

Supplementary Table 2. Statistically over-represented ($p < 0.1$) processes from DAVID analysis when comparing a list of genes with HTE-selective DHS in their promoter to all human genes.

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030855~epithelial cell differentiation	24	2.274881517	1.46E-06	727	136	13114	3.183267255	0.004005499	0.004005499	0.002603367
GOTERM_BP_FAT	GO:0060429~epithelium development	32	3.033175355	2.64E-06	727	226	13114	2.554125939	0.00722096	0.003617022	0.004700787
GOTERM_CC_FAT	GO:0044459~plasma membrane part	171	16.20853081	6.19E-06	713	2163	12337	1.367916619	0.002696242	0.002696242	0.008745068
KEGG_PATHWAY	hsa04080:Neuroactive ligand-receptor interaction	33	3.127962085	7.97E-06	280	255	5042	2.330336134	0.001354196	0.001354196	0.009724331
GOTERM_BP_FAT	GO:0007398~ectoderm development	28	2.654028436	9.69E-06	727	195	13114	2.590145664	0.026285225	0.008839651	0.017276612
GOTERM_BP_FAT	GO:0008544~epidermis development	26	2.464454976	2.14E-05	727	181	13114	2.591167821	0.057224832	0.014623879	0.03821622
GOTERM_CC_FAT	GO:0030054~cell junction	53	5.023696682	5.38E-05	713	515	12337	1.780691458	0.023169856	0.011652822	0.075906008
GOTERM_CC_FAT	GO:0016327~apicolateral plasma membrane	18	1.706161137	6.02E-05	713	101	12337	3.083693222	0.025891017	0.008705912	0.084934776
GOTERM_BP_FAT	GO:0009913~epidermal cell differentiation	14	1.327014218	1.21E-04	727	71	13114	3.556890172	0.28385072	0.064592793	0.216329602
GOTERM_CC_FAT	GO:0043296~apical junction complex	17	1.611374408	1.43E-04	713	98	12337	3.001531328	0.060337434	0.0154382	0.201386465
GOTERM_BP_FAT	GO:0030216~keratinocyte differentiation	13	1.232227488	2.03E-04	727	65	13114	3.607702889	0.427357777	0.088729675	0.360967749
GOTERM_CC_FAT	GO:0005911~cell-cell junction	25	2.369668246	2.08E-04	713	188	12337	2.300923577	0.086641139	0.017962009	0.293126235
SP_PIR_KEYWORDS	cell junction	41	3.886255924	3.19E-04	1037	398	18289	1.81682036	0.160161888	0.160161888	0.464234149
GOTERM_CC_FAT	GO:0005576~extracellular region	144	13.6492891	3.76E-04	713	1906	12337	1.30725295	0.151081616	0.026929463	0.529150101
UP_SEQ_FEATURE	site:Stutter	9	0.853080569	4.06E-04	1037	33	18267	4.804155343	0.658523769	0.658523769	0.717671921

GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	98	9.289099526	4.08E-04	713	1207	12337	1.40487874	0.162856376	0.025074511	0.574143656
SP_PIR_KEYWORDS	palmoplantar keratoderma	7	0.663507109	4.67E-04	1037	19	18289	6.497639953	0.225299988	0.119829555	0.67822803
SP_PIR_KEYWORDS	Secreted	125	11.84834123	5.23E-04	1037	1643	18289	1.341787226	0.24889175	0.090992407	0.760079664
SP_PIR_KEYWORDS	signal	219	20.75829384	6.87E-04	1037	3158	18289	1.22304713	0.31341799	0.089723974	0.997433532
UP_SEQ_FEATURE	signal peptide	219	20.75829384	7.52E-04	1037	3158	18267	1.221575915	0.863642101	0.630733296	1.326743814
SP_PIR_KEYWORDS	disease mutation	119	11.27962085	0.00105123	1037	1580	18289	1.328315003	0.437475853	0.108691119	1.522022576
SP_PIR_KEYWORDS	glycoprotein	281	26.63507109	0.00105427	1037	4209	18289	1.177439491	0.438400461	0.091682272	1.52634115
GOTERM_CC_FAT	GO:0001533~cornified envelope	7	0.663507109	0.001216105	713	22	12337	5.505482596	0.411715488	0.064166846	1.703855019
SP_PIR_KEYWORDS	developmental protein	65	6.161137441	0.001380506	1037	771	18289	1.486860356	0.530298904	0.102328643	1.994323298
PIR_SUPERFAMILY	PIRSF002282:cytoskeletal keratin	11	1.042654028	0.001442185	397	60	7196	3.32308984	0.449812067	0.449812067	2.002767843
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	93	8.815165877	0.001572016	713	1180	12337	1.363706706	0.496382557	0.073383382	2.197386278
SP_PIR_KEYWORDS	nitration	7	0.663507109	0.001814657	1037	24	18289	5.143964963	0.629728686	0.116787904	2.613813232
GOTERM_BP_FAT	GO:0051896~regulation of protein kinase B signaling cascade	6	0.568720379	0.001816546	727	17	13114	6.366534509	0.993250093	0.510334297	3.190126329
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc..)	267	25.30805687	0.002209801	1037	4021	18267	1.16967622	0.997149444	0.858210779	3.852165983
GOTERM_BP_FAT	GO:0051897~positive regulation of protein kinase B signaling cascade	5	0.473933649	0.002247701	727	11	13114	8.199324747	0.99794172	0.538482619	3.933063974
UP_SEQ_FEATURE	region of interest:Head	12	1.137440758	0.002323703	1037	72	18267	2.93587271	0.997893344	0.785761057	4.046877047

UP_SEQ_FEATUR E	region of interest:Coil 2	11	1.042654028	0.0027135 56	1037	63	18267	3.075676172	0.999251905	0.762976553	4.710501877
UP_SEQ_FEATUR E	region of interest:Linker 12	11	1.042654028	0.0027135 56	1037	63	18267	3.075676172	0.999251905	0.762976553	4.710501877
GOTERM_MF_FA T	GO:0005200~structural constituent of cytoskeleton	12	1.137440758	0.0027874 79	710	74	12549	2.866159117	0.913052424	0.913052424	4.242568408
UP_SEQ_FEATUR E	region of interest:Tail	12	1.137440758	0.0028996 86	1037	74	18267	2.856524799	0.99954373	0.72253792	5.02581011
SP_PIR_KEYWOR DS	gamma-carboxyglutamic acid	6	0.568720379	0.0034476 49	1037	19	18289	5.569405674	0.848795551	0.189336709	4.911419817
INTERPRO	IPR013090:Phospholipase A2, active site	6	0.568720379	0.0037935 47	933	19	16090	5.445929937	0.993742753	0.993742753	6.036205713
INTERPRO	IPR002383:Coagulation factor, Gla region	5	0.473933649	0.0038055 87	933	12	16090	7.185602001	0.993842902	0.921532825	6.054806937
UP_SEQ_FEATUR E	sequence variant	710	67.2985782	0.0041237 19	1037	11801	18267	1.059809994	0.999982377	0.79065246	7.074954672
GOTERM_CC_FAT	GO:0044463~cell projection part	25	2.369668246	0.0042124 65	713	233	12337	1.856539195	0.841264163	0.168106945	5.787549548
SP_PIR_KEYWOR DS	polymorphism	684	64.83412322	0.0044011 92	1037	11351	18289	1.06275506	0.91043274	0.214375663	6.229594075
GOTERM_CC_FAT	GO:0030057~desmosome	6	0.568720379	0.0047358 36	713	20	12337	5.19088359	0.873780085	0.171515566	6.484462468
SP_PIR_KEYWOR DS	rna editing	5	0.473933649	0.0048470 41	1037	13	18289	6.783250501	0.929896165	0.21464243	6.840076393
GOTERM_BP_FAT	GO:0051967~negative regulation of synaptic transmission, glutamatergic	4	0.379146919	0.0049994 1	727	7	13114	10.30772254	0.999998962	0.783653053	8.54933666
UP_SEQ_FEATUR E	DNA-binding region:Homeobox	21	1.990521327	0.0050852 39	1037	188	18267	1.967659369	0.999998636	0.815138022	8.655292755
GOTERM_BP_FAT	GO:0007409~axonogenesis	21	1.990521327	0.0051384 89	727	193	13114	1.962739913	0.999999293	0.757368726	8.777004991
UP_SEQ_FEATUR E	region of interest:Coil 1B	11	1.042654028	0.0053189 78	1037	69	18267	2.80822607	0.999999268	0.791898841	9.035611542

