Table S1: The information of the ingredients from *Sparganii Rhizoma* .

No.	Ingredients	Molecular formula	CAS No.	Number of target gene
1	adenosine	C10H13N5O4	58-61-7	6
2	1-hexanoic acid	C6H12O2	142-62-1	4
3	docosanoic acid	C22H44O2	112-85-6	4
4	lauric acid	C12H24O2	143-07-7	4
5	linoleic acid	C18H32O2	60-33-3	4
6	1-hydroxy-2-acetyl-4-methylbenzene	C9H10O2	1450-72-2	3
7	1-octanol	C8H18O	111-87-5	3
8	4-hydroxybenzoic acid	C7H6O3	99-96-7	3
9	4-hydroxycinnamic acid	C9H8O3	7400-08-0	3
10	betulinic acid	C30H48O3	472-15-1	3
11	ethyl linoleate	C20H36O2	544-35-4	3
12	hexadecan-1-ol	C16H34O	36653-82-4	3
13	lily aldehyde	C14H20O	80-54-6	3
14	methyl linoleate	C19H34O2	112-63-0	3
15	octadecan-1-ol	C18H38O	8034-90-0	3
16	(7E)-6,9,10-trihydroxy-7-octadecenoic acid	C18H34O5	/	2
17	2-acetylpyrrole	C6H7NO	1072-83-9	2
18	4-hydroxybenzaldehyde	C7H6O2	123-08-0	2
19	9(S),12(S),13(S)-trihydroxy-10(E)-octadecenoic a	C18H34O5	/	2
20	butyric Acid	C4H8O2	107-92-6	2
21	cyclo(Tyr-Leu)	C15H20N2O3	82863-65-8	2
22	dehydrocostus lactone	C15H18O2	477-43-0	2
23	phenanthrene-9,10-dione	C14H8O2	84-11-7	2
24	sparstolonin B	C15H8O5	1259330-61-4	2
25	succinic acid	C4H6O4	110-15-6	2
26	(-)-β-caryophyllene	C15H24	87-44-5	1
27	(+)-alpha-longipinene	C15H24	5989-08-2	1
28	(+)-borneol	C10H18O	464-43-7	1
29	(+)-R-limonene	C10H16	95327-98-3	1
30	(±)-myrtenol	C10H16O	515-00-4	1
31	(±)-trans-nerolidol	C15H26O	40716-66-3	1
32	(1R,2R,4S)-2,4-diisopropenyl-1-methyl-1-vinylcy	C19H38O5	33880-83-0	1
33	1,3,6-trihydroxy-8-methylxanthone	C15H10O5	20716-98-7	1
34	1-docosanol	C22H44	1599-67-3	1
35	1-methyl-4-(1,2,2-trimethylcyclopentyl)-1,3-cyclo	C15H24	5046-93-5	1
36	1-methyl-4-isopropyl-1-cyclohexene	C10H18	61585-35-1	1
37	2,7-dihydroxyxanthone	C13H8O4	64632-72-0	1
38	24-methylenecycloartanol	C31H52O	1449-09-8	1
39	2-benzylphenol	C13H12O	28994-41-4	1
40	3-ethylphenol	C8H10O	620-17-7	1
41	4-ethyl-2-methoxyphenol	C9H12O2	2785-89-9	1
42	alpha-selinene	C15H24	473-13-2	1
43	beta-pinene	C10H16	18172-67-3	1
44	beta-selinene	C15H24	17066-67-0	1
45	beta-Sitosterol	C29H50O	83-46-5	1
46	cedran-9-one	C15H24O	13794-73-5	1
47	chrysophanic acid	C15H10O4	481-74-3	1
48	cis-zimtsaeure	C9H8O2	621-82-9	1
49	emodin	C15H10O5	518-82-1	1
50	hydroquinone	C6H6O2	123-31-9	1

51	L-(-)-camphor	C10H16O	464-48-2	1
52	methyl palmitate	C17H34O2	112-39-0	1
53	octadec-1-ene	C18H36	112-88-9	1
54	orcinol	C7H8O2	504-15-4	1
55	stigmasterol	C29H48O	83-48-7	1
56	β-eudesmol	C15H26O	473-15-4	1
57	β-pinene	C10H16	127-91-3	1
58	(E)-β-farnesene	C15H24	18794-84-8	/
59	1,3-O-diferuloyl glycerol	C23H24O9	83008-46-2	/
60	1,4,6-trimethylnaphthalene	C13H14	2131-42-2	/
61	1,4-cineole	C10H18O	470-67-7	/
62	16-hexadecanolactone	C16H30O2	109-29-5	/
63	1-isopropyl-4,7-dimethyl-1,2,3,5,6,8a-hexahydron	C15H24	483-76-1	/
64	1-O-feruloyl-3-O-p-coumaryl glycerol	C22H22O8	108026-21-7	/
65	1-palmitoylglycerol	C19H38O4	542-44-9	/
66	2-(3,4-dihydroxyphenyl) ethyl acetate	C10H12O4	69039-02-7	/
67	2,6,10,14-tetramethylpentadecane	C19H40	1921-70-6	/
68	2,6,8-trimethyldecane	C13H28	62108-26-3	/
69	2-methylbutanal	C5H10O	96-17-3	/
70	2-Methylfuran	C5H6O	534-22-5	/
71	2-octanone	C8H16O	111-13-7	/
72	3,5,24-trimethyltetracontane	C43H88	55162-61-3	/
73	3,5-dihydroxy-4-methoxybenzoic acid	C8H8O5	4319-02-2	/
74	4,5-dimethylnonane	C11H24	17302-23-7	/
75	4-hydroxy-4-methyl-2-pentanone	C6H12O2	123-42-2	/
76	4-methoxy-4-oxobutanoic acid	C5H8O4	3878-55-5	/
77	5-hydroxy-2-(hydroxymethyl) pyridine	C6H7NO2	/	/
78	5-hydroxymethyl-2-furaldehyde	C6H6O3	67-47-0	/
79	apiole	C12H14O4	523-80-8	/
80	azelaic acid	C9H16O4	123-99-9	/
81	benzoic acid	C7H6O2	65-85-0	/
82	bornyl acetate	C12H20O2	5655-61-8	/
83	caffeic acid	C9H8O4	331-39-5	/
84	camphene	C10H16	79-92-5	/
85	cis-anethol	C10H12O	104-46-1	/
86	coumaran	C8H8O	496-16-2	/
87	cyclo-(Phe-Phe)	C18H18N2O2	2862-51-3	/
88	cyclopentadecanolide	C15H28O2	106-02-5	/
89	daucosterol	C35H60O6	474-58-8	/
90	decanoic acid	C10H20O2	334-48-5	/
91	D-erythritol	C4H10O4	149-32-6	/
92	diphenylamine	C12H11N	122-39-4	/
93	emodin-3-methyl ether	C16H12O5	521-61-9	/
94	ergosterol peroxide	C28H44O3	2061-64-5	/
95	formononetin	C16H12O4	485-72-3	/
96	fumaric acid	C4H4O4	110-17-8	/
97	furfural	C5H4O2	98-01-1	/
98	furfuryl alcohol	C5H6O2	98-00-0	/
99	glycerol ferulate	C13H16O6	120601-69-6	/
100	heneicosanoic acid 2,3-dihydroxypropyl ester	C24H48O4	245117-31-1	/
101	heptadecane	C17H36	629-78-7	/
102	hexadecane	C16H34	544-76-3	/
103	hexyl formate	C7H14O2	629-33-4	/

104	hydroxytyrosol	C8H10O3	10597-60-1	/
105	iovaleraldehyde	C5H10O	590-86-3	/
106	isopropyl palmitate	C19H38O2	142-91-6	/
107	L-alpha-palmitin	C15H25	5309-46-6	/
108	methyleugenol	C11H14O2	93-15-2	/
109	Myristic acid	C14H28O2	544-63-8	/
110	n-butyl-O-β-D-fructopyranoside	C10H20O6	/	/
111	n-butyl-α-D-fructofuranoside	C10H20O6	80971-59-1	/
112	N-decylhydroxylamine	C10H23NO	26228-72-8	/
113	N-docosane	C22H46	629-97-0	/
114	nectriapyrone	C11H14O3	57685-79-7	/
115	nonyl aldehyde	C9H18O	124-19-6	/
116	N-pentadecyl mercaptan	C15H32S	25276-70-4	/
117	palmitic acid	C16H32O2	57-10-3	/
118	phenethyl alcohol	C8H10O	60-12-8	/
119	pichtosin	C12H20O2	125-12-2	/
120	rhamnazin-3-O-rutinoside	C29H34O16	/	/
121	rosenonolactone	C20H28O3	508-71-4	/
122	rutin	C27H30O16	153-18-4	/
123	R-γ-decalactone	C10H18O2	706-14-9	/
124	syringaldehyde	C9H10O4	134-96-3	/
125	trans-ferulic acid	C10H10O4	537-98-4	/
126	turmerone	C15H22O	82508-15-4	/
127	vanillic acid	C8H8O4	121-34-6	/
128	vanillin	C8H8O3	121-33-5	/
129	β-sitosterol palmitate	C45H80O2	/	/

Table S2: The Gene Ontology (GO) and KEGG enrichment analysis data of the targets for *Sparganii Rhizoma* on lung cancer.

