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Supplemental Table S2. Statistically over-represented ($p < 0.05$) processes from DAVID analysis when comparing a list of genes with Epididymis-selective DHS in their promoter to all human genes.

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	glycoprotein	169	31.8267420	0.0000016	529	4209	18289	1.3881681	0.0006730	0.0006730	0.0022515
SP_PIR_KEYWORDS	cell junction	30	5.6497175	0.0000053	529	398	18289	2.6059884	0.0022086	0.0011049	0.0073946
KEGG_PATHWAY	hsa00830:Retinol metabolism	10	1.8832392	0.0000131	140	54	5042	6.6693122	0.0016551	0.0016551	0.0152233
GOTERM_CC_FAT	GO:0030054~cell junction	34	6.4030132	0.0000223	364	515	12337	2.2375867	0.0071754	0.0071754	0.0301237
SP_PIR_KEYWORDS	signal	129	24.2937853	0.0000233	529	3158	18289	1.4122509	0.0097264	0.0032527	0.0326842
GOTERM_CC_FAT	GO:0005886~plasma membrane	145	27.3069680	0.0000240	364	3663	12337	1.3416501	0.0077188	0.0038669	0.0324134
GOTERM_CC_FAT	GO:0044459~plasma membrane part	95	17.8907721	0.0000330	364	2163	12337	1.4885906	0.0106181	0.0035520	0.0446510
GOTERM_CC_FAT	GO:0005912~adherens junction	15	2.8248588	0.0001921	364	155	12337	3.2799539	0.0601784	0.0153966	0.2593278
SP_PIR_KEYWORDS	transmembrane	175	32.9566855	0.0002431	529	4781	18289	1.2654751	0.0970911	0.0252102	0.3410072
SP_PIR_KEYWORDS	membrane	214	40.3013183	0.0003110	529	6079	18289	1.2170710	0.1224803	0.0257927	0.4360303
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	17	3.2015066	0.0003310	364	203	12337	2.8383181	0.1014140	0.0211595	0.4463797
GOTERM_CC_FAT	GO:0070161~anchoring junction	15	2.8248588	0.0005594	364	172	12337	2.9557724	0.1653430	0.0296732	0.7532936
GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	186	35.0282486	0.0006028	364	5244	12337	1.2021494	0.1769659	0.0274390	0.8115039
GOTERM_MF_FAT	GO:0005275~amine transmembrane transporter	9	1.6949153	0.0007208	342	72	12549	4.5866228	0.3403720	0.3403720	1.0537326

	activity										
SP_PIR_KEYWORDS	cell membrane	87	16.3841808	0.0007891	529	2131	18289	1.4114649	0.2821771	0.0537565	1.1026981
KEGG_PATHWAY	hsa00053:Ascorbate and aldarate metabolism	5	0.9416196	0.0009955	140	17	5042	10.5924370	0.1179447	0.0608220	1.1468474
KEGG_PATHWAY	hsa00983:Drug metabolism	7	1.3182674	0.0010368	140	43	5042	5.8627907	0.1225204	0.0426318	1.1940910
GOTERM_CC_FAT	GO:0016021~integral to membrane	179	33.7099812	0.0010482	364	5061	12337	1.1987397	0.2873475	0.0414611	1.4072920
GOTERM_MF_FAT	GO:0015293~symporter activity	12	2.2598870	0.0011995	342	136	12549	3.2376161	0.4997023	0.2926827	1.7477601
KEGG_PATHWAY	hsa04080:Neuroactive ligand-receptor interaction	17	3.2015066	0.0015835	140	255	5042	2.4009524	0.1810087	0.0486949	1.8185360
INTERPRO	IPR000233:Cadherin cytoplasmic region	5	0.9416196	0.0016620	450	19	16090	9.4093567	0.7489991	0.7489991	2.5334565
GOTERM_CC_FAT	GO:0045211~postsynaptic membrane	12	2.2598870	0.0021211	364	135	12337	3.0126984	0.4963317	0.0733730	2.8285869
PIR_SUPERFAMILY	PIRSF002504:cadherin	5	0.9416196	0.0022431	208	20	7196	8.6490385	0.4087322	0.4087322	2.8456894
GOTERM_CC_FAT	GO:0005576~extracellular region	77	14.5009416	0.0028580	364	1906	12337	1.3692288	0.6032561	0.0883020	3.7938735
COG_ONTOLOGY	Secondary metabolites biosynthesis, transport, and catabolism	7	1.3182674	0.0032351	46	65	1944	4.5511706	0.0443513	0.0443513	2.1770906
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	17	3.2015066	0.0036494	360	274	13114	2.2601176	0.9992525	0.9992525	6.0817034
GOTERM_BP_FAT	GO:0050801~ion homeostasis	22	4.1431262	0.0039770	360	406	13114	1.9739190	0.9996088	0.9802211	6.6102273
GOTERM_MF_FAT	GO:0015294~solute:cation symporter activity	9	1.6949153	0.0040086	342	94	12549	3.5131579	0.9014931	0.5381628	5.7298917

