

## Supporting Information

### Isolation of oligostilbenes from *Iris lactea* Pall. var. *chinensis* (Fisch.)

#### Koidz and their anti-inflammatory activities

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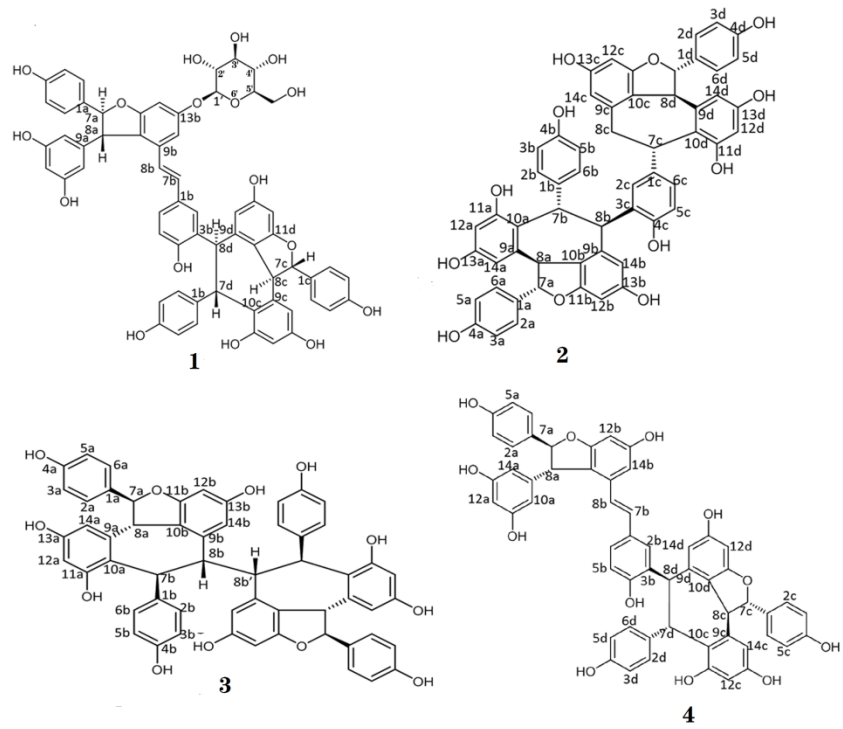


Figure S1. Chemical structures of isolated oligostilbenes from seeds of *Iris lactea*.

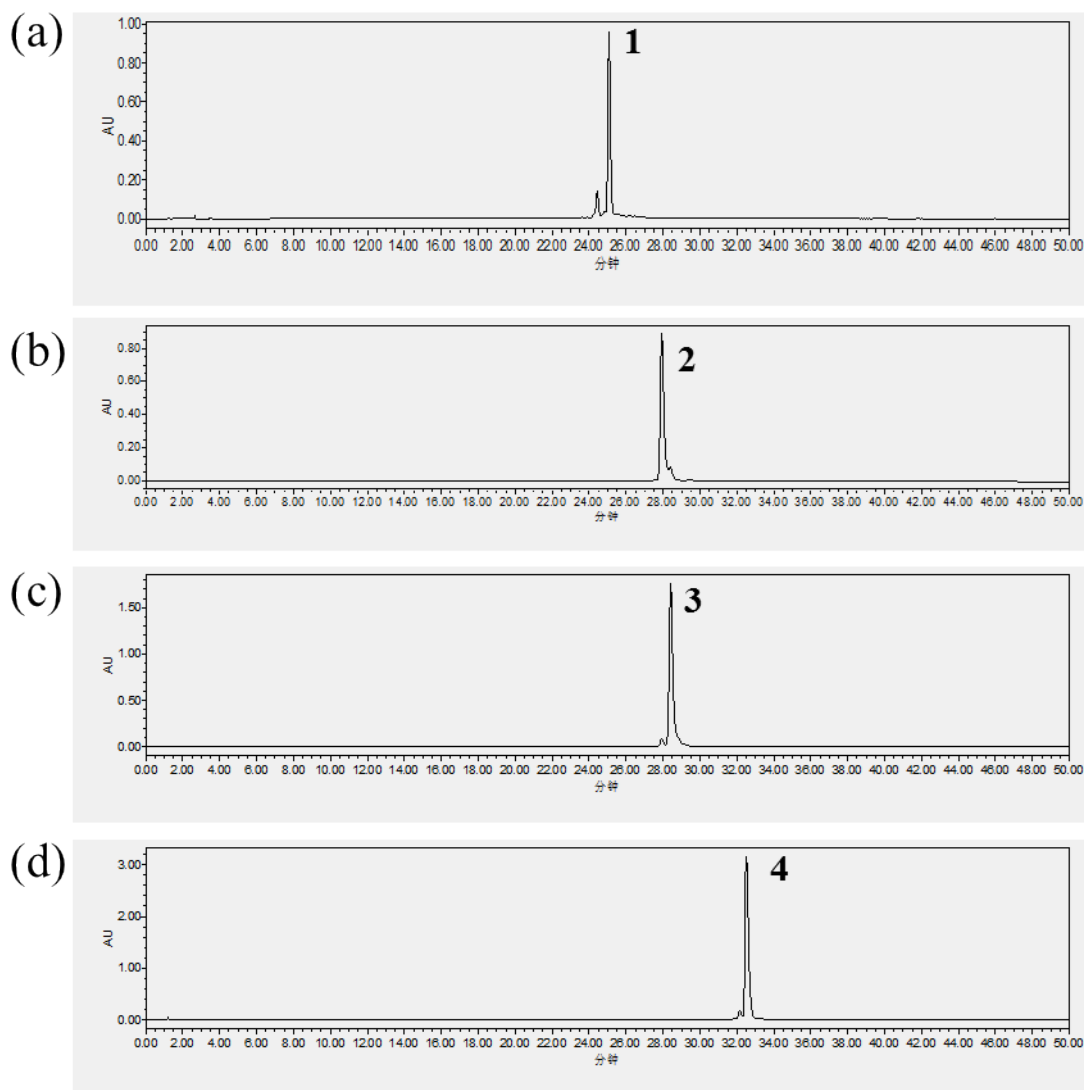


Figure S2. The purity HPLC chromatograms of compounds 1, 2, 3 and 4

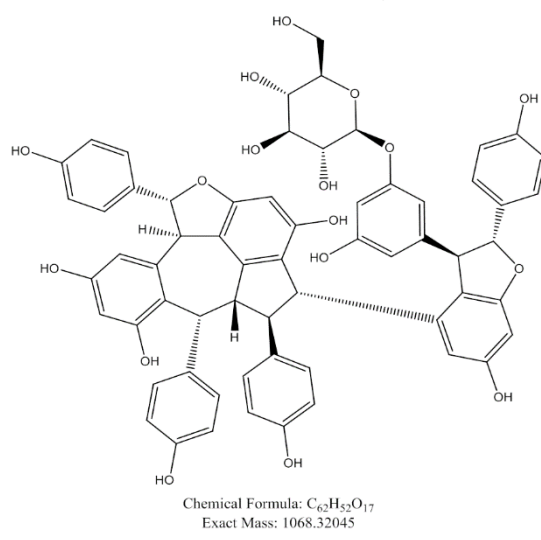
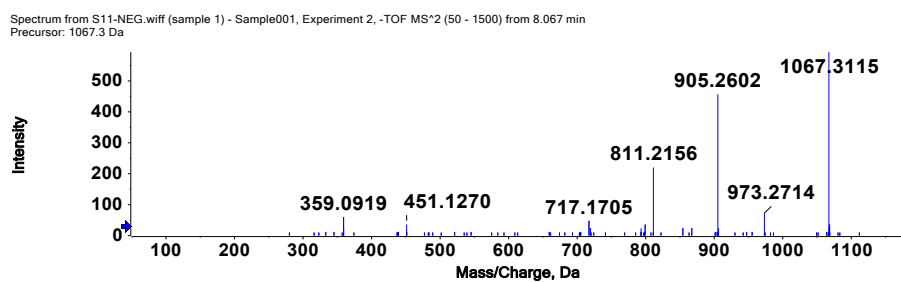
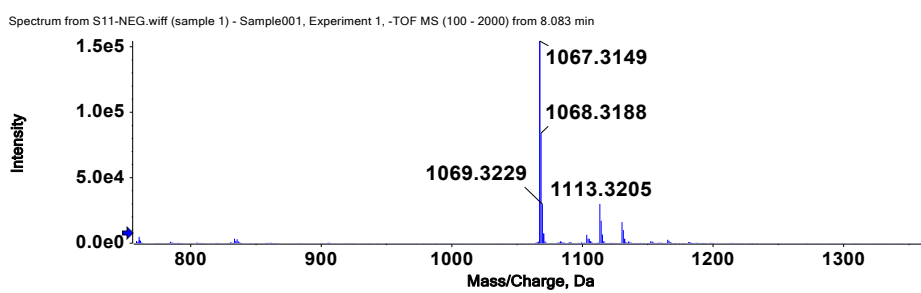


Figure S3 The primary and secondary mass spectra and chemical structure of the impurity

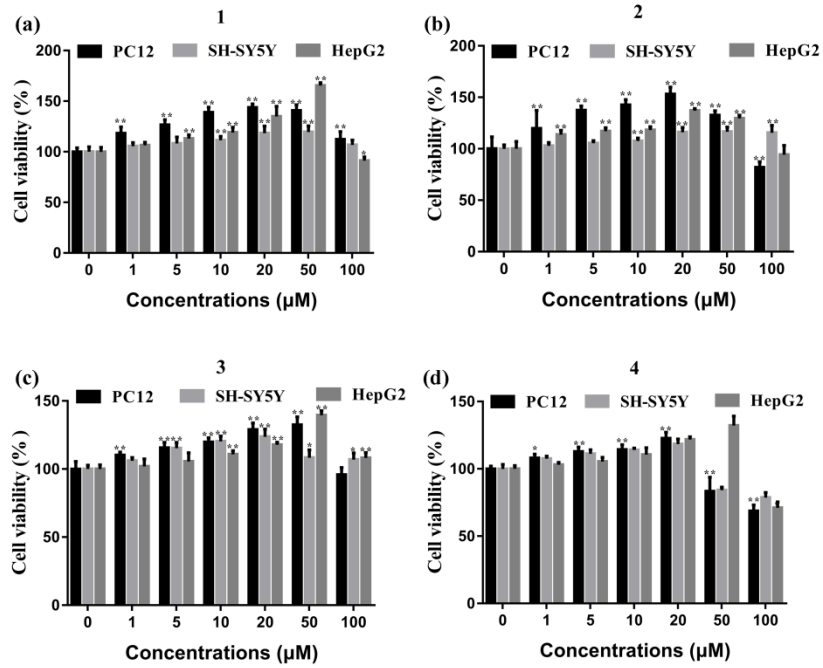


Figure S4. The effects of compounds 1, 2, 3 and 4 on the viability of cells *in vitro*. (a) The effects of compound 1 on the viability cells (PC12, SH-SY5Y and HepG2), (b) The effects of compound 2 on the viability cells (PC12, SH-SY5Y and HepG2), (c) The effects of compound 3 on the viability cells (PC12, SH-SY5Y and HepG2), (d) The effects of compound 4 on the viability cells (PC12, SH-SY5Y and HepG2). \* $P < 0.05$  and \*\* $P < 0.01$  compared to the control group.