No	Category	Description	target	Enrichment	P
001	KEGG Pathway	Drug metabolism - other enzymes	CES1|CYP2E1|CYP3A4|MPO|RRM1|UGT1A1	83.23	8E-11
002	KEGG Pathway	Steroid hormone biosynthesis	CYP1A2|CYP2E1|CYP3A4|CYP19A1|UGT1A1	90.61	2E-09
003	KEGG Pathway	Chemical carcinogenesis - DNA adducts	CYP1A2|CYP2E1|CYP3A4|PTGS2|UGT1A1	79.13	5E-09
004	KEGG Pathway	Pathways in cancer	ALK|BCL2|NQO1|EGFR|FGFR2|MAP2K1|PTGS2|RET	16.86	1E-08
005	KEGG Pathway	Bile secretion	ABCC2|CYP3A4|ABCB1|ABCB11|UGT1A1	62.42	2E-08
006	KEGG Pathway	Chemical carcinogenesis - receptor activation	BCL2|CYP1A2|CYP3A4|EGFR|MAP2K1|UGT1A1	31.36	3E-08
007	KEGG Pathway	Chemical carcinogenesis - reactive oxygen species	CYP1A2|CYP2E1|NQO1|EGFR|MAP2K1|SOD1	29.83	4E-08
008	KEGG Pathway	Gastric cancer	BCL2|EGFR|FGFR2|ABCB1|MAP2K1	37.45	2E-07
009	KEGG Pathway	Central carbon metabolism in cancer	EGFR|FGFR2|MAP2K1|RET	63.30	5E-07
010	KEGG Pathway	Drug metabolism - cytochrome P450	CYP1A2|CYP2E1|CYP3A4|UGT1A1	61.57	5E-07
011	KEGG Pathway	Non-small cell lung cancer	ALK|EGFR|MAP2K1|RET	61.57	5E-07
012	KEGG Pathway	Metabolism of xenobiotics by cytochrome P450	CYP1A2|CYP2E1|CYP3A4|UGT1A1	56.89	7E-07
013	KEGG Pathway	EGFR tyrosine kinase inhibitor resistance	BCL2|EGFR|FGFR2|MAP2K1	56.18	8E-07
014	KEGG Pathway	Prostate cancer	BCL2|EGFR|FGFR2|MAP2K1	45.86	2E-06
015	KEGG Pathway	Endocrine resistance	BCL2|EGFR|MAP2K1|ABCB11	45.40	2E-06
016	KEGG Pathway	Linoleic acid metabolism	CYP1A2|CYP2E1|CYP3A4	112.36	3E-06
017	KEGG Pathway	MicroRNAs in cancer	BCL2|EGFR|ABCB1|MAP2K1|PTGS2	18.01	7E-06
018	KEGG Pathway	ABC transporters	ABCC2|ABCB1|ABCB11	74.91	9E-06
019	KEGG Pathway	PI3K-Akt signaling pathway	BCL2|EGFR|FGFR2|MAP2K1|RET	15.52	2E-05
020	KEGG Pathway	Arachidonic acid metabolism	CYP2E1|PTGS1|PTGS2	55.26	2E-05
021	KEGG Pathway	Retinol metabolism	CYP1A2|CYP3A4|UGT1A1	49.57	3E-05
022	KEGG Pathway	Colorectal cancer	BCL2|EGFR|MAP2K1	38.74	6E-05
023	KEGG Pathway	PD-L1 expression and PD-1 checkpoint pathway in cancer	ALK|EGFR|MAP2K1	37.45	7E-05
024	KEGG Pathway	HIF-1 signaling pathway	BCL2|EGFR|MAP2K1	30.92	0.0001
025	KEGG Pathway	MAPK signaling pathway	EGFR|FGFR2|MAP2K1|RET	14.98	0.0001
026	KEGG Pathway	Parathyroid hormone synthesis, secretion and action	BCL2|EGFR|MAP2K1	29.31	0.0001
027	KEGG Pathway	Serotonergic synapse	MAP2K1|PTGS1|PTGS2	29.31	0.0001
028	KEGG Pathway	Estrogen signaling pathway	BCL2|EGFR|MAP2K1	24.25	0.0003
029	KEGG Pathway	Oxytocin signaling pathway	EGFR|MAP2K1|PTGS2	21.89	0.0003
030	KEGG Pathway	Hepatocellular carcinoma	NQO1|EGFR|MAP2K1	19.83	0.0005
031	KEGG Pathway	Thyroid cancer	MAP2K1|RET	60.73	0.0005
032	KEGG Pathway	Bladder cancer	EGFR|MAP2K1	54.81	0.0006
033	KEGG Pathway	Alcoholism	SLC29A1|SLC29A2|MAP2K1	17.93	0.0006
034	KEGG Pathway	Focal adhesion	BCL2|EGFR|MAP2K1	16.60	0.0008
035	KEGG Pathway	Pathways of neurodegeneration - multiple diseases	BCL2|MAP2K1|PTGS2|SOD1	9.31	0.0008
036	KEGG Pathway	Rap1 signaling pathway	EGFR|FGFR2|MAP2K1	15.90	0.0009
037	KEGG Pathway	Ovarian steroidogenesis	CYP19A1|PTGS2	44.06	0.0009
038	KEGG Pathway	Human cytomegalovirus infection	EGFR|MAP2K1|PTGS2	14.91	0.001
039	KEGG Pathway	Regulation of actin cytoskeleton	EGFR|FGFR2|MAP2K1	14.66	0.0011
040	KEGG Pathway	Ras signaling pathway	EGFR|FGFR2|MAP2K1	14.16	0.0012
041	KEGG Pathway	Pyrimidine metabolism	DCK|RRM1	38.74	0.0012
042	KEGG Pathway	Endometrial cancer	EGFR|MAP2K1	38.09	0.0013
043	KEGG Pathway	Regulation of lipolysis in adipocytes	PTGS1|PTGS2	38.09	0.0013
044	KEGG Pathway	VEGF signaling pathway	MAP2K1|PTGS2	37.45	0.0013
045	KEGG Pathway	Calcium signaling pathway	EGFR|FGFR2|RET	13.27	0.0015
046	KEGG Pathway	Acute myeloid leukemia	MPO|MAP2K1	33.05	0.0017
047	KEGG Pathway	Melanoma	EGFR|MAP2K1	30.78	0.0019
048	KEGG Pathway	Platinum drug resistance	BCL2|ABCC2	29.96	0.002
049	KEGG Pathway	Glioma	EGFR|MAP2K1	29.57	0.0021
050	KEGG Pathway	Pancreatic cancer	EGFR|MAP2K1	29.18	0.0021
051	KEGG Pathway	Nucleotide metabolism	DCK|RRM1	26.44	0.0026
052	KEGG Pathway	ErbB signaling pathway	EGFR|MAP2K1	26.13	0.0027
053	KEGG Pathway	Gap junction	EGFR|MAP2K1	24.43	0.003
054	KEGG Pathway	Small cell lung cancer	BCL2|PTGS2	24.16	0.0031
055	KEGG Pathway	GnRH signaling pathway	EGFR|MAP2K1	24.16	0.0031
056	KEGG Pathway	Human papillomavirus infection	EGFR|MAP2K1|PTGS2	10.12	0.0032
057	KEGG Pathway	Choline metabolism in cancer	EGFR|MAP2K1	22.70	0.0035
058	KEGG Pathway	NF-kappa B signaling pathway	BCL2|PTGS2	21.40	0.0039
059	KEGG Pathway	Cholinergic synapse	BCL2|MAP2K1	19.54	0.0047
060	KEGG Pathway	TNF signaling pathway	MAP2K1|PTGS2	18.88	0.005
061	KEGG Pathway	Neurotrophin signaling pathway	BCL2|MAP2K1	18.73	0.0051
062	KEGG Pathway	Sphingolipid signaling pathway	BCL2|MAP2K1	18.42	0.0053
063	KEGG Pathway	Purine metabolism	DCK|RRM1	17.56	0.0058
064	KEGG Pathway	Relaxin signaling pathway	EGFR|MAP2K1	17.29	0.006
065	KEGG Pathway	FoxO signaling pathway	EGFR|MAP2K1	16.90	0.0062
066	KEGG Pathway	Apoptosis	BCL2|MAP2K1	16.52	0.0065
067	KEGG Pathway	Fluid shear stress and atherosclerosis	BCL2|NQO1	15.94	0.007
068	KEGG Pathway	Signaling pathways regulating pluripotency of stem cells	FGFR2|MAP2K1	15.61	0.0073
069	KEGG Pathway	Breast cancer	EGFR|MAP2K1	15.18	0.0077
070	KEGG Pathway	Phospholipase D signaling pathway	EGFR|MAP2K1	15.08	0.0078
071	KEGG Pathway	Biosynthesis of cofactors	NQO1|UGT1A1	14.69	0.0082
072	KEGG Pathway	Cushing syndrome	EGFR|MAP2K1	14.50	0.0084
073	KEGG Pathway	Efferocytosis	MAP2K1|PTGS2	14.41	0.0085
074	KEGG Pathway	Hepatitis C	EGFR|MAP2K1	14.13	0.0088
075	KEGG Pathway	Hepatitis B	BCL2|MAP2K1	13.79	0.0092
076	KEGG Pathway	JAK-STAT signaling pathway	BCL2|EGFR	13.38	0.0098
077	KEGG Pathway	Autophagy - animal	BCL2|MAP2K1	13.30	0.0099
078	KEGG Pathway	Neutrophil extracellular trap formation	MPO|MAP2K1	11.70	0.0126
079	KEGG Pathway	Kaposi sarcoma-associated herpesvirus infection	MAP2K1|PTGS2	11.47	0.0131
080	KEGG Pathway	Proteoglycans in cancer	EGFR|MAP2K1	11.02	0.0141
081	KEGG Pathway	Human immunodeficiency virus 1 infection	BCL2|MAP2K1	10.55	0.0153
082	KEGG Pathway	Shigellosis	BCL2|EGFR	9.02	0.0206
083	KEGG Pathway	Salmonella infection	BCL2|MAP2K1	8.95	0.0209
084	KEGG Pathway	Endocytosis	EGFR|FGFR2	8.92	0.021
085	KEGG Pathway	Amyotrophic lateral sclerosis	BCL2|SOD1	6.06	0.0428
086	KEGG Pathway	Alzheimer disease	MAP2K1|PTGS2	5.75	0.0471

001	GO Molecular Functions	heme binding	CYP1A2|CYP2E1|CYP3A4|CYP19A1|MPO|PTGS1|PTGS2	55.39	3E-11
002	GO Molecular Functions	tetrapyrrole binding	CYP1A2|CYP2E1|CYP3A4|CYP19A1|MPO|PTGS1|PTGS2	51.74	6E-11
003	GO Molecular Functions	oxidoreductase activity	CYP1A2|CYP2E1|CYP3A4|CYP19A1|NQO1|MPO|PTGS1|PT	15.48	3E-10
004	GO Molecular Functions	aromatase activity	CYP1A2|CYP2E1|CYP3A4|CYP19A1	172.86	7E-09
005	GO Molecular Functions	oxidoreductase activity, acting on paired donors, with incorporati	CYP1A2|CYP2E1|CYP3A4|CYP19A1|PTGS1|PTGS2	37.66	1E-08
006	GO Molecular Functions	antioxidant activity	NQO1|MPO|PTGS1|PTGS2|SOD1	66.09	1E-08
007	GO Molecular Functions	uridine transmembrane transporter activity	SLC29A1|SLC29A2|SLC28A3	561.80	1E-08
008	GO Molecular Functions	pyrimidine nucleobase transmembrane transporter activity	SLC29A1|SLC29A2|SLC28A3	481.54	2E-08
009	GO Molecular Functions	pyrimidine nucleoside transmembrane transporter activity	SLC29A1|SLC29A2|SLC28A3	421.35	4E-08
010	GO Molecular Functions	oxidoreductase activity, acting on paired donors, with incorporati	CYP1A2|CYP2E1|CYP3A4|CYP19A1	107.01	5E-08
011	GO Molecular Functions	nucleoside transmembrane transporter activity	SLC29A1|SLC29A2|SLC28A3	337.08	8E-08
012	GO Molecular Functions	purine nucleobase transmembrane transporter activity	SLC29A1|SLC29A2|SLC28A3	337.08	8E-08
013	GO Molecular Functions	oxidoreductase activity, acting on CH or CH2 groups	CYP1A2|CYP3A4|RRM1	306.43	1E-07
014	GO Molecular Functions	nucleobase transmembrane transporter activity	SLC29A1|SLC29A2|SLC28A3	306.43	1E-07
015	GO Molecular Functions	protein tyrosine kinase activity	ALK|EGFR|FGFR2|MAP2K1|RET	40.71	1E-07
016	GO Molecular Functions	ABC-type xenobiotic transporter activity	ABCC2|ABCB1|ABCB11	240.77	2E-07
017	GO Molecular Functions	transmembrane receptor protein tyrosine kinase activity	ALK|EGFR|FGFR2|RET	74.91	2E-07
018	GO Molecular Functions	transmembrane receptor protein kinase activity	ALK|EGFR|FGFR2|RET	56.89	7E-07
019	GO Molecular Functions	prostaglandin-endoperoxide synthase activity	PTGS1|PTGS2	1123.59	8E-07
020	GO Molecular Functions	phosphotransferase activity, alcohol group as acceptor	ALK|DCK|EGFR|FGFR2|MAP2K1|RET|TOP1	11.70	2E-06
021	GO Molecular Functions	steroid hydroxylase activity	CYP1A2|CYP3A4|CYP19A1	129.65	2E-06
022	GO Molecular Functions	monooxygenase activity	CYP1A2|CYP2E1|CYP3A4|CYP19A1	42.80	2E-06
023	GO Molecular Functions	uracil transmembrane transporter activity	SLC29A1|SLC29A2	749.06	2E-06
024	GO Molecular Functions	kinase activity	ALK|DCK|EGFR|FGFR2|MAP2K1|RET|TOP1	10.83	3E-06
025	GO Molecular Functions	xenobiotic transmembrane transporter activity	ABCC2|ABCB1|ABCB11	105.34	3E-06
026	GO Molecular Functions	oxygen binding	CYP2E1|CYP3A4|CYP19A1	99.14	4E-06
027	GO Molecular Functions	oxidoreductase activity, acting on CH or CH2 groups, quinone or	CYP1A2|CYP3A4	561.80	5E-06
028	GO Molecular Functions	caffeine oxidase activity	CYP1A2|CYP3A4	561.80	5E-06
029	GO Molecular Functions	nucleoside:sodium symporter activity	SLC29A1|SLC28A3	561.80	5E-06
030	GO Molecular Functions	guanine transmembrane transporter activity	SLC29A1|SLC29A2	561.80	5E-06
031	GO Molecular Functions	purine nucleoside transmembrane transporter activity	SLC29A1|SLC29A2	561.80	5E-06