SP_PIR_KEYWORDS	transmembrane protein	31	5.8380414	0.0045113	529	623	18289	1.7203148	0.8502890	0.2376067	6.1539420
SP_PIR_KEYWORDS	Symport	10	1.8832392	0.0045838	529	110	18289	3.1429799	0.8547963	0.2143173	6.2498413
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	20	3.7664783	0.0049078	360	360	13114	2.0237654	0.9999379	0.9604075	8.0968703
GOTERM_BP_FAT	GO:0007155~cell adhesion	32	6.0263653	0.0049989	360	694	13114	1.6796670	0.9999482	0.9151511	8.2410943
INTERPRO	IPR002213:UDP-glucuronosyl/UDP-glucosyltransferase	4	0.7532957	0.0050111	450	13	16090	11.0017094	0.9846196	0.8759822	7.4571536
GOTERM_BP_FAT	GO:0022610~biological adhesion	32	6.0263653	0.0051046	360	695	13114	1.6772502	0.9999580	0.8667271	8.4082916
INTERPRO	IPR013106:Immunoglobulin V-set	13	2.4482109	0.0051323	450	182	16090	2.5539683	0.9861006	0.7595644	7.6309318
GOTERM_MF_FAT	GO:0008289~lipid binding	23	4.3314501	0.0051927	342	446	12549	1.8922390	0.9504110	0.5281041	7.3629018
PIR_SUPERFAMILY	PIRSF005678:glucuronosyltransferase	4	0.7532957	0.0054209	208	13	7196	10.6449704	0.7197104	0.4705762	6.7492929
SP_PIR_KEYWORDS	neurotransmitter receptor	7	1.3182674	0.0058726	529	57	18289	4.2457799	0.9157324	0.2403230	7.9405653
GOTERM_BP_FAT	GO:0030817~regulation of cAMP biosynthetic process	9	1.6949153	0.0064681	360	101	13114	3.2460396	0.9999972	0.8811060	10.5388559
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	25	4.7080979	0.0065392	360	507	13114	1.7962415	0.9999975	0.8420403	10.6485553
GOTERM_BP_FAT	GO:0046942~carboxylic acid transport	11	2.0715631	0.0065541	360	145	13114	2.7634866	0.9999976	0.8017922	10.6716094
GOTERM_MF_FAT	GO:0042165~neurotransmitter binding	9	1.6949153	0.0065569	342	102	12549	3.2376161	0.9775350	0.5319404	9.2116977
GOTERM_BP_FAT	GO:0007389~pattern specification process	16	3.0131827	0.0068139	360	267	13114	2.1829380	0.9999986	0.7759378	11.0716602

GOTERM_BP_FAT	GO:0015849~organic acid transport	11	2.0715631	0.0068703	360	146	13114	2.7445586	0.9999987	0.7426786	11.1582811
GOTERM_BP_FAT	GO:0030814~regulation of cAMP metabolic process	9	1.6949153	0.0072618	360	103	13114	3.1830097	0.9999994	0.7287178	11.7573462
GOTERM_MF_FAT	GO:0015276~ligand-gated ion channel activity	10	1.8832392	0.0073981	342	126	12549	2.9121415	0.9862208	0.5103668	10.3345153
GOTERM_MF_FAT	GO:0022834~ligand-gated channel activity	10	1.8832392	0.0073981	342	126	12549	2.9121415	0.9862208	0.5103668	10.3345153
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	51	9.6045198	0.0079862	364	1207	12337	1.4320926	0.9249714	0.2097802	10.2690105
SP_PIR_KEYWORDS	Secreted	65	12.2410546	0.0084541	529	1643	18289	1.3677606	0.9717261	0.2999347	11.2423099
SMART	SM00112:CA	9	1.6949153	0.0085155	243	106	8828	3.0845563	0.7909154	0.7909154	10.0242366
GOTERM_BP_FAT	GO:0060541~respiratory system development	9	1.6949153	0.0085871	360	106	13114	3.0929245	1.0000000	0.7570939	13.7574434
GOTERM_CC_FAT	GO:0014704~intercalated disc	4	0.7532957	0.0088347	364	15	12337	9.0380952	0.9430902	0.2124728	11.3006764
GOTERM_CC_FAT	GO:0045202~synapse	20	3.7664783	0.0089705	364	355	12337	1.9094567	0.9455545	0.2005960	11.4647957
GOTERM_BP_FAT	GO:0007156~homophilic cell adhesion	10	1.8832392	0.0090005	360	129	13114	2.8238587	1.0000000	0.7457400	14.3725355
SP_PIR_KEYWORDS	synapse	14	2.6365348	0.0091689	529	213	18289	2.2723892	0.9791144	0.2965086	12.1368809
INTERPRO	IPR002126:Cadherin	9	1.6949153	0.0096348	450	106	16090	3.0358491	0.9996794	0.8661893	13.8735279
GOTERM_CC_FAT	GO:0005911~cell-cell junction	13	2.4482109	0.0097166	364	188	12337	2.3436550	0.9573104	0.2017006	12.3612303
GOTERM_CC_FAT	GO:0005925~focal adhesion	9	1.6949153	0.0103438	364	102	12337	2.9905462	0.9652109	0.2006023	13.1083928
GOTERM_BP_FAT	GO:0030808~regulation of nucleotide biosynthetic	9	1.6949153	0.0106259	360	110	13114	2.9804545	1.0000000	0.7774168	16.7511560

	process										
GOTERM_BP_FAT	GO:0030802~regulation of cyclic nucleotide biosynthetic process	9	1.6949153	0.0106259	360	110	13114	2.9804545	1.0000000	0.7774168	16.7511560
GOTERM_BP_FAT	GO:0015718~monocarboxylic acid transport	6	1.1299435	0.0115501	360	50	13114	4.3713333	1.0000000	0.7823718	18.0757130
GOTERM_BP_FAT	GO:0055080~cation homeostasis	16	3.0131827	0.0116150	360	284	13114	2.0522692	1.0000000	0.7625352	18.1679649
KEGG_PATHWAY	hsa00860:Porphyrin and chlorophyll metabolism	5	0.9416196	0.0121713	140	33	5042	5.4567100	0.7862583	0.2655236	13.2218972
KEGG_PATHWAY	hsa00040:Pentose and glucuronate interconversions	4	0.7532957	0.0123514	140	18	5042	8.0031746	0.7911132	0.2297143	13.4049522
GOTERM_BP_FAT	GO:0030799~regulation of cyclic nucleotide metabolic process	9	1.6949153	0.0123754	360	113	13114	2.9013274	1.0000000	0.7636168	19.2416772
INTERPRO	IPR016044:Filament	7	1.3182674	0.0124542	450	69	16090	3.6273752	0.9999700	0.8754298	17.5793053
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	49	9.2278719	0.0128032	364	1180	12337	1.4074153	0.9844255	0.2290506	15.9814103
GOTERM_CC_FAT	GO:0005924~cell-substrate adherens junction	9	1.6949153	0.0128672	364	106	12337	2.8776954	0.9847484	0.2181271	16.0550310
INTERPRO	IPR018039:Intermediate filament protein, conserved site	7	1.3182674	0.0133109	450	70	16090	3.5755556	0.9999854	0.8436950	18.6754968
INTERPRO	IPR001664:Intermediate filament protein	7	1.3182674	0.0133109	450	70	16090	3.5755556	0.9999854	0.8436950	18.6754968
GOTERM_BP_FAT	GO:0055066~di-, tri-valent inorganic cation homeostasis	14	2.6365348	0.0136321	360	237	13114	2.1518519	1.0000000	0.7771956	20.9873191
GOTERM_BP_FAT	GO:0006140~regulation of nucleotide metabolic process	9	1.6949153	0.0143277	360	116	13114	2.8262931	1.0000000	0.7758726	21.9381032