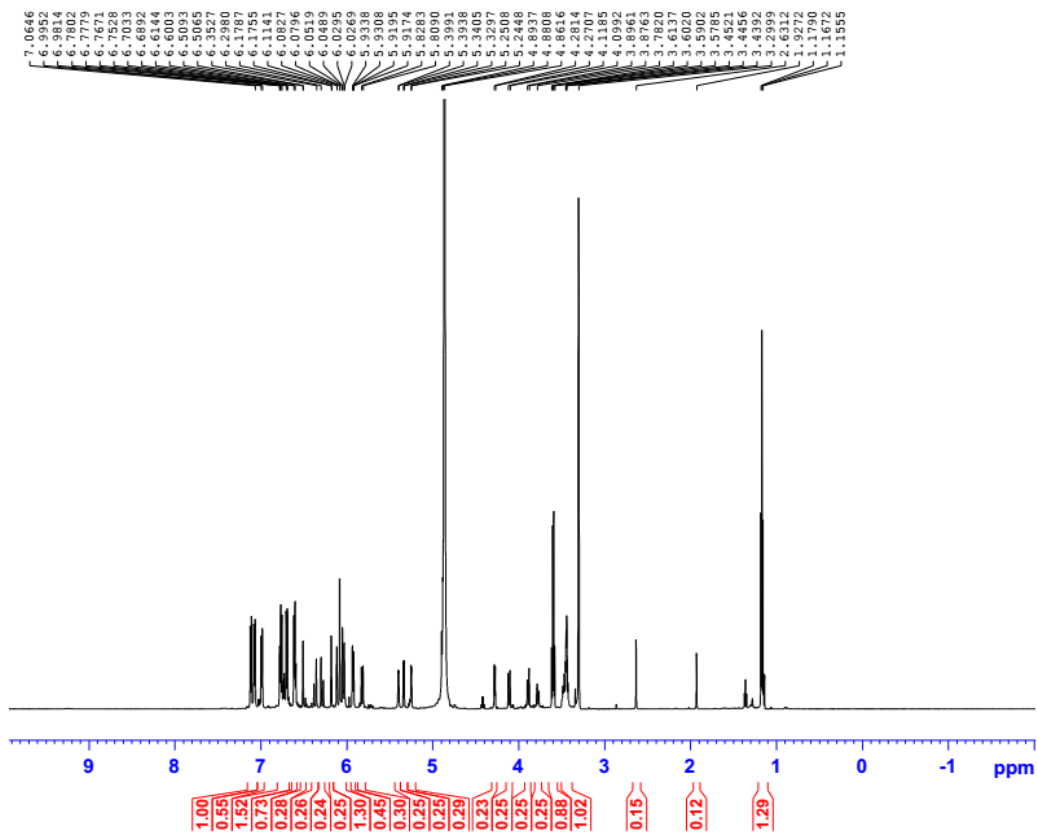


Figure S5. The  $^1\text{H}$ -NMR chromatography of compound 1

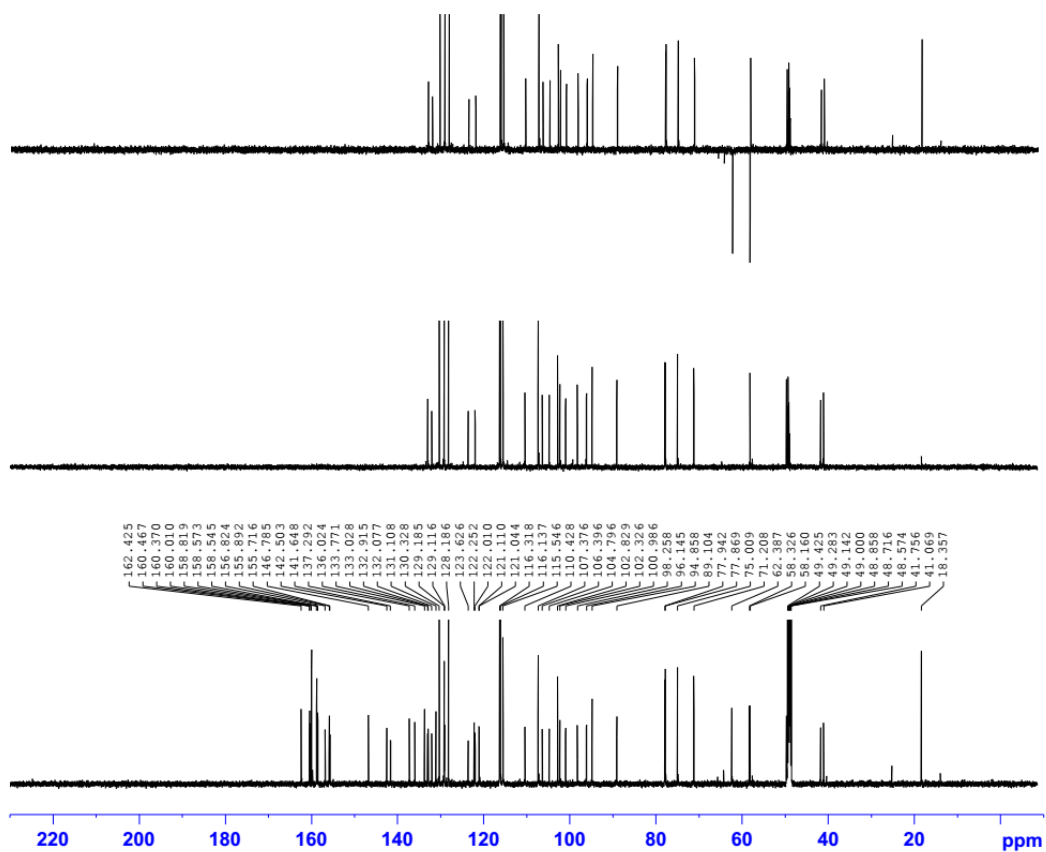


Figure S6. The  $^{13}\text{C}$ -NMR and DEPT chromatography of compound 1



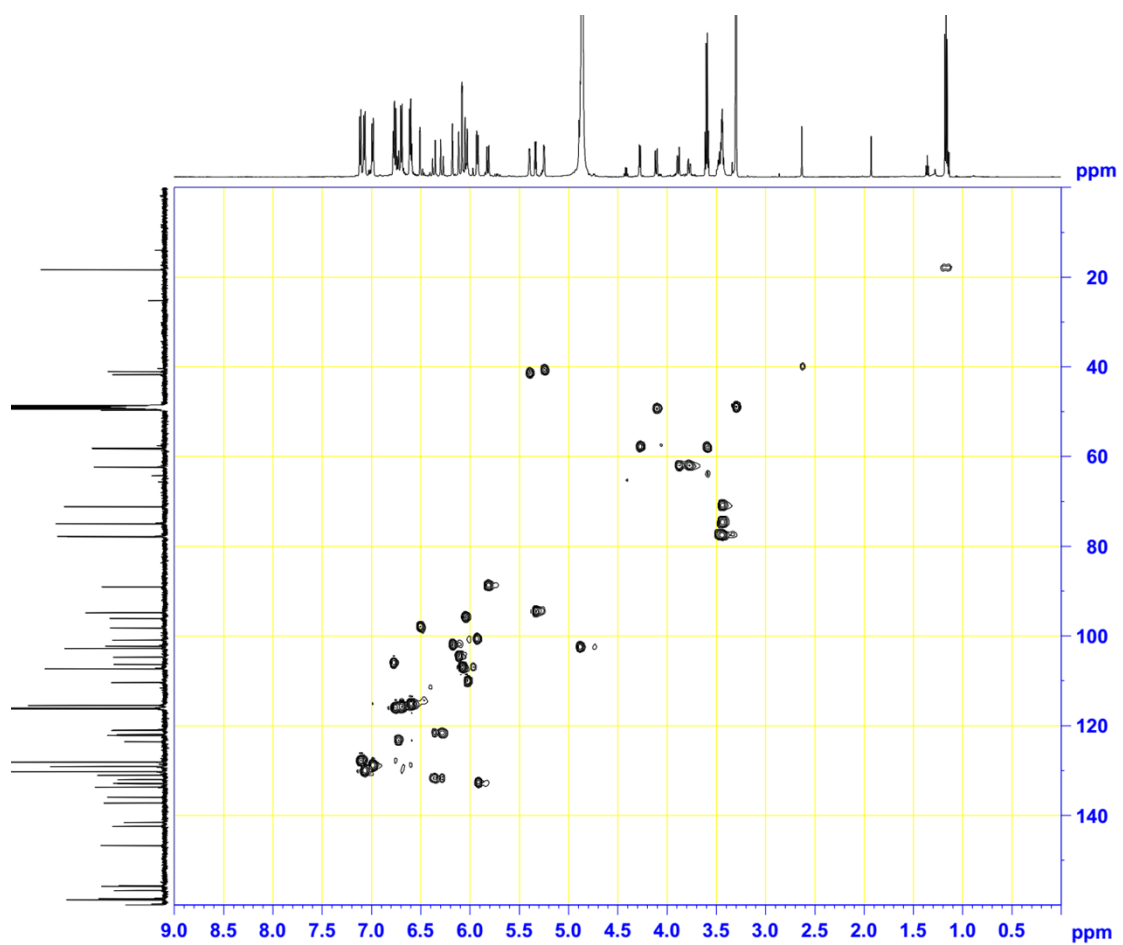


Figure S7. The HSQC chromatography of compound 1

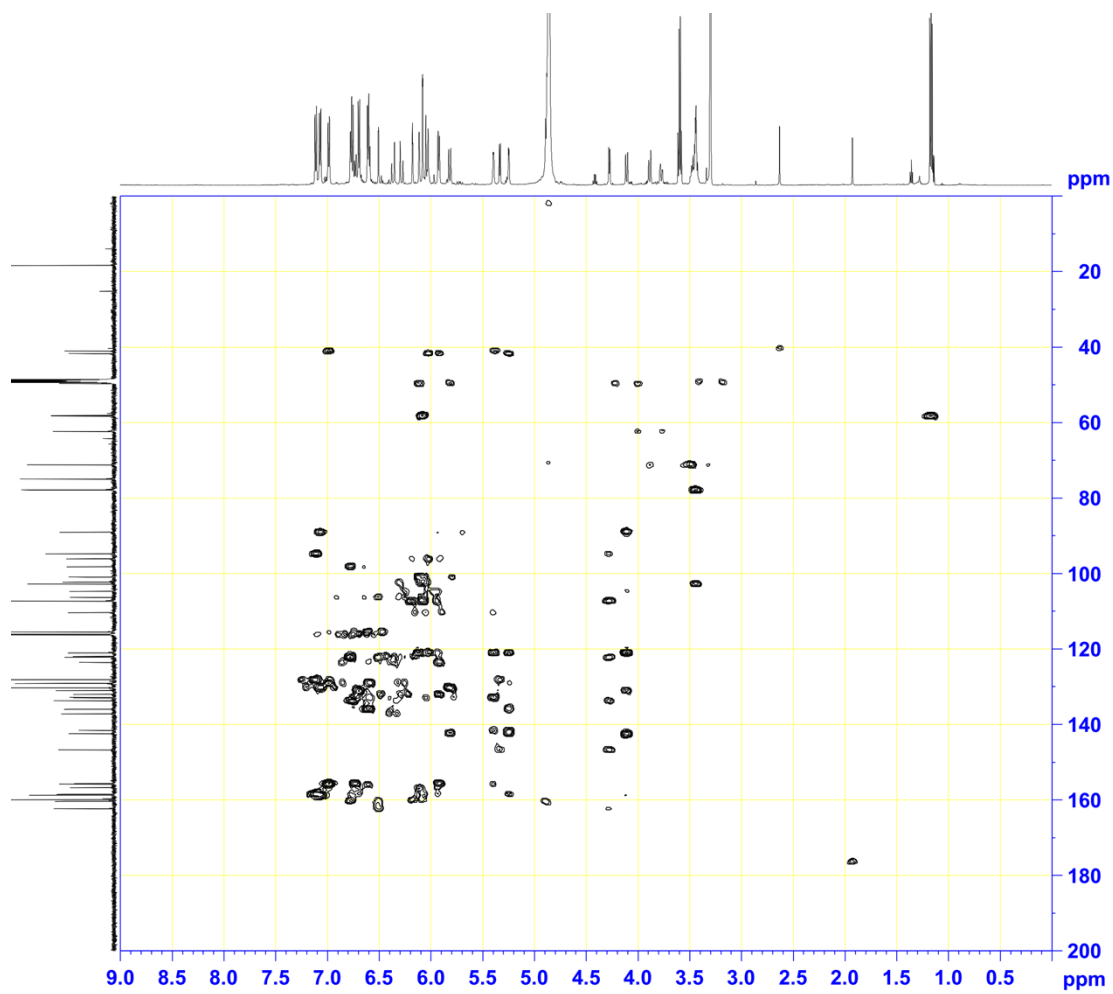


Figure S8. The HMBC chromatography of compound 1

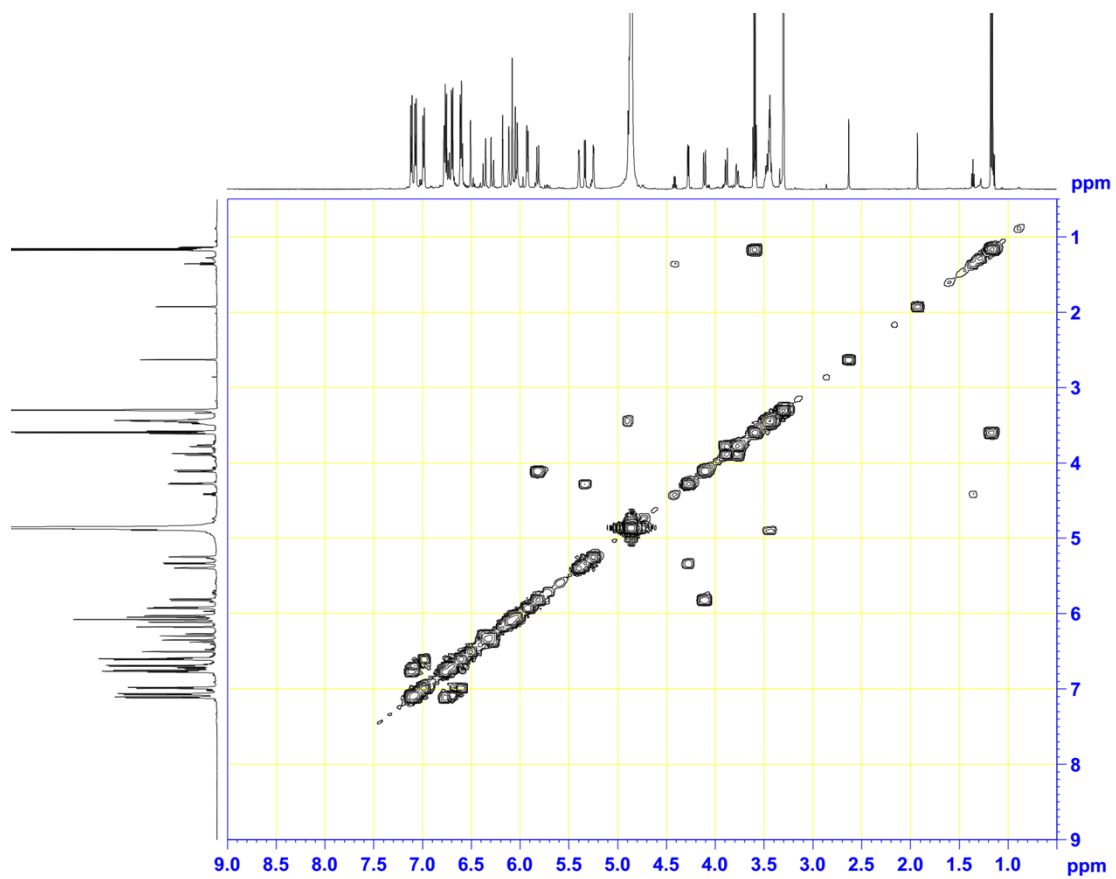


Figure S9. The H-H COSY chromatography of compound 1

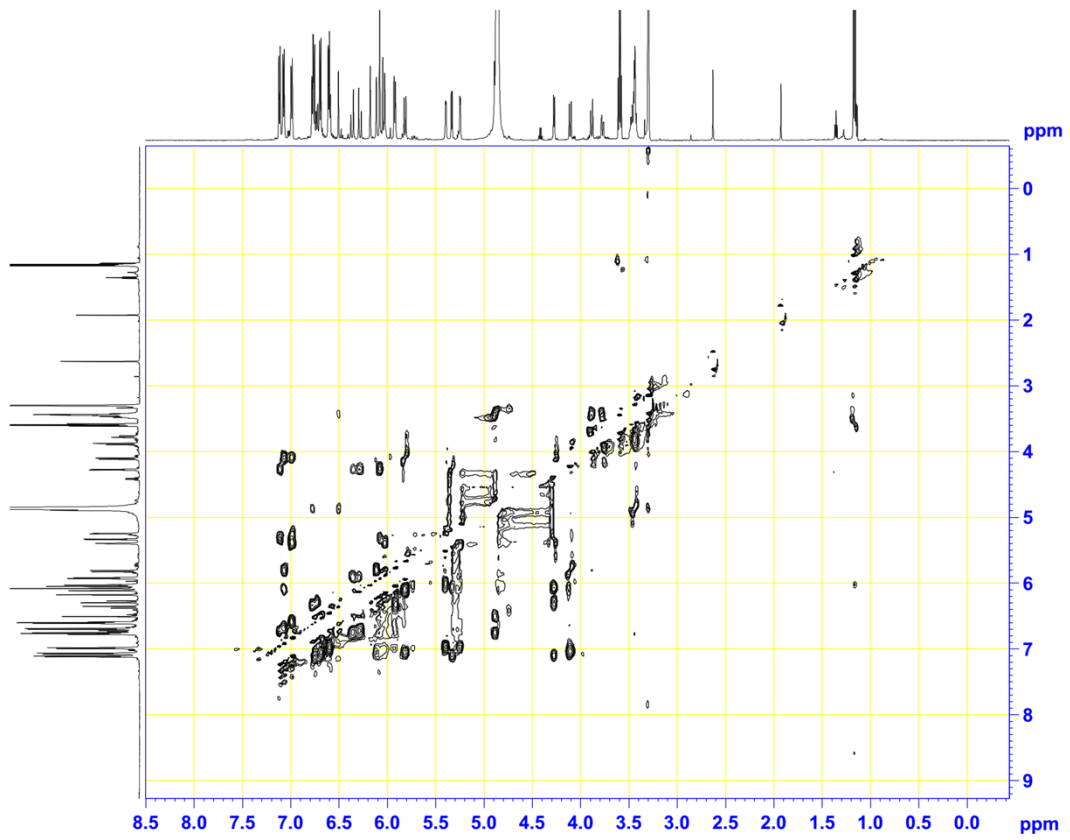
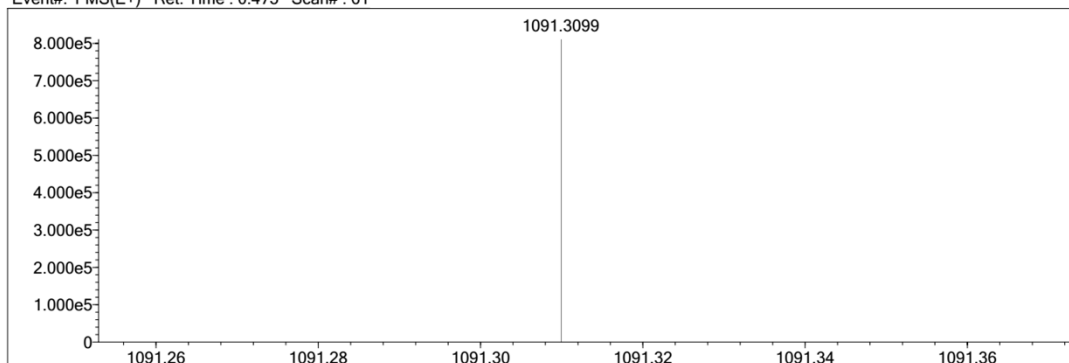
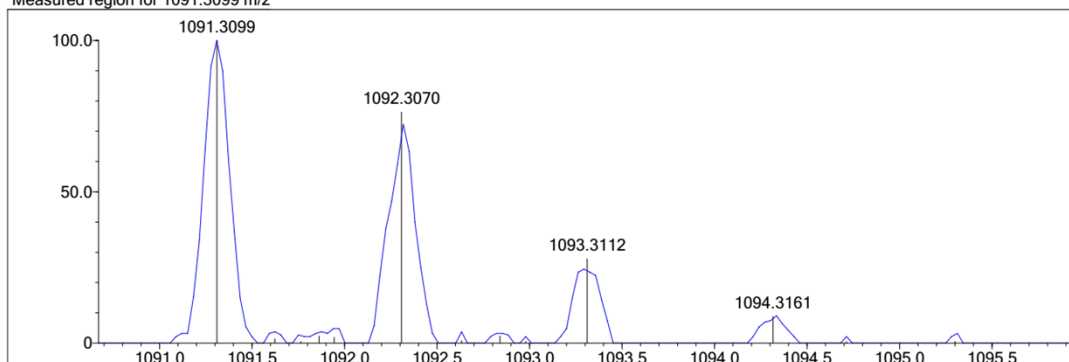


Figure S10. The ROESY chromatography of compound 1

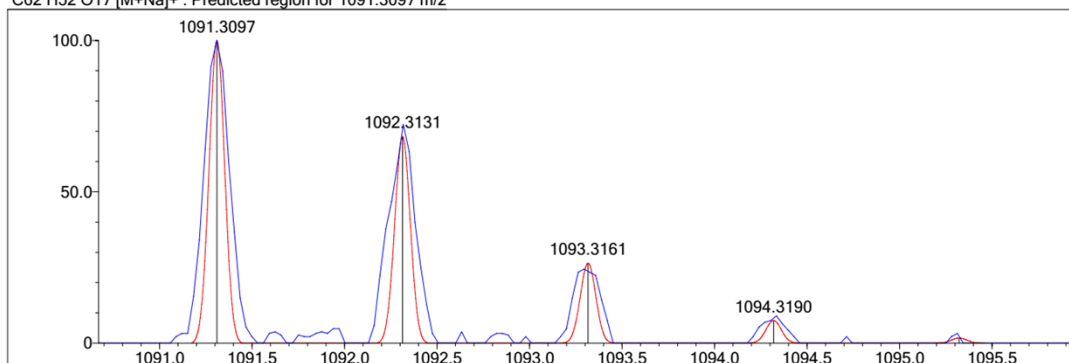
Event#: 1 MS(E+) Ret. Time : 0.475 Scan#: 61



Measured region for 1091.3099 m/z



C62 H52 O17 [M+Na]<sup>+</sup> : Predicted region for 1091.3097 m/z



Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	DBE
C62 H52 O17	[M+Na] <sup>+</sup>	1091.3099	1091.3097	0.2	0.18	37.0

