_Member	GO Biological Processes	GO:1901615	organic hydroxy compound metabolic process	-38.7444	-36.190
18_Member	GO Biological Processes	GO:0008202	steroid metabolic process	-24.5327	-22.469
18_Member	GO Biological Processes	GO:1901617	organic hydroxy compound biosynthetic process	-17.5685	-15.789
18_Member	GO Biological Processes	GO:0006066	alcohol metabolic process	-16.287	-14.578
18_Member	GO Biological Processes	GO:0006694	steroid biosynthetic process	-15.1728	-13.523
18_Member	GO Biological Processes	GO:0016125	sterol metabolic process	-11.8458	-10.383
18_Member	GO Biological Processes	GO:0008203	cholesterol metabolic process	-10.6713	-9.276
18_Member	GO Biological Processes	GO:1902652	secondary alcohol metabolic process	-10.0417	-8.682
18_Member	GO Biological Processes	GO:0046165	alcohol biosynthetic process	-8.14297	-6.904
18_Member	GO Biological Processes	GO:0016126	sterol biosynthetic process	-5.03025	-4.025
18_Member	GO Biological Processes	GO:0006695	cholesterol biosynthetic process	-4.43443	-3.480
18_Member	GO Biological Processes	GO:1902653	secondary alcohol biosynthetic process	-4.43443	-3.480
19_Summary	GO Biological Processes	GO:0007610	behavior	-38.5725	-36.028

19_Member	GO Biological Processes	GO:0007610	behavior	-38.5725	-36.028
19_Member	GO Biological Processes	GO:0050890	cognition	-22.9403	-20.939
19_Member	GO Biological Processes	GO:0007611	learning or memory	-22.3624	-20.386
19_Member	GO Biological Processes	GO:0007612	learning	-13.6085	-12.036
19_Member	GO Biological Processes	GO:0008306	associative learning	-11.8393	-10.378
19_Member	GO Biological Processes	GO:0007632	visual behavior	-9.78953	-8.441
19_Member	GO Biological Processes	GO:0008542	visual learning	-9.35932	-8.031
19_Member	GO Biological Processes	GO:0007613	memory	-7.5027	-6.305
20_Summary	GO Biological Processes	GO:0051046	regulation of secretion	-37.3932	-34.915
20_Member	GO Biological Processes	GO:0051046	regulation of secretion	-37.3932	-34.915
20_Member	GO Biological Processes	GO:1903530	regulation of secretion by cell	-36.2118	-33.775
20_Member	GO Biological Processes	GO:0070201	regulation of establishment of protein localization	-30.2769	-28.034
20_Member	GO Biological Processes	GO:0051223	regulation of protein transport	-26.4956	-24.352
20_Member	GO Biological Processes	GO:1903829	positive regulation of protein localization	-23.7185	-21.687
20_Member	GO Biological Processes	GO:0050708	regulation of protein secretion	-21.8253	-19.878
20_Member	GO Biological Processes	GO:1904951	positive regulation of establishment of protein localization	-21.7818	-19.840
20_Member	GO Biological Processes	GO:0046883	regulation of hormone secretion	-21.6978	-19.758
20_Member	GO Biological Processes	GO:0051047	positive regulation of secretion	-21.4444	-19.512
20_Member	GO Biological Processes	GO:0051222	positive regulation of protein transport	-20.9859	-19.076
20_Member	GO Biological Processes	GO:1903532	positive regulation of secretion by cell	-20.6756	-18.779
20_Member	GO Biological Processes	GO:0090087	regulation of peptide transport	-16.7288	-14.989
20_Member	GO Biological Processes	GO:0002791	regulation of peptide secretion	-15.8554	-14.169
20_Member	GO Biological Processes	GO:0090276	regulation of peptide hormone secretion	-15.0465	-13.401
20_Member	GO Biological Processes	GO:0050796	regulation of insulin secretion	-13.7853	-12.202
20_Member	GO Biological Processes	GO:0050714	positive regulation of protein secretion	-11.9666	-10.492
20_Member	GO Biological Processes	GO:0046887	positive regulation of hormone secretion	-9.28041	-7.957

20_Member	GO Biological Processes	GO:0002793	positive regulation of peptide secretion	-7.10835	-5.942
20_Member	GO Biological Processes	GO:0090277	positive regulation of peptide hormone secretion	-6.31146	-5.207
20_Member	GO Biological Processes	GO:0032024	positive regulation of insulin secretion	-4.76422	-3.783