SP_PIR_KEYWORDS	postsynaptic cell membrane	9	1.6949153	0.0143930	529	110	18289	2.8286819	0.9977323	0.3979501	18.4250748
SP_PIR_KEYWORDS	disulfide bond	101	19.0207156	0.0151118	529	2819	18289	1.2386842	0.9983308	0.3885686	19.2567715
GOTERM_BP_FAT	GO:0045761~regulation of adenylate cyclase activity	8	1.5065913	0.0161757	360	96	13114	3.0356481	1.0000000	0.7992154	24.4122099
GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signaling pathway	41	7.7212806	0.0167477	360	1036	13114	1.4416399	1.0000000	0.7947648	25.1628853
GOTERM_BP_FAT	GO:0035295~tube development	13	2.4482109	0.0169665	360	218	13114	2.1722987	1.0000000	0.7837961	25.4481488
GOTERM_BP_FAT	GO:0030324~lung development	8	1.5065913	0.0170388	360	97	13114	3.0043528	1.0000000	0.7703586	25.5421137
GOTERM_BP_FAT	GO:0007409~axonogenesis	12	2.2598870	0.0172635	360	193	13114	2.2649396	1.0000000	0.7603791	25.8337764
INTERPRO	IPR001828:Extracellular ligand-binding receptor	5	0.9416196	0.0174109	450	36	16090	4.9660494	0.9999995	0.8757086	23.7351624
GOTERM_CC_FAT	GO:0030055~cell-substrate junction	9	1.6949153	0.0174590	364	112	12337	2.7235332	0.9966173	0.2709838	21.1809606
GOTERM_BP_FAT	GO:0030182~neuron differentiation	21	3.9548023	0.0175327	360	437	13114	1.7505339	1.0000000	0.7517013	26.1816044
KEGG_PATHWAY	hsa00150:Androgen and estrogen metabolism	5	0.9416196	0.0180531	140	37	5042	4.8667954	0.8992859	0.2795824	19.0206928
GOTERM_BP_FAT	GO:0043129~surfactant homeostasis	3	0.5649718	0.0187602	360	8	13114	13.6604167	1.0000000	0.7616997	27.7486231
GOTERM_BP_FAT	GO:0048875~chemical homeostasis within a tissue	3	0.5649718	0.0187602	360	8	13114	13.6604167	1.0000000	0.7616997	27.7486231
GOTERM_BP_FAT	GO:0015909~long-chain fatty acid transport	4	0.7532957	0.0187686	360	21	13114	6.9386243	1.0000000	0.7488550	27.7591749
GOTERM_CC_FAT	GO:0005913~cell-cell	5	0.9416196	0.0188056	364	35	12337	4.8418367	0.9978278	0.2758369	22.6282228

	adherens junction										
GOTERM_BP_FAT	GO:0031279~regulation of cyclase activity	8	1.5065913	0.0188614	360	99	13114	2.9436588	1.0000000	0.7379006	27.8763890
GOTERM_MF_FAT	GO:0015171~amino acid transmembrane transporter activity	6	1.1299435	0.0190022	342	57	12549	3.8624192	0.9999844	0.7943126	24.5600302
GOTERM_CC_FAT	GO:0030424~axon	11	2.0715631	0.0191382	364	159	12337	2.3447889	0.9980532	0.2680756	22.9819509
GOTERM_BP_FAT	GO:0030323~respiratory tube development	8	1.5065913	0.0198222	360	100	13114	2.9142222	1.0000000	0.7431794	29.0789247
SP_PIR_KEYWORDS	cell adhesion	21	3.9548023	0.0199808	529	419	18289	1.7327646	0.9997918	0.4541954	24.6867331
GOTERM_BP_FAT	GO:0051339~regulation of lyase activity	8	1.5065913	0.0208167	360	101	13114	2.8853685	1.0000000	0.7485944	30.3037137
SMART	SM00181:EGF	12	2.2598870	0.0208786	243	199	8828	2.1907066	0.9789580	0.8549414	22.9419998
GOTERM_MF_FAT	GO:0015020~glucuronosyltransferase activity	4	0.7532957	0.0208862	342	22	12549	6.6714514	0.9999949	0.7818066	26.6606516
SP_PIR_KEYWORDS	Intermediate filament	7	1.3182674	0.0211760	529	75	18289	3.2267927	0.9998753	0.4508014	25.9666813
GOTERM_BP_FAT	GO:0034754~cellular hormone metabolic process	6	1.1299435	0.0223893	360	59	13114	3.7045198	1.0000000	0.7626562	32.2000769
INTERPRO	IPR004841:Amino acid permease-associated region	4	0.7532957	0.0224179	450	22	16090	6.5010101	1.0000000	0.9051220	29.5150002
GOTERM_MF_FAT	GO:0051378~serotonin binding	3	0.5649718	0.0233599	342	9	12549	12.2309942	0.9999988	0.7802792	29.3359748
GOTERM_MF_FAT	GO:0005283~sodium:amino acid symporter activity	3	0.5649718	0.0233599	342	9	12549	12.2309942	0.9999988	0.7802792	29.3359748
GOTERM_MF_FAT	GO:0005326~neurotransmitter transporter activity	4	0.7532957	0.0235465	342	23	12549	6.3813883	0.9999989	0.7471309	29.5340571