Figure S11. The HR-ESI mass spectrum of compound 1

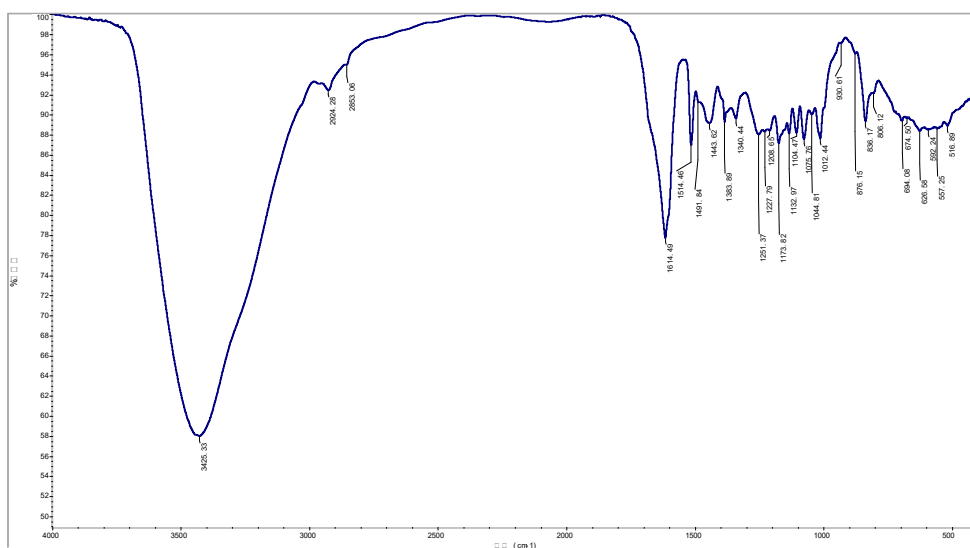


Figure S12. Experimental IR Spectrum of compound 1

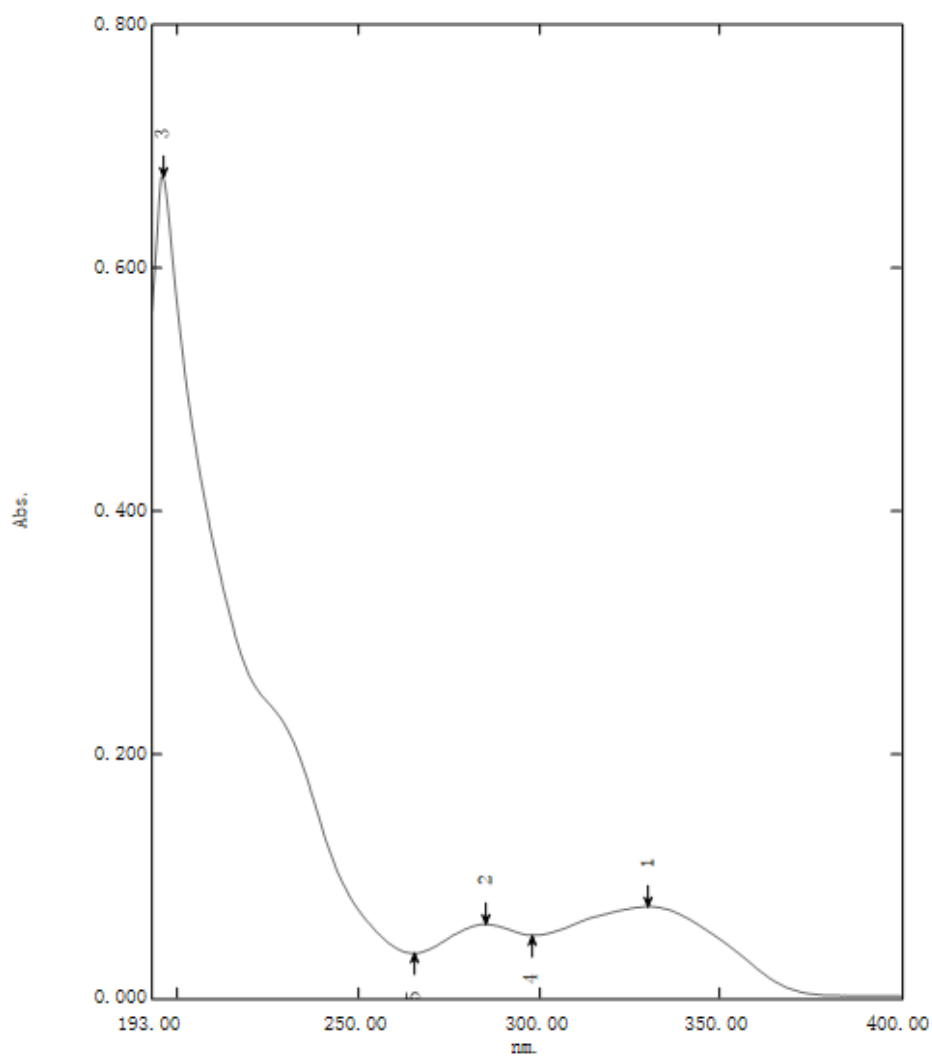


Figure S13. Experimental UV Spectrum of compound 1

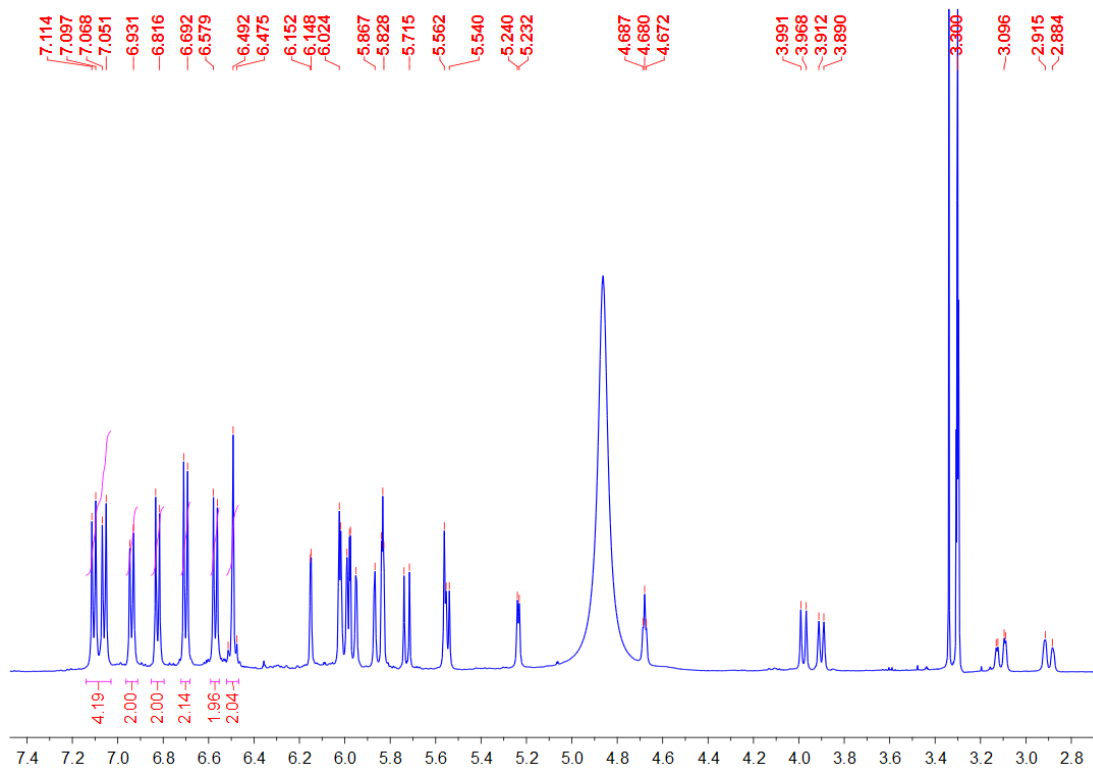


Figure S14. The  $^1\text{H}$ -NMR chromatography of compound 2

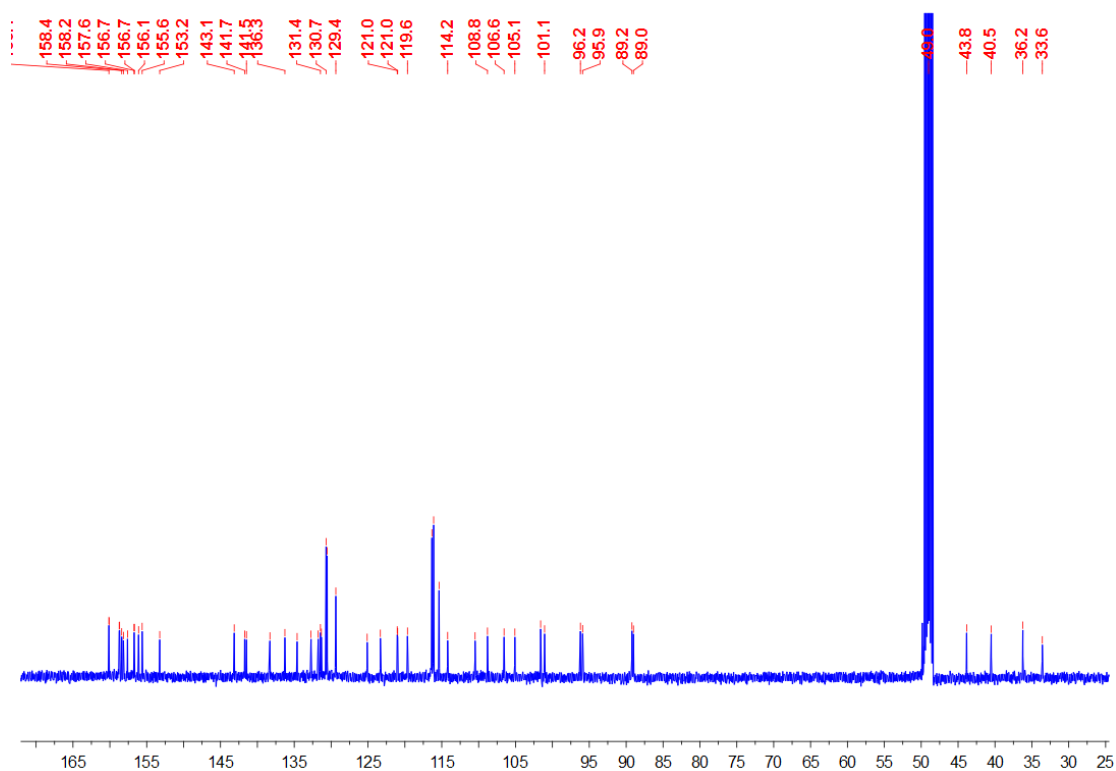


Figure S15. The  $^{13}\text{C}$ -NMR chromatography of compound 2

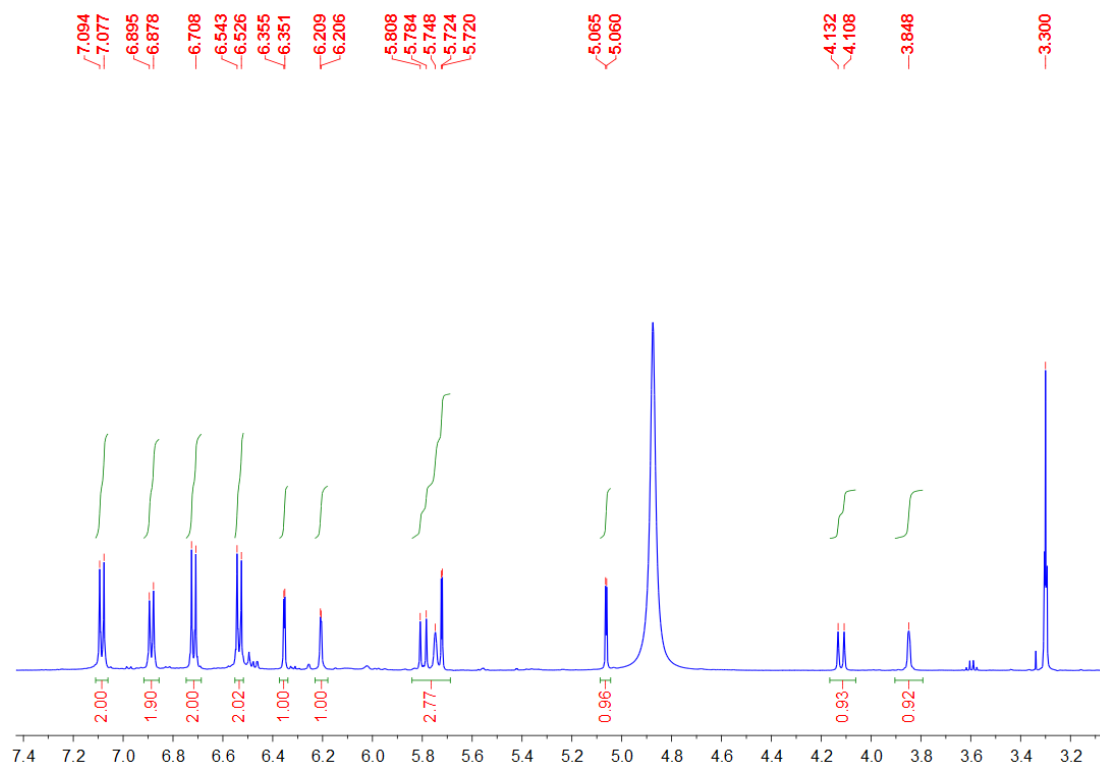


Figure S16. The  $^1\text{H}$ -NMR chromatography of compound 3

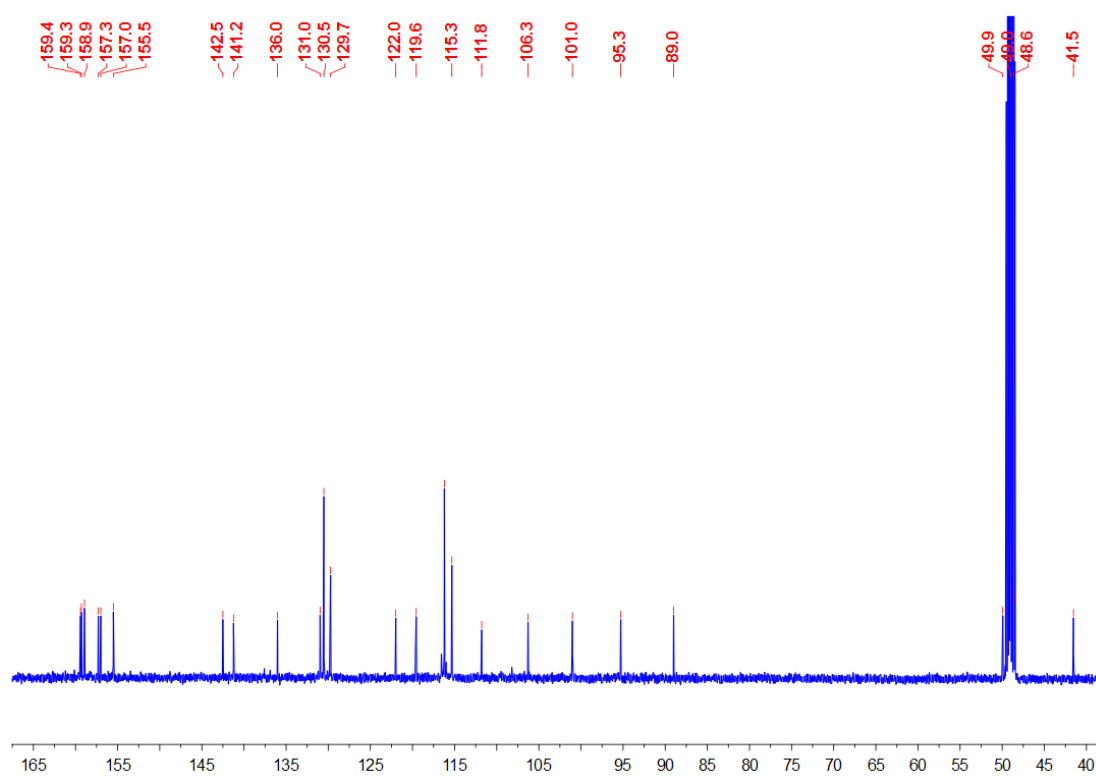


Figure S17. The  $^{13}\text{C}$ -NMR chromatography of compound 3



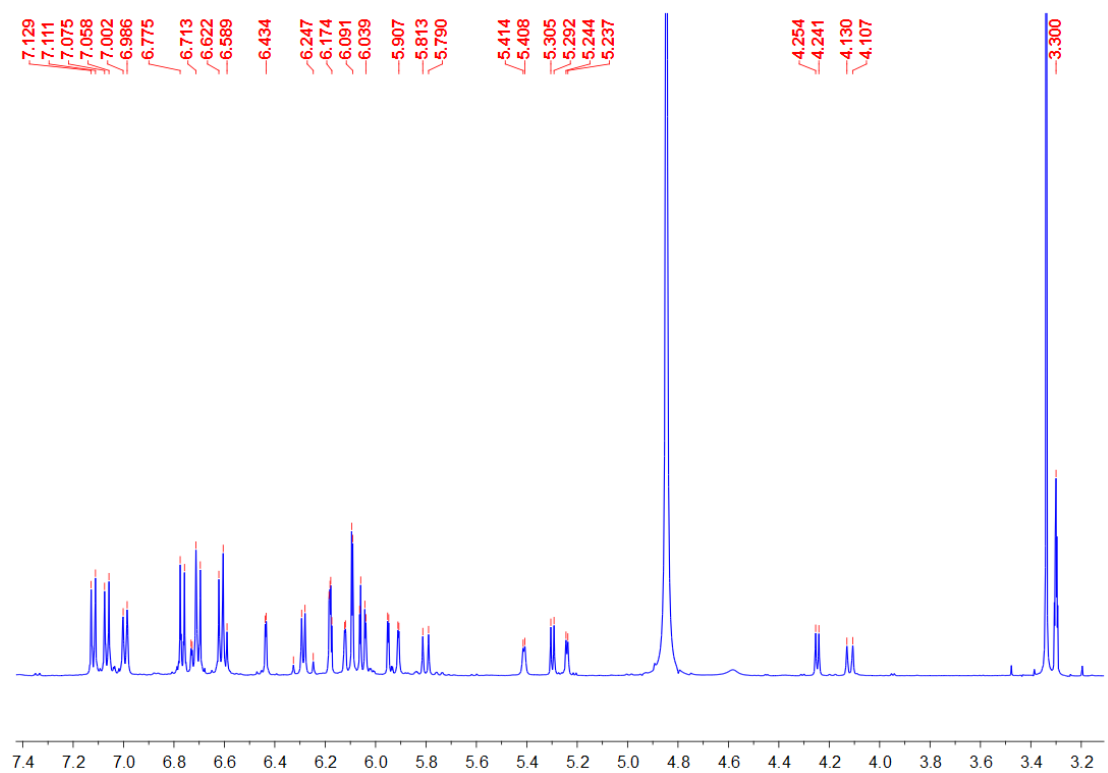


Figure S18. The  $^1\text{H-NMR}$  chromatography of compound 4

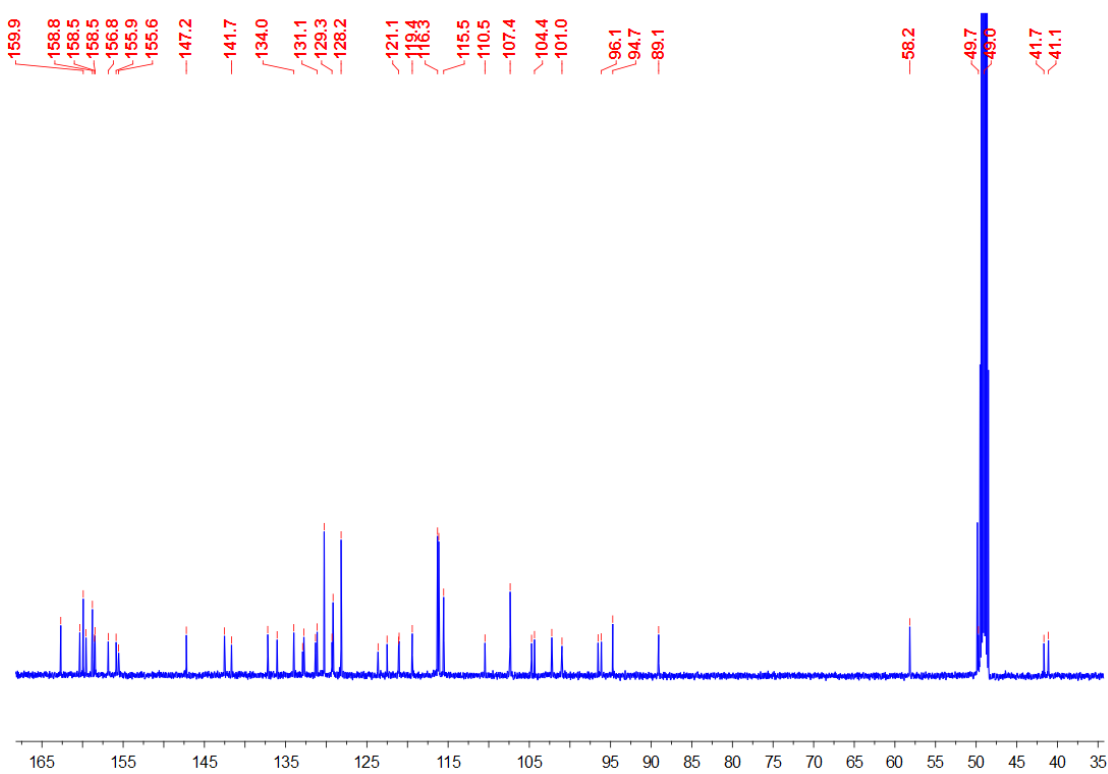


Figure S19. The  $^{13}\text{C-NMR}$  chromatography of compound 4

Table S1. The degree of the compounds and targets in the compound-target network.

No.	Name	Degree	No.	Name	Degree	No.	Compound	Degree
1	P12643	4	70	P80188	4	1	<b>2</b>	123
2	P00918	4	71	O75469	4	2	<b>4</b>	122
3	P02766	4	72	P43403	4	3	<b>1</b>	117
4	P02768	4	73	P04150	4	4	<b>3</b>	108
5	P55210	4	74	Q04759	4			
6	P06276	4	75	P06702	4			
7	P28482	4	76	P08473	4			
8	P48736	4	77	P07900	4			
9	P02774	4	78	P11362	4			
10	P45452	4	79	P60568	4			
11	P00742	4	80	P43235	4			
12	P42768	4	81	P11473	4			
13	P00734	4	82	P23946	4			
14	P37231	4	83	P15056	4			
15	P45983	4	84	Q02763	4			
16	P10275	4	85	Q13231	4			
17	P04278	4	86	Q03181	4			
18	P12931	4	87	P09960	4			
19	P42574	4	88	P09601	4			
20	Q06124	4	89	P25774	4			
21	P15090	4	90	P98170	4			
22	O15496	4	91	P08311	4			
23	P78536	4	92	P10721	4			
24	P29474	4	93	P07858	4			
25	P49841	4	94	P61812	4			
26	P28845	4	95	P11511	3			
27	Q08499	4	96	P06126	3			
28	Q16539	4	97	P00749	3			
29	Q07343	4	98	Q92731	3			
30	P08235	4	99	P54577	3			
31	P03372	4	100	Q9UM07	3			
32	P35398	4	101	P12821	3			
33	P15559	4	102	P14780	3			
34	P08758	4	103	P29466	3			
35	P00533	4	104	O60674	3			
36	P04035	4	105	P31749	3			
37	P08581	4	106	P11474	3			
38	P36897	4	107	P05230	2			
39	P10632	4	108	Q07817	2			
40	P01009	4	109	P14210	2			
41	P21802	4	110	P24752	2			

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42	P14555	4	111	P35520	2
43	P49763	4	112	P27986	2
44	P09211	4	113	P09488	2
45	P35968	4	114	P05089	2
46	P20701	4	115	Q9UNN8	2
47	P27487	4	116	Q03518	2
48	Q01469	4	117	Q06187	2
49	P22894	4	118	P63000	2
50	P02753	4	119	P00751	2
51	P39900	4	120	P13598	2
52	Q08881	4	121	Q9NP99	2
53	P06239	4	122	P14174	2
54	P52333	4	123	P00736	2
55	Q96RI1	4	124	O00244	2
56	Q07869	4	125	P15153	2
57	P00797	4	126	P68400	2
58	Q13133	4	127	P61586	2
59	P55055	4	128	P16109	2
60	P50135	4	129	P09871	2
61	P08254	4	130	P12724	2
62	P11712	4	131	P13501	2
63	P43405	4	132	P35228	2
64	P08253	4	133	P78540	1
65	P09874	4	134	P17931	1
66	P04179	4	135	Q9Y5Y6	1
67	P00374	4	136	P09237	1
68	P08709	4	137	P42224	1
69	P08246	4	138	P09486	1

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Table S2. Result of KEGG enrichment analysis

No.	ID	Description	LogP
1	hsa05200	Pathways in cancer	-39.38648017
2	hsa04014	Ras signaling pathway	-22.04012741
3	hsa04015	Rap1 signaling pathway	-20.08348863
4	hsa04151	PI3K-Akt signaling pathway	-19.29281724
5	hsa04010	MAPK signaling pathway	-17.17914784
6	hsa04020	Calcium signaling pathway	-5.76592454
7	hsa05417	Lipid and atherosclerosis	-25.77632691
8	hsa04657	IL-17 signaling pathway	-12.21813636
9	hsa05133	Pertussis	-11.67623147
10	hsa04668	TNF signaling pathway	-9.963617162
11	hsa05130	Pathogenic Escherichia coli infection	-8.715640126
12	hsa05132	Salmonella infection	-7.657710736
13	hsa05010	Alzheimer disease	-6.662116425
14	hsa04215	Apoptosis - multiple species	-6.471241779
15	hsa05022	Pathways of neurodegeneration - multiple diseases	-4.896432483
16	hsa05134	Legionellosis	-2.641828902
17	hsa05014	Amyotrophic lateral sclerosis	-2.174651062
18	hsa05205	Proteoglycans in cancer	-20.29489101
19	hsa05215	Prostate cancer	-16.74820967
20	hsa01521	EGFR tyrosine kinase inhibitor resistance	-16.36239205
21	hsa05135	Yersinia infection	-16.05659485
22	hsa05210	Colorectal cancer	-15.85589428
23	hsa04062	Chemokine signaling pathway	-15.1911414
24	hsa04380	Osteoclast differentiation	-15.0063179
25	hsa04933	AGE-RAGE signaling pathway in diabetic complications	-14.96713898
26	hsa05212	Pancreatic cancer	-14.90962327
27	hsa04510	Focal adhesion	-14.87493592
28	hsa05225	Hepatocellular carcinoma	-14.71374731
29	hsa05208	Chemical carcinogenesis - reactive oxygen species	-14.16283536
30	hsa04917	Prolactin signaling pathway	-13.68174332
31	hsa05161	Hepatitis B	-13.56167908
32	hsa04625	C-type lectin receptor signaling pathway	-13.21057158
33	hsa04660	T cell receptor signaling pathway	-13.21057158
34	hsa04613	Neutrophil extracellular trap formation	-12.60123784
35	hsa05142	Chagas disease	-11.81988751
36	hsa04210	Apoptosis	-11.79679189
37	hsa05226	Gastric cancer	-11.32339453
38	hsa05167	Kaposi sarcoma-associated herpesvirus infection	-11.20789014
39	hsa04370	VEGF signaling pathway	-11.1605345

40	hsa05131	Shigellosis	-11.05126911
41	hsa04664	Fc epsilon RI signaling pathway	-10.58210184
42	hsa05211	Renal cell carcinoma	-10.52307645
43	hsa05166	Human T-cell leukemia virus 1 infection	-10.47071433
44	hsa05163	Human cytomegalovirus infection	-10.39784676
45	hsa05218	Melanoma	-10.35146691
46	hsa05224	Breast cancer	-10.07338514
47	hsa05169	Epstein-Barr virus infection	-9.77351741
48	hsa04722	Neurotrophin signaling pathway	-9.701200213
49	hsa04068	FoxO signaling pathway	-9.288222794
50	hsa05162	Measles	-9.035188724
51	hsa05230	Central carbon metabolism in cancer	-8.938361775
52	hsa04620	Toll-like receptor signaling pathway	-8.896036856
53	hsa05223	Non-small cell lung cancer	-8.838618419
54	hsa01524	Platinum drug resistance	-8.789872347
55	hsa05220	Chronic myeloid leukemia	-8.647883511
56	hsa05160	Hepatitis C	-8.519670014
57	hsa04662	B cell receptor signaling pathway	-8.381354032
58	hsa04071	Sphingolipid signaling pathway	-8.374513092
59	hsa04012	ErbB signaling pathway	-8.255932461
60	hsa04024	cAMP signaling pathway	-8.193115102
61	hsa05231	Choline metabolism in cancer	-7.763002637
62	hsa04550	Signaling pathways regulating pluripotency of stem cells	-7.673459679
63	hsa05170	Human immunodeficiency virus 1 infection	-7.274022307
64	hsa04630	JAK-STAT signaling pathway	-7.204271914
65	hsa04935	Growth hormone synthesis, secretion and action	-7.1003686
66	hsa05213	Endometrial cancer	-6.56571319
67	hsa04666	Fc gamma R-mediated phagocytosis	-6.487231785
68	hsa04914	Progesterone-mediated oocyte maturation	-6.337847294
69	hsa05020	Prion disease	-6.256800418
70	hsa05221	Acute myeloid leukemia	-6.188424872
71	hsa05164	Influenza A	-5.894907367
72	hsa04919	Thyroid hormone signaling pathway	-5.83521409
73	hsa04140	Autophagy - animal	-5.392017912
74	hsa05222	Small cell lung cancer	-5.375014846
75	hsa05168	Herpes simplex virus 1 infection	-4.739367421
76	hsa05214	Glioma	-4.606640009
77	hsa04910	Insulin signaling pathway	-4.386308652
78	hsa04150	mTOR signaling pathway	-4.072688682
79	hsa04218	Cellular senescence	-4.072688682
80	hsa04725	Cholinergic synapse	-3.75666373
81	hsa04929	GnRH secretion	-3.668664214
82	hsa04960	Aldosterone-regulated sodium reabsorption	-3.188764589