032	GO Molecular Functions	cytidine transmembrane transporter activity	SLC29A1|SLC29A2	561.80	5E-06
033	GO Molecular Functions	pyrimidine- and adenosine-specific:sodium symporter activity	SLC29A1|SLC28A3	561.80	5E-06
034	GO Molecular Functions	nucleobase:monoatomic cation symporter activity	SLC29A1|SLC28A3	561.80	5E-06
035	GO Molecular Functions	superoxide dismutase activity	NQO1|SOD1	449.44	8E-06
036	GO Molecular Functions	oxidoreductase activity, acting on superoxide radicals as acceptor	NQO1|SOD1	449.44	8E-06
037	GO Molecular Functions	estrogen 2-hydroxylase activity	CYP1A2|CYP3A4	449.44	8E-06
038	GO Molecular Functions	adenine transmembrane transporter activity	SLC29A1|SLC29A2	449.44	8E-06
039	GO Molecular Functions	protein kinase activity	ALK|EGFR|FGFR2|MAP2K1|RET|TOP1	11.95	9E-06
040	GO Molecular Functions	iron ion binding	CYP1A2|CYP2E1|CYP3A4|CYP19A1	29.37	1E-05
041	GO Molecular Functions	ABC-type transporter activity	ABCC2|ABCB1|ABCB11	70.22	1E-05
042	GO Molecular Functions	nucleobase-containing compound transmembrane transporter acti	SLC29A1|SLC29A2|SLC28A3	59.14	2E-05
043	GO Molecular Functions	carbohydrate derivative transmembrane transporter activity	SLC29A1|SLC29A2|SLC28A3	59.14	2E-05
044	GO Molecular Functions	peroxidase activity	MPO|PTGS1|PTGS2	59.14	2E-05
045	GO Molecular Functions	oxidoreductase activity, acting on peroxide as acceptor	MPO|PTGS1|PTGS2	57.13	2E-05
046	GO Molecular Functions	estrogen 16-alpha-hydroxylase activity	CYP1A2|CYP3A4	280.90	2E-05
047	GO Molecular Functions	active transmembrane transporter activity	ABCC2|SLC29A1|ABCB1|ABCB11|SLC28A3	12.27	5E-05
048	GO Molecular Functions	ATPase-coupled transmembrane transporter activity	ABCC2|ABCB1|ABCB11	34.40	9E-05
049	GO Molecular Functions	neurotransmitter transmembrane transporter activity	SLC29A1|SLC29A2	107.01	0.0002
050	GO Molecular Functions	oxidoreductase activity, acting on single donors with incorporatio	PTGS1|PTGS2	93.63	0.0002
051	GO Molecular Functions	oxidoreductase activity, acting on single donors with incorporatio	PTGS1|PTGS2	89.89	0.0002
052	GO Molecular Functions	protein kinase activator activity	ALK|EGFR|MAP2K1	25.16	0.0002
053	GO Molecular Functions	kinase activator activity	ALK|EGFR|MAP2K1	23.74	0.0003
054	GO Molecular Functions	protein phosphatase binding	BCL2|EGFR|SOD1	23.57	0.0003
055	GO Molecular Functions	protein tyrosine kinase activator activity	ALK|EGFR	70.22	0.0004
056	GO Molecular Functions	oxidoreductase activity, acting on paired donors, with incorporati	CYP2E1|CYP3A4	66.09	0.0004
057	GO Molecular Functions	primary active transmembrane transporter activity	ABCC2|ABCB1|ABCB11	20.31	0.0004
058	GO Molecular Functions	heparin binding	ALK|FGFR2|MPO	19.37	0.0005
059	GO Molecular Functions	carboxylic acid transmembrane transporter activity	ABCC2|ABCB1|ABCB11	18.22	0.0006
060	GO Molecular Functions	organic acid transmembrane transporter activity	ABCC2|ABCB1|ABCB11	18.12	0.0006
061	GO Molecular Functions	phosphatase binding	BCL2|EGFR|SOD1	17.83	0.0006
062	GO Molecular Functions	protein kinase regulator activity	ALK|EGFR|MAP2K1	13.99	0.0013
063	GO Molecular Functions	glycosaminoglycan binding	ALK|FGFR2|MPO	13.93	0.0013
064	GO Molecular Functions	organic anion transmembrane transporter activity	ABCC2|ABCB1|ABCB11	12.58	0.0017
065	GO Molecular Functions	sulfur compound binding	ALK|FGFR2|MPO	12.44	0.0018
066	GO Molecular Functions	kinase regulator activity	ALK|EGFR|MAP2K1	12.08	0.0019
067	GO Molecular Functions	solute:sodium symporter activity	SLC29A1|SLC28A3	28.45	0.0023
068	GO Molecular Functions	ubiquitin protein ligase binding	BCL2|EGFR|ABCB1	11.05	0.0025
069	GO Molecular Functions	ubiquitin-like protein ligase binding	BCL2|EGFR|ABCB1	10.40	0.0029
070	GO Molecular Functions	dioxygenase activity	PTGS1|PTGS2	24.16	0.0031
071	GO Molecular Functions	protein homodimerization activity	DCK|FGFR2|PTGS2|UGT1A1	6.29	0.0035
072	GO Molecular Functions	steroid binding	CYP3A4|UGT1A1	21.00	0.0041
073	GO Molecular Functions	solute:monoatomic cation symporter activity	SLC29A1|SLC28A3	19.37	0.0048
074	GO Molecular Functions	electron transfer activity	CYP1A2|CYP19A1	19.21	0.0049
075	GO Molecular Functions	ATP hydrolysis activity	ABCC2|ABCB1|ABCB11	8.04	0.006
076	GO Molecular Functions	protein-folding chaperone binding	CYP2E1|SOD1	16.90	0.0062
077	GO Molecular Functions	protein serine/threonine kinase activity	EGFR|MAP2K1|TOP1	7.89	0.0063
078	GO Molecular Functions	growth factor binding	EGFR|FGFR2	16.65	0.0064
079	GO Molecular Functions	symporter activity	SLC29A1|SLC28A3	15.29	0.0076
080	GO Molecular Functions	sodium ion transmembrane transporter activity	SLC29A1|SLC28A3	13.87	0.0091
081	GO Molecular Functions	lipid transporter activity	ABCB1|ABCB11	13.46	0.0097
082	GO Molecular Functions	ATP-dependent activity	ABCC2|ABCB1|ABCB11	5.78	0.0147
083	GO Molecular Functions	enzyme activator activity	ALK|EGFR|MAP2K1	5.56	0.0162
084	GO Molecular Functions	chromatin binding	EGFR|MPO|TOP1	5.33	0.0182
085	GO Molecular Functions	protein domain specific binding	BCL2|RRM1|TOP1	5.15	0.0199
086	GO Molecular Functions	active monoatomic ion transmembrane transporter activity	SLC29A1|SLC28A3	7.86	0.0266
087	GO Molecular Functions	inorganic molecular entity transmembrane transporter activity	ABCC2|SLC29A1|SLC28A3	4.59	0.0268
088	GO Molecular Functions	secondary active transmembrane transporter activity	SLC29A1|SLC28A3	7.80	0.027
089	GO Molecular Functions	ribonucleoside triphosphate phosphatase activity	ABCC2|ABCB1|ABCB11	4.51	0.028

090	GO Molecular Functions	protein heterodimerization activity	BCL2|UGT1A1	6.42	0.0385
001	GO Cellular Components	apical plasma membrane	ABCC2|EGFR|SLC29A1|SLC29A2|ABCB1|ABCB11	16.65	1E-06
002	GO Cellular Components	apical part of cell	ABCC2|EGFR|SLC29A1|SLC29A2|ABCB1|ABCB11	14.31	3E-06
003	GO Cellular Components	intercellular canaliculus	ABCC2|ABCB11	374.53	1E-05
004	GO Cellular Components	neuronal cell body	NQO1|RET|RRM1|SOD1|TOP1	11.42	7E-05
005	GO Cellular Components	cell body	NQO1|RET|RRM1|SOD1|TOP1	10.05	0.0001
006	GO Cellular Components	nuclear envelope	BCL2|EGFR|PTGS2|RRM1	8.97	0.001
007	GO Cellular Components	receptor complex	ALK|EGFR|FGFR2|RET	8.28	0.0013
008	GO Cellular Components	basolateral plasma membrane	EGFR|SLC29A1|SLC29A2	13.07	0.0015
009	GO Cellular Components	basal plasma membrane	EGFR|SLC29A1|SLC29A2	11.58	0.0022
010	GO Cellular Components	basal part of cell	EGFR|SLC29A1|SLC29A2	10.87	0.0026
011	GO Cellular Components	nuclear membrane	BCL2|EGFR|PTGS2	10.70	0.0027
012	GO Cellular Components	early endosome	EGFR|MAP2K1|RET	7.70	0.0068
013	GO Cellular Components	endosome membrane	EGFR|RET|ABCB11	5.85	0.0142
014	GO Cellular Components	dendrite	NQO1|RET|SOD1	5.41	0.0175
015	GO Cellular Components	dendritic tree	NQO1|RET|SOD1	5.39	0.0176
016	GO Cellular Components	organelle outer membrane	BCL2|PTGS2	8.95	0.0209
017	GO Cellular Components	outer membrane	BCL2|PTGS2	8.88	0.0212
018	GO Cellular Components	membrane raft	EGFR|PTGS2	7.80	0.027
019	GO Cellular Components	membrane microdomain	EGFR|PTGS2	7.75	0.0273
020	GO Cellular Components	endoplasmic reticulum lumen	CES1|PTGS2	7.18	0.0314
021	GO Cellular Components	late endosome	EGFR|MAP2K1	7.13	0.0318
022	GO Cellular Components	vesicle lumen	EGFR|MPO	6.85	0.0342
023	GO Cellular Components	endocytic vesicle	EGFR|MPO	6.38	0.0389
024	GO Cellular Components	cell projection membrane	EGFR|SLC28A3	6.33	0.0395
001	GO Biological Processes	response to xenobiotic stimulus	BCL2|ABCC2|CYP1A2|CYP2E1|CYP3A4|NQO1|EGFR|SLC2	44.22	2E-25
002	GO Biological Processes	cellular response to xenobiotic stimulus	ABCC2|CYP1A2|CYP2E1|CYP3A4|NQO1|EGFR|SLC29A1|A	69.86	5E-20
003	GO Biological Processes	xenobiotic metabolic process	ABCC2|CYP1A2|CYP2E1|CYP3A4|NQO1|SLC29A1|ABCB1	98.09	5E-20
004	GO Biological Processes	xenobiotic transport	ABCC2|SLC29A1|SLC29A2|ABCB1|ABCB11|NR1I2|SLC28A	163.86	1E-14
005	GO Biological Processes	xenobiotic transmembrane transport	ABCC2|SLC29A1|SLC29A2|ABCB11|SLC28A3	330.47	2E-12
006	GO Biological Processes	response to toxic substance	BCL2|CES1|NQO1|MPO|ABCB1|PTGS1|PTGS2|SOD1	36.39	3E-11
007	GO Biological Processes	steroid metabolic process	CES1|CYP1A2|CYP2E1|CYP3A4|CYP19A1|ABCB11|NR1I2	34.71	5E-11
008	GO Biological Processes	small molecule biosynthetic process	CES1|CYP1A2|CYP2E1|CYP3A4|CYP19A1|MPO|PTGS1|PT	21.89	1E-10
009	GO Biological Processes	reactive oxygen species metabolic process	BCL2|CYP1A2|NQO1|EGFR|MPO|SOD1	61.85	5E-10
010	GO Biological Processes	response to oxidative stress	BCL2|NQO1|EGFR|MPO|PTGS1|PTGS2|SOD1|ABCB11	24.43	8E-10
011	GO Biological Processes	gland development	BCL2|CYP19A1|EGFR|SLC29A1|FGFR2|MAP2K1|SOD1|UG	21.15	2E-09
012	GO Biological Processes	detoxification	NQO1|MPO|ABCB1|PTGS1|PTGS2|SOD1	46.82	3E-09
013	GO Biological Processes	olefinic compound metabolic process	CYP1A2|CYP2E1|CYP3A4|CYP19A1|PTGS1|PTGS2	46.49	3E-09
014	GO Biological Processes	vascular process in circulatory system	ABCC2|EGFR|SLC29A1|SLC29A2|ABCB1|PTGS2|SOD1	28.70	3E-09
015	GO Biological Processes	xenobiotic catabolic process	CYP1A2|CYP3A4|NR1I2|UGT1A1	179.77	6E-09
016	GO Biological Processes	purine nucleoside transmembrane transport	SLC29A1|SLC29A2|SLC28A3	674.16	6E-09
017	GO Biological Processes	organic hydroxy compound metabolic process	BCL2|CES1|CYP1A2|CYP2E1|CYP3A4|CYP19A1|NQO1|AB	18.61	7E-09
018	GO Biological Processes	monocarboxylic acid biosynthetic process	CYP1A2|CYP2E1|CYP3A4|PTGS1|PTGS2|ABCB11	40.37	7E-09