GOTERM_BP_FAT	GO:0001523~retinoid metabolic process	4	0.7532957	0.0240099	360	23	13114	6.3352657	1.0000000	0.7758372	34.1032601
GOTERM_BP_FAT	GO:0016101~diterpenoid metabolic process	4	0.7532957	0.0240099	360	23	13114	6.3352657	1.0000000	0.7758372	34.1032601
GOTERM_BP_FAT	GO:0006776~vitamin A metabolic process	4	0.7532957	0.0240099	360	23	13114	6.3352657	1.0000000	0.7758372	34.1032601
KEGG_PATHWAY	hsa00980:Metabolism of xenobiotics by cytochrome P450	6	1.1299435	0.0240484	140	60	5042	3.6014286	0.9534451	0.3184532	24.5650201
INTERPRO	IPR006210:EGF-like	12	2.2598870	0.0241747	450	199	16090	2.1561139	1.0000000	0.8956026	31.4438440
INTERPRO	IPR002231:5-Hydroxytryptamine receptor	3	0.5649718	0.0245642	450	9	16090	11.9185185	1.0000000	0.8734068	31.8648272
GOTERM_BP_FAT	GO:0055065~metal ion homeostasis	12	2.2598870	0.0248430	360	204	13114	2.1428105	1.0000000	0.7770976	35.0619731
KEGG_PATHWAY	hsa04514:Cell adhesion molecules (CAMs)	9	1.6949153	0.0253068	140	129	5042	2.5126246	0.9604308	0.3015251	25.6838536
GOTERM_CC_FAT	GO:0043296~apical junction complex	8	1.5065913	0.0253916	364	98	12337	2.7667638	0.9997533	0.3267179	29.3590389
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	18	3.3898305	0.0268763	360	371	13114	1.7673854	1.0000000	0.7935618	37.3470361
GOTERM_BP_FAT	GO:0050905~neuromuscular process	6	1.1299435	0.0270997	360	62	13114	3.5252688	1.0000000	0.7868145	37.5934303
KEGG_PATHWAY	hsa00982:Drug metabolism	6	1.1299435	0.0272838	140	62	5042	3.4852535	0.9693624	0.2942914	27.4108547
GOTERM_MF_FAT	GO:0030246~carbohydrate binding	17	3.2015066	0.0274345	342	347	12549	1.7976389	0.9999999	0.7675709	33.5453080
KEGG_PATHWAY	hsa00500:Starch and sucrose metabolism	5	0.9416196	0.0275419	140	42	5042	4.2874150	0.9703698	0.2737823	27.6335525

GOTERM_BP_FAT	GO:0022604~regulation of cell morphogenesis	9	1.6949153	0.0275519	360	131	13114	2.5026718	1.0000000	0.7830491	38.0893113
PIR_SUPERFAMILY	PIRSF002282:cytoskeletal keratin	6	1.1299435	0.0285227	208	60	7196	3.4596154	0.9988538	0.8953481	31.0652896
GOTERM_BP_FAT	GO:0001654~eye development	9	1.6949153	0.0286596	360	132	13114	2.4837121	1.0000000	0.7872078	39.2885545
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	12	2.2598870	0.0289728	360	209	13114	2.0915470	1.0000000	0.7820362	39.6236191
GOTERM_BP_FAT	GO:0008210~estrogen metabolic process	3	0.5649718	0.0290817	360	10	13114	10.9283333	1.0000000	0.7746333	39.7397187
GOTERM_CC_FAT	GO:0016327~apicolateral plasma membrane	8	1.5065913	0.0293283	364	101	12337	2.6845827	0.9999333	0.3540499	33.1189634
GOTERM_MF_FAT	GO:0005343~organic acid:sodium symporter activity	4	0.7532957	0.0293907	342	25	12549	5.8708772	1.0000000	0.7617390	35.4821736
SP_PIR_KEYWORDS	Immunoglobulin domain	21	3.9548023	0.0296508	529	437	18289	1.6613921	0.9999968	0.5462038	34.4794930
GOTERM_BP_FAT	GO:0006721~terpenoid metabolic process	4	0.7532957	0.0299601	360	25	13114	5.8284444	1.0000000	0.7762731	40.6685144
GOTERM_CC_FAT	GO:0019898~extrinsic to membrane	23	4.3314501	0.0300279	364	486	12337	1.6039830	0.9999471	0.3482910	33.7674522
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	19	3.5781544	0.0300968	360	405	13114	1.7089575	1.0000000	0.7695165	40.8118200
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	18	3.3898305	0.0305653	360	377	13114	1.7392573	1.0000000	0.7666662	41.3005888
GOTERM_MF_FAT	GO:0005044~scavenger receptor activity	5	0.9416196	0.0309900	342	44	12549	4.1696571	1.0000000	0.7527221	37.0263073
SP_PIR_KEYWORDS	microsome	8	1.5065913	0.0310185	529	104	18289	2.6594445	0.9999982	0.5408948	35.7648286

GOTERM_BP_FAT	GO:0001655~urogenital system development	8	1.5065913	0.0313652	360	110	13114	2.6492929	1.0000000	0.7675878	42.1263492
GOTERM_BP_FAT	GO:0006720~isoprenoid metabolic process	5	0.9416196	0.0317348	360	44	13114	4.1395202	1.0000000	0.7638179	42.5040717
GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduction	62	11.6760829	0.0323017	360	1769	13114	1.2767226	1.0000000	0.7622913	43.0790928
GOTERM_BP_FAT	GO:0006022~aminoglycan metabolic process	6	1.1299435	0.0323978	360	65	13114	3.3625641	1.0000000	0.7557906	43.1760633
GOTERM_BP_FAT	GO:0007610~behavior	21	3.9548023	0.0324190	360	467	13114	1.6380799	1.0000000	0.7485852	43.1973889
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	12	2.2598870	0.0324474	360	213	13114	2.0522692	1.0000000	0.7415596	43.2259630
GOTERM_MF_FAT	GO:0019212~phosphatase inhibitor activity	4	0.7532957	0.0325734	342	26	12549	5.6450742	1.0000000	0.7445788	38.5211839
GOTERM_BP_FAT	GO:0055074~calcium ion homeostasis	11	2.0715631	0.0331686	360	187	13114	2.1428105	1.0000000	0.7421665	43.9479073
GOTERM_CC_FAT	GO:0005916~fascia adherens	3	0.5649718	0.0332337	364	10	12337	10.1678571	0.9999819	0.3654701	36.6651397
GOTERM_CC_FAT	GO:0042995~cell projection	30	5.6497175	0.0350787	364	693	12337	1.4672233	0.9999902	0.3695724	38.2791804
GOTERM_BP_FAT	GO:0031344~regulation of cell projection organization	7	1.3182674	0.0351640	360	89	13114	2.8651061	1.0000000	0.7557812	45.9004725
GOTERM_BP_FAT	GO:0042592~homeostatic process	30	5.6497175	0.0353505	360	745	13114	1.4668904	1.0000000	0.7508041	46.0797215
OMIM_DISEASE	Asthma, susceptibility to	3	0.5649718	0.0354021	104	9	3023	9.6891026	0.9994839	0.9994839	36.5794061
GOTERM_MF_FAT	GO:0005509~calcium ion binding	35	6.5913371	0.0359468	342	910	12549	1.4112686	1.0000000	0.7554218	41.5963740
KEGG_PATHWAY	hsa00140:Steroid hormone biosynthesis	5	0.9416196	0.0369281	140	46	5042	3.9145963	0.9912703	0.3263776	35.3218973