83	hsa04211	Longevity regulating pathway	-3.122282021
84	hsa05165	Human papillomavirus infection	-3.071000788
85	hsa04930	Type II diabetes mellitus	-2.910941679
86	hsa04923	Regulation of lipolysis in adipocytes	-2.663866989
87	hsa04152	AMPK signaling pathway	-2.642648247
88	hsa04213	Longevity regulating pathway - multiple species	-2.537592175
89	hsa05017	Spinocerebellar ataxia	-2.369414538
90	hsa04934	Cushing syndrome	-2.246183801
91	hsa05418	Fluid shear stress and atherosclerosis	-18.98974721
92	hsa05415	Diabetic cardiomyopathy	-16.15568796
93	hsa04670	Leukocyte transendothelial migration	-9.886857966
94	hsa05171	Coronavirus disease - COVID-19	-15.17945733
95	hsa04659	Th17 cell differentiation	-14.51872172
96	hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	-14.04766115
97	hsa05152	Tuberculosis	-12.92540283
98	hsa05145	Toxoplasmosis	-12.81656913
99	hsa04658	Th1 and Th2 cell differentiation	-10.82487539
100	hsa04621	NOD-like receptor signaling pathway	-9.028844865
101	hsa04217	Necroptosis	-6.133314986
102	hsa05140	Leishmaniasis	-5.828866894
103	hsa04520	Adherens junction	-13.61031462
104	hsa04810	Regulation of actin cytoskeleton	-10.56957245
105	hsa04360	Axon guidance	-6.771702393
106	hsa05203	Viral carcinogenesis	-5.324761659
107	hsa05100	Bacterial invasion of epithelial cells	-4.551102765
108	hsa04530	Tight junction	-3.881845422
109	hsa04144	Endocytosis	-2.219205566
110	hsa01522	Endocrine resistance	-13.52846935
111	hsa04926	Relaxin signaling pathway	-13.49574553
112	hsa05207	Chemical carcinogenesis - receptor activation	-11.94927403
113	hsa04915	Estrogen signaling pathway	-10.37124712
114	hsa05219	Bladder cancer	-7.492381392
115	hsa04912	GnRH signaling pathway	-5.347674365
116	hsa04921	Oxytocin signaling pathway	-4.103632737
117	hsa04540	Gap junction	-2.11233501
118	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	-12.04749033
119	hsa04750	Inflammatory mediator regulation of TRP channels	-4.048220287
120	hsa04137	Mitophagy - animal	-3.471627169
121	hsa04650	Natural killer cell mediated cytotoxicity	-11.99215173
122	hsa05416	Viral myocarditis	-3.777465917
123	hsa04611	Platelet activation	-10.87943496
124	hsa04072	Phospholipase D signaling pathway	-8.768860987

125	hsa04066	HIF-1 signaling pathway	-7.3985211
126	hsa04371	Apelin signaling pathway	-4.351078329
127	hsa04022	cGMP-PKG signaling pathway	-2.981040543
128	hsa04261	Adrenergic signaling in cardiomyocytes	-2.296141321
129	hsa04064	NF-kappa B signaling pathway	-10.28631625
130	hsa05340	Primary immunodeficiency	-6.084156723
131	hsa04931	Insulin resistance	-10.12171346
132	hsa04932	Non-alcoholic fatty liver disease	-9.82485916
133	hsa04920	Adipocytokine signaling pathway	-6.112049883
134	hsa04936	Alcoholic liver disease	-4.299276582
135	hsa04728	Dopaminergic synapse	-2.493310636
136	hsa04610	Complement and coagulation cascades	-9.688587929
137	hsa05150	Staphylococcus aureus infection	-4.090776771
138	hsa05322	Systemic lupus erythematosus	-2.446934511
139	hsa04928	Parathyroid hormone synthesis, secretion and action	-8.821928227
140	hsa05146	Amoebiasis	-7.62553578
141	hsa00220	Arginine biosynthesis	-5.542914711
142	hsa00330	Arginine and proline metabolism	-4.05398091
143	hsa01230	Biosynthesis of amino acids	-2.304560478
144	hsa04614	Renin-angiotensin system	-7.233927615
145	hsa04924	Renin secretion	-2.406113959
146	hsa05206	MicroRNAs in cancer	-6.693951516
147	hsa04310	Wnt signaling pathway	-5.972260602
148	hsa03320	PPAR signaling pathway	-5.896565452
149	hsa05144	Malaria	-5.477836204
150	hsa05323	Rheumatoid arthritis	-5.347674365
151	hsa00590	Arachidonic acid metabolism	-5.046962281
152	hsa00591	Linoleic acid metabolism	-5.0422319
153	hsa04270	Vascular smooth muscle contraction	-4.440239837
154	hsa04972	Pancreatic secretion	-3.965897427
155	hsa04975	Fat digestion and absorption	-2.996523184
156	hsa05204	Chemical carcinogenesis - DNA adducts	-4.783424718
157	hsa00982	Drug metabolism - cytochrome P450	-3.471627169
158	hsa00980	Metabolism of xenobiotics by cytochrome P450	-3.338890684
159	hsa05202	Transcriptional misregulation in cancer	-4.505168893
160	hsa04350	TGF-beta signaling pathway	-4.134316611
161	hsa04390	Hippo signaling pathway	-3.101051963
162	hsa04726	Serotonergic synapse	-3.721046073
163	hsa05216	Thyroid cancer	-3.188764589
164	hsa05321	Inflammatory bowel disease	-3.642613753
165	hsa04612	Antigen processing and presentation	-3.338890684
166	hsa04142	Lysosome	-2.493310636
167	hsa04145	Phagosome	-2.275929828

168	hsa04978	Mineral absorption	-2.578150419
169	hsa04976	Bile secretion	-2.098876582

Table S3. Result of GO enrichment analysis

Biological Process

ID	Description	LogP
GO:0009725	response to hormone	-30.61415109
GO:0071396	cellular response to lipid	-27.97422208
GO:0032870	cellular response to hormone stimulus	-22.22513717
GO:0071407	cellular response to organic cyclic compound	-20.45864386
GO:0030522	intracellular receptor signaling pathway	-20.32313914
GO:0009755	hormone-mediated signaling pathway	-16.5619981
GO:0048545	response to steroid hormone	-15.16280867
GO:0043401	steroid hormone mediated signaling pathway	-13.47073761
GO:0071383	cellular response to steroid hormone stimulus	-12.79273257
GO:0030518	intracellular steroid hormone receptor signaling pathway	-9.937473371
GO:0031347	regulation of defense response	-30.24042097
GO:0050727	regulation of inflammatory response	-28.44524614
GO:0032102	negative regulation of response to external stimulus	-19.85341502
GO:0031348	negative regulation of defense response	-17.93765725
GO:0050728	negative regulation of inflammatory response	-15.52393472
GO:0001959	regulation of cytokine-mediated signaling pathway	-12.07187815
GO:0060759	regulation of response to cytokine stimulus	-11.68347148
GO:0001960	negative regulation of cytokine-mediated signaling pathway	-9.551316374
GO:0060761	negative regulation of response to cytokine stimulus	-9.333478224
GO:0002831	regulation of response to biotic stimulus	-8.976431021
GO:0045088	regulation of innate immune response	-7.897490632
GO:0030335	positive regulation of cell migration	-29.00950329
GO:2000147	positive regulation of cell motility	-28.38709217
GO:0051272	positive regulation of cellular component movement	-28.0615005
GO:0040017	positive regulation of locomotion	-28.01209727
GO:0035239	tube morphogenesis	-16.39136709
GO:0050678	regulation of epithelial cell proliferation	-16.1472847
GO:0010634	positive regulation of epithelial cell migration	-14.48522115
GO:0070848	response to growth factor	-13.86000188
GO:0010632	regulation of epithelial cell migration	-13.57478814
GO:0071363	cellular response to growth factor stimulus	-13.31715135
GO:0050679	positive regulation of epithelial cell proliferation	-13.27283202
GO:0010595	positive regulation of endothelial cell migration	-11.99215173



GO:0001936	regulation of endothelial cell proliferation	-11.68347148
GO:0010594	regulation of endothelial cell migration	-11.468685
GO:0001525	angiogenesis	-10.57766692
GO:0001938	positive regulation of endothelial cell proliferation	-10.00255824
GO:0048514	blood vessel morphogenesis	-9.962702849
GO:0001568	blood vessel development	-9.746947717
GO:0001944	vasculature development	-9.476287431
GO:0045765	regulation of angiogenesis	-7.136120043
GO:1901342	regulation of vasculature development	-7.055419378
GO:0043535	regulation of blood vessel endothelial cell migration	-6.32556126
GO:0043536	positive regulation of blood vessel endothelial cell migration	-5.896565452
GO:0045766	positive regulation of angiogenesis	-5.656736283
GO:1904018	positive regulation of vasculature development	-5.656736283
GO:0009611	response to wounding	-28.66849709
GO:0042060	wound healing	-23.96840122
GO:0050878	regulation of body fluid levels	-14.06987454
GO:0007596	blood coagulation	-13.19921058
GO:0050817	coagulation	-13.12947612
GO:0007599	hemostasis	-13.02649646
GO:0030168	platelet activation	-6.518113894
GO:0009617	response to bacterium	-26.24787723
GO:0032496	response to lipopolysaccharide	-25.77628589
GO:0002237	response to molecule of bacterial origin	-25.02771014
GO:0071216	cellular response to biotic stimulus	-20.34227405
GO:0071222	cellular response to lipopolysaccharide	-17.65187
GO:0071219	cellular response to molecule of bacterial origin	-17.19616425
GO:0007167	enzyme-linked receptor protein signaling pathway	-25.37740259
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	-24.26556203
GO:0006468	protein phosphorylation	-19.96953793
GO:0048534	hematopoietic or lymphoid organ development	-19.74140463
GO:0002520	immune system development	-18.9732106
GO:0030097	hemopoiesis	-18.42692047
GO:0018108	peptidyl-tyrosine phosphorylation	-15.63506253
GO:0018212	peptidyl-tyrosine modification	-15.50082505
GO:0001775	cell activation	-14.59057313
GO:0046777	protein autophosphorylation	-14.01824325
GO:0045321	leukocyte activation	-12.37737438
GO:0002521	leukocyte differentiation	-12.09215781
GO:0042110	T cell activation	-10.64244193
GO:0046649	lymphocyte activation	-10.02359068
GO:1903131	mononuclear cell differentiation	-8.949005199
GO:0030217	T cell differentiation	-8.628440228

GO:0030098	lymphocyte differentiation	-8.579435909
GO:0042113	B cell activation	-3.867856281
GO:0030183	B cell differentiation	-3.634926326
GO:0030155	regulation of cell adhesion	-22.93223024
GO:0050865	regulation of cell activation	-19.8830662
GO:0002694	regulation of leukocyte activation	-17.58939832
GO:1903037	regulation of leukocyte cell-cell adhesion	-16.57051771
GO:0022407	regulation of cell-cell adhesion	-16.42824304
GO:0045785	positive regulation of cell adhesion	-14.33523146
GO:0050863	regulation of T cell activation	-14.219541
GO:0071345	cellular response to cytokine stimulus	-13.70634039
GO:0070663	regulation of leukocyte proliferation	-13.25358083
GO:0007162	negative regulation of cell adhesion	-13.21689815
GO:0051249	regulation of lymphocyte activation	-12.91507804
GO:0022409	positive regulation of cell-cell adhesion	-11.90776951
GO:1903039	positive regulation of leukocyte cell-cell adhesion	-11.80215737
GO:0050670	regulation of lymphocyte proliferation	-11.44320582
GO:0032944	regulation of mononuclear cell proliferation	-11.36748866
GO:0042129	regulation of T cell proliferation	-10.49878848
GO:0050867	positive regulation of cell activation	-10.40237322
GO:0050870	positive regulation of T cell activation	-9.981955309
GO:2000106	regulation of leukocyte apoptotic process	-9.688587929
GO:0070228	regulation of lymphocyte apoptotic process	-9.673603132
GO:0002696	positive regulation of leukocyte activation	-9.667784501
GO:0051251	positive regulation of lymphocyte activation	-9.421425286
GO:0070229	negative regulation of lymphocyte apoptotic process	-8.087850438
GO:0070665	positive regulation of leukocyte proliferation	-7.274208925
GO:2000107	negative regulation of leukocyte apoptotic process	-6.958748065
GO:0050671	positive regulation of lymphocyte proliferation	-6.507428677
GO:0032946	positive regulation of mononuclear cell proliferation	-6.460924539
GO:0070232	regulation of T cell apoptotic process	-6.333992384
GO:0042102	positive regulation of T cell proliferation	-6.280313163
GO:0070233	negative regulation of T cell apoptotic process	-5.718752183
GO:0019221	cytokine-mediated signaling pathway	-5.183423092
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	-3.566996298
GO:2000515	negative regulation of CD4-positive, alpha-beta T cell activation	-3.417757237
GO:0046636	negative regulation of alpha-beta T cell activation	-3.026484409
GO:0032103	positive regulation of response to external stimulus	-22.8808739
GO:0031349	positive regulation of defense response	-12.07950528
GO:0050729	positive regulation of inflammatory response	-8.656119157
GO:0048608	reproductive structure development	-22.46910082
GO:0061458	reproductive system development	-22.38826386

GO:0007548	sex differentiation	-12.72240701
GO:0008406	gonad development	-11.7303654
GO:0045137	development of primary sexual characteristics	-11.59793099
GO:0046660	female sex differentiation	-9.774425465
GO:0008585	female gonad development	-9.128026859
GO:0046545	development of primary female sexual characteristics	-8.971712316
GO:0022602	ovulation cycle process	-7.067738962
GO:0001541	ovarian follicle development	-6.705781387
GO:0008584	male gonad development	-6.651377823
GO:0046546	development of primary male sexual characteristics	-6.626908074
GO:0034405	response to fluid shear stress	-6.333992384
GO:0046661	male sex differentiation	-6.1126988
GO:0042698	ovulation cycle	-6.112049883
GO:0048771	tissue remodeling	-5.293941743
GO:0048863	stem cell differentiation	-4.042186803
GO:0007276	gamete generation	-2.153483435
GO:0001934	positive regulation of protein phosphorylation	-20.42059355
GO:0001819	positive regulation of cytokine production	-19.810826
GO:0043549	regulation of kinase activity	-19.80775099
GO:0043408	regulation of MAPK cascade	-19.16010247
GO:0051347	positive regulation of transferase activity	-17.89381664
GO:0033674	positive regulation of kinase activity	-17.31762786
GO:0043410	positive regulation of MAPK cascade	-17.25712509
GO:0045859	regulation of protein kinase activity	-14.40033004
GO:0045860	positive regulation of protein kinase activity	-12.22640589
GO:0071900	regulation of protein serine/threonine kinase activity	-11.53464025
GO:0043405	regulation of MAP kinase activity	-11.5299948
GO:0071902	positive regulation of protein serine/threonine kinase activity	-10.42201666
GO:0070372	regulation of ERK1 and ERK2 cascade	-9.705209483
GO:0070374	positive regulation of ERK1 and ERK2 cascade	-9.324260724
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	-8.929948732
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	-8.560430379
GO:0043406	positive regulation of MAP kinase activity	-8.472870371
GO:0009410	response to xenobiotic stimulus	-19.30097994
GO:0036293	response to decreased oxygen levels	-17.29566579
GO:0070482	response to oxygen levels	-16.56781487
GO:0001666	response to hypoxia	-16.39733095
GO:0010942	positive regulation of cell death	-15.23603218
GO:0043068	positive regulation of programmed cell death	-13.12874643
GO:0043065	positive regulation of apoptotic process	-11.34069512
GO:0048511	rhythmic process	-10.62063458
GO:0022617	extracellular matrix disassembly	-17.76091099
GO:0030574	collagen catabolic process	-14.91767342

GO:0032963	collagen metabolic process	-14.63948025
GO:0030198	extracellular matrix organization	-10.51293975
GO:0043062	extracellular structure organization	-10.49166442
GO:0045229	external encapsulating structure organization	-10.44937211
GO:0022411	cellular component disassembly	-8.931177664
GO:1904645	response to amyloid-beta	-8.219438111
GO:0006935	chemotaxis	-16.980079
GO:0042330	taxis	-16.94119533
GO:0050900	leukocyte migration	-15.2423965
GO:0060326	cell chemotaxis	-9.650921305
GO:0097529	myeloid leukocyte migration	-9.489311998
GO:0030595	leukocyte chemotaxis	-8.855624789
GO:0033628	regulation of cell adhesion mediated by integrin	-8.648182486
GO:0030593	neutrophil chemotaxis	-8.511866349
GO:0071621	granulocyte chemotaxis	-8.297197646
GO:1990266	neutrophil migration	-8.095990489
GO:0097530	granulocyte migration	-7.798323649
GO:0033630	positive regulation of cell adhesion mediated by integrin	-3.932113785
GO:0002683	negative regulation of immune system process	-16.254587
GO:0050777	negative regulation of immune response	-11.5299948
GO:0050866	negative regulation of cell activation	-9.438241111
GO:0022408	negative regulation of cell-cell adhesion	-8.66947871
GO:0002695	negative regulation of leukocyte activation	-7.659334066
GO:1903038	negative regulation of leukocyte cell-cell adhesion	-7.647101957
GO:0002700	regulation of production of molecular mediator of immune response	-7.090818429
GO:0002718	regulation of cytokine production involved in immune response	-6.456694159
GO:0051250	negative regulation of lymphocyte activation	-6.092224523
GO:0050868	negative regulation of T cell activation	-5.740423278
GO:0070664	negative regulation of leukocyte proliferation	-5.402680918
GO:0002719	negative regulation of cytokine production involved in immune response	-5.170556276
GO:0002698	negative regulation of immune effector process	-4.881757815
GO:0002701	negative regulation of production of molecular mediator of immune response	-4.563621458
GO:0050672	negative regulation of lymphocyte proliferation	-4.368389267
GO:0032945	negative regulation of mononuclear cell proliferation	-4.343647301
GO:0046006	regulation of activated T cell proliferation	-4.231385806
GO:0002823	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	-2.709251562
GO:0002820	negative regulation of adaptive immune response	-2.598984718

GO:0002704	negative regulation of leukocyte mediated immunity	-2.442135686
GO:0042130	negative regulation of T cell proliferation	-2.423979776
GO:0010817	regulation of hormone levels	-16.02162897
GO:0042445	hormone metabolic process	-13.61758849
GO:0000302	response to reactive oxygen species	-15.99652924
GO:0006979	response to oxidative stress	-14.19796632
GO:0062197	cellular response to chemical stress	-14.16505199
GO:0010035	response to inorganic substance	-13.47737931
GO:0034599	cellular response to oxidative stress	-13.00511939
GO:0034614	cellular response to reactive oxygen species	-12.54071619
GO:0046686	response to cadmium ion	-11.1605345
GO:0010038	response to metal ion	-10.0712723
GO:0071241	cellular response to inorganic substance	-8.213609384
GO:0071276	cellular response to cadmium ion	-7.772351068
GO:0071248	cellular response to metal ion	-7.723996604
GO:0006954	inflammatory response	-15.56171256
GO:0051090	regulation of DNA-binding transcription factor activity	-9.511982904
GO:0051091	positive regulation of DNA-binding transcription factor activity	-7.381102715
GO:0016485	protein processing	-15.33690367
GO:0051604	protein maturation	-13.20096053
GO:0008015	blood circulation	-12.28023701
GO:0003013	circulatory system process	-11.81213653
GO:0008217	regulation of blood pressure	-11.3226546
GO:0140448	signaling receptor ligand precursor processing	-11.27175812
GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	-10.53819703
GO:0003073	regulation of systemic arterial blood pressure	-9.24988813
GO:0001990	regulation of systemic arterial blood pressure by hormone	-7.925116092
GO:0016486	peptide hormone processing	-7.925116092
GO:0043603	cellular amide metabolic process	-7.615024831
GO:0003081	regulation of systemic arterial blood pressure by renin-angiotensin	-7.449166496
GO:0002002	regulation of angiotensin levels in blood	-7.28670494
GO:0002003	angiotensin maturation	-7.28670494
GO:0050886	endocrine process	-7.012638408
GO:0001991	regulation of systemic arterial blood pressure by circulatory renin-angiotensin	-6.538943171
GO:0006518	peptide metabolic process	-5.992728233
GO:0050435	amyloid-beta metabolic process	-4.066733811
GO:0009991	response to extracellular stimulus	-15.27808387
GO:0031667	response to nutrient levels	-14.80315541
GO:0007584	response to nutrient	-10.17040996