UP_SEQ_FEATUR E	region of interest:Linker 1	11	1.042654028	0.0053189 78	1037	69	18267	2.80822607	0.999999268	0.791898841	9.035611542
UP_SEQ_FEATUR E	region of interest:Coil 1A	11	1.042654028	0.0053189 78	1037	69	18267	2.80822607	0.999999268	0.791898841	9.035611542
SP_PIR_KEYWOR DS	keratinization	8	0.758293839	0.0057345 95	1037	39	18289	3.6177336	0.956969754	0.230607729	8.044362213
UP_SEQ_FEATUR E	region of interest:Rod	11	1.042654028	0.0058981 32	1037	70	18267	2.768108555	0.999999844	0.79133829	9.971529305
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	22	2.085308057	0.0059867 91	727	209	13114	1.898790994	0.999999932	0.777014823	10.15410736
UP_SEQ_FEATUR E	domain:Gla	5	0.473933649	0.0065126 56	1037	14	18267	6.291155807	0.99999997	0.792680765	10.95466674
GOTERM_BP_FAT	GO:0030182~neuron differentiation	38	3.601895735	0.0065194 89	727	437	13114	1.568566473	0.999999984	0.776511658	11.00881525
GOTERM_MF_FA T	GO:0008376~acetylgalactosami nyltransferase activity	7	0.663507109	0.0069666 75	710	31	12549	3.991049523	0.997795322	0.953046	10.28892686
INTERPRO	IPR000294:Gamma- carboxyglutamic acid-rich (GLA) domain	5	0.473933649	0.0070135 7	933	14	16090	6.159087429	0.999916953	0.956371082	10.8896597
GOTERM_BP_FAT	GO:0006811~ion transport	59	5.592417062	0.0072145 91	727	757	13114	1.405907995	0.999999998	0.783710729	12.11256067
GOTERM_CC_FAT	GO:0045095~keratin filament	12	1.137440758	0.0072527 5	713	82	12337	2.532138337	0.958152451	0.232392572	9.769534682
GOTERM_CC_FAT	GO:0031012~extracellular matrix	32	3.033175355	0.0073433 16	713	339	12337	1.633316371	0.959784359	0.219009468	9.885718341
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	22	2.085308057	0.0074005 4	727	213	13114	1.863132947	0.999999999	0.767427334	12.40562768
GOTERM_BP_FAT	GO:0031424~keratinization	8	0.758293839	0.0076643 21	727	42	13114	3.435907513	0.999999999	0.75586281	12.81978292
GOTERM_BP_FAT	GO:0001655~urogenital system development	14	1.327014218	0.0076787 47	727	110	13114	2.295810929	0.999999999	0.734036458	12.84237858
SMART	SM00069:GLA	5	0.473933649	0.0078772 33	530	14	8828	5.948787062	0.880849238	0.880849238	9.870368755

SP_PIR_KEYWORD	cysteine proteinase inhibitor	4	0.379146919	0.0081858 94	1037	8	18289	8.818225651	0.98884772	0.292384716	11.29553046
GOTERM_CC_FAT	GO:0044421~extracellular region part	73	6.91943128	0.0087099 84	713	946	12337	1.335216709	0.977944384	0.238482405	11.62216719
INTERPRO	IPR003267:Small proline-rich	6	0.568720379	0.0090583 54	933	23	16090	4.498811687	0.999994701	0.952021462	13.84842768
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	24	2.274881517	0.0092546 61	727	245	13114	1.76703815	1	0.777649686	15.27782783
SP_PIR_KEYWORD	Intermediate filament	11	1.042654028	0.0094892 83	1037	75	18289	2.586679524	0.994567863	0.311011147	12.98030563
INTERPRO	IPR019412:Outer membrane protein, IML2, mitochondrial/Tetratricopeptide repeat protein 39	3	0.28436019	0.0096679 38	933	3	16090	17.2454448	0.99999767	0.925271862	14.71247737
UP_SEQ_FEATURE	compositionally biased region:Gly-rich	23	2.180094787	0.0100522 38	1037	227	18267	1.784803674	1	0.89249951	16.42305863
GOTERM_MF_FAT	GO:0001653~peptide receptor activity	14	1.327014218	0.0104325 36	710	112	12549	2.209330986	0.99989655	0.953056311	15.03031682
GOTERM_MF_FAT	GO:0008528~peptide receptor activity, G-protein coupled	14	1.327014218	0.0104325 36	710	112	12549	2.209330986	0.99989655	0.953056311	15.03031682
SP_PIR_KEYWORD	ion transport	47	4.454976303	0.0112495 56	1037	574	18289	1.444099671	0.997946852	0.338045686	15.20837449
GOTERM_BP_FAT	GO:0006812~cation transport	44	4.170616114	0.0120099 23	727	545	13114	1.456320432	1	0.842019764	19.38224769
INTERPRO	IPR003117:cAMP-dependent protein kinase, regulatory subunit, type I/II alpha/beta	4	0.379146919	0.0125040 79	933	9	16090	7.664642134	0.999999949	0.939171579	18.62661972
SMART	SM00394:RIIa	4	0.379146919	0.0136933 2	530	9	8828	7.40293501	0.975496894	0.843465321	16.5716003
GOTERM_MF_FAT	GO:0004623~phospholipase A2 activity	6	0.568720379	0.0138685 52	710	26	12549	4.078764897	0.999995069	0.952876292	19.49861604
SP_PIR_KEYWORD	G protein-coupled receptor	14	1.327014218	0.0141774 45	1037	116	18289	2.128537226	0.99959457	0.386245381	18.79703379
GOTERM_CC_FAT	GO:0005886~plasma	239	22.65402844	0.0145350	713	3663	12337	1.128966401	0.998311314	0.346613847	18.6804648