Supplement table 6

Supplementary Table 6 106 cellular component (CC) terms

GO:1903426	Category	Term	Description	LogP	Log(q-value)
1_Summary	GO Cellular Components	GO:0045121	membrane raft	-29.0996	-26.053
1_Member	GO Cellular Components	GO:0045121	membrane raft	-29.0996	-26.053
1_Member	GO Cellular Components	GO:0098857	membrane microdomain	-29.032	-26.053
1_Member	GO Cellular Components	GO:0005901	caveola	-13.4542	-11.554
1_Member	GO Cellular Components	GO:0044853	plasma membrane raft	-13.1761	-11.311
2_Summary	GO Cellular Components	GO:0030425	dendrite	-27.0903	-24.336
2_Member	GO Cellular Components	GO:0030425	dendrite	-27.0903	-24.336
2_Member	GO Cellular Components	GO:0097447	dendritic tree	-27.0142	-24.336
2_Member	GO Cellular Components	GO:0097060	synaptic membrane	-25.676	-23.095
2_Member	GO Cellular Components	GO:0098794	postsynapse	-25.1646	-22.662
2_Member	GO Cellular Components	GO:0098793	presynapse	-24.7873	-22.352
2_Member	GO Cellular Components	GO:0044297	cell body	-22.6722	-20.381
2_Member	GO Cellular Components	GO:0043025	neuronal cell body	-22.6609	-20.381
2_Member	GO Cellular Components	GO:0042734	presynaptic membrane	-22.3492	-20.148
2_Member	GO Cellular Components	GO:0030424	axon	-21.0048	-18.871
2_Member	GO Cellular Components	GO:0045211	postsynaptic membrane	-17.6183	-15.593
2_Member	GO Cellular Components	GO:0098978	glutamatergic synapse	-12.6356	-10.802
3_Summary	GO Cellular Components	GO:0043235	receptor complex	-24.6737	-22.296
3_Member	GO Cellular Components	GO:0043235	receptor complex	-24.6737	-22.296
3_Member	GO Cellular Components	GO:0098797	plasma membrane protein complex	-13.8644	-11.927
3_Member	GO Cellular Components	GO:0098802	plasma membrane signaling receptor complex	-4.80789	-3.523
4_Summary	GO Cellular Components	GO:0000307	cyclin-dependent protein kinase holoenzyme complex	-22.3586	-20.148
4_Member	GO Cellular Components	GO:0000307	cyclin-dependent protein kinase holoenzyme complex	-22.3586	-20.148
4_Member	GO Cellular Components	GO:1902911	protein kinase complex	-21.5501	-19.384
4_Member	GO Cellular Components	GO:1902554	serine/threonine protein kinase complex	-20.4296	-18.353
4_Member	GO Cellular Components	GO:0061695	transferase complex, transferring	-17.9408	-15.891

			phosphorus-containing groups		
5_Summary	GO Cellular Components	GO:0048471	perinuclear region of cytoplasm	-20.6616	-18.557
5_Member	GO Cellular Components	GO:0048471	perinuclear region of cytoplasm	-20.6616	-18.557
6_Summary	GO Cellular Components	GO:0005813	centrosome	-16.0398	-14.052
6_Member	GO Cellular Components	GO:0005813	centrosome	-16.0398	-14.052
7_Summary	GO Cellular Components	GO:0045177	apical part of cell	-16.0312	-14.052
7_Member	GO Cellular Components	GO:0045177	apical part of cell	-16.0312	-14.052
7_Member	GO Cellular Components	GO:0016324	apical plasma membrane	-12.0819	-10.307
7_Member	GO Cellular Components	GO:0045178	basal part of cell	-7.04516	-5.571
7_Member	GO Cellular Components	GO:0009925	basal plasma membrane	-6.84799	-5.381
7_Member	GO Cellular Components	GO:0016323	basolateral plasma membrane	-5.63003	-4.269
8_Summary	GO Cellular Components	GO:1902710	GABA receptor complex	-13.9842	-12.026
8_Member	GO Cellular Components	GO:1902710	GABA receptor complex	-13.9842	-12.026
8_Member	GO Cellular Components	GO:1902711	GABA-A receptor complex	-11.0186	-9.306
8_Member	GO Cellular Components	GO:0032589	neuron projection membrane	-10.6202	-8.942
8_Member	GO Cellular Components	GO:0098982	GABA-ergic synapse	-10.1384	-8.491
8_Member	GO Cellular Components	GO:0034707	chloride channel complex	-8.5942	-7.013
8_Member	GO Cellular Components	GO:0032590	dendrite membrane	-6.46974	-5.015
9_Summary	GO Cellular Components	GO:0031983	vesicle lumen	-13.7859	-11.867
9_Member	GO Cellular Components	GO:0031983	vesicle lumen	-13.7859	-11.867
9_Member	GO Cellular Components	GO:0060205	cytoplasmic vesicle lumen	-13.0186	-11.170
9_Member	GO Cellular Components	GO:0034774	secretory granule lumen	-12.3328	-10.530
9_Member	GO Cellular Components	GO:1904813	ficolin-1-rich granule lumen	-9.34935	-7.741
9_Member	GO Cellular Components	GO:0101002	ficolin-1-rich granule	-7.61364	-6.081
10_Summary	GO Cellular Components	GO:0150034	distal axon	-13.3654	-11.483
10_Member	GO Cellular Components	GO:0150034	distal axon	-13.3654	-11.483
10_Member	GO Cellular Components	GO:0044306	neuron projection terminus	-11.08	-9.331
10_Member	GO Cellular Components	GO:0043679	axon terminus	-10.024	-8.387
10_Member	GO Cellular Components	GO:0044305	calyx of Held	-6.2535	-4.830