GO:0033273	response to vitamin	-5.828866894
GO:2001233	regulation of apoptotic signaling pathway	-15.24603219
GO:2001234	negative regulation of apoptotic signaling pathway	-12.6937992
GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	-12.06460194
GO:2001236	regulation of extrinsic apoptotic signaling pathway	-11.186745
GO:1902041	regulation of extrinsic apoptotic signaling pathway via death domain receptors	-6.958748065
GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	-6.543434086
GO:0090199	regulation of release of cytochrome c from mitochondria	-4.19429302
GO:0010823	negative regulation of mitochondrion organization	-4.05398091
GO:0090201	negative regulation of release of cytochrome c from mitochondria	-3.997606803
GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	-2.967301303
GO:0031644	regulation of nervous system process	-2.380218931
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	-14.69697509
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	-14.41229536
GO:1904892	regulation of receptor signaling pathway via STAT	-5.516753227
GO:0071346	cellular response to interferon-gamma	-5.066523799
GO:0034341	response to interferon-gamma	-4.590863974
GO:0046425	regulation of receptor signaling pathway via JAK-STAT	-4.578672946
GO:0046427	positive regulation of receptor signaling pathway via JAK-STAT	-4.563621458
GO:1904894	positive regulation of receptor signaling pathway via STAT	-4.388971116
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	-3.591792775
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	-3.256454688
GO:0048660	regulation of smooth muscle cell proliferation	-14.59839173
GO:0048661	positive regulation of smooth muscle cell proliferation	-9.208808115
GO:0034612	response to tumor necrosis factor	-6.388814949
GO:0031663	lipopolysaccharide-mediated signaling pathway	-6.143833237
GO:0071356	cellular response to tumor necrosis factor	-5.764254059
GO:0048732	gland development	-14.55945095
GO:0008285	negative regulation of cell population proliferation	-11.84505922
GO:0002685	regulation of leukocyte migration	-14.28644142
GO:0050920	regulation of chemotaxis	-12.80508424
GO:0002688	regulation of leukocyte chemotaxis	-9.523847485
GO:0050921	positive regulation of chemotaxis	-9.004680611
GO:0002687	positive regulation of leukocyte migration	-8.974409356
GO:0002690	positive regulation of leukocyte chemotaxis	-6.580941646
GO:0010758	regulation of macrophage chemotaxis	-5.170556276
GO:1905521	regulation of macrophage migration	-4.430899217

GO:1901652	response to peptide	-13.80023289
GO:1901699	cellular response to nitrogen compound	-11.76198328
GO:0071417	cellular response to organonitrogen compound	-11.60211447
GO:1903829	positive regulation of protein localization	-11.56433151
GO:0051223	regulation of protein transport	-10.84773567
GO:0070201	regulation of establishment of protein localization	-10.49733981
GO:0043434	response to peptide hormone	-10.01971019
GO:0060341	regulation of cellular localization	-9.789714846
GO:0051222	positive regulation of protein transport	-8.984863675
GO:1904951	positive regulation of establishment of protein localization	-8.705369812
GO:0071375	cellular response to peptide hormone stimulus	-7.859657
GO:1900182	positive regulation of protein localization to nucleus	-6.918553397
GO:1901653	cellular response to peptide	-6.764531882
GO:1900180	regulation of protein localization to nucleus	-6.751267874
GO:0032868	response to insulin	-6.29966918
GO:0032869	cellular response to insulin stimulus	-5.23382086
GO:0032386	regulation of intracellular transport	-4.632557242
GO:0033157	regulation of intracellular protein transport	-4.096494249
GO:0090316	positive regulation of intracellular protein transport	-4.072688682
GO:0046822	regulation of nucleocytoplasmic transport	-3.926057035
GO:0046824	positive regulation of nucleocytoplasmic transport	-3.777465917
GO:0032388	positive regulation of intracellular transport	-3.510233948
GO:0042307	positive regulation of protein import into nucleus	-3.121184104
GO:0042306	regulation of protein import into nucleus	-2.641828902
GO:0050778	positive regulation of immune response	-13.77571313
GO:0002764	immune response-regulating signaling pathway	-9.736491901
GO:0002253	activation of immune response	-8.330832001
GO:0002768	immune response-regulating cell surface receptor signaling pathway	-8.008884027
GO:0002429	immune response-activating cell surface receptor signaling pathway	-5.494937956
GO:0002757	immune response-activating signal transduction	-5.494937956
GO:0050851	antigen receptor-mediated signaling pathway	-5.340477368
GO:0050852	T cell receptor signaling pathway	-5.090708846
GO:0050853	B cell receptor signaling pathway	-3.774735282
GO:0001655	urogenital system development	-13.72386201
GO:0072001	renal system development	-10.00555495
GO:0001822	kidney development	-9.094100882
GO:2000027	regulation of animal organ morphogenesis	-4.590863974
GO:0001823	mesonephros development	-4.29510201
GO:0019218	regulation of steroid metabolic process	-3.945870798
GO:0003156	regulation of animal organ formation	-3.648256523
GO:0072073	kidney epithelium development	-3.505116636

GO:0110110	positive regulation of animal organ morphogenesis	-3.460510079
GO:0061326	renal tubule development	-3.297108752
GO:0001657	ureteric bud development	-3.256454688
GO:0072163	mesonephric epithelium development	-3.236533122
GO:0072164	mesonephric tubule development	-3.236533122
GO:0072006	nephron development	-2.54131655
GO:0050810	regulation of steroid biosynthetic process	-2.371219039
GO:0072080	nephron tubule development	-2.288506924
GO:0051046	regulation of secretion	-13.13424077
GO:1903530	regulation of secretion by cell	-12.96034976
GO:1903532	positive regulation of secretion by cell	-9.301142639
GO:0051047	positive regulation of secretion	-8.808240449
GO:0050708	regulation of protein secretion	-8.675713583
GO:0046883	regulation of hormone secretion	-6.907834949
GO:0046887	positive regulation of hormone secretion	-5.811197723
GO:0090087	regulation of peptide transport	-5.674382207
GO:0050714	positive regulation of protein secretion	-5.671488577
GO:0050796	regulation of insulin secretion	-5.27247342
GO:0090276	regulation of peptide hormone secretion	-4.746366359
GO:0002791	regulation of peptide secretion	-4.699317536
GO:0032024	positive regulation of insulin secretion	-3.591792775
GO:0090277	positive regulation of peptide hormone secretion	-3.08607163
GO:0002793	positive regulation of peptide secretion	-3.050728521
GO:1902532	negative regulation of intracellular signal transduction	-13.03642147
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	-6.906017302
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	-4.621809367
GO:0048729	tissue morphogenesis	-12.91507804
GO:0002009	morphogenesis of an epithelium	-12.6219437
GO:0061180	mammary gland epithelium development	-9.673603132
GO:0030879	mammary gland development	-9.558687627
GO:0022612	gland morphogenesis	-8.971712316
GO:0060562	epithelial tube morphogenesis	-8.739409474
GO:0061138	morphogenesis of a branching epithelium	-8.387896728
GO:0001763	morphogenesis of a branching structure	-8.161571002
GO:0030855	epithelial cell differentiation	-8.009049865
GO:0048754	branching morphogenesis of an epithelial tube	-7.948682988
GO:0060065	uterus development	-7.449166496
GO:0060443	mammary gland morphogenesis	-7.427062266
GO:0035265	organ growth	-6.918553397
GO:0060736	prostate gland growth	-6.697100865
GO:0060603	mammary gland duct morphogenesis	-6.695815484
GO:0030850	prostate gland development	-5.809329102
GO:0048806	genitalia development	-5.660591272



GO:0060444	branching involved in mammary gland duct morphogenesis	-5.542914711
GO:0060745	mammary gland branching involved in pregnancy	-5.491517955
GO:0060740	prostate gland epithelium morphogenesis	-5.461481729
GO:0060512	prostate gland morphogenesis	-5.309661703
GO:0040007	growth	-5.049192521
GO:0048589	developmental growth	-5.049192521
GO:0043627	response to estrogen	-4.783424718
GO:0060571	morphogenesis of an epithelial fold	-4.300505605
GO:0030540	female genitalia development	-4.13991307
GO:0060688	regulation of morphogenesis of a branching structure	-4.05398091
GO:0030520	intracellular estrogen receptor signaling pathway	-3.997606803
GO:0002064	epithelial cell development	-3.746002342
GO:1905330	regulation of morphogenesis of an epithelium	-3.642613753
GO:0003382	epithelial cell morphogenesis	-3.297846025
GO:0048645	animal organ formation	-3.224038362
GO:2000377	regulation of reactive oxygen species metabolic process	-12.75419558
GO:2000379	positive regulation of reactive oxygen species metabolic process	-6.038037251
GO:0032653	regulation of interleukin-10 production	-3.695159677
GO:0090322	regulation of superoxide metabolic process	-3.297846025
GO:0032655	regulation of interleukin-12 production	-2.517844054
GO:0044057	regulation of system process	-12.53392151
GO:0090257	regulation of muscle system process	-5.578005572
GO:0062012	regulation of small molecule metabolic process	-12.35011022
GO:0019216	regulation of lipid metabolic process	-11.32376123
GO:0045834	positive regulation of lipid metabolic process	-11.08678946
GO:1905952	regulation of lipid localization	-10.27177678
GO:0062013	positive regulation of small molecule metabolic process	-10.0098941
GO:0032368	regulation of lipid transport	-9.885655747
GO:1905953	negative regulation of lipid localization	-9.257340565
GO:0010887	negative regulation of cholesterol storage	-9.077109052
GO:0010743	regulation of macrophage derived foam cell differentiation	-8.173372195
GO:0010565	regulation of cellular ketone metabolic process	-7.977441712
GO:0060331	negative regulation of response to interferon-gamma	-7.839919449
GO:0060336	negative regulation of interferon-gamma-mediated signaling pathway	-7.839919449
GO:0010885	regulation of cholesterol storage	-7.689013834
GO:0010888	negative regulation of lipid storage	-7.338787904
GO:0010883	regulation of lipid storage	-6.705781387
GO:0019217	regulation of fatty acid metabolic process	-6.645240103
GO:0010745	negative regulation of macrophage derived foam cell differentiation	-6.538943171
GO:0060330	regulation of response to interferon-gamma	-6.261202294

GO:0060334	regulation of interferon-gamma-mediated signaling pathway	-6.261202294
GO:0045923	positive regulation of fatty acid metabolic process	-6.026164049
GO:0046890	regulation of lipid biosynthetic process	-5.782565661
GO:0032369	negative regulation of lipid transport	-5.660591272
GO:0032370	positive regulation of lipid transport	-5.516753227
GO:0046889	positive regulation of lipid biosynthetic process	-5.48770807
GO:0042632	cholesterol homeostasis	-5.190083413
GO:0055092	sterol homeostasis	-5.164833848
GO:0043030	regulation of macrophage activation	-5.012035481
GO:1905954	positive regulation of lipid localization	-4.881757815
GO:0002832	negative regulation of response to biotic stimulus	-4.859684539
GO:0046470	phosphatidylcholine metabolic process	-4.846083842
GO:0055088	lipid homeostasis	-4.810509219
GO:0042752	regulation of circadian rhythm	-4.752445487
GO:0045824	negative regulation of innate immune response	-4.606640009
GO:0010874	regulation of cholesterol efflux	-4.02075444
GO:0046486	glycerolipid metabolic process	-3.607592279
GO:0010875	positive regulation of cholesterol efflux	-3.598556005
GO:0006644	phospholipid metabolic process	-3.559018779
GO:0006650	glycerophospholipid metabolic process	-3.392184112
GO:0032371	regulation of sterol transport	-3.297108752
GO:0032374	regulation of cholesterol transport	-3.297108752
GO:1905897	regulation of response to endoplasmic reticulum stress	-3.256454688
GO:0032373	positive regulation of sterol transport	-3.121184104
GO:0032376	positive regulation of cholesterol transport	-3.121184104
GO:0042789	mRNA transcription by RNA polymerase II	-3.057221553
GO:0055090	acylglycerol homeostasis	-3.026484409
GO:0070328	triglyceride homeostasis	-3.026484409
GO:0090207	regulation of triglyceride metabolic process	-2.996523184
GO:1903573	negative regulation of response to endoplasmic reticulum stress	-2.967301303
GO:0009299	mRNA transcription	-2.910941679
GO:0120163	negative regulation of cold-induced thermogenesis	-2.883742534
GO:0042304	regulation of fatty acid biosynthetic process	-2.83116673
GO:0060193	positive regulation of lipase activity	-12.17908013
GO:0051345	positive regulation of hydrolase activity	-11.65667311
GO:0060191	regulation of lipase activity	-10.92205192
GO:0010518	positive regulation of phospholipase activity	-8.219438111
GO:0010517	regulation of phospholipase activity	-7.653500333
GO:0010863	positive regulation of phospholipase C activity	-5.969764989
GO:1900274	regulation of phospholipase C activity	-5.861421458
GO:0048145	regulation of fibroblast proliferation	-4.497111344
GO:0060964	regulation of miRNA-mediated gene silencing	-3.057221553

GO:1900368	regulation of post-transcriptional gene silencing by RNA	-2.996523184
GO:0060147	regulation of post-transcriptional gene silencing	-2.967301303
GO:0060966	regulation of gene silencing by RNA	-2.938784718
GO:0048146	positive regulation of fibroblast proliferation	-2.857159545
GO:0002444	myeloid leukocyte mediated immunity	-11.76313485
GO:0002252	immune effector process	-10.76721729
GO:0002446	neutrophil mediated immunity	-9.24148916
GO:0042742	defense response to bacterium	-8.042860852
GO:0070942	neutrophil mediated cytotoxicity	-7.28670494
GO:0070943	neutrophil-mediated killing of symbiont cell	-7.28670494
GO:0070944	neutrophil-mediated killing of bacterium	-7.28670494
GO:0002443	leukocyte mediated immunity	-7.201584248
GO:0050829	defense response to Gram-negative bacterium	-6.882876887
GO:0070945	neutrophil-mediated killing of gram-negative bacterium	-6.429151568
GO:0051873	killing by host of symbiont cells	-5.170556276
GO:0051702	biological process involved in interaction with symbiont	-5.164833848
GO:0009620	response to fungus	-5.118712187
GO:0006959	humoral immune response	-5.086188203
GO:0001909	leukocyte mediated cytotoxicity	-4.02075444
GO:0019730	antimicrobial humoral response	-3.774735282
GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	-3.494919094
GO:0002526	acute inflammatory response	-3.403810574
GO:0001906	cell killing	-3.068294072
GO:0050832	defense response to fungus	-2.857159545
GO:0019731	antibacterial humoral response	-2.686335833
GO:0009411	response to UV	-11.35818208
GO:0009314	response to radiation	-10.75156466
GO:0070141	response to UV-A	-10.62371139
GO:0009416	response to light stimulus	-9.778659818
GO:0071492	cellular response to UV-A	-6.871648786
GO:0071214	cellular response to abiotic stimulus	-6.624655511
GO:0104004	cellular response to environmental stimulus	-6.624655511
GO:0071478	cellular response to radiation	-5.746056577
GO:0034644	cellular response to UV	-5.430679991
GO:0071482	cellular response to light stimulus	-4.816174602
GO:0048013	ephrin receptor signaling pathway	-4.087917396
GO:0007566	embryo implantation	-3.057221553
GO:0035987	endodermal cell differentiation	-3.057221553
GO:0150077	regulation of neuroinflammatory response	-3.057221553
GO:1904707	positive regulation of vascular associated smooth muscle cell proliferation	-2.883742534
GO:0060324	face development	-2.857159545

GO:0001706	endoderm formation	-2.780855605
GO:0001704	formation of primary germ layer	-2.723786282
GO:0007492	endoderm development	-2.320851758
GO:0007369	gastrulation	-2.188651941
GO:1901654	response to ketone	-11.20789014
GO:0031960	response to corticosteroid	-7.227424888
GO:1901655	cellular response to ketone	-6.456694159
GO:0051384	response to glucocorticoid	-5.433119651
GO:0071548	response to dexamethasone	-4.430899217
GO:0071384	cellular response to corticosteroid stimulus	-3.695159677
GO:0071549	cellular response to dexamethasone stimulus	-3.648256523
GO:0071385	cellular response to glucocorticoid stimulus	-2.732631226
GO:0045596	negative regulation of cell differentiation	-11.04190608
GO:0040008	regulation of growth	-10.54686563
GO:0045927	positive regulation of growth	-9.598754249
GO:0001558	regulation of cell growth	-9.009694606
GO:0030307	positive regulation of cell growth	-8.235530811
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	-10.93194826
GO:2000116	regulation of cysteine-type endopeptidase activity	-10.30233488
GO:0030162	regulation of proteolysis	-9.666576751
GO:0052547	regulation of peptidase activity	-8.511287502
GO:0052548	regulation of endopeptidase activity	-7.967894363
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	-5.740423278
GO:2001056	positive regulation of cysteine-type endopeptidase activity	-5.351554927
GO:0045862	positive regulation of proteolysis	-5.089900538
GO:0010950	positive regulation of endopeptidase activity	-4.794318788
GO:0010952	positive regulation of peptidase activity	-4.519572169
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	-3.360223118
GO:2001235	positive regulation of apoptotic signaling pathway	-2.469925039
GO:0008283	cell population proliferation	-10.89113188
GO:0050673	epithelial cell proliferation	-8.057224672
GO:0080135	regulation of cellular response to stress	-10.76887381
GO:0051129	negative regulation of cellular component organization	-9.349154664
GO:0010639	negative regulation of organelle organization	-4.531823314
GO:0030324	lung development	-10.52796053
GO:0030323	respiratory tube development	-10.41235365
GO:0060541	respiratory system development	-9.874018577
GO:0000902	cell morphogenesis	-10.47745816
GO:0000904	cell morphogenesis involved in differentiation	-7.728264592
GO:0061564	axon development	-5.802249407

GO:0031175	neuron projection development	-5.085367178
GO:0032990	cell part morphogenesis	-3.416548964
GO:0007409	axonogenesis	-2.988651126
GO:0048812	neuron projection morphogenesis	-2.924996159
GO:0120039	plasma membrane bounded cell projection morphogenesis	-2.90086338
GO:0048858	cell projection morphogenesis	-2.87699874
GO:0032989	cellular component morphogenesis	-2.874578644
GO:0048667	cell morphogenesis involved in neuron differentiation	-2.543518055
GO:0006809	nitric oxide biosynthetic process	-10.20100239
GO:0046209	nitric oxide metabolic process	-9.522661152
GO:2001057	reactive nitrogen species metabolic process	-9.378162529
GO:0006527	arginine catabolic process	-7.28670494
GO:0006525	arginine metabolic process	-6.13780614
GO:0009063	cellular amino acid catabolic process	-6.114690297
GO:1901606	alpha-amino acid catabolic process	-5.375014846
GO:0009065	glutamine family amino acid catabolic process	-5.309661703
GO:0006520	cellular amino acid metabolic process	-5.245708372
GO:0046395	carboxylic acid catabolic process	-5.084509487
GO:0016054	organic acid catabolic process	-5.027527274
GO:0019627	urea metabolic process	-4.823930581
GO:0071941	nitrogen cycle metabolic process	-4.823930581
GO:1901605	alpha-amino acid metabolic process	-4.476613983
GO:0044282	small molecule catabolic process	-3.648832041
GO:0009064	glutamine family amino acid metabolic process	-3.51857078
GO:0001890	placenta development	-10.10548493
GO:0007507	heart development	-9.290459653
GO:0009792	embryo development ending in birth or egg hatching	-6.471305844
GO:0043009	chordate embryonic development	-5.884509546
GO:0001701	in utero embryonic development	-4.959453215
GO:0048568	embryonic organ development	-4.394517462
GO:0001892	embryonic placenta development	-4.319220707
GO:0060711	labyrinthine layer development	-4.19429302
GO:0007423	sensory organ development	-3.610167822
GO:0048598	embryonic morphogenesis	-3.48262788
GO:0002697	regulation of immune effector process	-9.98560673
GO:0002703	regulation of leukocyte mediated immunity	-7.897490632
GO:0002699	positive regulation of immune effector process	-7.657710736
GO:0031341	regulation of cell killing	-5.164833848
GO:0031343	positive regulation of cell killing	-4.910802172
GO:0002705	positive regulation of leukocyte mediated immunity	-4.36862254
GO:0002706	regulation of lymphocyte mediated immunity	-2.890820235
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	-2.620206303
GO:0001910	regulation of leukocyte mediated cytotoxicity	-2.15375782

GO:0002709	regulation of T cell mediated immunity	-2.11233501
GO:0044089	positive regulation of cellular component biogenesis	-9.92104654
GO:0031334	positive regulation of protein-containing complex assembly	-8.833337619
GO:0043254	regulation of protein-containing complex assembly	-8.217880939
GO:0006909	phagocytosis	-4.889985371
GO:0045806	negative regulation of endocytosis	-3.894414272
GO:0060627	regulation of vesicle-mediated transport	-3.737496337
GO:0030100	regulation of endocytosis	-3.396359546
GO:0051098	regulation of binding	-9.801800955
GO:0030099	myeloid cell differentiation	-7.859657
GO:0060391	positive regulation of SMAD protein signal transduction	-7.820043856
GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	-7.072067127
GO:0051099	positive regulation of binding	-6.981046717
GO:0060390	regulation of SMAD protein signal transduction	-6.543434086
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	-6.100831869
GO:0051101	regulation of DNA binding	-5.83521409
GO:0043388	positive regulation of DNA binding	-5.193141575
GO:0002573	myeloid leukocyte differentiation	-4.79473041
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	-4.563296057
GO:0001818	negative regulation of cytokine production	-9.801800955
GO:0051897	positive regulation of protein kinase B signaling	-9.701200213
GO:0051896	regulation of protein kinase B signaling	-8.954454623
GO:0010631	epithelial cell migration	-9.506688451
GO:0090132	epithelium migration	-9.376009864
GO:0090130	tissue migration	-9.128026859
GO:0001667	ameboidal-type cell migration	-6.711372043
GO:0043542	endothelial cell migration	-6.188424872
GO:0007565	female pregnancy	-9.394535214
GO:0044703	multi-organism reproductive process	-8.881363746
GO:0044706	multi-multicellular organism process	-8.66947871
GO:0060135	maternal process involved in female pregnancy	-8.053631677
GO:0001893	maternal placenta development	-4.812136674
GO:0046697	decidualization	-3.810653527
GO:0043086	negative regulation of catalytic activity	-9.262902146
GO:0045861	negative regulation of proteolysis	-7.068760082
GO:0051346	negative regulation of hydrolase activity	-6.822437729
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	-5.828866894
GO:2000117	negative regulation of cysteine-type endopeptidase activity	-5.57594833
GO:0010466	negative regulation of peptidase activity	-4.538012652