	membrane			84							
SP_PIR_KEYWORD	heterotetramer	7	0.663507109	0.0147369 88	1037	36	18289	3.429309975	0.999702805	0.37979982	19.46654383
UP_SEQ_FEATURE	metal ion-binding site:Calcium; via carbonyl oxygen	7	0.663507109	0.0148175 81	1037	36	18267	3.425184828	1	0.952258793	23.28609384
PIR_SUPERFAMILY	PIRSF005670:polypeptide N- acetylgalactosaminyltransferase	4	0.379146919	0.0148513 06	397	10	7196	7.250377834	0.997959487	0.954827962	18.9209102
SP_PIR_KEYWORD	calcium	61	5.781990521	0.0149752 99	1037	798	18289	1.348149786	0.999739639	0.367784275	19.75012684
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	24	2.274881517	0.0150968 69	727	256	13114	1.691110729	1	0.889300317	23.75760545
GOTERM_BP_FAT	GO:0031175~neuron projection development	24	2.274881517	0.0150968 69	727	256	13114	1.691110729	1	0.889300317	23.75760545
GOTERM_CC_FAT	GO:0031526~brush border membrane	6	0.568720379	0.0150971 71	713	26	12337	3.992987377	0.998683212	0.339352595	19.33307865
GOTERM_BP_FAT	GO:0007411~axon guidance	13	1.232227488	0.0151078 78	727	107	13114	2.191595213	1	0.87661232	23.7728007
INTERPRO	IPR012287:Homeodomain- related	23	2.180094787	0.0151170 71	933	231	16090	1.71707892	0.999999999	0.945254227	22.08292971
INTERPRO	IPR000832:GPCR, family 2, secretin-like	8	0.758293839	0.0158470 98	933	46	16090	2.999207792	0.999999999	0.930446718	23.02364005
GOTERM_MF_FAT	GO:0004653~polypeptide N- acetylgalactosaminyltransferase activity	5	0.473933649	0.0163827 64	710	18	12549	4.909624413	0.999999472	0.94446423	22.62782727
PIR_SUPERFAMILY	PIRSF000548:PK_regulatory	3	0.28436019	0.0168302 49	397	4	7196	13.59445844	0.999112431	0.903897627	21.17438518
PIR_SUPERFAMILY	PIRSF000548:cAMP-dependent protein kinase, regulatory subunit	3	0.28436019	0.0168302 49	397	4	7196	13.59445844	0.999112431	0.903897627	21.17438518
UP_SEQ_FEATURE	binding site:cAMP 1	3	0.28436019	0.0178569 69	1037	4	18267	13.21142719	1	0.966936496	27.38179624
UP_SEQ_FEATURE	region of interest:Dimerization and phosphorylation	3	0.28436019	0.0178569 69	1037	4	18267	13.21142719	1	0.966936496	27.38179624

UP_SEQ_FEATUR E	binding site:cAMP 2	3	0.28436019	0.0178569 69	1037	4	18267	13.21142719	1	0.966936496	27.38179624
INTERPRO	IPR003302:Cornefin (SPRR)	3	0.28436019	0.0185944 09	933	4	16090	12.9340836	1	0.938217572	26.46909712
INTERPRO	IPR012198:cAMP-dependent protein kinase regulatory subunit	3	0.28436019	0.0185944 09	933	4	16090	12.9340836	1	0.938217572	26.46909712
UP_SEQ_FEATUR E	domain:PDZ 3	6	0.568720379	0.0192117 01	1037	28	18267	3.774693484	1	0.967476766	29.14006853
UP_SEQ_FEATUR E	topological domain:Cytoplasmic	213	20.18957346	0.0193147 86	1037	3287	18267	1.141480171	1	0.960406495	29.27220125
INTERPRO	IPR017970:Homeobox, conserved site	22	2.085308057	0.0194040 49	933	223	16090	1.70134433	1	0.926898255	27.45652086
SP_PIR_KEYWOR DS	keratin	15	1.421800948	0.0197104 56	1037	134	18289	1.974229623	0.999981343	0.436236612	25.1955628
INTERPRO	IPR017983:GPCR, family 2, secretin-like, conserved site	8	0.758293839	0.0197392 57	933	48	16090	2.8742408	1	0.911041716	27.86167784
UP_SEQ_FEATUR E	region of interest:Catalytic subdomain A	5	0.473933649	0.0201267 6	1037	19	18267	4.635588489	1	0.957921308	30.30488318
UP_SEQ_FEATUR E	region of interest:Catalytic subdomain B	5	0.473933649	0.0201267 6	1037	19	18267	4.635588489	1	0.957921308	30.30488318
GOTERM_MF_FA T	GO:0030414~peptidase inhibitor activity	16	1.516587678	0.0201340 35	710	148	12549	1.910772745	0.999999981	0.948500087	27.085775
INTERPRO	IPR001356:Homeobox	22	2.085308057	0.0202887 26	933	224	16090	1.693749043	1	0.897749774	28.52121555
UP_SEQ_FEATUR E	compositionally biased region:Ala-rich	16	1.516587678	0.0209674 97	1037	148	18267	1.904349866	1	0.955777694	31.35914154
GOTERM_BP_FAT	GO:0030001~metal ion transport	37	3.507109005	0.0217759 55	727	459	13114	1.454085042	1	0.943981391	32.46931445
GOTERM_CC_FAT	GO:0005923~tight junction	10	0.947867299	0.0221690 51	713	72	12337	2.403186847	0.999943114	0.437277126	27.13878682
GOTERM_CC_FAT	GO:0070160~occluding junction	10	0.947867299	0.0221690 51	713	72	12337	2.403186847	0.999943114	0.437277126	27.13878682

SP_PIR_KEYWORD	Homeobox	22	2.085308057	0.0222188 99	1037	231	18289	1.679662029	0.999995406	0.459110157	27.93884032
GOTERM_BP_FAT	GO:0044259~multicellular organismal macromolecule metabolic process	6	0.568720379	0.0231011 22	727	30	13114	3.607702889	1	0.946090819	34.08210175
GOTERM_CC_FAT	GO:0042734~presynaptic membrane	6	0.568720379	0.0236519 47	713	29	12337	3.579919718	0.999970648	0.439982141	28.68386541
INTERPRO	IPR001478:PDZ/DHR/GLGF	16	1.516587678	0.0246946 96	933	148	16090	1.864372411	1	0.923295342	33.60875275
PIR_SUPERFAMILY	PIRSF005503:G protein-coupled receptor, peptide hormone receptor type	4	0.379146919	0.0250871 46	397	12	7196	6.041981528	0.99997297	0.927895907	29.96357956
GOTERM_BP_FAT	GO:0030198~extracellular matrix organization	12	1.137440758	0.0253285 44	727	102	13114	2.12217817	1	0.953407248	36.71134635
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	46	4.360189573	0.0254246 25	710	592	12549	1.37336791	1	0.960012042	32.96588572
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	28	2.654028436	0.0257826 33	713	315	12337	1.538039582	0.999988677	0.450861349	30.85066051
PIR_SUPERFAMILY	PIRSF800007:secretin receptor-like G protein-coupled receptors	7	0.663507109	0.0261207 08	397	42	7196	3.020990764	0.999982577	0.888255827	30.99724981
INTERPRO	IPR000372:Leucine-rich repeat, cysteine-rich flanking region, N-terminal	12	1.137440758	0.0261490 21	933	98	16090	2.111687119	1	0.920075825	35.21200434
GOTERM_BP_FAT	GO:0015672~monovalent inorganic cation transport	27	2.559241706	0.0261715 29	727	314	13114	1.551082452	1	0.952052871	37.68033162
GOTERM_BP_FAT	GO:0015909~long-chain fatty acid transport	5	0.473933649	0.0262501 06	727	21	13114	4.294884391	1	0.94633654	37.76993595
GOTERM_MF_FAT	GO:0004866~endopeptidase inhibitor activity	15	1.421800948	0.0268245 89	710	140	12549	1.893712274	1	0.948901928	34.44588563
SP_PIR_KEYWORD	epidermolysis bullosa	4	0.379146919	0.0271385 64	1037	12	18289	5.878817101	0.999999709	0.511621319	33.04906342
SMART	SM00389:HOX	22	2.085308057	0.0273512 29	530	224	8828	1.635916442	0.999424328	0.916812422	30.53988515
GOTERM_BP_FAT	GO:0042574~retinal metabolic	3	0.28436019	0.0273657	727	5	13114	10.82310867	1	0.946801772	39.02911395