11_Summary	GO Cellular Components	GO:0005667	transcription regulator complex	-12.5224	-10.704
11_Member	GO Cellular Components	GO:0005667	transcription regulator complex	-12.5224	-10.704
11_Member	GO Cellular Components	GO:0090575	RNA polymerase II transcription regulator complex	-6.28449	-4.855
12_Summary	GO Cellular Components	GO:0031253	cell projection membrane	-12.0857	-10.307
12_Member	GO Cellular Components	GO:0031253	cell projection membrane	-12.0857	-10.307
12_Member	GO Cellular Components	GO:0031252	cell leading edge	-10.7703	-9.081
12_Member	GO Cellular Components	GO:0031256	leading edge membrane	-10.3667	-8.710
12_Member	GO Cellular Components	GO:0001726	ruffle	-2.89964	-1.812
12_Member	GO Cellular Components	GO:0032587	ruffle membrane	-2.76702	-1.694
13_Summary	GO Cellular Components	GO:0034702	monoatomic ion channel complex	-11.6148	-9.853
13_Member	GO Cellular Components	GO:0034702	monoatomic ion channel complex	-11.6148	-9.853
13_Member	GO Cellular Components	GO:1902495	transmembrane transporter complex	-8.99091	-7.392
13_Member	GO Cellular Components	GO:1990351	transporter complex	-8.40801	-6.844
13_Member	GO Cellular Components	GO:0034703	cation channel complex	-5.55699	-4.201
13_Member	GO Cellular Components	GO:0008076	voltage-gated potassium channel complex	-2.36171	-1.344
13_Member	GO Cellular Components	GO:0034705	potassium channel complex	-2.11768	-1.138
14_Summary	GO Cellular Components	GO:0000323	lytic vacuole	-11.0353	-9.311
14_Member	GO Cellular Components	GO:0000323	lytic vacuole	-11.0353	-9.311
14_Member	GO Cellular Components	GO:0005764	lysosome	-11.0353	-9.311
14_Member	GO Cellular Components	GO:0005775	vacuolar lumen	-10.5013	-8.834
14_Member	GO Cellular Components	GO:0043202	lysosomal lumen	-5.9993	-4.594
14_Member	GO Cellular Components	GO:0005766	primary lysosome	-5.52095	-4.175
14_Member	GO Cellular Components	GO:0042582	azurophil granule	-5.52095	-4.175
14_Member	GO Cellular Components	GO:0035578	azurophil granule lumen	-4.56551	-3.310
15_Summary	GO Cellular Components	GO:0098552	side of membrane	-10.9833	-9.283
15_Member	GO Cellular Components	GO:0098552	side of membrane	-10.9833	-9.283
15_Member	GO Cellular Components	GO:0009897	external side of plasma membrane	-9.89766	-8.271