SP_PIR_KEYWORDS	pharmaceutical	5	0.9416196	0.0375622	529	44	18289	3.9287249	0.9999999	0.5907118	41.5970266
GOTERM_BP_FAT	GO:0007187~G-protein signaling, coupled to cyclic nucleotide second messenger	8	1.5065913	0.0385469	360	115	13114	2.5341063	1.0000000	0.7742822	49.0652034
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	11	2.0715631	0.0385504	360	192	13114	2.0870081	1.0000000	0.7678845	49.0683737
GOTERM_BP_FAT	GO:0010648~negative regulation of cell communication	13	2.4482109	0.0393877	360	247	13114	1.9172515	1.0000000	0.7689782	49.8242827
GOTERM_BP_FAT	GO:0015908~fatty acid transport	4	0.7532957	0.0401998	360	28	13114	5.2039683	1.0000000	0.7698169	50.5472961
GOTERM_BP_FAT	GO:0000272~polysaccharide catabolic process	4	0.7532957	0.0401998	360	28	13114	5.2039683	1.0000000	0.7698169	50.5472961
GOTERM_MF_FAT	GO:0005416~cation:amino acid symporter activity	3	0.5649718	0.0405941	342	12	12549	9.1732456	1.0000000	0.7756321	45.5985052
GOTERM_BP_FAT	GO:0048048~embryonic eye morphogenesis	3	0.5649718	0.0411484	360	12	13114	9.1069444	1.0000000	0.7717733	51.3793797
GOTERM_BP_FAT	GO:0042573~retinoic acid metabolic process	3	0.5649718	0.0411484	360	12	13114	9.1069444	1.0000000	0.7717733	51.3793797
GOTERM_BP_FAT	GO:0006875~cellular metal ion homeostasis	11	2.0715631	0.0420772	360	195	13114	2.0549003	1.0000000	0.7734922	52.1814059
GOTERM_BP_FAT	GO:0006811~ion transport	30	5.6497175	0.0424424	360	757	13114	1.4436372	1.0000000	0.7706069	52.4933209
GOTERM_MF_FAT	GO:0030594~neurotransmitter receptor activity	7	1.3182674	0.0427499	342	94	12549	2.7324561	1.0000000	0.7730239	47.3668876
GOTERM_CC_FAT	GO:0044463~cell projection part	13	2.4482109	0.0429599	364	233	12337	1.8910178	0.9999993	0.4204464	44.7541067
GOTERM_CC_FAT	GO:0031012~extracellular matrix	17	3.2015066	0.0429952	364	339	12337	1.6996418	0.9999993	0.4088788	44.7815991

GOTERM_MF_FAT	GO:0042277~peptide binding	11	2.0715631	0.0430664	342	197	12549	2.0488467	1.0000000	0.7561318	47.6219669
GOTERM_MF_FAT	GO:0042562~hormone binding	5	0.9416196	0.0435793	342	49	12549	3.7441819	1.0000000	0.7415718	48.0328277
INTERPRO	IPR007110:Immunoglobulin-like	19	3.5781544	0.0439235	450	416	16090	1.6330662	1.0000000	0.9664024	49.9889293
GOTERM_MF_FAT	GO:0008509~anion transmembrane transporter activity	9	1.6949153	0.0442781	342	145	12549	2.2774955	1.0000000	0.7292523	48.5878428
GOTERM_CC_FAT	GO:0043005~neuron projection	17	3.2015066	0.0445422	364	341	12337	1.6896732	0.9999996	0.4088120	45.9757378
GOTERM_BP_FAT	GO:0010517~regulation of phospholipase activity	6	1.1299435	0.0448192	360	71	13114	3.0784038	1.0000000	0.7835293	54.4768659
SP_PIR_KEYWORDS	ion transport	25	4.7080979	0.0451909	529	574	18289	1.5057830	1.0000000	0.6402093	47.7740389
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	17	3.2015066	0.0455467	360	367	13114	1.6873903	1.0000000	0.7834214	55.0683191
GOTERM_MF_FAT	GO:0005230~extracellular ligand-gated ion channel activity	6	1.1299435	0.0458880	342	72	12549	3.0577485	1.0000000	0.7249143	49.8454944
GOTERM_MF_FAT	GO:0004993~serotonin receptor activity	3	0.5649718	0.0471304	342	13	12549	8.4676113	1.0000000	0.7180933	50.7963703
GOTERM_BP_FAT	GO:0032102~negative regulation of response to external stimulus	5	0.9416196	0.0474645	360	50	13114	3.6427778	1.0000000	0.7918809	56.5927877
GOTERM_BP_FAT	GO:0048854~brain morphogenesis	3	0.5649718	0.0477674	360	13	13114	8.4064103	1.0000000	0.7886902	56.8291050
GOTERM_BP_FAT	GO:0007605~sensory perception of sound	7	1.3182674	0.0480022	360	96	13114	2.6561921	1.0000000	0.7850745	57.0114214
GOTERM_MF_FAT	GO:0015370~solute:sodium	5	0.9416196	0.0493086	342	51	12549	3.5973512	1.0000000	0.7187588	52.4231190