019	GO Biological Processes	circulatory system process	ABCC2|EGFR|SLC29A1|SLC29A2|ABCB1|PTGS1|PTGS2|S	17.66	1E-08
020	GO Biological Processes	fatty acid metabolic process	CES1|CYP1A2|CYP2E1|CYP3A4|PTGS1|PTGS2|ABCB11	24.28	1E-08
021	GO Biological Processes	monocarboxylic acid metabolic process	CES1|CYP1A2|CYP2E1|CYP3A4|PTGS1|PTGS2|ABCB11|U	17.25	1E-08
022	GO Biological Processes	monoterpenoid metabolic process	CYP1A2|CYP2E1|CYP3A4	561.80	1E-08
023	GO Biological Processes	uridine transmembrane transport	SLC29A1|SLC29A2|SLC28A3	561.80	1E-08
024	GO Biological Processes	pyrimidine nucleoside transport	SLC29A1|SLC29A2|SLC28A3	561.80	1E-08
025	GO Biological Processes	cellular oxidant detoxification	NQO1|MPO|PTGS1|PTGS2|SOD1	61.74	2E-08
026	GO Biological Processes	pyrimidine nucleobase transport	SLC29A1|SLC29A2|SLC28A3	481.54	2E-08
027	GO Biological Processes	terpenoid metabolic process	CYP1A2|CYP2E1|CYP3A4|EGFR|UGT1A1	56.75	3E-08
028	GO Biological Processes	lipid biosynthetic process	CES1|CYP1A2|CYP2E1|CYP3A4|CYP19A1|PTGS1|PTGS2|A	15.03	3E-08
029	GO Biological Processes	nucleoside transport	SLC29A1|SLC29A2|SLC28A3	421.35	4E-08
030	GO Biological Processes	nucleoside transmembrane transport	SLC29A1|SLC29A2|SLC28A3	421.35	4E-08
031	GO Biological Processes	purine nucleobase transmembrane transport	SLC29A1|SLC29A2|SLC28A3	421.35	4E-08
032	GO Biological Processes	long-chain fatty acid metabolic process	CYP1A2|CYP2E1|CYP3A4|PTGS1|PTGS2	51.54	4E-08
033	GO Biological Processes	estrogen metabolic process	CYP1A2|CYP3A4|CYP19A1|UGT1A1	112.36	4E-08
034	GO Biological Processes	hydrogen peroxide metabolic process	CYP1A2|EGFR|MPO|SOD1	109.62	5E-08
035	GO Biological Processes	cellular detoxification	NQO1|MPO|PTGS1|PTGS2|SOD1	48.02	6E-08
036	GO Biological Processes	fatty acid biosynthetic process	CYP1A2|CYP2E1|CYP3A4|PTGS1|PTGS2	48.02	6E-08
037	GO Biological Processes	response to estradiol	CYP19A1|NQO1|EGFR|PTGS2|UGT1A1	47.61	6E-08
038	GO Biological Processes	response to ethanol	NQO1|FGFR2|SOD1|ABCB11|UGT1A1	44.59	9E-08
039	GO Biological Processes	cellular response to toxic substance	NQO1|MPO|PTGS1|PTGS2|SOD1	44.24	9E-08
040	GO Biological Processes	response to alcohol	CES1|NQO1|FGFR2|SOD1|ABCB11|UGT1A1	25.63	1E-07
041	GO Biological Processes	isoprenoid metabolic process	CYP1A2|CYP2E1|CYP3A4|EGFR|UGT1A1	41.61	1E-07
042	GO Biological Processes	carboxylic acid biosynthetic process	CYP1A2|CYP2E1|CYP3A4|PTGS1|PTGS2|ABCB11	24.79	1E-07
043	GO Biological Processes	organic acid biosynthetic process	CYP1A2|CYP2E1|CYP3A4|PTGS1|PTGS2|ABCB11	24.51	1E-07
044	GO Biological Processes	purine nucleobase transport	SLC29A1|SLC29A2|SLC28A3	280.90	1E-07
045	GO Biological Processes	nucleobase transport	SLC29A1|SLC29A2|SLC28A3	259.29	2E-07
046	GO Biological Processes	placenta development	EGFR|FGFR2|MAP2K1|PTGS2|SOD1	37.70	2E-07
047	GO Biological Processes	arachidonic acid metabolic process	CYP1A2|CYP2E1|PTGS1|PTGS2	77.49	2E-07
048	GO Biological Processes	xenobiotic export from cell	ABCC2|ABCB1|ABCB11	240.77	2E-07
049	GO Biological Processes	removal of superoxide radicals	NQO1|MPO|SOD1	224.72	3E-07
050	GO Biological Processes	carboxylic acid metabolic process	CES1|CYP1A2|CYP2E1|CYP3A4|PTGS1|PTGS2|ABCB11|U	11.35	3E-07
051	GO Biological Processes	pyrimidine-containing compound transmembrane transport	SLC29A1|SLC29A2|SLC28A3	210.67	3E-07
052	GO Biological Processes	reactive oxygen species biosynthetic process	CYP1A2|MPO|SOD1	210.67	3E-07
053	GO Biological Processes	regulation of lipid metabolic process	ALK|CES1|PTGS2|SOD1|ABCB11|UGT1A1	20.62	4E-07
054	GO Biological Processes	cellular response to oxygen radical	NQO1|MPO|SOD1	198.28	4E-07
055	GO Biological Processes	cellular response to superoxide	NQO1|MPO|SOD1	198.28	4E-07
056	GO Biological Processes	response to reactive oxygen species	BCL2|NQO1|EGFR|MPO|SOD1	30.87	5E-07
057	GO Biological Processes	response to superoxide	NQO1|MPO|SOD1	168.54	7E-07
058	GO Biological Processes	thymine transport	SLC29A1|SLC29A2	1123.59	8E-07
059	GO Biological Processes	response to oxygen radical	NQO1|MPO|SOD1	160.51	8E-07
060	GO Biological Processes	positive regulation of phosphorylation	ALK|BCL2|EGFR|FGFR2|MAP2K1|PTGS2|RET	12.81	8E-07
061	GO Biological Processes	vascular transport	ABCC2|SLC29A1|SLC29A2|ABCB1	52.26	1E-06
062	GO Biological Processes	transport across blood-brain barrier	ABCC2|SLC29A1|SLC29A2|ABCB1	52.26	1E-06
063	GO Biological Processes	diterpenoid metabolic process	CYP1A2|CYP3A4|EGFR|UGT1A1	51.07	1E-06
064	GO Biological Processes	positive regulation of peptidyl-serine phosphorylation	BCL2|EGFR|PTGS2|RET	49.94	1E-06

065	GO Biological Processes	steroid catabolic process	CYP1A2|CYP3A4|CYP19A1	134.83	1E-06
066	GO Biological Processes	molting cycle	BCL2|EGFR|FGFR2|PTGS2	46.33	2E-06
067	GO Biological Processes	hair cycle	BCL2|EGFR|FGFR2|PTGS2	46.33	2E-06
068	GO Biological Processes	hematopoietic or lymphoid organ development	BCL2|MAP2K1|RET|SOD1	45.40	2E-06
069	GO Biological Processes	long-chain fatty acid biosynthetic process	CYP1A2|CYP2E1|CYP3A4	124.84	2E-06
070	GO Biological Processes	positive regulation of phosphorus metabolic process	ALK|BCL2|EGFR|FGFR2|MAP2K1|PTGS2|RET	11.35	2E-06
071	GO Biological Processes	positive regulation of phosphate metabolic process	ALK|BCL2|EGFR|FGFR2|MAP2K1|PTGS2|RET	11.35	2E-06
072	GO Biological Processes	unsaturated fatty acid metabolic process	CYP1A2|CYP2E1|PTGS1|PTGS2	43.22	2E-06
073	GO Biological Processes	regulation of steroid metabolic process	CES1|SOD1|ABCB11|UGT1A1	43.22	2E-06
074	GO Biological Processes	uracil transport	SLC29A1|SLC29A2	749.06	2E-06
075	GO Biological Processes	uracil transmembrane transport	SLC29A1|SLC29A2	749.06	2E-06
076	GO Biological Processes	pyrimidine nucleobase transmembrane transport	SLC29A1|SLC29A2	749.06	2E-06
077	GO Biological Processes	positive regulation of neuron maturation	BCL2|RET	749.06	2E-06
078	GO Biological Processes	steroid biosynthetic process	CES1|CYP3A4|CYP19A1|ABCB11	39.08	3E-06
079	GO Biological Processes	icosanoid metabolic process	CYP1A2|CYP2E1|PTGS1|PTGS2	38.74	3E-06
080	GO Biological Processes	response to nutrient levels	BCL2|NQO1|EGFR|MPO|PTGS2|UGT1A1	13.76	4E-06
081	GO Biological Processes	regulation of peptidyl-serine phosphorylation	BCL2|EGFR|PTGS2|RET	36.24	4E-06
082	GO Biological Processes	guanine transport	SLC29A1|SLC29A2	561.80	5E-06
083	GO Biological Processes	cytidine transport	SLC29A1|SLC29A2	561.80	5E-06
084	GO Biological Processes	inosine transport	SLC29A1|SLC29A2	561.80	5E-06
085	GO Biological Processes	hypoxanthine transport	SLC29A1|SLC29A2	561.80	5E-06
086	GO Biological Processes	guanine transmembrane transport	SLC29A1|SLC29A2	561.80	5E-06
087	GO Biological Processes	cellular response to chemical stress	NQO1|EGFR|MPO|PTGS2|SOD1	19.85	5E-06
088	GO Biological Processes	regulation of kinase activity	ALK|EGFR|FGFR2|MAP2K1|RET|SOD1	13.04	5E-06
089	GO Biological Processes	positive regulation of kinase activity	ALK|EGFR|FGFR2|MAP2K1|RET	19.24	5E-06
090	GO Biological Processes	digestive tract development	BCL2|EGFR|FGFR2|RET	34.05	6E-06
091	GO Biological Processes	purine-containing compound transmembrane transport	SLC29A1|SLC29A2|SLC28A3	86.43	6E-06
092	GO Biological Processes	sterol metabolic process	CES1|CYP1A2|CYP3A4|CYP19A1	33.79	6E-06
093	GO Biological Processes	reproductive structure development	BCL2|CYP19A1|FGFR2|RRM1|SOD1	18.92	6E-06
094	GO Biological Processes	cellular response to reactive oxygen species	NQO1|EGFR|MPO|SOD1	33.29	6E-06
095	GO Biological Processes	response to glucocorticoid	BCL2|EGFR|PTGS2|UGT1A1	33.05	6E-06
096	GO Biological Processes	reproductive system development	BCL2|CYP19A1|FGFR2|RRM1|SOD1	18.66	6E-06
097	GO Biological Processes	cellular response to hypoxia	BCL2|SLC29A1|FGFR2|PTGS2	32.10	7E-06
098	GO Biological Processes	adenosine transport	SLC29A1|SLC29A2	449.44	8E-06
099	GO Biological Processes	digestive system development	BCL2|EGFR|FGFR2|RET	31.43	8E-06
100	GO Biological Processes	cellular response to decreased oxygen levels	BCL2|SLC29A1|FGFR2|PTGS2	30.57	9E-06
101	GO Biological Processes	superoxide metabolic process	NQO1|MPO|SOD1	74.91	9E-06
102	GO Biological Processes	secondary metabolic process	BCL2|CYP1A2|CYP3A4	71.72	1E-05
103	GO Biological Processes	sensory organ development	BCL2|EGFR|FGFR2|RET|RRM1|SOD1	11.58	1E-05
104	GO Biological Processes	response to lipopolysaccharide	NQO1|FGFR2|MPO|PTGS2|UGT1A1	16.87	1E-05
105	GO Biological Processes	porphyrin-containing compound metabolic process	ABCC2|CYP1A2|UGT1A1	70.22	1E-05
106	GO Biological Processes	epidermis development	BCL2|EGFR|FGFR2|MAP2K1|SOD1	16.72	1E-05
107	GO Biological Processes	thymus development	BCL2|MAP2K1|SOD1	68.79	1E-05
108	GO Biological Processes	digestive tract morphogenesis	BCL2|EGFR|FGFR2	68.79	1E-05
109	GO Biological Processes	response to corticosteroid	BCL2|EGFR|PTGS2|UGT1A1	28.45	1E-05
110	GO Biological Processes	xenobiotic transport across blood-brain barrier	ABCC2|ABCB1	374.53	1E-05
111	GO Biological Processes	adenine transport	SLC29A1|SLC29A2	374.53	1E-05
112	GO Biological Processes	regulation of bile acid secretion	CES1|ABCB11	374.53	1E-05
113	GO Biological Processes	response to nutrient	NQO1|EGFR|PTGS2|UGT1A1	28.09	1E-05
114	GO Biological Processes	response to metal ion	BCL2|CYP1A2|NQO1|EGFR|PTGS2	16.19	1E-05
115	GO Biological Processes	cellular response to oxygen levels	BCL2|SLC29A1|FGFR2|PTGS2	27.74	1E-05
116	GO Biological Processes	lipid transport	CES1|ABCC2|ABCB1|PTGS2|ABCB11	16.14	1E-05