16_Summary	GO Cellular Components	GO:0070765	gamma-secretase complex	-9.76566	-8.148
16_Member	GO Cellular Components	GO:0070765	gamma-secretase complex	-9.76566	-8.148
16_Member	GO Cellular Components	GO:0005769	early endosome	-5.76979	-4.382
16_Member	GO Cellular Components	GO:0010008	endosome membrane	-2.67458	-1.614
17_Summary	GO Cellular Components	GO:0031968	organelle outer membrane	-8.6126	-7.022
17_Member	GO Cellular Components	GO:0031968	organelle outer membrane	-8.6126	-7.022
17_Member	GO Cellular Components	GO:0019867	outer membrane	-8.54998	-6.977
17_Member	GO Cellular Components	GO:0005741	mitochondrial outer membrane	-7.27294	-5.763
17_Member	GO Cellular Components	GO:0031966	mitochondrial membrane	-6.30074	-4.865
18_Summary	GO Cellular Components	GO:0099572	postsynaptic specialization	-8.17323	-6.617
18_Member	GO Cellular Components	GO:0099572	postsynaptic specialization	-8.17323	-6.617
18_Member	GO Cellular Components	GO:0032279	asymmetric synapse	-7.15086	-5.656
18_Member	GO Cellular Components	GO:0098984	neuron to neuron synapse	-7.08558	-5.598
18_Member	GO Cellular Components	GO:0014069	postsynaptic density	-5.6344	-4.269
18_Member	GO Cellular Components	GO:0099634	postsynaptic specialization membrane	-4.35841	-3.123
18_Member	GO Cellular Components	GO:0098839	postsynaptic density membrane	-2.79219	-1.713
19_Summary	GO Cellular Components	GO:0008021	synaptic vesicle	-8.15522	-6.607
19_Member	GO Cellular Components	GO:0008021	synaptic vesicle	-8.15522	-6.607
19_Member	GO Cellular Components	GO:0070382	exocytic vesicle	-7.55709	-6.033
19_Member	GO Cellular Components	GO:0030133	transport vesicle	-5.66795	-4.296
19_Member	GO Cellular Components	GO:0030672	synaptic vesicle membrane	-4.12028	-2.908
19_Member	GO Cellular Components	GO:0099501	exocytic vesicle membrane	-4.12028	-2.908
19_Member	GO Cellular Components	GO:0030658	transport vesicle membrane	-3.04045	-1.930
20_Summary	GO Cellular Components	GO:0098685	Schaffer collateral - CA1 synapse	-8.14297	-6.603
20_Member	GO Cellular Components	GO:0098685	Schaffer collateral - CA1 synapse	-8.14297	-6.603

Supplement table 7

Supplementary Table 7 188 signaling pathways of KEGG

GroupID	Category	Term	Description	LogP	Log(q-value)
1_Summary	KEGG Pathway	hsa05200	Pathways in cancer	-83.1829	-80.633
1_Member	KEGG Pathway	hsa05200	Pathways in cancer	-83.1829	-80.633
2_Summary	KEGG Pathway	hsa05417	Lipid and atherosclerosis	-48.8775	-46.628
2_Member	KEGG Pathway	hsa05417	Lipid and atherosclerosis	-48.8775	-46.628
3_Summary	KEGG Pathway	hsa04080	Neuroactive ligand-receptor interaction	-47.6435	-45.570
3_Member	KEGG Pathway	hsa04080	Neuroactive ligand-receptor interaction	-47.6435	-45.570
1_Member	KEGG Pathway	hsa05161	Hepatitis B	-46.2977	-44.350
1_Member	KEGG Pathway	hsa05215	Prostate cancer	-42.5637	-40.712
2_Member	KEGG Pathway	hsa04933	AGE-RAGE signaling pathway in diabetic complications	-41.9316	-40.159
4_Summary	KEGG Pathway	hsa05207	Chemical carcinogenesis - receptor activation	-40.0009	-38.296
4_Member	KEGG Pathway	hsa05207	Chemical carcinogenesis - receptor activation	-40.0009	-38.296
2_Member	KEGG Pathway	hsa05418	Fluid shear stress and atherosclerosis	-39.6747	-38.028
1_Member	KEGG Pathway	hsa05169	Epstein-Barr virus infection	-37.2393	-35.643
3_Member	KEGG Pathway	hsa04020	Calcium signaling pathway	-36.058	-34.508
1_Member	KEGG Pathway	hsa04151	PI3K-Akt signaling pathway	-35.9126	-34.404
1_Member	KEGG Pathway	hsa05223	Non-small cell lung cancer	-35.0485	-33.577
1_Member	KEGG Pathway	hsa05162	Measles	-34.2033	-32.767
1_Member	KEGG Pathway	hsa05166	Human T-cell leukemia virus 1 infection	-34.043	-32.639
5_Summary	KEGG Pathway	hsa04024	cAMP signaling pathway	-33.7711	-32.397
5_Member	KEGG Pathway	hsa04024	cAMP signaling pathway	-33.7711	-32.397
6_Summary	KEGG Pathway	hsa04010	MAPK signaling pathway	-33.4137	-32.068
6_Member	KEGG Pathway	hsa04010	MAPK signaling pathway	-33.4137	-32.068
1_Member	KEGG Pathway	hsa01522	Endocrine resistance	-33.0244	-31.705
1_Member	KEGG Pathway	hsa05163	Human cytomegalovirus infection	-32.5811	-31.292
1_Member	KEGG Pathway	hsa05222	Small cell lung cancer	-32.5631	-31.292
1_Member	KEGG Pathway	hsa04218	Cellular senescence	-31.9931	-30.744
1_Member	KEGG Pathway	hsa05167	Kaposi sarcoma-associated herpesvirus infection	-31.8106	-30.583