GO:0010951	negative regulation of endopeptidase activity	-3.790278081
GO:1905114	cell surface receptor signaling pathway involved in cell-cell signaling	-3.109546336
GO:0016055	Wnt signaling pathway	-2.142507837
GO:0198738	cell-cell signaling by wnt	-2.142507837
GO:0019725	cellular homeostasis	-9.255887293
GO:0055082	cellular chemical homeostasis	-7.739252798
GO:0055080	cation homeostasis	-7.266678635
GO:0098771	inorganic ion homeostasis	-7.168471926
GO:0050801	ion homeostasis	-6.988569488
GO:0055065	metal ion homeostasis	-6.484750597
GO:0030003	cellular cation homeostasis	-5.672686326
GO:0006873	cellular ion homeostasis	-5.517096473
GO:0055076	transition metal ion homeostasis	-5.496011604
GO:0006875	cellular metal ion homeostasis	-4.801382538
GO:0046916	cellular transition metal ion homeostasis	-3.848849255
GO:0072507	divalent inorganic cation homeostasis	-3.779680595
GO:0072503	cellular divalent inorganic cation homeostasis	-3.267802072
GO:0055074	calcium ion homeostasis	-2.563556743
GO:0055072	iron ion homeostasis	-2.15375782
GO:0002250	adaptive immune response	-9.167706854
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	-2.300126015
GO:0048872	homeostasis of number of cells	-8.956998904
GO:0002262	myeloid cell homeostasis	-5.859448924
GO:0034101	erythrocyte homeostasis	-5.215612988
GO:0030218	erythrocyte differentiation	-4.24775971
GO:0001776	leukocyte homeostasis	-3.426082434
GO:0043029	T cell homeostasis	-3.297846025
GO:0097194	execution phase of apoptosis	-2.83116673
GO:0002260	lymphocyte homeostasis	-2.663866989
GO:0097305	response to alcohol	-8.93630579
GO:1903426	regulation of reactive oxygen species biosynthetic process	-5.567153769
GO:0045471	response to ethanol	-4.731597802
GO:1903579	negative regulation of ATP metabolic process	-3.460510079
GO:2000378	negative regulation of reactive oxygen species metabolic process	-2.883742534
GO:1903578	regulation of ATP metabolic process	-2.07245992
GO:0001501	skeletal system development	-8.817575438
GO:0001503	ossification	-6.256800418
GO:0009612	response to mechanical stimulus	-5.340477368
GO:0060348	bone development	-5.24746245

GO:0045936	negative regulation of phosphate metabolic process	-8.720921622
GO:0010563	negative regulation of phosphorus metabolic process	-8.707565302
GO:0042326	negative regulation of phosphorylation	-5.802249407
GO:0001933	negative regulation of protein phosphorylation	-5.401431576
GO:0051348	negative regulation of transferase activity	-5.335196965
GO:0031400	negative regulation of protein modification process	-5.290649318
GO:0071901	negative regulation of protein serine/threonine kinase activity	-4.670193976
GO:0006469	negative regulation of protein kinase activity	-4.233686037
GO:0033673	negative regulation of kinase activity	-3.944015866
GO:0043407	negative regulation of MAP kinase activity	-3.777465917
GO:0043409	negative regulation of MAPK cascade	-2.021836371
GO:1901214	regulation of neuron death	-8.621340543
GO:0097190	apoptotic signaling pathway	-8.338565027
GO:0048662	negative regulation of smooth muscle cell proliferation	-7.344447048
GO:1904705	regulation of vascular associated smooth muscle cell proliferation	-6.812871715
GO:0043523	regulation of neuron apoptotic process	-6.29966918
GO:1901215	negative regulation of neuron death	-5.24746245
GO:1904706	negative regulation of vascular associated smooth muscle cell proliferation	-4.388971116
GO:0097193	intrinsic apoptotic signaling pathway	-4.183005797
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	-3.566996298
GO:0010660	regulation of muscle cell apoptotic process	-3.2766443
GO:0043524	negative regulation of neuron apoptotic process	-3.257114236
GO:0010543	regulation of platelet activation	-8.51903376
GO:0034110	regulation of homotypic cell-cell adhesion	-6.205291712
GO:0090330	regulation of platelet aggregation	-5.0422319
GO:0034112	positive regulation of homotypic cell-cell adhesion	-4.300505605
GO:0042119	neutrophil activation	-3.598556005
GO:0036230	granulocyte activation	-3.417757237
GO:0002548	monocyte chemotaxis	-2.938784718
GO:0038093	Fc receptor signaling pathway	-8.51903376
GO:0002274	myeloid leukocyte activation	-6.60263341
GO:0038095	Fc-epsilon receptor signaling pathway	-5.383841545
GO:0046903	secretion	-4.77998074
GO:0002366	leukocyte activation involved in immune response	-4.699317536
GO:0002263	cell activation involved in immune response	-4.637939042
GO:0045579	positive regulation of B cell differentiation	-4.484681481
GO:0002279	mast cell activation involved in immune response	-3.932113785
GO:0002902	regulation of B cell apoptotic process	-3.932113785
GO:0043303	mast cell degranulation	-3.932113785
GO:0002275	myeloid cell activation involved in immune response	-3.894414272



GO:0002448	mast cell mediated immunity	-3.810653527
GO:0045576	mast cell activation	-3.700049736
GO:0030888	regulation of B cell proliferation	-3.668664214
GO:0045577	regulation of B cell differentiation	-3.417757237
GO:0043299	leukocyte degranulation	-3.297846025
GO:0002673	regulation of acute inflammatory response	-2.883742534
GO:0032418	lysosome localization	-2.756492868
GO:1990849	vacuolar localization	-2.756492868
GO:0002702	positive regulation of production of molecular mediator of immune response	-2.642648247
GO:0050864	regulation of B cell activation	-2.63701341
GO:0045055	regulated exocytosis	-2.517103536
GO:0006887	exocytosis	-2.418013114
GO:0050871	positive regulation of B cell activation	-2.275929828
GO:0032940	secretion by cell	-2.097946359
GO:0046456	icosanoid biosynthetic process	-8.51903376
GO:0006690	icosanoid metabolic process	-8.506273005
GO:0071466	cellular response to xenobiotic stimulus	-8.235530811
GO:0044283	small molecule biosynthetic process	-7.91689543
GO:0046394	carboxylic acid biosynthetic process	-7.364439906
GO:0016053	organic acid biosynthetic process	-7.331324229
GO:0006631	fatty acid metabolic process	-6.489754039
GO:0006805	xenobiotic metabolic process	-6.16877933
GO:0008610	lipid biosynthetic process	-5.63549519
GO:0032787	monocarboxylic acid metabolic process	-5.535254779
GO:0042178	xenobiotic catabolic process	-5.309661703
GO:0033559	unsaturated fatty acid metabolic process	-5.090708846
GO:0042759	long-chain fatty acid biosynthetic process	-5.0422319
GO:0006633	fatty acid biosynthetic process	-4.752445487
GO:0006575	cellular modified amino acid metabolic process	-4.714901986
GO:0006692	prostanoid metabolic process	-4.518163071
GO:0006693	prostaglandin metabolic process	-4.518163071
GO:0072330	monocarboxylic acid biosynthetic process	-3.997238423
GO:0001676	long-chain fatty acid metabolic process	-3.792986253
GO:0006749	glutathione metabolic process	-2.498434788
GO:0044272	sulfur compound biosynthetic process	-2.402092399
GO:0018209	peptidyl-serine modification	-8.511848544
GO:0018105	peptidyl-serine phosphorylation	-7.879362112
GO:0043393	regulation of protein binding	-6.480454685
GO:0018107	peptidyl-threonine phosphorylation	-5.966250708
GO:0018210	peptidyl-threonine modification	-5.667640153
GO:0051100	negative regulation of binding	-4.94392675
GO:0032091	negative regulation of protein binding	-4.090776771

GO:0010906	regulation of glucose metabolic process	-3.585147496
GO:0010675	regulation of cellular carbohydrate metabolic process	-3.151522286
GO:0010907	positive regulation of glucose metabolic process	-3.026484409
GO:0006109	regulation of carbohydrate metabolic process	-2.78452125
GO:0010676	positive regulation of cellular carbohydrate metabolic process	-2.663866989
GO:0008286	insulin receptor signaling pathway	-2.578150419
GO:0005976	polysaccharide metabolic process	-2.288506924
GO:0045913	positive regulation of carbohydrate metabolic process	-2.241710754
GO:0043269	regulation of ion transport	-8.477303986
GO:0051924	regulation of calcium ion transport	-6.481365199
GO:0010959	regulation of metal ion transport	-5.496859706
GO:0043270	positive regulation of ion transport	-4.355828848
GO:0051928	positive regulation of calcium ion transport	-2.578453323
GO:0010810	regulation of cell-substrate adhesion	-8.254909162
GO:0001952	regulation of cell-matrix adhesion	-8.216439272
GO:0150116	regulation of cell-substrate junction organization	-6.112049883
GO:0034446	substrate adhesion-dependent cell spreading	-5.231422398
GO:0051893	regulation of focal adhesion assembly	-4.943974638
GO:0090109	regulation of cell-substrate junction assembly	-4.943974638
GO:0150117	positive regulation of cell-substrate junction organization	-4.923165698
GO:0043550	regulation of lipid kinase activity	-4.783424718
GO:0090218	positive regulation of lipid kinase activity	-4.610387768
GO:0031589	cell-substrate adhesion	-4.563296057
GO:0001954	positive regulation of cell-matrix adhesion	-3.925064108
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	-3.864349935
GO:0051894	positive regulation of focal adhesion assembly	-3.648256523
GO:0010811	positive regulation of cell-substrate adhesion	-3.601588866
GO:1901888	regulation of cell junction assembly	-3.46390458
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	-3.33651332
GO:0007160	cell-matrix adhesion	-2.481567703
GO:0032355	response to estradiol	-8.2474917
GO:0043200	response to amino acid	-7.128930794
GO:0001101	response to acid chemical	-6.725987508
GO:0071392	cellular response to estradiol stimulus	-4.473943562
GO:0071230	cellular response to amino acid stimulus	-2.241710754
GO:0071229	cellular response to acid chemical	-2.098876582
GO:0007159	leukocyte cell-cell adhesion	-8.163095614
GO:0098609	cell-cell adhesion	-5.920458802
GO:0071674	mononuclear cell migration	-4.926560597
GO:0070486	leukocyte aggregation	-4.823930581
GO:0072678	T cell migration	-3.504816454
GO:0072676	lymphocyte migration	-3.403810574
GO:0045123	cellular extravasation	-3.026484409

GO:0038127	ERBB signaling pathway	-8.000432293
GO:0007173	epidermal growth factor receptor signaling pathway	-7.067738962
GO:0033135	regulation of peptidyl-serine phosphorylation	-5.331557269
GO:1903076	regulation of protein localization to plasma membrane	-5.090708846
GO:1905475	regulation of protein localization to membrane	-4.826804822
GO:1904375	regulation of protein localization to cell periphery	-4.630175874
GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	-4.19429302
GO:0070849	response to epidermal growth factor	-4.19429302
GO:1904031	positive regulation of cyclin-dependent protein kinase activity	-4.05398091
GO:1905477	positive regulation of protein localization to membrane	-3.945870798
GO:0033138	positive regulation of peptidyl-serine phosphorylation	-3.867851957
GO:0032768	regulation of monooxygenase activity	-3.864349935
GO:1903078	positive regulation of protein localization to plasma membrane	-3.777465917
GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	-3.738768372
GO:1904029	regulation of cyclin-dependent protein kinase activity	-3.686108516
GO:0045787	positive regulation of cell cycle	-3.599428221
GO:1904377	positive regulation of protein localization to cell periphery	-3.591792775
GO:0032770	positive regulation of monooxygenase activity	-3.376455779
GO:0050999	regulation of nitric-oxide synthase activity	-3.026484409
GO:0071364	cellular response to epidermal growth factor stimulus	-2.996523184
GO:0051341	regulation of oxidoreductase activity	-2.80986657
GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	-2.686335833
GO:0051353	positive regulation of oxidoreductase activity	-2.578150419
GO:0045931	positive regulation of mitotic cell cycle	-2.529156705
GO:1902808	positive regulation of cell cycle G1/S phase transition	-2.423979776
GO:0042058	regulation of epidermal growth factor receptor signaling pathway	-2.337387332
GO:1901184	regulation of ERBB signaling pathway	-2.241710754
GO:1902893	regulation of miRNA transcription	-7.94820614
GO:0001837	epithelial to mesenchymal transition	-7.142785982
GO:0048762	mesenchymal cell differentiation	-7.068576747
GO:0060485	mesenchyme development	-6.925294287
GO:0030278	regulation of ossification	-5.83521409
GO:0003206	cardiac chamber morphogenesis	-5.717245075
GO:1902895	positive regulation of miRNA transcription	-5.660591272
GO:0071560	cellular response to transforming growth factor beta stimulus	-5.195738897
GO:0071559	response to transforming growth factor beta	-5.066729504
GO:0008544	epidermis development	-4.946077483
GO:0003205	cardiac chamber development	-4.909904966
GO:0060389	pathway-restricted SMAD protein phosphorylation	-4.389226998
GO:0060412	ventricular septum morphogenesis	-4.388971116

GO:0010862	positive regulation of pathway-restricted SMAD protein phosphorylation	-4.12259354
GO:0045778	positive regulation of ossification	-3.956321576
GO:0003007	heart morphogenesis	-3.800924933
GO:0055008	cardiac muscle tissue morphogenesis	-3.777465917
GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	-3.722114756
GO:0043588	skin development	-3.706847735
GO:0060317	cardiac epithelial to mesenchymal transition	-3.550789691
GO:0048565	digestive tract development	-3.520840466
GO:0007435	salivary gland morphogenesis	-3.504816454
GO:0060411	cardiac septum morphogenesis	-3.494919094
GO:0003281	ventricular septum development	-3.448684857
GO:0060415	muscle tissue morphogenesis	-3.448684857
GO:0007431	salivary gland development	-3.417757237
GO:0031069	hair follicle morphogenesis	-3.417757237
GO:0061061	muscle structure development	-3.397024311
GO:0001942	hair follicle development	-3.360223118
GO:0055123	digestive system development	-3.340727355
GO:0048644	muscle organ morphogenesis	-3.297108752
GO:0022404	molting cycle process	-3.2766443
GO:0022405	hair cycle process	-3.2766443
GO:0098773	skin epidermis development	-3.2766443
GO:0048730	epidermis morphogenesis	-3.26037759
GO:1905207	regulation of cardiocyte differentiation	-3.26037759
GO:0060537	muscle tissue development	-3.246177213
GO:0003203	endocardial cushion morphogenesis	-3.224038362
GO:1905314	semi-lunar valve development	-3.057221553
GO:0007179	transforming growth factor beta receptor signaling pathway	-3.033370362
GO:0042303	molting cycle	-3.033370362
GO:0042633	hair cycle	-3.033370362
GO:0035272	exocrine system development	-2.996523184
GO:0003197	endocardial cushion development	-2.910941679
GO:0048738	cardiac muscle tissue development	-2.901835172
GO:0055010	ventricular cardiac muscle tissue morphogenesis	-2.883742534
GO:0014706	striated muscle tissue development	-2.847476443
GO:0003279	cardiac septum development	-2.839754762
GO:0072132	mesenchyme morphogenesis	-2.780855605
GO:0010718	positive regulation of epithelial to mesenchymal transition	-2.709251562
GO:0003179	heart valve morphogenesis	-2.686335833
GO:0003229	ventricular cardiac muscle tissue development	-2.663866989
GO:0007517	muscle organ development	-2.630942793
GO:0003231	cardiac ventricle development	-2.5659631

GO:0072175	epithelial tube formation	-2.517103536
GO:0043583	ear development	-2.48481191
GO:0003170	heart valve development	-2.479353688
GO:1904888	cranial skeletal system development	-2.371219039
GO:0016331	morphogenesis of embryonic epithelium	-2.369414538
GO:0003208	cardiac ventricle morphogenesis	-2.354174047
GO:0035148	tube formation	-2.337515912
GO:0030509	BMP signaling pathway	-2.196841192
GO:0001843	neural tube closure	-2.098876582
GO:0060606	tube closure	-2.08558614
GO:0014020	primary neural tube formation	-2.021526278
GO:0038083	peptidyl-tyrosine autophosphorylation	-7.820043856
GO:0044403	biological process involved in symbiotic interaction	-7.729973951
GO:0051701	biological process involved in interaction with host	-3.203514987
GO:0044409	entry into host	-2.80986657
GO:0052126	movement in host environment	-2.458381135
GO:0016032	viral process	-2.240840068
GO:0032642	regulation of chemokine production	-7.798323649
GO:0002886	regulation of myeloid leukocyte mediated immunity	-5.118712187
GO:0032722	positive regulation of chemokine production	-3.51857078
GO:0043304	regulation of mast cell degranulation	-3.376455779
GO:0033006	regulation of mast cell activation involved in immune response	-3.297846025
GO:0033003	regulation of mast cell activation	-2.938784718
GO:0043300	regulation of leukocyte degranulation	-2.83116673
GO:1903305	regulation of regulated secretory pathway	-2.402092399
GO:0008202	steroid metabolic process	-7.569183404
GO:1901615	organic hydroxy compound metabolic process	-7.446637666
GO:0016125	sterol metabolic process	-2.481567703
GO:1901617	organic hydroxy compound biosynthetic process	-2.106896887
GO:0042542	response to hydrogen peroxide	-7.493811982
GO:1990748	cellular detoxification	-6.251996584
GO:0097237	cellular response to toxic substance	-6.035538036
GO:0009636	response to toxic substance	-5.934156
GO:0098754	detoxification	-5.582287344
GO:0098869	cellular oxidant detoxification	-5.430679991
GO:0019430	removal of superoxide radicals	-4.58796101
GO:0006801	superoxide metabolic process	-4.473943562
GO:0071450	cellular response to oxygen radical	-4.389226998
GO:0071451	cellular response to superoxide	-4.389226998
GO:0051602	response to electrical stimulus	-4.388971116
GO:0000303	response to superoxide	-4.13991307
GO:0000305	response to oxygen radical	-4.066733811
GO:0007568	aging	-3.93875277

GO:0045454	cell redox homeostasis	-3.088773975
GO:0014075	response to amine	-2.996523184
GO:0072593	reactive oxygen species metabolic process	-2.965924416
GO:0070301	cellular response to hydrogen peroxide	-2.423979776
GO:0046634	regulation of alpha-beta T cell activation	-7.461725629
GO:0043366	beta selection	-7.029752835
GO:0046632	alpha-beta T cell differentiation	-5.15558001
GO:0046635	positive regulation of alpha-beta T cell activation	-4.814504723
GO:1903706	regulation of hemopoiesis	-4.78726531
GO:0046637	regulation of alpha-beta T cell differentiation	-4.783424718
GO:0046640	regulation of alpha-beta T cell proliferation	-4.610387768
GO:0046631	alpha-beta T cell activation	-4.523918936
GO:1902105	regulation of leukocyte differentiation	-4.064663945
GO:0046641	positive regulation of alpha-beta T cell proliferation	-3.810653527
GO:0045621	positive regulation of lymphocyte differentiation	-3.536703187
GO:0045619	regulation of lymphocyte differentiation	-3.46390458
GO:0045058	T cell selection	-3.026484409
GO:0045580	regulation of T cell differentiation	-2.924085708
GO:1902107	positive regulation of leukocyte differentiation	-2.869006791
GO:1903708	positive regulation of hemopoiesis	-2.869006791
GO:0046638	positive regulation of alpha-beta T cell differentiation	-2.805739715
GO:0045582	positive regulation of T cell differentiation	-2.737775421
GO:0050848	regulation of calcium-mediated signaling	-2.211592639
GO:0051769	regulation of nitric-oxide synthase biosynthetic process	-7.449166496
GO:0060416	response to growth hormone	-6.40147965
GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	-6.022842965
GO:0060396	growth hormone receptor signaling pathway	-3.997606803
GO:0071378	cellular response to growth hormone stimulus	-3.932113785
GO:0007259	receptor signaling pathway via JAK-STAT	-2.938784718
GO:0097696	receptor signaling pathway via STAT	-2.910941679
GO:0009895	negative regulation of catabolic process	-7.402572752
GO:0031330	negative regulation of cellular catabolic process	-4.456762875
GO:0042177	negative regulation of protein catabolic process	-3.536703187
GO:0042176	regulation of protein catabolic process	-3.301129466
GO:1903362	regulation of cellular protein catabolic process	-2.156155259
GO:0009896	positive regulation of catabolic process	-2.020137108
GO:0015908	fatty acid transport	-7.386577474
GO:0015909	long-chain fatty acid transport	-6.80384732
GO:0010876	lipid localization	-5.258079936
GO:0032309	icosanoid secretion	-5.170556276
GO:0006869	lipid transport	-4.779738372
GO:0071715	icosanoid transport	-4.708150754