117	GO Biological Processes	response to molecule of bacterial origin	NQO1|FGFR2|MPO|PTGS2|UGT1A1	15.87	1E-05
118	GO Biological Processes	immune system development	BCL2|MAP2K1|RET|SOD1	27.07	1E-05
119	GO Biological Processes	regulation of transferase activity	ALK|EGFR|FGFR2|MAP2K1|RET|SOD1	10.82	2E-05
120	GO Biological Processes	positive regulation of transferase activity	ALK|EGFR|FGFR2|MAP2K1|RET	15.43	2E-05
121	GO Biological Processes	organic hydroxy compound biosynthetic process	CES1|CYP3A4|CYP19A1|ABCB11	26.13	2E-05
122	GO Biological Processes	lipid hydroxylation	CYP2E1|CYP3A4	321.03	2E-05
123	GO Biological Processes	alkaloid metabolic process	CYP1A2|CYP3A4	321.03	2E-05
124	GO Biological Processes	mycotoxin metabolic process	CYP1A2|CYP3A4	321.03	2E-05
125	GO Biological Processes	aflatoxin metabolic process	CYP1A2|CYP3A4	321.03	2E-05
126	GO Biological Processes	organic heteropentacyclic compound metabolic process	CYP1A2|CYP3A4	321.03	2E-05
127	GO Biological Processes	tetrapyrrole metabolic process	ABCC2|CYP1A2|UGT1A1	60.19	2E-05
128	GO Biological Processes	lipid localization	CES1|ABCC2|ABCB1|PTGS2|ABCB11	14.67	2E-05
129	GO Biological Processes	regulation of neuron maturation	BCL2|RET	280.90	2E-05
130	GO Biological Processes	cellular response to metal ion	CYP1A2|NQO1|EGFR|PTGS2	23.91	2E-05
131	GO Biological Processes	lung development	CYP1A2|EGFR|FGFR2|MAP2K1	23.53	2E-05
132	GO Biological Processes	respiratory tube development	CYP1A2|EGFR|FGFR2|MAP2K1	23.05	3E-05
133	GO Biological Processes	peptidyl-tyrosine phosphorylation	ALK|EGFR|FGFR2	51.86	3E-05
134	GO Biological Processes	pigment metabolic process	BCL2|ABCC2|UGT1A1	51.86	3E-05
135	GO Biological Processes	cyclooxygenase pathway	PTGS1|PTGS2	249.69	3E-05
136	GO Biological Processes	positive regulation of cell maturation	BCL2|RET	249.69	3E-05
137	GO Biological Processes	peptidyl-tyrosine modification	ALK|EGFR|FGFR2	50.31	3E-05
138	GO Biological Processes	response to bacterium	CYP2E1|NQO1|FGFR2|MPO|PTGS2|UGT1A1	9.46	3E-05
139	GO Biological Processes	hormone metabolic process	CYP1A2|CYP3A4|CYP19A1|UGT1A1	21.82	3E-05
140	GO Biological Processes	cell surface receptor protein tyrosine kinase signaling pathway	ALK|EGFR|FGFR2|MAP2K1|RET	13.28	3E-05
141	GO Biological Processes	cell population proliferation	BCL2|EGFR|FGFR2|ABCB1|MAP2K1|RRM1	9.38	3E-05
142	GO Biological Processes	oxidative demethylation	CYP1A2|CYP3A4	224.72	3E-05
143	GO Biological Processes	hydrogen peroxide biosynthetic process	CYP1A2|SOD1	224.72	3E-05
144	GO Biological Processes	brain development	ALK|BCL2|EGFR|FGFR2|MAP2K1|RRM1	9.22	4E-05
145	GO Biological Processes	respiratory system development	CYP1A2|EGFR|FGFR2|MAP2K1	20.62	4E-05
146	GO Biological Processes	prostate gland growth	CYP19A1|FGFR2	204.29	4E-05
147	GO Biological Processes	cellular response to oxidative stress	NQO1|EGFR|MPO|SOD1	19.89	5E-05
148	GO Biological Processes	gonad development	BCL2|CYP19A1|RRM1|SOD1	19.80	5E-05
149	GO Biological Processes	midgut development	EGFR|RET	187.27	5E-05
150	GO Biological Processes	development of primary sexual characteristics	BCL2|CYP19A1|RRM1|SOD1	19.37	5E-05
151	GO Biological Processes	hair follicle development	BCL2|EGFR|FGFR2	41.61	5E-05
152	GO Biological Processes	positive regulation of MAPK cascade	EGFR|FGFR2|MAP2K1|RET|SOD1	12.03	5E-05
153	GO Biological Processes	head development	ALK|BCL2|EGFR|FGFR2|MAP2K1|RRM1	8.63	5E-05

154	GO Biological Processes	retinoid metabolic process	CYP1A2|CYP3A4|UGT1A1	40.61	6E-05
155	GO Biological Processes	cellular catabolic process	BCL2|CYP1A2|CYP3A4|MPO|NR1I2|UGT1A1	8.53	6E-05
156	GO Biological Processes	response to hormone	BCL2|NQO1|EGFR|PTGS2|ABCB11|UGT1A1	8.48	6E-05
157	GO Biological Processes	negative regulation of smooth muscle contraction	PTGS2|SOD1	172.86	6E-05
158	GO Biological Processes	porphyrin-containing compound catabolic process	ABCC2|UGT1A1	172.86	6E-05
159	GO Biological Processes	tetrapyrrole catabolic process	ABCC2|UGT1A1	172.86	6E-05
160	GO Biological Processes	molting cycle process	BCL2|EGFR|FGFR2	39.66	6E-05
161	GO Biological Processes	hair cycle process	BCL2|EGFR|FGFR2	39.66	6E-05
162	GO Biological Processes	embryonic placenta development	EGFR|FGFR2|MAP2K1	39.20	6E-05
163	GO Biological Processes	protein phosphorylation	ALK|EGFR|FGFR2|RET|TOP1	11.49	6E-05
164	GO Biological Processes	ureteric bud development	BCL2|FGFR2|RET	38.30	7E-05
165	GO Biological Processes	carbohydrate derivative transport	SLC29A1|SLC29A2|SLC28A3	37.87	7E-05
166	GO Biological Processes	post-embryonic development	BCL2|CYP1A2|FGFR2	37.87	7E-05
167	GO Biological Processes	mesonephric epithelium development	BCL2|FGFR2|RET	37.87	7E-05
168	GO Biological Processes	mesonephric tubule development	BCL2|FGFR2|RET	37.87	7E-05
169	GO Biological Processes	peptidyl-tyrosine autophosphorylation	ALK|EGFR	160.51	7E-05
170	GO Biological Processes	deoxyribonucleotide biosynthetic process	DCK|RRM1	160.51	7E-05
171	GO Biological Processes	2'-deoxyribonucleotide biosynthetic process	DCK|RRM1	160.51	7E-05
172	GO Biological Processes	deoxyribose phosphate biosynthetic process	DCK|RRM1	160.51	7E-05
173	GO Biological Processes	female gonad development	BCL2|CYP19A1|SOD1	36.24	8E-05
174	GO Biological Processes	mesonephros development	BCL2|FGFR2|RET	36.24	8E-05
175	GO Biological Processes	toxin metabolic process	CYP1A2|CYP3A4	149.81	8E-05
176	GO Biological Processes	regulation of bile acid metabolic process	CES1|ABCB11	149.81	8E-05
177	GO Biological Processes	development of primary female sexual characteristics	BCL2|CYP19A1|SOD1	34.75	9E-05
178	GO Biological Processes	response to hydrogen peroxide	BCL2|NQO1|SOD1	34.40	9E-05
179	GO Biological Processes	regulation of response to osmotic stress	ABCB1|PTGS2	140.45	9E-05
180	GO Biological Processes	positive regulation of smooth muscle cell proliferation	EGFR|FGFR2|PTGS2	33.71	1E-04
181	GO Biological Processes	cellular response to lipid	CES1|EGFR|FGFR2|RET|UGT1A1	10.48	1E-04
182	GO Biological Processes	regulation of hormone levels	CYP1A2|CYP3A4|CYP19A1|EGFR|UGT1A1	10.38	0.0001
183	GO Biological Processes	skin development	BCL2|EGFR|FGFR2|MAP2K1	15.94	0.0001
184	GO Biological Processes	phosphorylation	ALK|EGFR|FGFR2|RET|TOP1	10.27	0.0001
185	GO Biological Processes	sex differentiation	BCL2|CYP19A1|RRM1|SOD1	15.88	0.0001
186	GO Biological Processes	gland morphogenesis	BCL2|EGFR|FGFR2	32.10	0.0001
187	GO Biological Processes	positive regulation of apoptotic process	BCL2|NQO1|PTGS2|RET|SOD1	10.18	0.0001
188	GO Biological Processes	response to steroid hormone	BCL2|EGFR|PTGS2|UGT1A1	15.71	0.0001
189	GO Biological Processes	epoxygenase P450 pathway	CYP1A2|CYP2E1	124.84	0.0001
190	GO Biological Processes	positive regulation of superoxide anion generation	EGFR|SOD1	124.84	0.0001
191	GO Biological Processes	morphogenesis of an epithelial fold	EGFR|FGFR2	124.84	0.0001
192	GO Biological Processes	organ growth	BCL2|CYP19A1|FGFR2	31.50	0.0001
193	GO Biological Processes	ossification	BCL2|EGFR|FGFR2|PTGS2	15.55	0.0001
194	GO Biological Processes	positive regulation of protein phosphorylation	BCL2|EGFR|MAP2K1|PTGS2|RET	9.87	0.0001
195	GO Biological Processes	positive regulation of programmed cell death	BCL2|NQO1|PTGS2|RET|SOD1	9.84	0.0001
196	GO Biological Processes	carboxylic acid transport	ABCC2|ABCB1|PTGS2|ABCB11	15.08	0.0001
197	GO Biological Processes	female sex differentiation	BCL2|CYP19A1|SOD1	30.10	0.0001
198	GO Biological Processes	negative regulation of lipid metabolic process	ALK|SOD1|UGT1A1	30.10	0.0001
199	GO Biological Processes	organic acid transport	ABCC2|ABCB1|PTGS2|ABCB11	15.03	0.0001
200	GO Biological Processes	lipid catabolic process	CES1|CYP1A2|CYP3A4|CYP19A1	14.98	0.0001
201	GO Biological Processes	response to hypoxia	BCL2|SLC29A1|FGFR2|PTGS2	14.88	0.0001
202	GO Biological Processes	demethylation	CYP1A2|CYP3A4	112.36	0.0001
203	GO Biological Processes	regulation of superoxide anion generation	EGFR|SOD1	112.36	0.0001
204	GO Biological Processes	skin epidermis development	BCL2|EGFR|FGFR2	28.81	0.0002
205	GO Biological Processes	prostaglandin biosynthetic process	PTGS1|PTGS2	107.01	0.0002
206	GO Biological Processes	prostanoid biosynthetic process	PTGS1|PTGS2	107.01	0.0002
207	GO Biological Processes	cholesterol metabolic process	CES1|CYP1A2|CYP3A4	28.33	0.0002
208	GO Biological Processes	response to decreased oxygen levels	BCL2|SLC29A1|FGFR2|PTGS2	14.22	0.0002
209	GO Biological Processes	programmed cell death involved in cell development	BCL2|SOD1	102.14	0.0002
210	GO Biological Processes	negative regulation of muscle contraction	PTGS2|SOD1	97.70	0.0002
211	GO Biological Processes	ERBB2 signaling pathway	EGFR|MAP2K1	97.70	0.0002
212	GO Biological Processes	behavior	ALK|BCL2|EGFR|PTGS2|SOD1	9.09	0.0002
213	GO Biological Processes	enzyme-linked receptor protein signaling pathway	ALK|EGFR|FGFR2|MAP2K1|RET	9.09	0.0002
214	GO Biological Processes	mammary gland development	CYP19A1|SLC29A1|FGFR2	26.54	0.0002
215	GO Biological Processes	glial cell development	EGFR|MAP2K1|SOD1	26.33	0.0002
216	GO Biological Processes	response to amino acid	NQO1|EGFR|PTGS2	26.33	0.0002
217	GO Biological Processes	regulation of small molecule metabolic process	CES1|PTGS2|SOD1|ABCB11	13.54	0.0002
218	GO Biological Processes	regulation of cell maturation	BCL2|RET	93.63	0.0002
219	GO Biological Processes	secondary alcohol metabolic process	CES1|CYP1A2|CYP3A4	25.93	0.0002
220	GO Biological Processes	response to oxygen levels	BCL2|SLC29A1|FGFR2|PTGS2	13.14	0.0002