2_Member	KEGG Pathway	hsa04210	Apoptosis	-31.7408	-30.533
6_Member	KEGG Pathway	hsa04066	HIF-1 signaling pathway	-31.2737	-30.085
7_Summary	KEGG Pathway	hsa05032	Morphine addiction	-31.2306	-30.061
7_Member	KEGG Pathway	hsa05032	Morphine addiction	-31.2306	-30.061
1_Member	KEGG Pathway	hsa05212	Pancreatic cancer	-30.941	-29.789
4_Member	KEGG Pathway	hsa05208	Chemical carcinogenesis - reactive oxygen species	-30.4068	-29.272
1_Member	KEGG Pathway	hsa05205	Proteoglycans in cancer	-28.4304	-27.311
1_Member	KEGG Pathway	hsa05160	Hepatitis C	-27.9574	-26.854
1_Member	KEGG Pathway	hsa05220	Chronic myeloid leukemia	-27.84	-26.752
2_Member	KEGG Pathway	hsa04668	TNF signaling pathway	-27.7898	-26.717
1_Member	KEGG Pathway	hsa05219	Bladder cancer	-27.7721	-26.713
1_Member	KEGG Pathway	hsa05203	Viral carcinogenesis	-27.3548	-26.310
8_Summary	KEGG Pathway	hsa05010	Alzheimer disease	-27.288	-26.256
8_Member	KEGG Pathway	hsa05010	Alzheimer disease	-27.288	-26.256
9_Summary	KEGG Pathway	hsa04750	Inflammatory mediator regulation of TRP channels	-27.2139	-26.195
9_Member	KEGG Pathway	hsa04750	Inflammatory mediator regulation of TRP channels	-27.2139	-26.195
10_Summary	KEGG Pathway	hsa04068	FoxO signaling pathway	-27.047	-26.041
10_Member	KEGG Pathway	hsa04068	FoxO signaling pathway	-27.047	-26.041
1_Member	KEGG Pathway	hsa05225	Hepatocellular carcinoma	-26.9792	-25.985
1_Member	KEGG Pathway	hsa04110	Cell cycle	-26.8187	-25.837
2_Member	KEGG Pathway	hsa05142	Chagas disease	-26.6498	-25.679
2_Member	KEGG Pathway	hsa04657	IL-17 signaling pathway	-26.3828	-25.424
11_Summary	KEGG Pathway	hsa04931	Insulin resistance	-25.8532	-24.905
11_Member	KEGG Pathway	hsa04931	Insulin resistance	-25.8532	-24.905
12_Summary	KEGG Pathway	hsa04919	Thyroid hormone signaling pathway	-25.5953	-24.658
12_Member	KEGG Pathway	hsa04919	Thyroid hormone signaling pathway	-25.5953	-24.658
1_Member	KEGG Pathway	hsa05206	MicroRNAs in cancer	-25.4586	-24.532
10_Member	KEGG Pathway	hsa04914	Progesterone-mediated oocyte maturation	-25.2749	-24.358
2_Member	KEGG Pathway	hsa05135	Yersinia infection	-25.1162	-24.209
1_Member	KEGG Pathway	hsa05214	Glioma	-25.0071	-24.120
2_Member	KEGG Pathway	hsa04625	C-type lectin receptor signaling pathway	-25.0147	-24.120
13_Summary	KEGG Pathway	hsa04726	Serotonergic synapse	-24.9899	-24.112
13_Member	KEGG Pathway	hsa04726	Serotonergic synapse	-24.9899	-24.112