	symporter activity										
GOTERM_BP_FAT	GO:0031175~neuron projection development	13	2.4482109	0.0493178	360	256	13114	1.8498481	1.0000000	0.7890185	58.0196249
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	13	2.4482109	0.0493178	360	256	13114	1.8498481	1.0000000	0.7890185	58.0196249
INTERPRO	IPR002293:Amino acid/polyamine transporter I	3	0.5649718	0.0494617	450	13	16090	8.2512821	1.0000000	0.9701877	54.2760518
GOTERM_MF_FAT	GO:0005543~phospholipid binding	10	1.8832392	0.0495598	342	175	12549	2.0967419	1.0000000	0.7053713	52.6074478
SP_PIR_KEYWORDS	acute phase	4	0.7532957	0.0501773	529	29	18289	4.7686591	1.0000000	0.6607708	51.4774936
GOTERM_BP_FAT	GO:0007423~sensory organ development	12	2.2598870	0.0505166	360	229	13114	1.9088792	1.0000000	0.7920110	58.9189451
GOTERM_MF_FAT	GO:0005200~structural constituent of cytoskeleton	6	1.1299435	0.0506085	342	74	12549	2.9751067	1.0000000	0.6983952	53.3698445
SP_PIR_KEYWORDS	G protein-coupled receptor	8	1.5065913	0.0510319	529	116	18289	2.3843296	1.0000000	0.6492218	52.0871299
GOTERM_MF_FAT	GO:0008066~glutamate receptor activity	4	0.7532957	0.0510331	342	31	12549	4.7345784	1.0000000	0.6872850	53.6752470
PIR_SUPERFAMILY	PIRSF006060:AA_transporter	3	0.5649718	0.0521517	208	13	7196	7.9837278	0.9999964	0.9564265	49.7701960
GOTERM_MF_FAT	GO:0019208~phosphatase regulator activity	5	0.9416196	0.0523214	342	52	12549	3.5281714	1.0000000	0.6828695	54.5906150
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	20	3.7664783	0.0530124	360	463	13114	1.5735541	1.0000000	0.8030886	60.7333281
GOTERM_BP_FAT	GO:0045744~negative regulation of G-protein coupled receptor protein signaling pathway	3	0.5649718	0.0547427	360	14	13114	7.8059524	1.0000000	0.8088110	61.9466001
INTERPRO	IPR002152:Glycoside	2	0.3766478	0.0550340	450	2	16090	35.7555556	1.0000000	0.9731759	58.2407469

	hydrolase, family 23										
GOTERM_MF_FAT	GO:0030247~polysaccharide binding	9	1.6949153	0.0555735	342	152	12549	2.1726108	1.0000000	0.6921872	56.8267600
GOTERM_MF_FAT	GO:0001871~pattern binding	9	1.6949153	0.0555735	342	152	12549	2.1726108	1.0000000	0.6921872	56.8267600
INTERPRO	IPR011500:GPCR, family 3, nine cysteines region	3	0.5649718	0.0566642	450	14	16090	7.6619048	1.0000000	0.9686480	59.3383591
INTERPRO	IPR000337:GPCR, family 3	3	0.5649718	0.0566642	450	14	16090	7.6619048	1.0000000	0.9686480	59.3383591
PIR_SUPERFAMILY	PIRSF001065:lysozyme g	2	0.3766478	0.0567084	208	2	7196	34.5961538	0.9999988	0.9349223	52.7875769
PIR_SUPERFAMILY	PIRSF001065:Lysozyme_g	2	0.3766478	0.0567084	208	2	7196	34.5961538	0.9999988	0.9349223	52.7875769
INTERPRO	IPR013783:Immunoglobulin-like fold	20	3.7664783	0.0570019	450	459	16090	1.5579763	1.0000000	0.9612831	59.5623082
GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	16	3.0131827	0.0572398	360	349	13114	1.6700414	1.0000000	0.8185466	63.6354719
GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	12	2.2598870	0.0572525	360	234	13114	1.8680912	1.0000000	0.8140735	63.6438528
SP_PIR_KEYWORDS	calcium	32	6.0263653	0.0575265	529	798	18289	1.3863771	1.0000000	0.6773180	56.4932016
GOTERM_BP_FAT	GO:0008360~regulation of cell shape	5	0.9416196	0.0599564	360	54	13114	3.3729424	1.0000000	0.8243325	65.3925236
GOTERM_CC_FAT	GO:0070160~occluding junction	6	1.1299435	0.0605867	364	72	12337	2.8244048	1.0000000	0.5014833	57.0265942
GOTERM_CC_FAT	GO:0005923~tight junction	6	1.1299435	0.0605867	364	72	12337	2.8244048	1.0000000	0.5014833	57.0265942
GOTERM_BP_FAT	GO:0006775~fat-soluble vitamin metabolic process	4	0.7532957	0.0606455	360	33	13114	4.4154882	1.0000000	0.8236007	65.8253536

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GOTERM_CC_FAT	GO:0044456~synapse part	13	2.4482109	0.0607026	364	246	12337	1.7910859	1.0000000	0.4904575	57.0981511
GOTERM_BP_FAT	GO:0050954~sensory perception of mechanical stimulus	7	1.3182674	0.0610430	360	102	13114	2.4999455	1.0000000	0.8213774	66.0726453
SMART	SM00198:SCP	3	0.5649718	0.0621541	243	15	8828	7.2658436	0.9999921	0.9800464	54.7328830
GOTERM_BP_FAT	GO:0006874~cellular calcium ion homeostasis	10	1.8832392	0.0629012	360	182	13114	2.0015263	1.0000000	0.8266283	67.2067069
GOTERM_BP_FAT	GO:0030203~glycosaminoglycan metabolic process	5	0.9416196	0.0633267	360	55	13114	3.3116162	1.0000000	0.8246061	67.4612958
INTERPRO	IPR002190:MAGE protein	4	0.7532957	0.0635465	450	33	16090	4.3340067	1.0000000	0.9669580	63.6816045
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	24	4.5197740	0.0636341	360	599	13114	1.4595437	1.0000000	0.8220279	67.6440679
SP_PIR_KEYWORDS	hexosyltransferase	4	0.7532957	0.0639787	529	32	18289	4.3215974	1.0000000	0.7010130	60.4953081
INTERPRO	IPR014044:SCP-like extracellular	3	0.5649718	0.0642050	450	15	16090	7.1511111	1.0000000	0.9609838	64.0736191
INTERPRO	IPR001283:Allergen V5/Tpx-1 related	3	0.5649718	0.0642050	450	15	16090	7.1511111	1.0000000	0.9609838	64.0736191
GOTERM_BP_FAT	GO:0007268~synaptic transmission	14	2.6365348	0.0650625	360	297	13114	1.7171343	1.0000000	0.8250002	68.4808321
KEGG_PATHWAY	hsa00650:Butanoate metabolism	4	0.7532957	0.0659358	140	34	5042	4.2369748	0.9998149	0.4837240	54.6118009
GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-mediated signaling	8	1.5065913	0.0662260	360	130	13114	2.2417094	1.0000000	0.8266036	69.1472291
GOTERM_BP_FAT	GO:0043627~response to estrogen stimulus	7	1.3182674	0.0682787	360	105	13114	2.4285185	1.0000000	0.8322474	70.2907498
GOTERM_BP_FAT	GO:0006825~copper ion	3	0.5649718	0.0696655	360	16	13114	6.8302083	1.0000000	0.8346668	71.0406012