	process			58								
GOTERM_BP_FAT	GO:0007598~blood coagulation, extrinsic pathway	3	0.28436019	0.0273657 58	727	5	13114	10.82310867		1	0.946801772	39.02911395
GOTERM_BP_FAT	GO:0043288~apocarotenoid metabolic process	3	0.28436019	0.0273657 58	727	5	13114	10.82310867		1	0.946801772	39.02911395
KEGG_PATHWAY	hsa04530:Tight junction	14	1.327014218	0.0282429 21	280	131	5042	1.924427481	0.992329721		0.912419869	29.49723129
GOTERM_MF_FAT	GO:0005509~calcium ion binding	66	6.255924171	0.0282567 54	710	910	12549	1.281897539		1	0.938378518	35.92825151
GOTERM_BP_FAT	GO:0042471~ear morphogenesis	9	0.853080569	0.0286161	727	66	13114	2.459797424		1	0.947975619	40.41171711
UP_SEQ_FEATURE	nucleotide phosphate-binding region:cAMP 2	3	0.28436019	0.0286493 57	1037	5	18267	10.56914176		1	0.982623869	40.31928304
UP_SEQ_FEATURE	nucleotide phosphate-binding region:cAMP 1	3	0.28436019	0.0286493 57	1037	5	18267	10.56914176		1	0.982623869	40.31928304
GOTERM_MF_FAT	GO:0042165~neurotransmitter binding	12	1.137440758	0.0288188 65	710	102	12549	2.07937034		1	0.922594684	36.50144833
GOTERM_BP_FAT	GO:0048568~embryonic organ development	17	1.611374408	0.0290823 78	727	172	13114	1.782876427		1	0.944845022	40.91970022
GOTERM_BP_FAT	GO:0007423~sensory organ development	21	1.990521327	0.0292731 14	727	229	13114	1.654186914		1	0.940173977	41.12631504
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	22	2.085308057	0.0300801 42	727	244	13114	1.626423433		1	0.939107778	41.99300746
INTERPRO	IPR000483:Cysteine-rich flanking region, C-terminal	11	1.042654028	0.0306530 81	933	88	16090	2.1556806		1	0.937388826	39.94973231
GOTERM_BP_FAT	GO:0051046~regulation of secretion	19	1.800947867	0.0314272 74	727	202	13114	1.696691953		1	0.941082756	43.41295999
SMART	SM00228:PDZ	16	1.516587678	0.0315152 78	530	148	8828	1.800713921	0.999818467		0.883924905	34.34752843
SMART	SM00013:LRRNT	12	1.137440758	0.0320481 7	530	98	8828	2.039584136	0.999843448		0.82664695	34.82063813
SP_PIR_KEYWORD	cleavage on pair of basic	24	2.274881517	0.032395	1037	269	18289	1.573512384	0.999999985		0.559036285	38.13481275

DS	residues										
GOTERM_MF_FAT	GO:0031420~alkali metal ion binding	21	1.990521327	0.032420239	710	227	12549	1.635099584	1	0.927314451	40.06153293
GOTERM_BP_FAT	GO:0048562~embryonic organ morphogenesis	14	1.327014218	0.032773934	727	133	13114	1.898790994	1	0.942883176	44.79957656
UP_SEQ_FEATURE	disulfide bond	176	16.68246445	0.033679725	1037	2715	18267	1.141908501	1	0.989302344	45.57572205
SP_PIR_KEYWORDS	synapse	20	1.895734597	0.033807238	1037	213	18289	1.656004817	0.999999993	0.558655501	39.43852201
GOTERM_BP_FAT	GO:0042472~inner ear morphogenesis	8	0.758293839	0.033972465	727	56	13114	2.576930635	1	0.943820182	46.00663527
GOTERM_MF_FAT	GO:0015267~channel activity	33	3.127962085	0.034249129	710	405	12549	1.440156495	1	0.921220332	41.79710835
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	26	2.464454976	0.034283501	727	307	13114	1.527691777	1	0.940426962	46.31578824
GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	22	2.085308057	0.03463656	727	248	13114	1.600190797	1	0.937255537	46.66468468
GOTERM_BP_FAT	GO:0030030~cell projection organization	30	2.843601896	0.034920432	727	368	13114	1.470531069	1	0.933744372	46.94365628
UP_SEQ_FEATURE	region of interest:Calmodulin-binding	8	0.758293839	0.034967653	1037	55	18267	2.562216183	1	0.988778074	46.84950112
GOTERM_MF_FAT	GO:0022803~passive transmembrane transporter activity	33	3.127962085	0.035326186	710	406	12549	1.436609311	1	0.911143987	42.79709302
GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	21	1.990521327	0.035612877	727	234	13114	1.61884104	1	0.932403878	47.61838184
GOTERM_BP_FAT	GO:0035270~endocrine system development	9	0.853080569	0.036111659	727	69	13114	2.35284971	1	0.930102793	48.09937212
GOTERM_BP_FAT	GO:0010518~positive regulation of phospholipase activity	9	0.853080569	0.036111659	727	69	13114	2.35284971	1	0.930102793	48.09937212
UP_SEQ_FEATURE	site:Reactive bond	7	0.663507109	0.036715758	1037	44	18267	2.80242395	1	0.988936595	48.53344632