8_Member	KEGG Pathway	hsa05022	Pathways of neurodegeneration - multiple diseases	-24.7994	-23.930
12_Member	KEGG Pathway	hsa01521	EGFR tyrosine kinase inhibitor resistance	-24.3579	-23.498
2_Member	KEGG Pathway	hsa04660	T cell receptor signaling pathway	-24.2996	-23.448
1_Member	KEGG Pathway	hsa05165	Human papillomavirus infection	-24.2889	-23.446
12_Member	KEGG Pathway	hsa04510	Focal adhesion	-24.0382	-23.204
1_Member	KEGG Pathway	hsa05226	Gastric cancer	-23.9292	-23.103
14_Summary	KEGG Pathway	hsa05202	Transcriptional misregulation in cancer	-23.6836	-22.866
14_Member	KEGG Pathway	hsa05202	Transcriptional misregulation in cancer	-23.6836	-22.866
12_Member	KEGG Pathway	hsa04012	ErbB signaling pathway	-23.4579	-22.648
2_Member	KEGG Pathway	hsa04620	Toll-like receptor signaling pathway	-23.1926	-22.398
2_Member	KEGG Pathway	hsa04659	Th17 cell differentiation	-23.1926	-22.398
2_Member	KEGG Pathway	hsa05164	Influenza A	-23.1686	-22.382
2_Member	KEGG Pathway	hsa04071	Sphingolipid signaling pathway	-23.024	-22.245
6_Member	KEGG Pathway	hsa04014	Ras signaling pathway	-22.8149	-22.043
12_Member	KEGG Pathway	hsa04062	Chemokine signaling pathway	-22.6456	-21.881
1_Member	KEGG Pathway	hsa04115	p53 signaling pathway	-22.2485	-21.491
1_Member	KEGG Pathway	hsa05210	Colorectal cancer	-21.9316	-21.181
12_Member	KEGG Pathway	hsa05230	Central carbon metabolism in cancer	-21.4267	-20.683
1_Member	KEGG Pathway	hsa05218	Melanoma	-21.1211	-20.384
11_Member	KEGG Pathway	hsa05415	Diabetic cardiomyopathy	-20.7798	-20.049
2_Member	KEGG Pathway	hsa04722	Neurotrophin signaling pathway	-20.7329	-20.009
1_Member	KEGG Pathway	hsa05224	Breast cancer	-20.5567	-19.839
12_Member	KEGG Pathway	hsa05221	Acute myeloid leukemia	-20.4506	-19.739
2_Member	KEGG Pathway	hsa04380	Osteoclast differentiation	-20.4296	-19.724
2_Member	KEGG Pathway	hsa05145	Toxoplasmosis	-20.3046	-19.606
15_Summary	KEGG Pathway	hsa04915	Estrogen signaling pathway	-20.252	-19.559
15_Member	KEGG Pathway	hsa04915	Estrogen signaling pathway	-20.252	-19.559
2_Member	KEGG Pathway	hsa05152	Tuberculosis	-20.2318	-19.545

2_Member	KEGG Pathway	hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	-20.1989	-19.518
2_Member	KEGG Pathway	hsa05170	Human immunodeficiency virus 1 infection	-20.1885	-19.513
2_Member	KEGG Pathway	hsa04917	Prolactin signaling pathway	-19.9984	-19.329
16_Summary	KEGG Pathway	hsa00140	Steroid hormone biosynthesis	-19.7898	-19.126
16_Member	KEGG Pathway	hsa00140	Steroid hormone biosynthesis	-19.7898	-19.126
2_Member	KEGG Pathway	hsa04926	Relaxin signaling pathway	-19.7837	-19.126
12_Member	KEGG Pathway	hsa04072	Phospholipase D signaling pathway	-19.3274	-18.675
17_Summary	KEGG Pathway	hsa04022	cGMP-PKG signaling pathway	-18.9913	-18.344
17_Member	KEGG Pathway	hsa04022	cGMP-PKG signaling pathway	-18.9913	-18.344
2_Member	KEGG Pathway	hsa04936	Alcoholic liver disease	-18.6742	-18.032
18_Summary	KEGG Pathway	hsa04064	NF-kappa B signaling pathway	-18.5345	-17.898
18_Member	KEGG Pathway	hsa04064	NF-kappa B signaling pathway	-18.5345	-17.898
1_Member	KEGG Pathway	hsa01524	Platinum drug resistance	-18.1964	-17.565
19_Summary	KEGG Pathway	hsa04540	Gap junction	-17.7103	-17.084
19_Member	KEGG Pathway	hsa04540	Gap junction	-17.7103	-17.084
2_Member	KEGG Pathway	hsa04932	Non-alcoholic fatty liver disease	-17.6803	-17.059
7_Member	KEGG Pathway	hsa04727	GABAergic synapse	-17.6003	-16.985
1_Member	KEGG Pathway	hsa05213	Endometrial cancer	-17.5249	-16.914
12_Member	KEGG Pathway	hsa04664	Fc epsilon RI signaling pathway	-17.4954	-16.890
12_Member	KEGG Pathway	hsa04370	VEGF signaling pathway	-17.3737	-16.773
2_Member	KEGG Pathway	hsa05131	Shigellosis	-17.1925	-16.596
7_Member	KEGG Pathway	hsa04723	Retrograde endocannabinoid signaling	-17.0983	-16.507
2_Member	KEGG Pathway	hsa05132	Salmonella infection	-17.0905	-16.504
2_Member	KEGG Pathway	hsa05171	Coronavirus disease - COVID-19	-17.022	-16.440
11_Member	KEGG Pathway	hsa04930	Type II diabetes mellitus	-16.5543	-15.977
2_Member	KEGG Pathway	hsa05133	Pertussis	-16.4931	-15.921
20_Summary	KEGG Pathway	hsa05140	Leishmaniasis	-16.3769	-15.809
20_Member	KEGG Pathway	hsa05140	Leishmaniasis	-16.3769	-15.809
20_Member	KEGG Pathway	hsa05146	Amoebiasis	-16.2933	-15.730