GO:0050482	arachidonic acid secretion	-3.754114469
GO:1903963	arachidonate transport	-3.754114469
GO:0015849	organic acid transport	-3.656221621
GO:0015718	monocarboxylic acid transport	-2.982496277
GO:0097006	regulation of plasma lipoprotein particle levels	-2.686335833
GO:0061383	trabecula morphogenesis	-7.301381528
GO:0046620	regulation of organ growth	-5.139858569
GO:0061384	heart trabecula morphogenesis	-4.923165698
GO:0055021	regulation of cardiac muscle tissue growth	-4.846083842
GO:0048638	regulation of developmental growth	-4.663475562
GO:0060420	regulation of heart growth	-4.635014918
GO:0060043	regulation of cardiac muscle cell proliferation	-4.12259354
GO:0060343	trabecula formation	-3.810653527
GO:0048705	skeletal system morphogenesis	-3.21662651
GO:0032526	response to retinoic acid	-2.795153446
GO:0050918	positive chemotaxis	-7.181790516
GO:0045744	negative regulation of G protein-coupled receptor signaling pathway	-2.83116673
GO:0008277	regulation of G protein-coupled receptor signaling pathway	-2.435583723
GO:0050680	negative regulation of epithelial cell proliferation	-7.158434033
GO:0001937	negative regulation of endothelial cell proliferation	-3.381860332
GO:0016525	negative regulation of angiogenesis	-3.203514987
GO:2000181	negative regulation of blood vessel morphogenesis	-3.177323238
GO:1901343	negative regulation of vasculature development	-3.164374566
GO:0010827	regulation of glucose transmembrane transport	-7.142785982
GO:0034762	regulation of transmembrane transport	-6.921571184
GO:0042593	glucose homeostasis	-6.370790296
GO:0033500	carbohydrate homeostasis	-6.352864372
GO:0010828	positive regulation of glucose transmembrane transport	-5.758533407
GO:0046324	regulation of glucose import	-5.082513923
GO:0034764	positive regulation of transmembrane transport	-4.971688255
GO:0046326	positive regulation of glucose import	-4.610387768
GO:0001678	cellular glucose homeostasis	-2.839754762
GO:2001242	regulation of intrinsic apoptotic signaling pathway	-7.002717175
GO:0051881	regulation of mitochondrial membrane potential	-6.038037251
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	-5.115152029
GO:0010043	response to zinc ion	-3.98821009
GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	-3.504816454
GO:0010212	response to ionizing radiation	-3.312411372
GO:0006974	cellular response to DNA damage stimulus	-3.286225761
GO:0010332	response to gamma radiation	-2.663866989
GO:0008637	apoptotic mitochondrial changes	-2.598984718

GO:0042391	regulation of membrane potential	-2.452269628
GO:0097306	cellular response to alcohol	-2.021526278
GO:0032680	regulation of tumor necrosis factor production	-6.751470684
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	-6.652116058
GO:0032760	positive regulation of tumor necrosis factor production	-5.066523799
GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	-4.972265791
GO:0032675	regulation of interleukin-6 production	-3.812816894
GO:0032755	positive regulation of interleukin-6 production	-2.982496277
GO:0097066	response to thyroid hormone	-6.695815484
GO:0097067	cellular response to thyroid hormone stimulus	-4.217639664
GO:0002244	hematopoietic progenitor cell differentiation	-2.046685718
GO:1900407	regulation of cellular response to oxidative stress	-6.612902956
GO:1902882	regulation of response to oxidative stress	-6.337847294
GO:1903201	regulation of oxidative stress-induced cell death	-5.795729341
GO:0048012	hepatocyte growth factor receptor signaling pathway	-5.114221558
GO:0001889	liver development	-4.670193976
GO:0061008	hepaticobiliary system development	-4.610433095
GO:1903202	negative regulation of oxidative stress-induced cell death	-3.925064108
GO:0010507	negative regulation of autophagy	-3.159399861
GO:1901031	regulation of response to reactive oxygen species	-3.088773975
GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	-6.611511541
GO:0032682	negative regulation of chemokine production	-5.238651716
GO:0071637	regulation of monocyte chemotactic protein-1 production	-3.932113785
GO:0010804	negative regulation of tumor necrosis factor-mediated signaling pathway	-3.550789691
GO:0032652	regulation of interleukin-1 production	-3.474076902
GO:0032651	regulation of interleukin-1 beta production	-2.766174948
GO:0032720	negative regulation of tumor necrosis factor production	-2.272684787
GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	-2.241710754
GO:0051051	negative regulation of transport	-6.527692166
GO:0051048	negative regulation of secretion	-2.946636282
GO:1903828	negative regulation of protein localization	-2.646438389
GO:0050709	negative regulation of protein secretion	-2.423979776
GO:1903531	negative regulation of secretion by cell	-2.337515912
GO:1903522	regulation of blood circulation	-6.465940124
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	-5.782565661
GO:0032660	regulation of interleukin-17 production	-5.613334692



GO:0002819	regulation of adaptive immune response	-5.519312186
GO:0032740	positive regulation of interleukin-17 production	-5.238651716
GO:0045822	negative regulation of heart contraction	-5.238651716
GO:1903523	negative regulation of blood circulation	-5.170556276
GO:0008016	regulation of heart contraction	-4.272513314
GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	-3.774735282
GO:0002821	positive regulation of adaptive immune response	-3.686108516
GO:0032649	regulation of interferon-gamma production	-3.686108516
GO:2000316	regulation of T-helper 17 type immune response	-3.460510079
GO:0032729	positive regulation of interferon-gamma production	-3.360223118
GO:0007204	positive regulation of cytosolic calcium ion concentration	-2.714008588
GO:2000191	regulation of fatty acid transport	-6.40147965
GO:0032890	regulation of organic acid transport	-6.038037251
GO:0090237	regulation of arachidonic acid secretion	-5.28885554
GO:0002532	production of molecular mediator involved in inflammatory response	-4.389226998
GO:0044070	regulation of anion transport	-4.224522423
GO:0032303	regulation of eicosanoid secretion	-3.869898183
GO:0042116	macrophage activation	-2.663866989
GO:0120161	regulation of cold-induced thermogenesis	-6.392483081
GO:0120162	positive regulation of cold-induced thermogenesis	-4.048220287
GO:0045428	regulation of nitric oxide biosynthetic process	-6.390713081
GO:0080164	regulation of nitric oxide metabolic process	-6.267311401
GO:0045429	positive regulation of nitric oxide biosynthetic process	-5.861421458
GO:1904407	positive regulation of nitric oxide metabolic process	-5.758533407
GO:0009408	response to heat	-4.048220287
GO:0009266	response to temperature stimulus	-3.881845422
GO:0046677	response to antibiotic	-2.910941679
GO:0034605	cellular response to heat	-2.756492868
GO:0031099	regeneration	-6.347703571
GO:0031100	animal organ regeneration	-4.910802172
GO:0010821	regulation of mitochondrion organization	-6.32556126
GO:0010506	regulation of autophagy	-3.759449635
GO:0010822	positive regulation of mitochondrion organization	-3.381860332
GO:0016241	regulation of macroautophagy	-3.088663012
GO:0010638	positive regulation of organelle organization	-6.236950521
GO:0010310	regulation of hydrogen peroxide metabolic process	-5.718752183
GO:0071622	regulation of granulocyte chemotaxis	-5.43461533
GO:0060491	regulation of cell projection assembly	-5.420383079
GO:0051492	regulation of stress fiber assembly	-5.375014846
GO:1902743	regulation of lamellipodium organization	-5.350857763

GO:0110020	regulation of actomyosin structure organization	-5.139858569
GO:0032231	regulation of actin filament bundle assembly	-5.018907987
GO:0120034	positive regulation of plasma membrane bounded cell projection assembly	-5.018907987
GO:0032970	regulation of actin filament-based process	-4.7965876
GO:1902745	positive regulation of lamellipodium organization	-4.658536989
GO:0031346	positive regulation of cell projection organization	-4.531823314
GO:0120035	regulation of plasma membrane bounded cell projection organization	-4.499126998
GO:0120032	regulation of plasma membrane bounded cell projection assembly	-4.462460603
GO:0051493	regulation of cytoskeleton organization	-4.46104278
GO:0010591	regulation of lamellipodium assembly	-4.430899217
GO:0031344	regulation of cell projection organization	-4.386591869
GO:0008360	regulation of cell shape	-4.135030735
GO:0022604	regulation of cell morphogenesis	-4.064663945
GO:0032956	regulation of actin cytoskeleton organization	-3.599428221
GO:0051495	positive regulation of cytoskeleton organization	-3.557652995
GO:0010592	positive regulation of lamellipodium assembly	-3.550789691
GO:0051497	negative regulation of stress fiber assembly	-3.33651332
GO:0090022	regulation of neutrophil chemotaxis	-3.33651332
GO:0032232	negative regulation of actin filament bundle assembly	-3.224038362
GO:0030041	actin filament polymerization	-3.188764589
GO:0032273	positive regulation of protein polymerization	-3.068294072
GO:0043277	apoptotic cell clearance	-2.967301303
GO:1902622	regulation of neutrophil migration	-2.938784718
GO:1902905	positive regulation of supramolecular fiber organization	-2.890820235
GO:0007015	actin filament organization	-2.833565222
GO:0051496	positive regulation of stress fiber assembly	-2.780855605
GO:0110053	regulation of actin filament organization	-2.760818361
GO:0007163	establishment or maintenance of cell polarity	-2.63701341
GO:0030865	cortical cytoskeleton organization	-2.578150419
GO:0032233	positive regulation of actin filament bundle assembly	-2.557690368
GO:0008154	actin polymerization or depolymerization	-2.517844054
GO:0097435	supramolecular fiber organization	-2.416193952
GO:0070507	regulation of microtubule cytoskeleton organization	-2.256024321
GO:0007264	small GTPase mediated signal transduction	-2.142507837
GO:0006897	endocytosis	-2.09100555
GO:1902903	regulation of supramolecular fiber organization	-2.081987197
GO:0051258	protein polymerization	-2.00916892
GO:1900076	regulation of cellular response to insulin stimulus	-6.112049883
GO:0031295	T cell costimulation	-5.914876393
GO:0031294	lymphocyte costimulation	-5.809329102

GO:1900078	positive regulation of cellular response to insulin stimulus	-5.309661703
GO:0046626	regulation of insulin receptor signaling pathway	-4.814504723
GO:0048011	neurotrophin TRK receptor signaling pathway	-4.58796101
GO:0046628	positive regulation of insulin receptor signaling pathway	-3.869898183
GO:0038179	neurotrophin signaling pathway	-3.648256523
GO:0061515	myeloid cell development	-3.51857078
GO:0098751	bone cell development	-3.460510079
GO:0007229	integrin-mediated signaling pathway	-3.050728521
GO:0045113	regulation of integrin biosynthetic process	-6.032669996
GO:0051092	positive regulation of NF-kappaB transcription factor activity	-2.256024321
GO:0050818	regulation of coagulation	-5.931152806
GO:0050819	negative regulation of coagulation	-5.522002094
GO:0030194	positive regulation of blood coagulation	-3.550789691
GO:1900048	positive regulation of hemostasis	-3.550789691
GO:0030193	regulation of blood coagulation	-3.542592824
GO:0050820	positive regulation of coagulation	-3.504816454
GO:1900046	regulation of hemostasis	-3.494919094
GO:0030195	negative regulation of blood coagulation	-2.938784718
GO:1900047	negative regulation of hemostasis	-2.910941679
GO:0090303	positive regulation of wound healing	-2.517844054
GO:0061041	regulation of wound healing	-2.435583723
GO:0061045	negative regulation of wound healing	-2.337387332
GO:1903036	positive regulation of response to wounding	-2.272684787
GO:1903034	regulation of response to wounding	-2.106896887
GO:1903035	negative regulation of response to wounding	-2.098876582
GO:0051054	positive regulation of DNA metabolic process	-5.911996219
GO:2000573	positive regulation of DNA biosynthetic process	-4.6638091
GO:0051972	regulation of telomerase activity	-4.19429302
GO:1904356	regulation of telomere maintenance via telomere lengthening	-3.749544794
GO:0051052	regulation of DNA metabolic process	-3.724493635
GO:2000278	regulation of DNA biosynthetic process	-3.651827575
GO:0051973	positive regulation of telomerase activity	-3.297846025
GO:0032204	regulation of telomere maintenance	-2.933336161
GO:0032210	regulation of telomere maintenance via telomerase	-2.732631226
GO:0031647	regulation of protein stability	-2.435986643
GO:0010469	regulation of signaling receptor activity	-5.856980018
GO:1902894	negative regulation of miRNA transcription	-4.066733811
GO:0090287	regulation of cellular response to growth factor stimulus	-3.830086401
GO:0046320	regulation of fatty acid oxidation	-3.376455779
GO:0043502	regulation of muscle adaptation	-3.016215128
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	-2.949538981
GO:1905562	regulation of vascular endothelial cell proliferation	-2.883742534

GO:2000272	negative regulation of signaling receptor activity	-2.479353688
GO:0010611	regulation of cardiac muscle hypertrophy	-2.423979776
GO:0014743	regulation of muscle hypertrophy	-2.371219039
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	-2.327050591
GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	-2.296141321
GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	-2.265939334
GO:0045926	negative regulation of growth	-2.262796115
GO:0000165	MAPK cascade	-5.727971916
GO:0031281	positive regulation of cyclase activity	-4.05398091
GO:0031098	stress-activated protein kinase signaling cascade	-3.591792775
GO:0031279	regulation of cyclase activity	-3.317855103
GO:0051403	stress-activated MAPK cascade	-2.517844054
GO:0007610	behavior	-5.618870018
GO:0099177	regulation of trans-synaptic signaling	-3.729103234
GO:0007611	learning or memory	-3.646231472
GO:0050890	cognition	-3.262847539
GO:0050804	modulation of chemical synaptic transmission	-3.04344013
GO:0014910	regulation of smooth muscle cell migration	-5.606116233
GO:0061098	positive regulation of protein tyrosine kinase activity	-3.956321576
GO:0061097	regulation of protein tyrosine kinase activity	-3.122282021
GO:0070555	response to interleukin-1	-2.493310636
GO:0035094	response to nicotine	-5.522002094
GO:0071496	cellular response to external stimulus	-4.889585467
GO:0031668	cellular response to extracellular stimulus	-4.758986389
GO:0031669	cellular response to nutrient levels	-4.246558691
GO:0042594	response to starvation	-2.646438389
GO:0009267	cellular response to starvation	-2.170028695
GO:1901216	positive regulation of neuron death	-5.48770807
GO:0060322	head development	-4.786693947
GO:0043525	positive regulation of neuron apoptotic process	-4.02075444
GO:0007420	brain development	-3.783237323
GO:0030900	forebrain development	-2.766540644
GO:0021537	telencephalon development	-2.255441216
GO:0021543	pallium development	-2.124618421
GO:0040013	negative regulation of locomotion	-5.466721552
GO:0002686	negative regulation of leukocyte migration	-5.392301184
GO:2000146	negative regulation of cell motility	-4.989086224
GO:0051271	negative regulation of cellular component movement	-4.910672
GO:0030336	negative regulation of cell migration	-4.32197564
GO:0002689	negative regulation of leukocyte chemotaxis	-3.810653527

GO:0050922	negative regulation of chemotaxis	-3.542592824
GO:0003018	vascular process in circulatory system	-5.44076812
GO:0009743	response to carbohydrate	-4.653141911
GO:0035296	regulation of tube diameter	-4.316407356
GO:0097746	blood vessel diameter maintenance	-4.316407356
GO:0035150	regulation of tube size	-4.299276582
GO:0034284	response to monosaccharide	-4.057383188
GO:0090066	regulation of anatomical structure size	-3.326722883
GO:0009749	response to glucose	-3.257114236
GO:0045777	positive regulation of blood pressure	-3.224038362
GO:0009746	response to hexose	-3.203514987
GO:0042311	vasodilation	-2.857159545
GO:0019229	regulation of vasoconstriction	-2.498434788
GO:0014823	response to activity	-2.460590562
GO:0097191	extrinsic apoptotic signaling pathway	-5.430679991
GO:0007005	mitochondrion organization	-3.773797276
GO:0038034	signal transduction in absence of ligand	-3.550789691
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	-3.550789691
GO:0007006	mitochondrial membrane organization	-2.642648247
GO:0046902	regulation of mitochondrial membrane permeability	-2.537592175
GO:0006839	mitochondrial transport	-2.296141321
GO:0090559	regulation of membrane permeability	-2.272684787
GO:0032872	regulation of stress-activated MAPK cascade	-5.420383079
GO:0070302	regulation of stress-activated protein kinase signaling cascade	-5.37217153
GO:1901224	positive regulation of NIK/NF-kappaB signaling	-3.591792775
GO:1901222	regulation of NIK/NF-kappaB signaling	-2.780590493
GO:0032874	positive regulation of stress-activated MAPK cascade	-2.493310636
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	-2.469925039
GO:0046328	regulation of JNK cascade	-2.380218931
GO:2001026	regulation of endothelial cell chemotaxis	-5.383841545
GO:2001028	positive regulation of endothelial cell chemotaxis	-4.389226998
GO:0003158	endothelium development	-3.033370362
GO:0045446	endothelial cell differentiation	-2.257088005
GO:0045598	regulation of fat cell differentiation	-5.371707728
GO:0045600	positive regulation of fat cell differentiation	-4.846083842
GO:0006006	glucose metabolic process	-4.027298015
GO:0061448	connective tissue development	-3.363427185
GO:0019318	hexose metabolic process	-3.312411372
GO:0005996	monosaccharide metabolic process	-3.052026281
GO:0005975	carbohydrate metabolic process	-2.924996159
GO:0046622	positive regulation of organ growth	-2.756492868
GO:0051216	cartilage development	-2.226722372

GO:0019395	fatty acid oxidation	-2.18228809
GO:0042692	muscle cell differentiation	-2.149315443
GO:0048639	positive regulation of developmental growth	-2.115726801
GO:0034440	lipid oxidation	-2.11233501
GO:0030258	lipid modification	-2.046755222
GO:0120254	olefinic compound metabolic process	-5.331557269
GO:0006720	isoprenoid metabolic process	-4.816174602
GO:0034754	cellular hormone metabolic process	-4.590863974
GO:0006721	terpenoid metabolic process	-4.069378208
GO:0001523	retinoid metabolic process	-3.236533122
GO:0006066	alcohol metabolic process	-3.188840502
GO:0008210	estrogen metabolic process	-3.188764589
GO:0016101	diterpenoid metabolic process	-3.178312401
GO:0042572	retinol metabolic process	-2.780855605
GO:0019369	arachidonic acid metabolic process	-2.620206303
GO:0034308	primary alcohol metabolic process	-2.021526278
GO:0035821	modulation of process of another organism	-5.309661703
GO:0051709	regulation of killing of cells of another organism	-5.28885554
GO:0032757	positive regulation of interleukin-8 production	-2.537592175
GO:0048678	response to axon injury	-5.231422398
GO:0031103	axon regeneration	-3.700049736
GO:0031102	neuron projection regeneration	-3.417757237
GO:0071695	anatomical structure maturation	-5.217124323
GO:0021700	developmental maturation	-4.695771097
GO:0048469	cell maturation	-3.02803249
GO:0009615	response to virus	-5.204578903
GO:0032481	positive regulation of type I interferon production	-5.012035481
GO:0098586	cellular response to virus	-4.156468705
GO:0032479	regulation of type I interferon production	-3.926057035
GO:0050691	regulation of defense response to virus by host	-3.026484409
GO:0050688	regulation of defense response to virus	-2.320851758
GO:0048010	vascular endothelial growth factor receptor signaling pathway	-4.981623907
GO:0035924	cellular response to vascular endothelial growth factor stimulus	-4.12259354
GO:0002040	sprouting angiogenesis	-3.805895085
GO:0050927	positive regulation of positive chemotaxis	-3.700049736
GO:0050926	regulation of positive chemotaxis	-3.648256523
GO:0043491	protein kinase B signaling	-3.154497773
GO:0001894	tissue homeostasis	-4.87660039
GO:0060249	anatomical structure homeostasis	-4.344848908
GO:0048871	multicellular organismal homeostasis	-4.331183651
GO:0048873	homeostasis of number of cells within a tissue	-3.504816454
GO:0061035	regulation of cartilage development	-3.494919094