	transport										
SMART	SM00352:POU	3	0.5649718	0.0697836	243	16	8828	6.8117284	0.9999982	0.9634644	59.0771727
GOTERM_BP_FAT	GO:0050885~neuromuscular process controlling balance	4	0.7532957	0.0699435	360	35	13114	4.1631746	1.0000000	0.8321445	71.1887698
GOTERM_BP_FAT	GO:0042445~hormone metabolic process	7	1.3182674	0.0707967	360	106	13114	2.4056080	1.0000000	0.8321907	71.6389835
GOTERM_MF_FAT	GO:0042626~ATPase activity, coupled to transmembrane movement of substances	7	1.3182674	0.0713130	342	107	12549	2.4004755	1.0000000	0.7705377	66.2717444
GOTERM_CC_FAT	GO:0005624~membrane fraction	32	6.0263653	0.0714237	364	801	12337	1.3540218	1.0000000	0.5379597	63.2629870
GOTERM_BP_FAT	GO:0042493~response to drug	11	2.0715631	0.0716243	360	215	13114	1.8637468	1.0000000	0.8321287	72.0694210
INTERPRO	IPR000327:POU-specific	3	0.5649718	0.0720598	450	16	16090	6.7041667	1.0000000	0.9683404	68.4542728
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	12	2.2598870	0.0724214	360	244	13114	1.7915301	1.0000000	0.8319400	72.4781394
GOTERM_BP_FAT	GO:0043010~camera-type eye development	7	1.3182674	0.0733676	360	107	13114	2.3831256	1.0000000	0.8323916	72.9559730
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	12	2.2598870	0.0738065	360	245	13114	1.7842177	1.0000000	0.8307007	73.1749792
GOTERM_BP_FAT	GO:0042060~wound healing	10	1.8832392	0.0738167	360	188	13114	1.9376478	1.0000000	0.8272114	73.1800338
GOTERM_MF_FAT	GO:0043492~ATPase activity, coupled to movement of substances	7	1.3182674	0.0738753	342	108	12549	2.3782489	1.0000000	0.7714701	67.6132603
INTERPRO	IPR001128:Cytochrome P450	5	0.9416196	0.0744382	450	57	16090	3.1364522	1.0000000	0.9660626	69.6787895

GOTERM_BP_FAT	GO:0050906~detection of stimulus involved in sensory perception	4	0.7532957	0.0748193	360	36	13114	4.0475309	1.0000000	0.8279583	73.6739471
GOTERM_BP_FAT	GO:0005976~polysaccharide metabolic process	7	1.3182674	0.0759914	360	108	13114	2.3610597	1.0000000	0.8293913	74.2405013
GOTERM_BP_FAT	GO:0050877~neurological system process	41	7.7212806	0.0764219	360	1160	13114	1.2875335	1.0000000	0.8277527	74.4457223
GOTERM_MF_FAT	GO:0016820~hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	7	1.3182674	0.0764896	342	109	12549	2.3564301	1.0000000	0.7726099	68.9306435
GOTERM_MF_FAT	GO:0005246~calcium channel regulator activity	3	0.5649718	0.0765736	342	17	12549	6.4752322	1.0000000	0.7622282	68.9721228
SMART	SM00233:PH	13	2.4482109	0.0770083	243	276	8828	1.7111588	0.9999996	0.9467598	62.8343732
GOTERM_BP_FAT	GO:0051241~negative regulation of multicellular organismal process	9	1.6949153	0.0772268	360	162	13114	2.0237654	1.0000000	0.8276719	74.8252199
GOTERM_BP_FAT	GO:0045785~positive regulation of cell adhesion	5	0.9416196	0.0777740	360	59	13114	3.0870998	1.0000000	0.8265505	75.0802319
INTERPRO	IPR008250:ATPase, P-type, ATPase-associated region	4	0.7532957	0.0783068	450	36	16090	3.9728395	1.0000000	0.9662274	71.5760035
INTERPRO	IPR018303:ATPase, P-type phosphorylation site	4	0.7532957	0.0783068	450	36	16090	3.9728395	1.0000000	0.9662274	71.5760035
INTERPRO	IPR001757:ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	4	0.7532957	0.0783068	450	36	16090	3.9728395	1.0000000	0.9662274	71.5760035
GOTERM_BP_FAT	GO:0007204~elevation of cytosolic calcium ion concentration	7	1.3182674	0.0786678	360	109	13114	2.3393986	1.0000000	0.8268469	75.4914815