12_Member	KEGG Pathway	hsa04015	Rap1 signaling pathway	-16.2776	-15.719
2_Member	KEGG Pathway	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	-15.8952	-15.341
1_Member	KEGG Pathway	hsa04630	JAK-STAT signaling pathway	-15.8693	-15.319
2_Member	KEGG Pathway	hsa04621	NOD-like receptor signaling pathway	-15.6661	-15.120
20_Member	KEGG Pathway	hsa05143	African trypanosomiasis	-15.1612	-14.620
18_Member	KEGG Pathway	hsa05134	Legionellosis	-14.9995	-14.462
11_Member	KEGG Pathway	hsa04910	Insulin signaling pathway	-14.6388	-14.110
2_Member	KEGG Pathway	hsa05130	Pathogenic Escherichia coli infection	-14.0363	-13.511
19_Member	KEGG Pathway	hsa04270	Vascular smooth muscle contraction	-13.7824	-13.266
9_Member	KEGG Pathway	hsa04912	GnRH signaling pathway	-13.5563	-13.043
1_Member	KEGG Pathway	hsa04934	Cushing syndrome	-13.4888	-12.980
2_Member	KEGG Pathway	hsa04920	Adipocytokine signaling pathway	-13.4264	-12.925
12_Member	KEGG Pathway	hsa05231	Choline metabolism in cancer	-13.1396	-12.646
20_Member	KEGG Pathway	hsa05144	Malaria	-13.0636	-12.574
12_Member	KEGG Pathway	hsa04935	Growth hormone synthesis, secretion and action	-12.6123	-12.126
12_Member	KEGG Pathway	hsa04613	Neutrophil extracellular trap formation	-12.5189	-12.048
2_Member	KEGG Pathway	hsa04658	Th1 and Th2 cell differentiation	-12.4893	-12.022
12_Member	KEGG Pathway	hsa04666	Fc gamma R-mediated phagocytosis	-12.0953	-11.638
12_Member	KEGG Pathway	hsa04662	B cell receptor signaling pathway	-12.0056	-11.552
18_Member	KEGG Pathway	hsa01523	Antifolate resistance	-11.8548	-11.405
8_Member	KEGG Pathway	hsa05020	Prion disease	-11.707	-11.261
7_Member	KEGG Pathway	hsa05033	Nicotine addiction	-11.6811	-11.238
12_Member	KEGG Pathway	hsa04611	Platelet activation	-11.3192	-10.883
20_Member	KEGG Pathway	hsa05323	Rheumatoid arthritis	-11.2918	-10.859
11_Member	KEGG Pathway	hsa04140	Autophagy - animal	-11.0201	-10.590
12_Member	KEGG Pathway	hsa04725	Cholinergic synapse	-10.9812	-10.555
12_Member	KEGG Pathway	hsa04650	Natural killer cell mediated cytotoxicity	-10.8496	-10.426
9_Member	KEGG Pathway	hsa04921	Oxytocin signaling pathway	-10.6369	-10.217