221	GO Biological Processes	benzene-containing compound metabolic process	CYP2E1|UGT1A1	86.43	0.0002
222	GO Biological Processes	regulation of MAPK cascade	EGFR|FGFR2|MAP2K1|RET|SOD1	8.50	0.0003
223	GO Biological Processes	cell proliferation in forebrain	FGFR2|RRM1	83.23	0.0003
224	GO Biological Processes	negative regulation of catabolic process	ALK|BCL2|NQO1|EGFR	12.62	0.0003
225	GO Biological Processes	kidney epithelium development	BCL2|FGFR2|RET	23.91	0.0003
226	GO Biological Processes	response to acid chemical	NQO1|EGFR|PTGS2	23.57	0.0003
227	GO Biological Processes	regulation of cellular ketone metabolic process	CES1|PTGS2|ABCB11	23.57	0.0003
228	GO Biological Processes	androgen metabolic process	CYP3A4|CYP19A1	77.49	0.0003
229	GO Biological Processes	regulation of superoxide metabolic process	EGFR|SOD1	77.49	0.0003
230	GO Biological Processes	salivary gland morphogenesis	EGFR|FGFR2	77.49	0.0003
231	GO Biological Processes	regulation of reactive oxygen species metabolic process	BCL2|EGFR|SOD1	22.78	0.0003
232	GO Biological Processes	cell morphogenesis	BCL2|EGFR|FGFR2|RET|SOD1	8.18	0.0003
233	GO Biological Processes	tube morphogenesis	BCL2|EGFR|FGFR2|PTGS2|RET	8.17	0.0003
234	GO Biological Processes	bile acid and bile salt transport	ABCC2|ABCB11	74.91	0.0003
235	GO Biological Processes	neurotransmitter uptake	SLC29A1|SLC29A2	74.91	0.0003
236	GO Biological Processes	neuron projection development	BCL2|EGFR|FGFR2|RET|SOD1	8.10	0.0003
237	GO Biological Processes	regulation of tube diameter	EGFR|PTGS2|SOD1	22.03	0.0003
238	GO Biological Processes	blood vessel diameter maintenance	EGFR|PTGS2|SOD1	22.03	0.0003
239	GO Biological Processes	regulation of tube size	EGFR|PTGS2|SOD1	21.89	0.0003
240	GO Biological Processes	eye development	BCL2|EGFR|RET|RRM1	11.77	0.0003
241	GO Biological Processes	retinoic acid metabolic process	CYP3A4|UGT1A1	72.49	0.0003
242	GO Biological Processes	regulation of osteoblast proliferation	BCL2|FGFR2	72.49	0.0003

243	GO Biological Processes	monocarboxylic acid transport	ABCC2|PTGS2|ABCB11	21.75	0.0003
244	GO Biological Processes	protein autophosphorylation	ALK|EGFR|FGFR2	21.75	0.0003
245	GO Biological Processes	visual system development	BCL2|EGFR|RET|RRM1	11.64	0.0004
246	GO Biological Processes	transepithelial transport	ABCC2|ABCB1	70.22	0.0004
247	GO Biological Processes	salivary gland development	EGFR|FGFR2	70.22	0.0004
248	GO Biological Processes	sensory system development	BCL2|EGFR|RET|RRM1	11.47	0.0004
249	GO Biological Processes	regulation of apoptotic signaling pathway	BCL2|PTGS2|RET|SOD1	11.35	0.0004
250	GO Biological Processes	positive regulation of vasoconstriction	EGFR|PTGS2	68.10	0.0004
251	GO Biological Processes	hair follicle morphogenesis	BCL2|FGFR2	68.10	0.0004
252	GO Biological Processes	regeneration	BCL2|EGFR|UGT1A1	20.81	0.0004
253	GO Biological Processes	organic anion transport	ABCC2|ABCB1|PTGS2|ABCB11	11.24	0.0004
254	GO Biological Processes	negative regulation of steroid metabolic process	SOD1|UGT1A1	66.09	0.0004
255	GO Biological Processes	organic hydroxy compound transport	CES1|ABCC2|ABCB11	20.18	0.0004
256	GO Biological Processes	forebrain development	ALK|EGFR|FGFR2|RRM1	10.99	0.0004
257	GO Biological Processes	positive regulation of synaptic transmission, glutamatergic	EGFR|PTGS2	62.42	0.0005
258	GO Biological Processes	female pregnancy	BCL2|PTGS2|SOD1	19.48	0.0005
259	GO Biological Processes	regulation of smooth muscle cell proliferation	EGFR|FGFR2|PTGS2	19.48	0.0005
260	GO Biological Processes	positive regulation of protein modification process	BCL2|EGFR|MAP2K1|PTGS2|RET	7.44	0.0005
261	GO Biological Processes	blood circulation	EGFR|PTGS1|PTGS2|SOD1	10.73	0.0005
262	GO Biological Processes	epithelial cell proliferation	EGFR|FGFR2|MAP2K1	19.37	0.0005
263	GO Biological Processes	mesenchymal cell differentiation	BCL2|FGFR2|RET	19.37	0.0005
264	GO Biological Processes	epidermis morphogenesis	BCL2|FGFR2	60.73	0.0005
265	GO Biological Processes	cellular response to cadmium ion	CYP1A2|EGFR	59.14	0.0005
266	GO Biological Processes	cellular response to estradiol stimulus	EGFR|UGT1A1	59.14	0.0005
267	GO Biological Processes	animal organ formation	FGFR2|MAP2K1	57.62	0.0006
268	GO Biological Processes	unsaturated fatty acid biosynthetic process	PTGS1|PTGS2	57.62	0.0006
269	GO Biological Processes	stem cell differentiation	BCL2|FGFR2|RET	18.42	0.0006
270	GO Biological Processes	prostaglandin metabolic process	PTGS1|PTGS2	56.18	0.0006
271	GO Biological Processes	response to carbohydrate	NQO1|SLC29A1|PTGS2	18.22	0.0006
272	GO Biological Processes	cell morphogenesis involved in neuron differentiation	BCL2|FGFR2|RET|SOD1	10.15	0.0006
273	GO Biological Processes	regulation of blood pressure	PTGS1|PTGS2|SOD1	18.03	0.0006
274	GO Biological Processes	regulation of G1/S transition of mitotic cell cycle	BCL2|EGFR|RRM1	18.03	0.0006
275	GO Biological Processes	prostanoid metabolic process	PTGS1|PTGS2	54.81	0.0006
276	GO Biological Processes	regulation of cholesterol metabolic process	CES1|SOD1	54.81	0.0006
277	GO Biological Processes	2'-deoxyribonucleotide metabolic process	DCK|RRM1	54.81	0.0006
278	GO Biological Processes	fat-soluble vitamin metabolic process	CYP3A4|NQO1	54.81	0.0006
279	GO Biological Processes	regulation of lipid biosynthetic process	CES1|PTGS2|SOD1	17.93	0.0006
280	GO Biological Processes	regulation of intrinsic apoptotic signaling pathway	BCL2|PTGS2|SOD1	17.83	0.0006
281	GO Biological Processes	Schwann cell development	MAP2K1|SOD1	53.50	0.0006
282	GO Biological Processes	neuron maturation	BCL2|RET	53.50	0.0006
283	GO Biological Processes	deoxyribonucleotide metabolic process	DCK|RRM1	53.50	0.0006
284	GO Biological Processes	deoxyribose phosphate metabolic process	DCK|RRM1	53.50	0.0006
285	GO Biological Processes	embryonic organ development	EGFR|FGFR2|MAP2K1|SOD1	9.94	0.0007
286	GO Biological Processes	regulation of neuron differentiation	ALK|BCL2|RET	17.56	0.0007
287	GO Biological Processes	multi-organism reproductive process	BCL2|PTGS2|SOD1	17.38	0.0007
288	GO Biological Processes	positive regulation of ERK1 and ERK2 cascade	EGFR|FGFR2|MAP2K1	17.38	0.0007
289	GO Biological Processes	morphogenesis of an epithelium	BCL2|EGFR|FGFR2|RET	9.81	0.0007
290	GO Biological Processes	positive regulation of cell development	BCL2|EGFR|MAP2K1|RET	9.79	0.0007
291	GO Biological Processes	exocrine system development	EGFR|FGFR2	51.07	0.0007
292	GO Biological Processes	cellular response to organic cyclic compound	CES1|EGFR|PTGS2|UGT1A1	9.62	0.0007
293	GO Biological Processes	embryo implantation	PTGS2|SOD1	49.94	0.0007
294	GO Biological Processes	multi-multicellular organism process	BCL2|PTGS2|SOD1	16.69	0.0008
295	GO Biological Processes	prostate gland development	CYP19A1|FGFR2	48.85	0.0008
296	GO Biological Processes	regulation of extrinsic apoptotic signaling pathway in absence of l	BCL2|RET	48.85	0.0008
297	GO Biological Processes	Schwann cell differentiation	MAP2K1|SOD1	47.81	0.0008
298	GO Biological Processes	labyrinthine layer development	FGFR2|MAP2K1	47.81	0.0008
299	GO Biological Processes	icosanoid transport	ABCC2|PTGS2	47.81	0.0008
300	GO Biological Processes	neuron projection morphogenesis	BCL2|EGFR|FGFR2|RET	9.25	0.0009
301	GO Biological Processes	export from cell	ABCC2|ABCB1|PTGS2|ABCB11	9.21	0.0009
302	GO Biological Processes	lung morphogenesis	FGFR2|MAP2K1	45.86	0.0009
303	GO Biological Processes	regulation of cell cycle G1/S phase transition	BCL2|EGFR|RRM1	15.83	0.0009
304	GO Biological Processes	plasma membrane bounded cell projection morphogenesis	BCL2|EGFR|FGFR2|RET	9.15	0.0009
305	GO Biological Processes	vasodilation	EGFR|SOD1	44.94	0.0009
306	GO Biological Processes	icosanoid biosynthetic process	PTGS1|PTGS2	44.94	0.0009
307	GO Biological Processes	cell projection morphogenesis	BCL2|EGFR|FGFR2|RET	9.06	0.0009
308	GO Biological Processes	MAPK cascade	EGFR|MAP2K1|RET	15.46	0.0009
309	GO Biological Processes	regulation of anatomical structure size	EGFR|PTGS2|RET|SOD1	8.97	0.001
310	GO Biological Processes	glial cell differentiation	EGFR|MAP2K1|SOD1	15.39	0.001
311	GO Biological Processes	response to mechanical stimulus	EGFR|MPO|PTGS2	15.32	0.001
312	GO Biological Processes	retinol metabolic process	CYP1A2|CYP3A4	43.22	0.001
313	GO Biological Processes	tissue homeostasis	BCL2|PTGS2|SOD1	15.18	0.001
314	GO Biological Processes	ear development	BCL2|FGFR2|SOD1	15.18	0.001
315	GO Biological Processes	anatomical structure homeostasis	BCL2|PTGS2|SOD1	15.18	0.001
316	GO Biological Processes	ovarian follicle development	BCL2|SOD1	42.40	0.001
317	GO Biological Processes	nucleobase-containing compound transport	SLC29A1|SLC29A2|SLC28A3	14.98	0.001
318	GO Biological Processes	peptidyl-amino acid modification	ALK|EGFR|FGFR2|TOP1	8.71	0.0011
319	GO Biological Processes	cellular response to glucocorticoid stimulus	EGFR|UGT1A1	40.86	0.0011
320	GO Biological Processes	response to axon injury	BCL2|SOD1	40.13	0.0011
321	GO Biological Processes	regulation of cellular response to stress	BCL2|EGFR|MAP2K1|PTGS2	8.54	0.0011
322	GO Biological Processes	positive regulation of G1/S transition of mitotic cell cycle	EGFR|RRM1	39.42	0.0012
323	GO Biological Processes	regulation of neuron apoptotic process	BCL2|NQO1|SOD1	13.76	0.0013
324	GO Biological Processes	mesenchyme development	BCL2|FGFR2|RET	13.65	0.0013
325	GO Biological Processes	regulation of smooth muscle contraction	PTGS2|SOD1	36.84	0.0014
326	GO Biological Processes	response to cadmium ion	CYP1A2|EGFR	36.84	0.0014