UP_SEQ_FEATUR E	topological domain:Extracellular	171	16.20853081	0.0369894 24	1037	2639	18267	1.14141925	1	0.986976589	48.79246601
SMART	SM00082:LRRCT	11	1.042654028	0.0370356 61	530	88	8828	2.082075472	0.999960993	0.815841895	39.09840092
UP_SEQ_FEATUR E	short sequence motif:Selectivity filter	8	0.758293839	0.0380848 99	1037	56	18267	2.516462323	1	0.986236845	49.81704291
GOTERM_MF_FA T	GO:0004857~enzyme inhibitor activity	23	2.180094787	0.0380884 44	710	260	12549	1.563526544	1	0.911702913	45.28870726
GOTERM_CC_FAT	GO:0005882~intermediate filament	17	1.611374408	0.0383906 83	713	171	12337	1.720175849	0.999999961	0.574038009	42.47032225
GOTERM_BP_FAT	GO:0051047~positive regulation of secretion	12	1.137440758	0.0387021 67	727	109	13114	1.985891498	1	0.938097788	50.53115208
INTERPRO	IPR003091:Voltage-dependent potassium channel	6	0.568720379	0.0397529 46	933	33	16090	3.135535418	1	0.966109328	48.54662781
INTERPRO	IPR002190:MAGE protein	6	0.568720379	0.0397529 46	933	33	16090	3.135535418	1	0.966109328	48.54662781
GOTERM_BP_FAT	GO:0016331~morphogenesis of embryonic epithelium	8	0.758293839	0.0401036 55	727	58	13114	2.488070958	1	0.939970098	51.80152328
GOTERM_CC_FAT	GO:0005615~extracellular space	51	4.834123223	0.0403971 46	713	675	12337	1.307333645	0.999999984	0.57519847	44.14261286
SP_PIR_KEYWOR DS	disulfide bond	181	17.1563981	0.0408772 81	1037	2819	18289	1.13238655	1	0.613737705	45.58922179
GOTERM_BP_FAT	GO:0030802~regulation of cyclic nucleotide biosynthetic process	12	1.137440758	0.0409503 01	727	110	13114	1.967837939	1	0.939400534	52.55397415
GOTERM_BP_FAT	GO:0030808~regulation of nucleotide biosynthetic process	12	1.137440758	0.0409503 01	727	110	13114	1.967837939	1	0.939400534	52.55397415
GOTERM_MF_FA T	GO:0019206~nucleoside kinase activity	4	0.379146919	0.0409819 23	710	14	12549	5.049899396	1	0.912924439	47.7895533
SP_PIR_KEYWOR DS	neurotransmitter receptor	8	0.758293839	0.0411534 7	1037	57	18289	2.475291411	1	0.601277886	45.81725248
SP_PIR_KEYWOR DS	voltage-gated ion channel	3	0.28436019	0.0412841 93	1037	6	18289	8.818225651	1	0.588107948	45.92487034

UP_SEQ_FEATUR E	domain:P-type	3	0.28436019	0.0413760 07	1037	6	18267	8.807618129	1	0.988638039	52.78003967
GOTERM_BP_FAT	GO:0007610~behavior	36	3.412322275	0.0417784 55	727	467	13114	1.390549293	1	0.938778906	53.27925217
GOTERM_BP_FAT	GO:0010517~regulation of phospholipase activity	9	0.853080569	0.0417836 47	727	71	13114	2.286572253	1	0.93469262	53.2837657
INTERPRO	IPR002373:cAMP/cGMP- dependent protein kinase	3	0.28436019	0.0430151 38	933	6	16090	8.622722401	1	0.9683418	51.33643093
GOTERM_CC_FAT	GO:0005903~brush border	7	0.663507109	0.0433108 07	713	45	12337	2.691569269	0.999999996	0.584172154	46.49072859
GOTERM_MF_FA T	GO:0004620~phospholipase activity	10	0.947867299	0.0440581 66	710	83	12549	2.129475649	1	0.914916397	50.33081632
INTERPRO	IPR016044:Filament	9	0.853080569	0.0453073 66	933	69	16090	2.249405844	1	0.967896807	53.21107132
GOTERM_CC_FAT	GO:0045111~intermediate filament cytoskeleton	17	1.611374408	0.0458494 61	713	175	12337	1.680857544	0.999999999	0.589221861	48.46151238
GOTERM_MF_FA T	GO:0005254~chloride channel activity	9	0.853080569	0.0461583 53	710	71	12549	2.240448324	1	0.91217218	51.9987765
GOTERM_BP_FAT	GO:0044243~multicellular organismal catabolic process	5	0.473933649	0.0466541 38	727	25	13114	3.607702889	1	0.949460966	57.34155031
GOTERM_BP_FAT	GO:0007215~glutamate signaling pathway	5	0.473933649	0.0466541 38	727	25	13114	3.607702889	1	0.949460966	57.34155031
GOTERM_BP_FAT	GO:0044236~multicellular organismal metabolic process	6	0.568720379	0.0466692 08	727	36	13114	3.006419074	1	0.946046968	57.35357238
GOTERM_BP_FAT	GO:0060042~retina morphogenesis in camera-type eye	4	0.379146919	0.0467077 16	727	15	13114	4.810270518	1	0.942650143	57.38427937
SP_PIR_KEYWOR DS	hydroxylation	9	0.853080569	0.0469037 38	1037	71	18289	2.235606503	1	0.622143983	50.36736403
GOTERM_CC_FAT	GO:0044456~synapse part	22	2.085308057	0.0469862 25	713	246	12337	1.547417872	0.999999999	0.582840887	49.32194503
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	44	4.170616114	0.0474070 93	727	599	13114	1.32503278	1	0.941614638	57.93834805

GOTERM_BP_FAT	GO:0030799~regulation of cyclic nucleotide metabolic process	12	1.137440758	0.0482329 41	727	113	13114	1.915594454	1	0.941056822	58.58385563
SP_PIR_KEYWORDS	Cardiomyopathy	7	0.663507109	0.0482504 79	1037	47	18289	2.626705513	1	0.619438403	51.38028618
INTERPRO	IPR018039:Intermediate filament protein, conserved site	9	0.853080569	0.0486734 55	933	70	16090	2.217271475	1	0.96998279	55.84140969
INTERPRO	IPR001664:Intermediate filament protein	9	0.853080569	0.0486734 55	933	70	16090	2.217271475	1	0.96998279	55.84140969
GOTERM_MF_FAT	GO:0005230~extracellular ligand-gated ion channel activity	9	0.853080569	0.0494770 87	710	72	12549	2.209330986	1	0.915133355	54.5280438
UP_SEQ_FEATURE	domain:PDZ 4	4	0.379146919	0.0496387 38	1037	15	18267	4.697396336	1	0.994412708	59.5082722
GOTERM_MF_FAT	GO:0005520~insulin-like growth factor binding	5	0.473933649	0.0496511 11	710	25	12549	3.534929577	1	0.904179764	54.65716691
UP_SEQ_FEATURE	domain:Ricin B-type lectin	5	0.473933649	0.0502884 38	1037	25	18267	3.523047252	1	0.993668607	59.99701354
UP_SEQ_FEATURE	domain:Collagen-like	6	0.568720379	0.0509417 99	1037	36	18267	2.93587271	1	0.992892104	60.48289034
GOTERM_BP_FAT	GO:0060191~regulation of lipase activity	10	0.947867299	0.0509438 98	727	87	13114	2.073392465	1	0.946785688	60.63771528
GOTERM_BP_FAT	GO:0006928~cell motion	36	3.412322275	0.0509601 57	727	475	13114	1.367129516	1	0.943623408	60.64973802
GOTERM_MF_FAT	GO:0022834~ligand-gated channel activity	13	1.232227488	0.0526007 6	710	126	12549	1.823574782	1	0.905958369	56.79424502
GOTERM_MF_FAT	GO:0015276~ligand-gated ion channel activity	13	1.232227488	0.0526007 6	710	126	12549	1.823574782	1	0.905958369	56.79424502
GOTERM_BP_FAT	GO:0030817~regulation of cAMP biosynthetic process	11	1.042654028	0.0526779 71	727	101	13114	1.964590682	1	0.945902583	61.90064327
GOTERM_BP_FAT	GO:0018149~peptide cross-linking	5	0.473933649	0.0528123 97	727	26	13114	3.468945085	1	0.943208891	61.99693162
INTERPRO	IPR017981:GPCR, family 2-like	8	0.758293839	0.0532179 43	933	59	16090	2.338365397	1	0.974017032	59.17284474