GO:0061037	negative regulation of cartilage development	-3.460510079
GO:0071675	regulation of mononuclear cell migration	-4.773488546
GO:2000401	regulation of lymphocyte migration	-3.668664214
GO:0071677	positive regulation of mononuclear cell migration	-3.616994367
GO:0044319	wound healing, spreading of cells	-3.550789691
GO:0090505	epiboly involved in wound healing	-3.550789691
GO:0090504	epiboly	-3.504816454
GO:2000406	positive regulation of T cell migration	-3.417757237
GO:2000403	positive regulation of lymphocyte migration	-3.188764589
GO:2000404	regulation of T cell migration	-2.938784718
GO:0002011	morphogenesis of an epithelial sheet	-2.780855605
GO:0001961	positive regulation of cytokine-mediated signaling pathway	-2.620206303
GO:0060760	positive regulation of response to cytokine stimulus	-2.479353688
GO:0071402	cellular response to lipoprotein particle stimulus	-4.708150754
GO:0036294	cellular response to decreased oxygen levels	-4.333673944
GO:0071453	cellular response to oxygen levels	-4.088104713
GO:0071456	cellular response to hypoxia	-3.443567003
GO:0055094	response to lipoprotein particle	-3.376455779
GO:0042476	odontogenesis	-4.690475264
GO:0045747	positive regulation of Notch signaling pathway	-4.158040881
GO:0008593	regulation of Notch signaling pathway	-4.069378208
GO:0032570	response to progesterone	-3.121184104
GO:0032147	activation of protein kinase activity	-2.446934511
GO:1902117	positive regulation of organelle assembly	-2.226547429
GO:0045216	cell-cell junction organization	-2.080770104
GO:0002833	positive regulation of response to biotic stimulus	-4.622828939
GO:0002861	regulation of inflammatory response to antigenic stimulus	-4.269357534
GO:0038094	Fc-gamma receptor signaling pathway	-3.550789691
GO:0002862	negative regulation of inflammatory response to antigenic stimulus	-3.417757237
GO:0045089	positive regulation of innate immune response	-3.270775606
GO:0034103	regulation of tissue remodeling	-3.178312401
GO:0002218	activation of innate immune response	-2.517844054
GO:1900015	regulation of cytokine production involved in inflammatory response	-4.606640009
GO:1900371	regulation of purine nucleotide biosynthetic process	-4.348104665
GO:0030808	regulation of nucleotide biosynthetic process	-4.308249183
GO:0045776	negative regulation of blood pressure	-4.12259354
GO:0030810	positive regulation of nucleotide biosynthetic process	-3.648256523
GO:1900373	positive regulation of purine nucleotide biosynthetic process	-3.648256523
GO:0007623	circadian rhythm	-3.443567003
GO:0043467	regulation of generation of precursor metabolites and energy	-3.384072629
GO:0019932	second-messenger-mediated signaling	-3.299163339

GO:1900542	regulation of purine nucleotide metabolic process	-3.122282021
GO:1900016	negative regulation of cytokine production involved in inflammatory response	-3.121184104
GO:0006140	regulation of nucleotide metabolic process	-3.08607163
GO:0045981	positive regulation of nucleotide metabolic process	-2.883742534
GO:1900544	positive regulation of purine nucleotide metabolic process	-2.883742534
GO:0044344	cellular response to fibroblast growth factor stimulus	-4.523918936
GO:0060602	branch elongation of an epithelium	-4.389226998
GO:0071774	response to fibroblast growth factor	-4.368389267
GO:0051781	positive regulation of cell division	-4.178883093
GO:0008543	fibroblast growth factor receptor signaling pathway	-4.12259354
GO:0003401	axis elongation	-3.810653527
GO:0051302	regulation of cell division	-3.618529669
GO:0060560	developmental growth involved in morphogenesis	-2.669176887
GO:0030901	midbrain development	-2.15375782
GO:0035303	regulation of dephosphorylation	-4.514268992
GO:0010921	regulation of phosphatase activity	-4.368389267
GO:0010923	negative regulation of phosphatase activity	-3.188764589
GO:0035305	negative regulation of dephosphorylation	-2.857159545
GO:0043666	regulation of phosphoprotein phosphatase activity	-2.598984718
GO:0035304	regulation of protein dephosphorylation	-2.07245992
GO:0003376	sphingosine-1-phosphate receptor signaling pathway	-4.389226998
GO:0090520	sphingolipid mediated signaling pathway	-4.300505605
GO:0045730	respiratory burst	-3.754114469
GO:0048015	phosphatidylinositol-mediated signaling	-3.426082434
GO:0048017	inositol lipid-mediated signaling	-3.338890684
GO:0014065	phosphatidylinositol 3-kinase signaling	-3.154497773
GO:0050994	regulation of lipid catabolic process	-2.557690368
GO:0051057	positive regulation of small GTPase mediated signal transduction	-2.388529752
GO:0051591	response to cAMP	-2.098876582
GO:0048286	lung alveolus development	-4.308249183
GO:0009791	post-embryonic development	-4.29510201
GO:0045165	cell fate commitment	-3.865865554
GO:0002053	positive regulation of mesenchymal cell proliferation	-3.810653527
GO:0010464	regulation of mesenchymal cell proliferation	-3.504816454
GO:0030177	positive regulation of Wnt signaling pathway	-4.26541474
GO:0030111	regulation of Wnt signaling pathway	-3.785702121
GO:0060828	regulation of canonical Wnt signaling pathway	-3.686460818
GO:0090263	positive regulation of canonical Wnt signaling pathway	-2.795153446
GO:0035306	positive regulation of dephosphorylation	-2.557690368
GO:0070613	regulation of protein processing	-2.423979776
GO:1903317	regulation of protein maturation	-2.371219039



GO:0010463	mesenchymal cell proliferation	-4.217639664
GO:0051147	regulation of muscle cell differentiation	-4.027098125
GO:0033688	regulation of osteoblast proliferation	-3.550789691
GO:0045667	regulation of osteoblast differentiation	-3.369505739
GO:0031214	biomineral tissue development	-3.016215128
GO:0110148	biomineralization	-2.933336161
GO:0062014	negative regulation of small molecule metabolic process	-2.901463698
GO:0030282	bone mineralization	-2.756492868
GO:0002065	columnar/cuboidal epithelial cell differentiation	-2.226547429
GO:0051153	regulation of striated muscle cell differentiation	-2.00916892
GO:1904035	regulation of epithelial cell apoptotic process	-4.134316611
GO:1904036	negative regulation of epithelial cell apoptotic process	-4.02075444
GO:0090049	regulation of cell migration involved in sprouting angiogenesis	-2.257088005
GO:0043279	response to alkaloid	-4.069378208
GO:0051402	neuron apoptotic process	-3.98821009
GO:0070997	neuron death	-3.749544794
GO:0071312	cellular response to alkaloid	-3.224038362
GO:0051900	regulation of mitochondrial depolarization	-4.066733811
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	-3.471627169
GO:0033146	regulation of intracellular estrogen receptor signaling pathway	-3.26037759
GO:0051385	response to mineralocorticoid	-3.224038362
GO:0003254	regulation of membrane depolarization	-2.883742534
GO:2000243	positive regulation of reproductive process	-2.15375782
GO:0006509	membrane protein ectodomain proteolysis	-3.932113785
GO:0033619	membrane protein proteolysis	-3.26037759
GO:1904996	positive regulation of leukocyte adhesion to vascular endothelial cell	-3.754114469
GO:1904994	regulation of leukocyte adhesion to vascular endothelial cell	-3.121184104
GO:0045666	positive regulation of neuron differentiation	-2.07245992
GO:0001816	cytokine production	-3.700049736
GO:0032663	regulation of interleukin-2 production	-3.695159677
GO:1901361	organic cyclic compound catabolic process	-3.48795999
GO:0032743	positive regulation of interleukin-2 production	-3.297846025
GO:0009187	cyclic nucleotide metabolic process	-3.121184104
GO:0009154	purine ribonucleotide catabolic process	-2.967301303
GO:1901136	carbohydrate derivative catabolic process	-2.946636282
GO:0006937	regulation of muscle contraction	-2.912923376
GO:0006195	purine nucleotide catabolic process	-2.857159545
GO:0009261	ribonucleotide catabolic process	-2.805739715
GO:0072523	purine-containing compound catabolic process	-2.732631226
GO:1904062	regulation of cation transmembrane transport	-2.721103078
GO:0072521	purine-containing compound metabolic process	-2.682984695

GO:0055086	nucleobase-containing small molecule metabolic process	-2.478683494
GO:0032409	regulation of transporter activity	-2.442581589
GO:0046700	heterocycle catabolic process	-2.435986643
GO:0044270	cellular nitrogen compound catabolic process	-2.396948386
GO:0019439	aromatic compound catabolic process	-2.297095376
GO:0009166	nucleotide catabolic process	-2.288506924
GO:0055117	regulation of cardiac muscle contraction	-2.272684787
GO:0046434	organophosphate catabolic process	-2.256024321
GO:0009150	purine ribonucleotide metabolic process	-2.237630331
GO:0006163	purine nucleotide metabolic process	-2.163462315
GO:1901292	nucleoside phosphate catabolic process	-2.15375782
GO:0009259	ribonucleotide metabolic process	-2.130362987
GO:0019693	ribose phosphate metabolic process	-2.076703732
GO:0034765	regulation of ion transmembrane transport	-2.064071376
GO:1903169	regulation of calcium ion transmembrane transport	-2.046755222
GO:0006942	regulation of striated muscle contraction	-2.00916892
GO:0010812	negative regulation of cell-substrate adhesion	-3.616994367
GO:0001953	negative regulation of cell-matrix adhesion	-3.088773975
GO:0006606	protein import into nucleus	-2.80986657
GO:0051170	import into nucleus	-2.751904129
GO:0034504	protein localization to nucleus	-2.0383936
GO:0042063	gliogenesis	-3.341772505
GO:0051651	maintenance of location in cell	-3.050728521
GO:0010001	glial cell differentiation	-2.981040543
GO:0048708	astrocyte differentiation	-2.756492868
GO:0051235	maintenance of location	-2.188651941
GO:0036314	response to sterol	-3.33651332
GO:0031670	cellular response to nutrient	-3.297846025
GO:0032092	positive regulation of protein binding	-3.216873055
GO:0060284	regulation of cell development	-2.657461249
GO:0051960	regulation of nervous system development	-2.360055011
GO:0034763	negative regulation of transmembrane transport	-2.265939334
GO:0006775	fat-soluble vitamin metabolic process	-3.154497773
GO:0006766	vitamin metabolic process	-2.933336161
GO:0019882	antigen processing and presentation	-3.050728521
GO:0019884	antigen processing and presentation of exogenous antigen	-2.883742534
GO:0048002	antigen processing and presentation of peptide antigen	-2.578150419
GO:0051150	regulation of smooth muscle cell differentiation	-2.996523184
GO:0051149	positive regulation of muscle cell differentiation	-2.18228809
GO:0002221	pattern recognition receptor signaling pathway	-2.982496277
GO:0002224	toll-like receptor signaling pathway	-2.620206303
GO:0050830	defense response to Gram-positive bacterium	-2.80986657
GO:0016042	lipid catabolic process	-2.706192581

GO:0006091	generation of precursor metabolites and energy	-2.014676917
GO:0045911	positive regulation of DNA recombination	-2.371219039
GO:0018958	phenol-containing compound metabolic process	-2.098876582

### Cellular Component

ID	Description	LogP
GO:0031983	vesicle lumen	-17.5176
GO:0034774	secretory granule lumen	-16.4092
GO:0060205	cytoplasmic vesicle lumen	-16.331
GO:0005775	vacuolar lumen	-10.528
GO:0000323	lytic vacuole	-7.28795
GO:0005764	lysosome	-7.28795
GO:0035578	azurophil granule lumen	-6.67796
GO:0005766	primary lysosome	-5.12123
GO:0042582	azurophil granule	-5.12123
GO:0031012	extracellular matrix	-13.7138
GO:0030312	external encapsulating structure	-13.6983
GO:0062023	collagen-containing extracellular matrix	-10.8461
GO:0045121	membrane raft	-12.7472
GO:0098857	membrane microdomain	-12.7256
GO:0005901	caveola	-4.41885
GO:0044853	plasma membrane raft	-3.75666
GO:0101002	ficolin-1-rich granule	-11.4699
GO:1904813	ficolin-1-rich granule lumen	-9.52385
GO:0070820	tertiary granule	-7.15843
GO:1904724	tertiary granule lumen	-5.27045
GO:0043235	receptor complex	-10.1786
GO:0098797	plasma membrane protein complex	-3.96607
GO:0098802	plasma membrane signaling receptor complex	-2.44258
GO:0098552	side of membrane	-8.60496
GO:0009897	external side of plasma membrane	-5.0347
GO:0005925	focal adhesion	-8.03242
GO:0030055	cell-substrate junction	-7.9169
GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	-6.42649
GO:0019897	extrinsic component of plasma membrane	-5.91406
GO:0009898	cytoplasmic side of plasma membrane	-5.85698
GO:0019898	extrinsic component of membrane	-5.70824
GO:0098562	cytoplasmic side of membrane	-5.32476
GO:0032587	ruffle membrane	-4.06938
GO:0031256	leading edge membrane	-3.78583

GO:0005884	actin filament	-3.75666
GO:0031252	cell leading edge	-3.16184
GO:0031253	cell projection membrane	-3.00338
GO:0001726	ruffle	-2.86901
GO:0030027	lamellipodium	-2.61833
GO:0005938	cell cortex	-2.50997
GO:0098978	glutamatergic synapse	-2.4492
GO:0098794	postsynapse	-2.13144
GO:0072562	blood microparticle	-6.39248
GO:0005788	endoplasmic reticulum lumen	-4.01597
GO:0030139	endocytic vesicle	-6.27099
GO:0045335	phagocytic vesicle	-4.36862
GO:0036021	endolysosome lumen	-6.03267
GO:0031904	endosome lumen	-4.70815
GO:0043202	lysosomal lumen	-4.06938
GO:0036019	endolysosome	-3.55079
GO:0045177	apical part of cell	-3.08874
GO:0016324	apical plasma membrane	-2.19158
GO:0031091	platelet alpha granule	-5.40268
GO:0031093	platelet alpha granule lumen	-4.84608
GO:0042581	specific granule	-5.03103
GO:0035580	specific granule lumen	-5.01204
GO:0030667	secretory granule membrane	-4.84515
GO:0101003	ficolin-1-rich granule membrane	-2.55769
GO:1904090	peptidase inhibitor complex	-4.82393
GO:0005911	cell-cell junction	-4.68334
GO:0048471	perinuclear region of cytoplasm	-4.54991
GO:0001772	immunological synapse	-4.30825
GO:0005667	transcription regulator complex	-4.01115
GO:0090575	RNA polymerase II transcription regulator complex	-2.28508
GO:0030425	dendrite	-2.69001
GO:0097447	dendritic tree	-2.68046
GO:0005813	centrosome	-2.64737
GO:0005741	mitochondrial outer membrane	-2.59071
GO:0031968	organelle outer membrane	-2.36186
GO:0019867	outer membrane	-2.34619
GO:0000791	euchromatin	-2.53759
GO:0009925	basal plasma membrane	-2.21206
GO:0045178	basal part of cell	-2.08918

## Molecular Function

ID	Description	LogP
GO:0004175	endopeptidase activity	-24.7553
GO:0008236	serine-type peptidase activity	-23.8807
GO:0017171	serine hydrolase activity	-23.6786
GO:0004252	serine-type endopeptidase activity	-23.285
GO:0008233	peptidase activity	-21.776
GO:0008237	metallopeptidase activity	-9.0039
GO:0004222	metalloendopeptidase activity	-8.60841
GO:0004879	nuclear receptor activity	-22.8528
GO:0098531	ligand-activated transcription factor activity	-22.8528
GO:0005496	steroid binding	-14.9671
GO:0003707	nuclear steroid receptor activity	-10.9364
GO:0061629	RNA polymerase II-specific DNA-binding transcription factor binding	-9.08809
GO:0016922	nuclear receptor binding	-7.78095
GO:0001223	transcription coactivator binding	-7.55947
GO:0140297	DNA-binding transcription factor binding	-7.43518
GO:0001221	transcription coregulator binding	-7.39852
GO:0008134	transcription factor binding	-6.98694
GO:0046965	nuclear retinoid X receptor binding	-6.2612
GO:0042974	nuclear retinoic acid receptor binding	-5.38384
GO:0008013	beta-catenin binding	-3.17831
GO:0001222	transcription corepressor binding	-2.9673
GO:0001228	DNA-binding transcription activator activity, RNA polymerase II-specific	-2.877
GO:0001216	DNA-binding transcription activator activity	-2.8534
GO:0008289	lipid binding	-22.739
GO:0004712	protein serine/threonine/tyrosine kinase activity	-18.2328
GO:0004672	protein kinase activity	-18.0806
GO:0016773	phosphotransferase activity, alcohol group as acceptor	-16.2194
GO:0004713	protein tyrosine kinase activity	-16.1053
GO:0016301	kinase activity	-15.3904
GO:0019199	transmembrane receptor protein kinase activity	-8.51187
GO:0004714	transmembrane receptor protein tyrosine kinase activity	-7.94821
GO:0019838	growth factor binding	-3.44357
GO:0031406	carboxylic acid binding	-13.1642
GO:0033293	monocarboxylic acid binding	-9.88006
GO:0043177	organic acid binding	-8.97441
GO:0005504	fatty acid binding	-8.58289
GO:0036041	long-chain fatty acid binding	-6.2612

GO:0019900	kinase binding	-12.9316
GO:0019901	protein kinase binding	-12.0797
GO:0019904	protein domain specific binding	-6.19417
GO:0004715	non-membrane spanning protein tyrosine kinase activity	-10.5382
GO:0016004	phospholipase activator activity	-8.44508
GO:0060229	lipase activator activity	-7.95978
GO:0043274	phospholipase binding	-7.23393
GO:0042169	SH2 domain binding	-5.91488
GO:0043548	phosphatidylinositol 3-kinase binding	-3.50482
GO:0008047	enzyme activator activity	-2.39269
GO:0008022	protein C-terminus binding	-2.03009
GO:0005126	cytokine receptor binding	-10.4917
GO:0001664	G protein-coupled receptor binding	-3.42802
GO:0042379	chemokine receptor binding	-2.37122
GO:0019902	phosphatase binding	-10.0028
GO:0019903	protein phosphatase binding	-7.54364
GO:0030235	nitric-oxide synthase regulator activity	-7.83992
GO:0051117	ATPase binding	-6.99131
GO:0030331	nuclear estrogen receptor binding	-3.12118
GO:0020037	heme binding	-7.78095
GO:0046906	tetrapyrrole binding	-7.51825
GO:0004497	monooxygenase activity	-5.09071
GO:0016712	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	-4.47394
GO:0016491	oxidoreductase activity	-4.4579
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	-3.77247
GO:0070330	aromatase activity	-3.70005
GO:0008395	steroid hydroxylase activity	-3.1545
GO:0005506	iron ion binding	-2.286
GO:0042803	protein homodimerization activity	-7.75527
GO:0097110	scaffold protein binding	-7.60723
GO:0005518	collagen binding	-7.5617
GO:0004197	cysteine-type endopeptidase activity	-4.71094
GO:0008234	cysteine-type peptidase activity	-3.69406
GO:0001968	fibronectin binding	-3.41776
GO:0043394	proteoglycan binding	-3.22404
GO:1901681	sulfur compound binding	-7.31487
GO:0008201	heparin binding	-5.91406
GO:0005539	glycosaminoglycan binding	-4.86328
GO:0001530	lipopolysaccharide binding	-3.26038

GO:0001784	phosphotyrosine residue binding	-7.30138
GO:0051219	phosphoprotein binding	-6.77852
GO:0045309	protein phosphorylated amino acid binding	-6.70578
GO:0005158	insulin receptor binding	-3.8699
GO:0030545	signaling receptor regulator activity	-6.65868
GO:0048018	receptor ligand activity	-6.37476
GO:0030546	signaling receptor activator activity	-6.30528
GO:0042056	chemoattractant activity	-6.20529
GO:0008083	growth factor activity	-4.99583
GO:0005125	cytokine activity	-2.33841
GO:0002020	protease binding	-6.65138
GO:0004674	protein serine/threonine kinase activity	-6.1416
GO:0004707	MAP kinase activity	-4.38923
GO:0106310	protein serine kinase activity	-4.34969
GO:0004708	MAP kinase kinase activity	-4.13991
GO:0005509	calcium ion binding	-5.9858
GO:0005543	phospholipid binding	-2.23748
GO:0042562	hormone binding	-5.51675
GO:0050661	NADP binding	-5.35086
GO:0034618	arginine binding	-5.28886
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	-2.99652
GO:0016597	amino acid binding	-2.66387
GO:0005178	integrin binding	-5.10293
GO:0070851	growth factor receptor binding	-4.35108
GO:0050839	cell adhesion molecule binding	-3.59776
GO:0051427	hormone receptor binding	-4.86671
GO:0016813	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines	-4.82393
GO:0030145	manganese ion binding	-2.47935
GO:0033218	amide binding	-4.75946
GO:0042277	peptide binding	-4.72632
GO:0019825	oxygen binding	-4.51816
GO:0016209	antioxidant activity	-4.34365
GO:0097153	cysteine-type endopeptidase activity involved in apoptotic process	-4.38923
GO:0004190	aspartic-type endopeptidase activity	-3.59856
GO:0070001	aspartic-type peptidase activity	-3.55079
GO:0019842	vitamin binding	-4.19924
GO:0072341	modified amino acid binding	-3.05073
GO:0019207	kinase regulator activity	-3.9102
GO:0046332	SMAD binding	-3.33889

GO:0016788	hydrolase activity, acting on ester bonds	-3.165
GO:0008081	phosphoric diester hydrolase activity	-3.14072
GO:0004620	phospholipase activity	-2.83975
GO:0016298	lipase activity	-2.5171
GO:0052689	carboxylic ester hydrolase activity	-2.29614
GO:0042578	phosphoric ester hydrolase activity	-2.1579
GO:0001046	core promoter sequence-specific DNA binding	-3.02648
GO:0051879	Hsp90 protein binding	-2.99652
GO:0031072	heat shock protein binding	-2.60378
GO:0008238	exopeptidase activity	-2.9825
GO:0050840	extracellular matrix binding	-2.66387
GO:0140272	exogenous protein binding	-2.27268