327	GO Biological Processes	bone mineralization	FGFR2|PTGS2	36.84	0.0014
328	GO Biological Processes	urogenital system development	CYP19A1|FGFR2	35.67	0.0014
329	GO Biological Processes	positive regulation of growth	BCL2|EGFR|FGFR2	13.07	0.0015
330	GO Biological Processes	regulation of multicellular organism growth	BCL2|SOD1	34.57	0.0015
331	GO Biological Processes	ERBB signaling pathway	EGFR|MAP2K1	34.57	0.0015

332	GO Biological Processes	cellular response to corticosteroid stimulus	EGFR|UGT1A1	34.57	0.0015
333	GO Biological Processes	regulation of system process	CYP19A1|EGFR|PTGS2|SOD1	7.87	0.0015
334	GO Biological Processes	tissue morphogenesis	BCL2|EGFR|FGFR2|RET	7.86	0.0016
335	GO Biological Processes	astrocyte differentiation	EGFR|MAP2K1	34.05	0.0016
336	GO Biological Processes	response to ischemia	BCL2|NQO1	34.05	0.0016
337	GO Biological Processes	regulation of lipid catabolic process	ALK|ABCB11	34.05	0.0016
338	GO Biological Processes	animal organ regeneration	EGFR|UGT1A1	33.54	0.0016
339	GO Biological Processes	cellular response to retinoic acid	FGFR2|RET	33.54	0.0016
340	GO Biological Processes	regulation of vasoconstriction	EGFR|PTGS2	33.05	0.0017
341	GO Biological Processes	embryonic morphogenesis	FGFR2|MAP2K1|RET|SOD1	7.63	0.0017
342	GO Biological Processes	positive regulation of reactive oxygen species metabolic process	EGFR|SOD1	32.10	0.0018
343	GO Biological Processes	positive regulation of cell cycle G1/S phase transition	EGFR|RRM1	32.10	0.0018
344	GO Biological Processes	positive regulation of cell migration	BCL2|EGFR|PTGS2|RET	7.55	0.0018
345	GO Biological Processes	negative regulation of calcium ion transport	BCL2|PTGS2	31.65	0.0018
346	GO Biological Processes	sensory organ morphogenesis	BCL2|FGFR2|SOD1	12.21	0.0019
347	GO Biological Processes	gliogenesis	EGFR|MAP2K1|SOD1	12.21	0.0019
348	GO Biological Processes	regulation of mitochondrial membrane potential	BCL2|SOD1	30.78	0.0019
349	GO Biological Processes	regulation of growth	BCL2|EGFR|FGFR2|SOD1	7.40	0.0019
350	GO Biological Processes	regulation of secretion	CES1|CYP19A1|EGFR|ABCB11	7.40	0.0019
351	GO Biological Processes	cellular response to mechanical stimulus	EGFR|PTGS2	30.37	0.002
352	GO Biological Processes	cellular response to external stimulus	EGFR|PTGS2	29.96	0.002
353	GO Biological Processes	multicellular organismal-level homeostasis	ALK|BCL2|PTGS2|SOD1	7.30	0.002
354	GO Biological Processes	regulation of ERK1 and ERK2 cascade	EGFR|FGFR2|MAP2K1	11.70	0.0021
355	GO Biological Processes	positive regulation of cell motility	BCL2|EGFR|PTGS2|RET	7.21	0.0021
356	GO Biological Processes	regulation of synaptic transmission, glutamatergic	EGFR|PTGS2	29.18	0.0021
357	GO Biological Processes	regulation of organic acid transport	CES1|ABCB11	28.81	0.0022
358	GO Biological Processes	epithelial cell differentiation	CES1|FGFR2|MAP2K1|SOD1	7.12	0.0022
359	GO Biological Processes	positive regulation of locomotion	BCL2|EGFR|PTGS2|RET	7.06	0.0023
360	GO Biological Processes	regulation of steroid biosynthetic process	CES1|SOD1	27.74	0.0024
361	GO Biological Processes	kidney development	BCL2|FGFR2|RET	11.09	0.0024
362	GO Biological Processes	peripheral nervous system development	MAP2K1|SOD1	26.75	0.0025
363	GO Biological Processes	response to vitamin	EGFR|PTGS2	26.75	0.0025
364	GO Biological Processes	stem cell development	BCL2|RET	26.75	0.0025
365	GO Biological Processes	cellular ketone metabolic process	CYP19A1|NQO1	26.75	0.0025
366	GO Biological Processes	metanephros development	BCL2|RET	26.44	0.0026
367	GO Biological Processes	pyrimidine-containing compound metabolic process	DCK|RRM1	26.44	0.0026
368	GO Biological Processes	positive regulation of secretion	CYP19A1|EGFR|ABCB11	10.77	0.0026
369	GO Biological Processes	positive regulation of lipid transport	CES1|CYP19A1	26.13	0.0027
370	GO Biological Processes	epithelial tube morphogenesis	BCL2|FGFR2|RET	10.73	0.0027
371	GO Biological Processes	renal system development	BCL2|FGFR2|RET	10.73	0.0027
372	GO Biological Processes	regulation of developmental growth	BCL2|FGFR2|SOD1	10.60	0.0028
373	GO Biological Processes	multicellular organismal response to stress	BCL2|RET	25.54	0.0028
374	GO Biological Processes	cellular response to amino acid stimulus	EGFR|PTGS2	24.97	0.0029
375	GO Biological Processes	alcohol metabolic process	CES1|CYP1A2|CYP3A4	10.37	0.0029
376	GO Biological Processes	primary alcohol metabolic process	CYP1A2|CYP3A4	24.69	0.003
377	GO Biological Processes	phenol-containing compound metabolic process	BCL2|CYP2E1	24.43	0.003
378	GO Biological Processes	cellular homeostasis	BCL2|NQO1|SLC29A1|SOD1	6.50	0.0031
379	GO Biological Processes	alcohol biosynthetic process	CES1|CYP3A4	24.16	0.0031
380	GO Biological Processes	response to heat	PTGS2|SOD1	23.91	0.0032
381	GO Biological Processes	camera-type eye development	EGFR|RET|RRM1	10.03	0.0032
382	GO Biological Processes	positive regulation of cell cycle	EGFR|FGFR2|RRM1	9.97	0.0033
383	GO Biological Processes	cellular response to acid chemical	EGFR|PTGS2	22.70	0.0035
384	GO Biological Processes	regulation of fatty acid metabolic process	PTGS2|ABCB11	22.70	0.0035
385	GO Biological Processes	regulation of organ growth	FGFR2|SOD1	22.03	0.0037
386	GO Biological Processes	positive regulation of mitotic cell cycle phase transition	EGFR|RRM1	22.03	0.0037
387	GO Biological Processes	cholesterol homeostasis	CES1|ABCB11	22.03	0.0037
388	GO Biological Processes	sterol homeostasis	CES1|ABCB11	21.82	0.0038
389	GO Biological Processes	vitamin metabolic process	CYP3A4|NQO1	21.82	0.0038
390	GO Biological Processes	neural precursor cell proliferation	FGFR2|RRM1	21.61	0.0039
391	GO Biological Processes	inner ear morphogenesis	FGFR2|SOD1	21.40	0.0039
392	GO Biological Processes	biomineral tissue development	FGFR2|PTGS2	21.40	0.0039
393	GO Biological Processes	positive regulation of cell projection organization	ALK|MAP2K1|RET	9.34	0.004
394	GO Biological Processes	regulation of mitotic cell cycle phase transition	BCL2|EGFR|RRM1	9.34	0.004
395	GO Biological Processes	cellular response to alcohol	CES1|UGT1A1	21.20	0.004
396	GO Biological Processes	response to retinoic acid	FGFR2|RET	21.20	0.004
397	GO Biological Processes	axonogenesis	BCL2|FGFR2|RET	9.21	0.0041
398	GO Biological Processes	membrane organization	BCL2|EGFR|ABCB1|SOD1	5.98	0.0042
399	GO Biological Processes	positive regulation of lipid localization	CES1|CYP19A1	20.24	0.0044
400	GO Biological Processes	negative regulation of intrinsic apoptotic signaling pathway	BCL2|PTGS2	19.89	0.0045
401	GO Biological Processes	positive regulation of canonical Wnt signaling pathway	EGFR|FGFR2	19.89	0.0045
402	GO Biological Processes	negative regulation of cell cycle	BCL2|EGFR|PTGS2	8.78	0.0047
403	GO Biological Processes	metencephalon development	BCL2|MAP2K1	19.21	0.0049
404	GO Biological Processes	negative regulation of protein catabolic process	NQO1|EGFR	19.21	0.0049
405	GO Biological Processes	negative regulation of cell population proliferation	BCL2|FGFR2|MAP2K1|PTGS2	5.68	0.005
406	GO Biological Processes	in utero embryonic development	EGFR|FGFR2|MAP2K1	8.56	0.005
407	GO Biological Processes	positive regulation of cell cycle phase transition	EGFR|RRM1	18.73	0.0051
408	GO Biological Processes	formation of primary germ layer	FGFR2|MAP2K1	18.27	0.0054
409	GO Biological Processes	positive regulation of protein serine/threonine kinase activity	EGFR|MAP2K1	18.12	0.0054
410	GO Biological Processes	positive regulation of lipid metabolic process	CES1|PTGS2	18.12	0.0054
411	GO Biological Processes	ear morphogenesis	FGFR2|SOD1	17.83	0.0056
412	GO Biological Processes	limbic system development	ALK|FGFR2	17.83	0.0056
413	GO Biological Processes	myelination	MAP2K1|SOD1	17.56	0.0058
414	GO Biological Processes	ensheathment of neurons	MAP2K1|SOD1	17.29	0.006
415	GO Biological Processes	axon ensheathment	MAP2K1|SOD1	17.29	0.006
416	GO Biological Processes	epithelial tube formation	FGFR2|RET	17.29	0.006
417	GO Biological Processes	axon development	BCL2|FGFR2|RET	8.01	0.0061
418	GO Biological Processes	negative regulation of monoatomic ion transport	BCL2|PTGS2	16.90	0.0062
419	GO Biological Processes	liver development	EGFR|UGT1A1	16.90	0.0062
420	GO Biological Processes	positive regulation of mitotic cell cycle	EGFR|RRM1	16.90	0.0062

421	GO Biological Processes	response to radiation	BCL2|EGFR|RRM1	7.91	0.0063
422	GO Biological Processes	growth	BCL2|CYP19A1|FGFR2	7.82	0.0065
423	GO Biological Processes	developmental growth	BCL2|CYP19A1|FGFR2	7.82	0.0065
424	GO Biological Processes	hepaticobiliary system development	EGFR|UGT1A1	16.52	0.0065
425	GO Biological Processes	regulation of inflammatory response	CYP19A1|PTGS2|SOD1	7.78	0.0065
426	GO Biological Processes	circadian rhythm	EGFR|TOP1	16.28	0.0067
427	GO Biological Processes	branching morphogenesis of an epithelial tube	BCL2|FGFR2	16.28	0.0067
428	GO Biological Processes	neurotransmitter transport	SLC29A1|SLC29A2	16.05	0.0069
429	GO Biological Processes	response to ionizing radiation	BCL2|RRM1	16.05	0.0069
430	GO Biological Processes	regulation of axonogenesis	MAP2K1|RET	15.94	0.007
431	GO Biological Processes	regulation of neuron projection development	ALK|MAP2K1|RET	7.57	0.0071
432	GO Biological Processes	positive regulation of apoptotic signaling pathway	RET|SOD1	15.71	0.0072
433	GO Biological Processes	positive regulation of hormone secretion	CYP19A1|EGFR	15.61	0.0073
434	GO Biological Processes	morphogenesis of embryonic epithelium	FGFR2|RET	15.61	0.0073