KEGG_PATHWAY	hsa00232:Caffeine metabolism	3	0.28436019	0.0532670 33	280	7	5042	7.717346939	0.999909077	0.95503323	48.71628578
GOTERM_BP_FAT	GO:0051491~positive regulation of filopodium assembly	3	0.28436019	0.0533830 57	727	7	13114	7.730791904	1	0.941895601	62.4031383
GOTERM_BP_FAT	GO:0051489~regulation of filopodium assembly	3	0.28436019	0.0533830 57	727	7	13114	7.730791904	1	0.941895601	62.4031383
GOTERM_BP_FAT	GO:0046033~AMP metabolic process	3	0.28436019	0.0533830 57	727	7	13114	7.730791904	1	0.941895601	62.4031383
GOTERM_BP_FAT	GO:0007216~metabotropic glutamate receptor signaling pathway	3	0.28436019	0.0533830 57	727	7	13114	7.730791904	1	0.941895601	62.4031383
GOTERM_BP_FAT	GO:0001503~ossification	12	1.137440758	0.0535487 73	727	115	13114	1.882279768	1	0.939295163	62.5203282
GOTERM_MF_FAT	GO:0042277~peptide binding	18	1.706161137	0.0539674 8	710	197	12549	1.614942447	1	0.900897168	57.75217342
BIOCARTA	h_no1Pathway:Actions of Nitric Oxide in the Heart	4	0.379146919	0.0543771 51	70	18	1406	4.463492063	0.999262747	0.999262747	47.80695691
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	16	1.516587678	0.0543809 21	727	172	13114	1.678001344	1	0.938870222	63.10360621
GOTERM_BP_FAT	GO:0060193~positive regulation of lipase activity	9	0.853080569	0.0548255 37	727	75	13114	2.164621733	1	0.937208543	63.41172793
BIOCARTA	h_nos1Pathway:Nitric Oxide Signaling Pathway	3	0.28436019	0.0548762 28	70	8	1406	7.532142857	0.999311283	0.973756589	48.12640792
UP_SEQ_FEATURE	DNA-binding region:H-T-H motif winged-type	3	0.28436019	0.0557832 35	1037	7	18267	7.549386968	1	0.994716406	63.91356104
SP_PIR_KEYWORDS	tumor antigen	6	0.568720379	0.0560302 77	1037	37	18289	2.859965076	1	0.662978742	56.86473027
GOTERM_BP_FAT	GO:0006140~regulation of nucleotide metabolic process	12	1.137440758	0.0563481 66	727	116	13114	1.866053218	1	0.939015263	64.44862172
SP_PIR_KEYWORDS	extracellular matrix	21	1.990521327	0.0564043 13	1037	241	18289	1.536786213	1	0.653052492	57.11329741
GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-	13	1.232227488	0.0564242	727	130	13114	1.803851444	1	0.936246211	64.4996969

	mediated signaling			46							
GOTERM_BP_FAT	GO:0015718~monocarboxylic acid transport	7	0.663507109	0.0566034 65	727	50	13114	2.525392022	1	0.933789805	64.61973858
GOTERM_CC_FAT	GO:0045202~synapse	29	2.748815166	0.0577685 54	713	355	12337	1.413480039	1	0.645751156	56.8450638
GOTERM_MF_FAT	GO:0008603~cAMP-dependent protein kinase regulator activity	4	0.379146919	0.0580170 55	710	16	12549	4.418661972	1	0.907184418	60.47514585
GOTERM_BP_FAT	GO:0008016~regulation of heart contraction	9	0.853080569	0.0584494 2	727	76	13114	2.136139868	1	0.936670878	65.83407536
GOTERM_BP_FAT	GO:0030814~regulation of cAMP metabolic process	11	1.042654028	0.0587317 75	727	103	13114	1.92644329	1	0.934629892	66.01631269
SP_PIR_KEYWORDS	cell membrane	138	13.08056872	0.0590679 88	1037	2131	18289	1.142107123	1	0.658468352	58.8452473
GOTERM_MF_FAT	GO:0005198~structural molecule activity	44	4.170616114	0.0593503 27	710	597	12549	1.302654116	1	0.90247741	61.33510232
GOTERM_BP_FAT	GO:0032963~collagen metabolic process	5	0.473933649	0.0593898 75	727	27	13114	3.340465638	1	0.933775581	66.4375079
INTERPRO	IPR003054:Type II keratin	5	0.473933649	0.0605639 69	933	26	16090	3.316431693	1	0.981157871	64.06356146
INTERPRO	IPR000772:Ricin B lectin	5	0.473933649	0.0605639 69	933	26	16090	3.316431693	1	0.981157871	64.06356146
SP_PIR_KEYWORDS	differentiation	35	3.317535545	0.0605844 07	1037	455	18289	1.3566501	1	0.656412454	59.8019084
GOTERM_BP_FAT	GO:0021510~spinal cord development	6	0.568720379	0.0623555 98	727	39	13114	2.775156068	1	0.939759639	68.27522223
GOTERM_BP_FAT	GO:0033555~multicellular organismal response to stress	6	0.568720379	0.0623555 98	727	39	13114	2.775156068	1	0.939759639	68.27522223
GOTERM_MF_FAT	GO:0022836~gated channel activity	25	2.369668246	0.0628644 71	710	305	12549	1.44874163	1	0.906251869	63.51858887
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	31	2.938388626	0.0632625 85	727	405	13114	1.380725797	1	0.939619222	68.81799443
GOTERM_MF_FAT	GO:0005253~anion channel activity	9	0.853080569	0.0642744 56	710	76	12549	2.093050408	1	0.902231944	64.36179478