19_Member	KEGG Pathway	hsa04730	Long-term depression	-10.6202	-10.204
8_Member	KEGG Pathway	hsa05012	Parkinson disease	-10.3254	-9.921
16_Member	KEGG Pathway	hsa04913	Ovarian steroidogenesis	-10.3019	-9.901
12_Member	KEGG Pathway	hsa04929	GnRH secretion	-10.2421	-9.844
20_Member	KEGG Pathway	hsa05321	Inflammatory bowel disease	-10.152	-9.757
19_Member	KEGG Pathway	hsa04720	Long-term potentiation	-9.97658	-9.585
10_Member	KEGG Pathway	hsa04114	Oocyte meiosis	-9.93422	-9.545
12_Member	KEGG Pathway	hsa04670	Leukocyte transendothelial migration	-9.84744	-9.462
12_Member	KEGG Pathway	hsa05211	Renal cell carcinoma	-9.80734	-9.424
2_Member	KEGG Pathway	hsa04622	RIG-I-like receptor signaling pathway	-9.64385	-9.267
11_Member	KEGG Pathway	hsa05017	Spinocerebellar ataxia	-9.32812	-8.957
12_Member	KEGG Pathway	hsa04150	mTOR signaling pathway	-8.73754	-8.372
17_Member	KEGG Pathway	hsa04371	Apelin signaling pathway	-8.60909	-8.252
7_Member	KEGG Pathway	hsa04742	Taste transduction	-8.57007	-8.216
19_Member	KEGG Pathway	hsa04970	Salivary secretion	-8.14297	-7.800
12_Member	KEGG Pathway	hsa04360	Axon guidance	-7.71943	-7.389
8_Member	KEGG Pathway	hsa05016	Huntington disease	-7.02116	-6.704
19_Member	KEGG Pathway	hsa04724	Glutamatergic synapse	-7.0172	-6.702
12_Member	KEGG Pathway	hsa04960	Aldosterone-regulated sodium reabsorption	-6.74939	-6.440
19_Member	KEGG Pathway	hsa04972	Pancreatic secretion	-6.71613	-6.409
12_Member	KEGG Pathway	hsa04810	Regulation of actin cytoskeleton	-6.27416	-5.972
18_Member	KEGG Pathway	hsa04623	Cytosolic DNA-sensing pathway	-6.20609	-5.909
20_Member	KEGG Pathway	hsa04061	Viral protein interaction with cytokine and cytokine receptor	-5.91092	-5.618
19_Member	KEGG Pathway	hsa04916	Melanogenesis	-5.86753	-5.580
19_Member	KEGG Pathway	hsa04971	Gastric acid secretion	-5.20734	-4.931
19_Member	KEGG Pathway	hsa04713	Circadian entrainment	-5.17121	-4.897
2_Member	KEGG Pathway	hsa05168	Herpes simplex virus 1 infection	-4.96638	-4.695
12_Member	KEGG Pathway	hsa04973	Carbohydrate digestion and absorption	-4.83438	-4.567
20_Member	KEGG Pathway	hsa04060	Cytokine-cytokine receptor interaction	-4.75639	-4.494
12_Member	KEGG Pathway	hsa04550	Signaling pathways regulating pluripotency of stem cells	-4.41279	-4.157
20_Member	KEGG Pathway	hsa05330	Allograft rejection	-4.3661	-4.115

19_Member	KEGG Pathway	hsa04918	Thyroid hormone synthesis	-4.35673	-4.108
20_Member	KEGG Pathway	hsa04640	Hematopoietic cell lineage	-4.2739	-4.029
8_Member	KEGG Pathway	hsa05014	Amyotrophic lateral sclerosis	-4.16504	-3.922
20_Member	KEGG Pathway	hsa05332	Graft-versus-host disease	-4.11251	-3.874
19_Member	KEGG Pathway	hsa04911	Insulin secretion	-3.9305	-3.696
19_Member	KEGG Pathway	hsa04925	Aldosterone synthesis and secretion	-3.53605	-3.306
12_Member	KEGG Pathway	hsa05100	Bacterial invasion of epithelial cells	-3.444	-3.216
20_Member	KEGG Pathway	hsa04940	Type I diabetes mellitus	-3.08525	-2.875
12_Member	KEGG Pathway	hsa04070	Phosphatidylinositol signaling system	-2.84354	-2.640
20_Member	KEGG Pathway	hsa04672	Intestinal immune network for IgA production	-2.82494	-2.623
20_Member	KEGG Pathway	hsa05310	Asthma	-2.72819	-2.532
19_Member	KEGG Pathway	hsa04961	Endocrine and other factor-regulated calcium reabsorption	-2.67176	-2.479