435	GO Biological Processes	positive regulation of small molecule metabolic process	CES1|PTGS2	15.61	0.0073
436	GO Biological Processes	tube formation	FGFR2|RET	15.50	0.0074
437	GO Biological Processes	mitotic cell cycle phase transition	BCL2|ABCB1	15.39	0.0075
438	GO Biological Processes	regulation of protein kinase activity	EGFR|MAP2K1|SOD1	7.41	0.0075
439	GO Biological Processes	male gonad development	BCL2|RRM1	15.29	0.0076
440	GO Biological Processes	development of primary male sexual characteristics	BCL2|RRM1	15.18	0.0077
441	GO Biological Processes	regulation of cell cycle phase transition	BCL2|EGFR|RRM1	7.33	0.0077
442	GO Biological Processes	positive regulation of Wnt signaling pathway	EGFR|FGFR2	15.08	0.0078
443	GO Biological Processes	regulation of membrane potential	BCL2|SLC29A1|SOD1	7.25	0.008
444	GO Biological Processes	regulation of monoatomic ion transport	BCL2|ABCB1|PTGS2	7.19	0.0082
445	GO Biological Processes	regulation of lipid transport	CES1|CYP19A1	14.69	0.0082
446	GO Biological Processes	cellular response to steroid hormone stimulus	EGFR|UGT1A1	14.59	0.0083
447	GO Biological Processes	response to hexose	SLC29A1|PTGS2	14.59	0.0083
448	GO Biological Processes	response to UV	BCL2|EGFR	14.50	0.0084
449	GO Biological Processes	retina development in camera-type eye	RET|RRM1	14.41	0.0085
450	GO Biological Processes	regulation of extrinsic apoptotic signaling pathway	BCL2|RET	14.31	0.0086
451	GO Biological Processes	hindbrain development	BCL2|MAP2K1	14.22	0.0087
452	GO Biological Processes	positive regulation of synaptic transmission	EGFR|PTGS2	14.13	0.0088
453	GO Biological Processes	cell cycle phase transition	BCL2|ABCB1	14.13	0.0088
454	GO Biological Processes	response to monosaccharide	SLC29A1|PTGS2	13.96	0.009
455	GO Biological Processes	positive regulation of neuron projection development	ALK|RET	13.87	0.0091
456	GO Biological Processes	positive regulation of cell growth	BCL2|EGFR	13.87	0.0091
457	GO Biological Processes	response to temperature stimulus	PTGS2|SOD1	13.79	0.0092
458	GO Biological Processes	negative regulation of neuron apoptotic process	BCL2|SOD1	13.70	0.0093
459	GO Biological Processes	regulation of muscle cell differentiation	BCL2|FGFR2	13.54	0.0095
460	GO Biological Processes	lipid modification	CYP2E1|CYP3A4	13.46	0.0097
461	GO Biological Processes	morphogenesis of a branching epithelium	BCL2|FGFR2	13.46	0.0097
462	GO Biological Processes	positive regulation of developmental growth	BCL2|FGFR2	13.30	0.0099
463	GO Biological Processes	male sex differentiation	BCL2|RRM1	13.14	0.0101
464	GO Biological Processes	regulation of muscle contraction	PTGS2|SOD1	13.07	0.0102
465	GO Biological Processes	gastrulation	FGFR2|MAP2K1	12.99	0.0103
466	GO Biological Processes	morphogenesis of a branching structure	BCL2|FGFR2	12.62	0.0109
467	GO Biological Processes	nucleotide metabolic process	DCK|NQO1|RRM1	6.42	0.0111
468	GO Biological Processes	lipid homeostasis	CES1|ABCB11	12.48	0.0111
469	GO Biological Processes	regulation of mitotic cell cycle	BCL2|EGFR|RRM1	6.38	0.0112
470	GO Biological Processes	blood vessel development	FGFR2|MAP2K1|PTGS2	6.32	0.0115
471	GO Biological Processes	nucleoside phosphate metabolic process	DCK|NQO1|RRM1	6.32	0.0115
472	GO Biological Processes	regulation of lipid localization	CES1|CYP19A1	12.21	0.0116
473	GO Biological Processes	positive regulation of phosphatidylinositol 3-kinase/protein kinase	EGFR|RET	12.02	0.012
474	GO Biological Processes	cell maturation	BCL2|RET	12.02	0.012
475	GO Biological Processes	secretion	SLC29A1|PTGS2|ABCB11	6.20	0.0122
476	GO Biological Processes	cell-cell adhesion	BCL2|EGFR|RET	6.14	0.0125
477	GO Biological Processes	pallium development	ALK|EGFR	11.70	0.0126
478	GO Biological Processes	vasculature development	FGFR2|MAP2K1|PTGS2	6.08	0.0128
479	GO Biological Processes	inner ear development	FGFR2|SOD1	11.52	0.013
480	GO Biological Processes	locomotory behavior	ALK|SOD1	11.41	0.0132
481	GO Biological Processes	DNA replication	RRM1|TOP1	11.24	0.0136
482	GO Biological Processes	negative regulation of inflammatory response	CYP19A1|SOD1	11.12	0.0139
483	GO Biological Processes	epidermal cell differentiation	MAP2K1|SOD1	11.02	0.0141
484	GO Biological Processes	intracellular chemical homeostasis	BCL2|SLC29A1|SOD1	5.80	0.0145
485	GO Biological Processes	response to starvation	BCL2|UGT1A1	10.40	0.0158
486	GO Biological Processes	nucleobase-containing small molecule metabolic process	DCK|NQO1|RRM1	5.62	0.0158
487	GO Biological Processes	response to ketone	NQO1|EGFR	10.26	0.0162
488	GO Biological Processes	positive regulation of epithelial cell proliferation	EGFR|FGFR2	10.21	0.0163
489	GO Biological Processes	regulation of transmembrane transporter activity	BCL2|ABCB1	10.21	0.0163
490	GO Biological Processes	protein ubiquitination	BCL2|NQO1|ABCB11	5.38	0.0178
491	GO Biological Processes	negative regulation of mitotic cell cycle	BCL2|EGFR	9.60	0.0183
492	GO Biological Processes	anatomical structure maturation	BCL2|RET	9.48	0.0188
493	GO Biological Processes	regulation of plasma membrane bounded cell projection organiza	ALK|MAP2K1|RET	5.23	0.0192
494	GO Biological Processes	chordate embryonic development	EGFR|FGFR2|MAP2K1	5.19	0.0195
495	GO Biological Processes	negative regulation of apoptotic signaling pathway	BCL2|PTGS2	9.21	0.0198
496	GO Biological Processes	positive regulation of protein kinase activity	EGFR|MAP2K1	9.13	0.0201
497	GO Biological Processes	positive regulation of neurogenesis	EGFR|MAP2K1	9.13	0.0201
498	GO Biological Processes	regulation of cell projection organization	ALK|MAP2K1|RET	5.09	0.0205
499	GO Biological Processes	regulation of transporter activity	BCL2|ABCB1	9.02	0.0206
500	GO Biological Processes	regulation of muscle system process	PTGS2|SOD1	8.92	0.021
501	GO Biological Processes	positive regulation of protein transport	EGFR|PTGS2	8.92	0.021
502	GO Biological Processes	embryo development ending in birth or egg hatching	EGFR|FGFR2|MAP2K1	5.03	0.0212
503	GO Biological Processes	regulation of calcium ion transport	BCL2|PTGS2	8.85	0.0214
504	GO Biological Processes	regulation of hormone secretion	CYP19A1|EGFR	8.81	0.0215
505	GO Biological Processes	cell fate commitment	BCL2|FGFR2	8.74	0.0218
506	GO Biological Processes	protein polyubiquitination	BCL2|NQO1	8.71	0.022
507	GO Biological Processes	regulation of blood circulation	EGFR|PTGS2	8.64	0.0223
508	GO Biological Processes	regulation of protein serine/threonine kinase activity	EGFR|MAP2K1	8.58	0.0226
509	GO Biological Processes	regulation of hydrolase activity	BCL2|FGFR2|SOD1	4.89	0.0228

510	GO Biological Processes	nucleotide biosynthetic process	DCK|RRM1	8.54	0.0228
511	GO Biological Processes	nucleoside phosphate biosynthetic process	DCK|RRM1	8.48	0.0231
512	GO Biological Processes	positive regulation of cell cycle process	EGFR|RRM1	8.35	0.0238
513	GO Biological Processes	regulation of canonical Wnt signaling pathway	EGFR|FGFR2	8.32	0.0239
514	GO Biological Processes	regulation of intracellular transport	MAP2K1|PTGS2	8.32	0.0239
515	GO Biological Processes	protein modification by small protein conjugation	BCL2|NQO1|ABCB11	4.79	0.0241
516	GO Biological Processes	rhythmic process	EGFR|TOP1	8.29	0.0241
517	GO Biological Processes	regulation of phosphatidylinositol 3-kinase/protein kinase B signa	EGFR|RET	8.23	0.0244
518	GO Biological Processes	telencephalon development	ALK|EGFR	8.14	0.0249
519	GO Biological Processes	learning or memory	EGFR|PTGS2	8.11	0.0251
520	GO Biological Processes	homeostasis of number of cells	BCL2|SOD1	7.97	0.0259
521	GO Biological Processes	developmental maturation	BCL2|RET	7.86	0.0266
522	GO Biological Processes	positive regulation of secretion by cell	CYP19A1|EGFR	7.72	0.0275
523	GO Biological Processes	negative regulation of defense response	CYP19A1|SOD1	7.64	0.028
524	GO Biological Processes	embryonic organ morphogenesis	FGFR2|SOD1	7.62	0.0282
525	GO Biological Processes	positive regulation of nervous system development	EGFR|MAP2K1	7.59	0.0284
526	GO Biological Processes	regulation of cell cycle process	BCL2|EGFR|RRM1	4.48	0.0285
527	GO Biological Processes	response to light stimulus	BCL2|EGFR	7.16	0.0316
528	GO Biological Processes	muscle organ development	BCL2|FGFR2	7.13	0.0318
529	GO Biological Processes	cellular response to abiotic stimulus	EGFR|PTGS2	7.02	0.0327
530	GO Biological Processes	cellular response to environmental stimulus	EGFR|PTGS2	7.02	0.0327
531	GO Biological Processes	cognition	EGFR|PTGS2	7.00	0.0329
532	GO Biological Processes	positive regulation of establishment of protein localization	EGFR|PTGS2	6.85	0.0342
533	GO Biological Processes	regulation of Wnt signaling pathway	EGFR|FGFR2	6.55	0.0371
534	GO Biological Processes	angiogenesis	FGFR2|PTGS2	6.53	0.0373
535	GO Biological Processes	regulation of monoatomic ion transmembrane transport	BCL2|ABCB1	6.40	0.0387
536	GO Biological Processes	muscle tissue development	BCL2|FGFR2	6.37	0.0391
537	GO Biological Processes	regulation of body fluid levels	EGFR|SLC29A1	6.33	0.0395
538	GO Biological Processes	regulation of protein catabolic process	NQO1|EGFR	6.19	0.0412
539	GO Biological Processes	regulation of neurogenesis	EGFR|MAP2K1	5.91	0.0447
540	GO Biological Processes	negative regulation of cell migration	BCL2|CYP19A1	5.88	0.0451
541	GO Biological Processes	negative regulation of cell motility	BCL2|CYP19A1	5.66	0.0484
542	GO Biological Processes	regulation of metal ion transport	BCL2|PTGS2	5.63	0.0488
543	GO Biological Processes	regulation of cell growth	BCL2|EGFR	5.59	0.0494