KEGG_PATHWAY	hsa00591:Linoleic acid metabolism	5	0.473933649	0.06596416	280	28	5042	3.215561224	0.999990842	0.944988879	56.50491886
GOTERM_BP_FAT	GO:0045017~glycerolipid biosynthetic process	9	0.853080569	0.066141519	727	78	13114	2.081367051	1	0.944649983	70.48336121
GOTERM_BP_FAT	GO:0007200~activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger	7	0.663507109	0.066198297	727	52	13114	2.42826156	1	0.942315174	70.51534529
GOTERM_BP_FAT	GO:0006081~cellular aldehyde metabolic process	5	0.473933649	0.066381304	727	28	13114	3.221163293	1	0.94028813	70.61821361
GOTERM_BP_FAT	GO:0015908~fatty acid transport	5	0.473933649	0.066381304	727	28	13114	3.221163293	1	0.94028813	70.61821361
INTERPRO	IPR000215:Protease inhibitor I4, serpin	6	0.568720379	0.066542246	933	38	16090	2.722964969	1	0.984678896	67.63186492
SMART	SM00458:RICIN	5	0.473933649	0.066861324	530	26	8828	3.203193033	0.999999992	0.930003712	59.72127516
GOTERM_MF_FAT	GO:0008188~neuropeptide receptor activity	6	0.568720379	0.066866716	710	39	12549	2.719176598	1	0.902615634	65.86464964
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	17	1.611374408	0.06698752	727	192	13114	1.597160133	1	0.939374407	70.95655282
GOTERM_MF_FAT	GO:0004867~serine-type endopeptidase inhibitor activity	10	0.947867299	0.067267749	710	90	12549	1.963849765	1	0.895310632	66.09178005
PIR_SUPERFAMILY	PIRSF001638:cystatin	3	0.28436019	0.067851919	397	8	7196	6.797229219	1	0.992157423	62.65406302
INTERPRO	IPR001879:GPCR, family 2, extracellular region	5	0.473933649	0.067973915	933	27	16090	3.193600889	1	0.983192672	68.43556433
SP_PIR_KEYWORDS	collagen degradation	4	0.379146919	0.068059614	1037	17	18289	4.149753247	1	0.689125498	64.22246396
BIOCARTA	h_dreampathway:Repression of Pain Sensation by the Transcriptional Regulator DREAM	3	0.28436019	0.068359953	70	9	1406	6.695238095	0.999892103	0.952393047	56.10933641
GOTERM_BP_FAT	GO:0051050~positive	19	1.800947867	0.0696740	727	223	13114	1.536913787	1	0.943713385	72.41218853

	regulation of transport			75							
SP_PIR_KEYWORDS	protease inhibitor	11	1.042654028	0.070186468	1037	104	18289	1.865393888	1	0.689868986	65.39483594
GOTERM_BP_FAT	GO:0048839~inner ear development	9	0.853080569	0.070211206	727	79	13114	2.055020633	1	0.942666745	72.69483329
GOTERM_MF_FAT	GO:0016494~C-X-C chemokine receptor activity	3	0.28436019	0.071140847	710	8	12549	6.627992958	1	0.900360102	68.21377041
GOTERM_MF_FAT	GO:0004372~glycine hydroxymethyltransferase activity	3	0.28436019	0.071140847	710	8	12549	6.627992958	1	0.900360102	68.21377041
SP_PIR_KEYWORDS	cAMP binding	3	0.28436019	0.071487328	1037	8	18289	6.613669238	1	0.68626001	66.09415981
UP_SEQ_FEATURE	domain:HP	3	0.28436019	0.071639865	1037	8	18267	6.605713597	1	0.998589525	73.28617673
INTERPRO	IPR000998:MAM	4	0.379146919	0.071793372	933	17	16090	4.057751718	1	0.984142508	70.48899887
GOTERM_MF_FAT	GO:0042923~neuropeptide binding	6	0.568720379	0.073037712	710	40	12549	2.651197183	1	0.898566125	69.20707974
KEGG_PATHWAY	hsa00340:Histidine metabolism	5	0.473933649	0.073335554	280	29	5042	3.104679803	0.999997619	0.924947525	60.51246489
UP_SEQ_FEATURE	domain:PDZ 1	6	0.568720379	0.074083778	1037	40	18267	2.642285439	1	0.998608455	74.50777061
UP_SEQ_FEATURE	domain:PDZ 2	6	0.568720379	0.074083778	1037	40	18267	2.642285439	1	0.998608455	74.50777061
GOTERM_BP_FAT	GO:0060491~regulation of cell projection assembly	4	0.379146919	0.074167582	727	18	13114	4.008558765	1	0.949395347	74.69407311
GOTERM_BP_FAT	GO:0046717~acid secretion	4	0.379146919	0.074167582	727	18	13114	4.008558765	1	0.949395347	74.69407311
INTERPRO	IPR003128:Villin headpiece	3	0.28436019	0.074360196	933	8	16090	6.467041801	1	0.983856267	71.79777904
SMART	SM00093:SERPIN	6	0.568720379	0.074493889	530	38	8828	2.62999007	0.999999999	0.925953651	63.84198234
GOTERM_CC_FAT	GO:0031253~cell projection	8	0.758293839	0.0746925	713	64	12337	2.162868163	1	0.727953486	66.59114026

	membrane			47							
SMART	SM00008:HormR	5	0.473933649	0.0749374 34	530	27	8828	3.084556254	0.999999999	0.902525285	64.06902853
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	12	1.137440758	0.0751778 69	727	122	13114	1.774280109	1	0.949407778	75.18198192
INTERPRO	IPR001173:Glycosyl transferase, family 2	5	0.473933649	0.0758285 03	933	28	16090	3.079543715	1	0.982560815	72.52173325
INTERPRO	IPR016160:Aldehyde dehydrogenase, conserved site	5	0.473933649	0.0758285 03	933	28	16090	3.079543715	1	0.982560815	72.52173325
SP_PIR_KEYWORDS	membrane	367	34.78672986	0.0759772 21	1037	6079	18289	1.064743811	1	0.698999408	68.40803784
SMART	SM00137:MAM	4	0.379146919	0.0777596 58	530	17	8828	3.919200888	1	0.886679961	65.48311973
GOTERM_MF_FAT	GO:0016646~oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	4	0.379146919	0.0778360 24	710	18	12549	3.927699531	1	0.905904008	71.5916483
GOTERM_MF_FAT	GO:0016702~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	8	0.758293839	0.0779004 99	710	66	12549	2.142381562	1	0.898649795	71.62248036
GOTERM_BP_FAT	GO:0060348~bone development	12	1.137440758	0.0786607 94	727	123	13114	1.759855068	1	0.9542777	76.79683103
SMART	SM00153:VHP	3	0.28436019	0.0789071 06	530	8	8828	6.246226415	1	0.866014855	66.04320923
GOTERM_BP_FAT	GO:0043583~ear development	10	0.947867299	0.0796970 94	727	95	13114	1.898790994	1	0.954283	77.2578248
GOTERM_BP_FAT	GO:0003002~regionalization	17	1.611374408	0.0801176 83	727	197	13114	1.556623074	1	0.953154615	77.44244455
GOTERM_BP_FAT	GO:0048663~neuron fate commitment	6	0.568720379	0.0806625 79	727	42	13114	2.576930635	1	0.952263556	77.67952588
KEGG_PATHWAY	hsa00512:O-Glycan biosynthesis	5	0.473933649	0.0811064 6	280	30	5042	3.001190476	0.999999431	0.908970821	64.36788905