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GOTERM_MF_FAT	GO:0005294~neutral L-amino acid secondary active transmembrane transporter activity	2	0.3766478	0.0793315	342	3	12549	24.4619883	1.0000000	0.7643043	70.3059486
INTERPRO	IPR013847:POU	3	0.5649718	0.0802053	450	17	16090	6.3098039	1.0000000	0.9634239	72.4659084
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	15	2.8248588	0.0811494	364	315	12337	1.6139456	1.0000000	0.5743985	68.1352060
INTERPRO	IPR001117:Multicopper oxidase, type 1	2	0.3766478	0.0814071	450	3	16090	23.8370370	1.0000000	0.9595370	73.0157003
INTERPRO	IPR004294:Carotenoid oxygenase	2	0.3766478	0.0814071	450	3	16090	23.8370370	1.0000000	0.9595370	73.0157003
INTERPRO	IPR009523:Prokineticin	2	0.3766478	0.0814071	450	3	16090	23.8370370	1.0000000	0.9595370	73.0157003
GOTERM_BP_FAT	GO:0048666~neuron development	15	2.8248588	0.0816286	360	338	13114	1.6166174	1.0000000	0.8351750	76.8086142
INTERPRO	IPR017972:Cytochrome P450, conserved site	5	0.9416196	0.0822159	450	59	16090	3.0301318	1.0000000	0.9549392	73.3799062
INTERPRO	IPR000742:EGF-like, type 3	10	1.8832392	0.0833094	450	189	16090	1.8918283	1.0000000	0.9508001	73.8649989
GOTERM_BP_FAT	GO:0007188~G-protein signaling, coupled to cAMP nucleotide second messenger	6	1.1299435	0.0834941	360	85	13114	2.5713725	1.0000000	0.8389893	77.6039612
PIR_SUPERFAMILY	PIRSF008887:human CAGR1 protein	2	0.3766478	0.0838506	208	3	7196	23.0641026	1.0000000	0.9671386	67.5623074
SP_PIR_KEYWORDS	glycosyltransferase	11	2.0715631	0.0841780	529	210	18289	1.8109551	1.0000000	0.7853683	70.9224581
GOTERM_MF_FAT	GO:0001653~peptide receptor activity	7	1.3182674	0.0846433	342	112	12549	2.2933114	1.0000000	0.7770712	72.7256732
GOTERM_MF_FAT	GO:0008528~peptide receptor activity, G-protein coupled	7	1.3182674	0.0846433	342	112	12549	2.2933114	1.0000000	0.7770712	72.7256732

GOTERM_BP_FAT	GO:0030003~cellular cation homeostasis	12	2.2598870	0.0862259	360	252	13114	1.7346561	1.0000000	0.8457115	78.7224128
INTERPRO	IPR001849:Pleckstrin homology	13	2.4482109	0.0868393	450	276	16090	1.6841385	1.0000000	0.9511809	75.3751220
GOTERM_BP_FAT	GO:0010033~response to organic substance	27	5.0847458	0.0871513	360	716	13114	1.3736732	1.0000000	0.8459141	79.0892157
GOTERM_BP_FAT	GO:0050878~regulation of body fluid levels	8	1.5065913	0.0874126	360	139	13114	2.0965627	1.0000000	0.8438247	79.1917107
GOTERM_BP_FAT	GO:0055085~transmembrane transport	22	4.1431262	0.0878909	360	560	13114	1.4310913	1.0000000	0.8425052	79.3780952
SP_PIR_KEYWORDS	cleavage on pair of basic residues	13	2.4482109	0.0891880	529	269	18289	1.6708034	1.0000000	0.7918374	73.0788946
BIOCARTA	h_nuclearRsPathway:Nuclear Receptors in Lipid Metabolism and Toxicity	4	0.7532957	0.0894332	43	36	1406	3.6330749	0.9997373	0.9997373	63.7521530
GOTERM_BP_FAT	GO:0060191~regulation of lipase activity	6	1.1299435	0.0901126	360	87	13114	2.5122605	1.0000000	0.8471345	80.2233801
GOTERM_BP_FAT	GO:0007613~memory	4	0.7532957	0.0903087	360	39	13114	3.7361823	1.0000000	0.8448958	80.2963930
SP_PIR_KEYWORDS	tumor antigen	4	0.7532957	0.0903605	529	37	18289	3.7375977	1.0000000	0.7834386	73.5616420
GOTERM_BP_FAT	GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	11	2.0715631	0.0903819	360	225	13114	1.7809136	1.0000000	0.8422550	80.3235921
SP_PIR_KEYWORDS	palmitate	11	2.0715631	0.0905270	529	213	18289	1.7854487	1.0000000	0.7714651	73.6295322
GOTERM_BP_FAT	GO:0003002~regionalization	10	1.8832392	0.0920435	360	197	13114	1.8491258	1.0000000	0.8449431	80.9313967
GOTERM_MF_FAT	GO:0031420~alkali metal ion binding	11	2.0715631	0.0921060	342	227	12549	1.7780740	1.0000000	0.7966804	75.8160769
GOTERM_MF_FAT	GO:0005328~neurotransmitt	3	0.5649718	0.0929640	342	19	12549	5.7936288	1.0000000	0.7906779	76.1496653

	er:sodium symporter activity										
GOTERM_CC_FAT	GO:0044421~extracellular region part	36	6.7796610	0.0943565	364	946	12337	1.2897916	1.0000000	0.6209444	73.7974553
INTERPRO	IPR012680:Laminin G, subdomain 2	4	0.7532957	0.0944094	450	39	16090	3.6672365	1.0000000	0.9579780	78.3428413
SP_PIR_KEYWORDS	Tight junction	5	0.9416196	0.0948690	529	60	18289	2.8810649	1.0000000	0.7757814	75.3439896
KEGG_PATHWAY	hsa04940:Type I diabetes mellitus	4	0.7532957	0.0968310	140	40	5042	3.6014286	0.9999973	0.6001277	69.2548577
INTERPRO	IPR000175:Sodium:neurotransmitter symporter	3	0.5649718	0.0972801	450	19	16090	5.6456140	1.0000000	0.9571432	79.3780564
BIOCARTA	h_no1Pathway:Actions of Nitric Oxide in the Heart	3	0.5649718	0.0985804	43	18	1406	5.4496124	0.9998920	0.9896059	67.5071594
OMIM_DISEASE	Association of three genetic loci with uric acid concentration and risk of gout: a genome-wide association study	2	0.3766478	0.0988047	104	3	3023	19.3782051	1.0000000	0.9999820	73.1354474
GOTERM_BP_FAT	GO:0015837~amine transport	7	1.3182674	0.0988615	360	116	13114	2.1982280	1.0000000	0.8632987	83.2451802
GOTERM_MF_FAT	GO:0031402~sodium ion binding	7	1.3182674	0.0992555	342	117	12549	2.1953066	1.0000000	0.8041019	78.4678568