GOTERM_MF_FAT	GO:0022838~substrate specific channel activity	30	2.843601896	0.081306407	710	391	12549	1.356111091	1	0.90161056	73.20738794
GOTERM_BP_FAT	GO:0034614~cellular response to reactive oxygen species	5	0.473933649	0.081576375	727	30	13114	3.006419074	1	0.952072058	78.07184219
GOTERM_MF_FAT	GO:0016701~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	8	0.758293839	0.082980914	710	67	12549	2.110405718	1	0.899432672	73.95586801
GOTERM_MF_FAT	GO:0030594~neurotransmitter receptor activity	10	0.947867299	0.083434258	710	94	12549	1.88028169	1	0.893764505	74.15511508
PIR_SUPERFAMILY	PIRSF005569:ultra-high-sulfur keratin	3	0.28436019	0.084143235	397	9	7196	6.041981528	1	0.994474486	70.83220664
GOTERM_BP_FAT	GO:0051966~regulation of synaptic transmission, glutamatergic	4	0.379146919	0.084595854	727	19	13114	3.797581988	1	0.955628928	79.32240404
GOTERM_BP_FAT	GO:0042220~response to cocaine	4	0.379146919	0.084595854	727	19	13114	3.797581988	1	0.955628928	79.32240404
GOTERM_BP_FAT	GO:0014073~response to tropane	4	0.379146919	0.084595854	727	19	13114	3.797581988	1	0.955628928	79.32240404
GOTERM_BP_FAT	GO:0030574~collagen catabolic process	4	0.379146919	0.084595854	727	19	13114	3.797581988	1	0.955628928	79.32240404
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	25	2.369668246	0.08464752	727	322	13114	1.40050578	1	0.953934875	79.34320475
GOTERM_BP_FAT	GO:0001976~neurological system process involved in regulation of systemic arterial blood pressure	3	0.28436019	0.085071838	727	9	13114	6.012838148	1	0.952884843	79.51328743
GOTERM_BP_FAT	GO:0045176~apical protein localization	3	0.28436019	0.085071838	727	9	13114	6.012838148	1	0.952884843	79.51328743
GOTERM_BP_FAT	GO:0032781~positive regulation of ATPase activity	3	0.28436019	0.085071838	727	9	13114	6.012838148	1	0.952884843	79.51328743
UP_SEQ_FEATURE	transmembrane region	290	27.48815166	0.085155396	1037	4755	18267	1.07432566	1	0.99936863	79.41087353
GOTERM_MF_FAT	GO:0030246~carbohydrate binding	27	2.559241706	0.086005195	710	347	12549	1.375260787	1	0.894417197	75.25834134

KEGG_PATHWAY	hsa00983:Drug metabolism	6	0.568720379	0.0866688 37	280	43	5042	2.512624585	0.999999797	0.889381044	66.91192244
GOTERM_BP_FAT	GO:0034599~cellular response to oxidative stress	6	0.568720379	0.0873357 83	727	43	13114	2.517002015	1	0.955019453	80.39864578
UP_SEQ_FEATUR E	domain:MAGE	5	0.473933649	0.0874684 37	1037	30	18267	2.93587271	1	0.999355845	80.3159234
GOTERM_BP_FAT	GO:0044057~regulation of system process	24	2.274881517	0.0881209 91	727	308	13114	1.405598528	1	0.954614233	80.69718818
GOTERM_MF_FA T	GO:0019958~C-X-C chemokine binding	3	0.28436019	0.0881320 87	710	9	12549	5.891549296	1	0.893800275	76.13755446
GOTERM_MF_FA T	GO:0016861~intramolecular oxidoreductase activity, interconverting aldoses and ketoses	3	0.28436019	0.0881320 87	710	9	12549	5.891549296	1	0.893800275	76.13755446
GOTERM_MF_FA T	GO:0004890~GABA-A receptor activity	4	0.379146919	0.0887093 3	710	19	12549	3.720978503	1	0.888841988	76.37108093
GOTERM_MF_FA T	GO:0002020~protease binding	4	0.379146919	0.0887093 3	710	19	12549	3.720978503	1	0.888841988	76.37108093
UP_SEQ_FEATUR E	site:Reactive site	3	0.28436019	0.0887354 94	1037	9	18267	5.871745419	1	0.99928249	80.79564798
UP_SEQ_FEATUR E	domain:EGF-like 1; calcium-binding	4	0.379146919	0.0895454 23	1037	19	18267	3.708470791	1	0.999175038	81.0964944
GOTERM_CC_FAT	GO:0045211~postsynaptic membrane	13	1.232227488	0.0899276 92	713	135	12337	1.666209548	1	0.781650821	73.57388456
GOTERM_MF_FA T	GO:0005216~ion channel activity	29	2.748815166	0.0903205 99	710	380	12549	1.348854707	1	0.886929216	77.01166465
UP_SEQ_FEATUR E	lipid moiety-binding region:S-palmitoyl cysteine	16	1.516587678	0.0906662 61	1037	181	18267	1.557147957	1	0.999082252	81.50549778
INTERPRO	IPR003150:DNA-binding RFX	3	0.28436019	0.0920333 73	933	9	16090	5.748481601	1	0.991551321	79.43453651
INTERPRO	IPR017857:Coagulation factor, subset, Gla region	3	0.28436019	0.0920333 73	933	9	16090	5.748481601	1	0.991551321	79.43453651
INTERPRO	IPR019794:Peroxidase, active site	3	0.28436019	0.0920333 73	933	9	16090	5.748481601	1	0.991551321	79.43453651

GOTERM_MF_FAT	GO:0019205~nucleobase, nucleoside, nucleotide kinase activity	6	0.568720379	0.093333274	710	43	12549	2.466229938	1	0.889005755	78.16602963
SP_PIR_KEYWORDS	postsynaptic cell membrane	11	1.042654028	0.093888742	1037	110	18289	1.76364513	1	0.767201091	76.25288918
INTERPRO	IPR004182:GRAM	4	0.379146919	0.094025982	933	19	16090	3.630619958	1	0.99097723	80.16151138
GOTERM_BP_FAT	GO:0006813~potassium ion transport	14	1.327014218	0.095506844	727	157	13114	1.60852995	1	0.964014956	83.3029053
GOTERM_BP_FAT	GO:0009126~purine nucleoside monophosphate metabolic process	4	0.379146919	0.095607479	727	20	13114	3.607702889	1	0.962698213	83.33600061
GOTERM_BP_FAT	GO:0009167~purine ribonucleoside monophosphate metabolic process	4	0.379146919	0.095607479	727	20	13114	3.607702889	1	0.962698213	83.33600061
PIR_SUPERFAMILY	PIRSF001630:serpin	5	0.473933649	0.096494189	397	32	7196	2.832178841	1	0.994758849	75.88730868
GOTERM_MF_FAT	GO:0008289~lipid binding	33	3.127962085	0.097024911	710	446	12549	1.307765427	1	0.892747492	79.50661293
GOTERM_BP_FAT	GO:0032956~regulation of actin cytoskeleton organization	9	0.853080569	0.097771471	727	85	13114	1.909960353	1	0.964117323	84.03285652
BIOCARTA	h_extrinsicPathway:Extrinsic Prothrombin Activation Pathway	3	0.28436019	0.098077808	70	11	1406	5.477922078	0.999998353	0.964173647	69.89491176