

**Supplementary Table 3 : Transcriptomic profiling singles out a subgroup of SLE kidney biopsy samples with decreased eGFR**

A cluster of SLE kidney biopsy samples, identified by hierarchical clustering algorithm (Pearson-centered algorithm, Ward's linkage rule) is characterized by the overexpression of 271 transcripts (by moderated t test, with Bonferroni correction for multiple comparisons) compared to the other lupus samples, significantly enriched in the indicated pathways.

**Transcripts**

Identifier	[Control]	[SLE]	Gene Symbol
ILMN_1654319	-0.3232504	1.9405183	HAPLN3
ILMN_1738116	-0.2354067	1.9201676	TMEM119
ILMN_1804601	-0.2589666	1.8242207	DKFZp686O16217
ILMN_1659800	-0.2759814	1.7896557	BCL11A
ILMN_1718936	-0.2632236	1.6821613	LST1
ILMN_1704286	-0.3620017	1.6446545	FXYD5
ILMN_2178226	-0.2631313	1.5874728	KRT86
ILMN_2316236	-0.3898594	1.5715406	HOPX
ILMN_1685403	-0.2286288	1.5471464	MMP7
ILMN_1701424	-0.4379956	1.504757	LAMC2
ILMN_1778977	-0.2593867	1.5005594	TYROBP
ILMN_3307693	-0.9245362	1.479397	WFDC2
ILMN_2325837	-0.4301998	1.4455804	CD3D
ILMN_1770673	-0.2988024	1.427377	AKNA
ILMN_1886655	-0.5120298	1.4127944	TCRVB
ILMN_1715760	-0.2148992	1.4113554	HUAT
ILMN_1727284	-0.1995767	1.3429725	CD4
ILMN_2280548	-0.3113598	1.32024	FYB
ILMN_1769129	-1.2588445	1.3199118	CCL19
ILMN_2254635	-0.901885	1.3150588	ITGAX
ILMN_1659688	-0.3078076	1.3150438	LGALS3BP
ILMN_1731233	-0.3580598	1.314427	GZMH
ILMN_1772359	-0.3015788	1.306691	LAPTM5
ILMN_1777190	-0.212863	1.2945279	CFD
ILMN_2320888	-0.2540839	1.2926085	CXCR4
ILMN_1740015	-0.2876653	1.27568	CD14
ILMN_2232177	-0.5919564	1.2677429	ACTN1
ILMN_1791726	-0.1165403	1.2661247	TUBB3
ILMN_1677505	-0.3786097	1.2465667	CCL21
ILMN_2393765	-1.3157812	1.2446996	IGLL1
ILMN_2192072	-0.4492103	1.2325146	MMP7
ILMN_2088124	-0.6159105	1.2310873	TMEM154
ILMN_2400947	-0.2970516	1.2233969	CELF2
ILMN_1682993	-0.3171521	1.2221096	NGK7
ILMN_1773964	-0.3415281	1.2133846	H1FX
ILMN_1656868	-0.5244166	1.2129158	NPIPL3
ILMN_1659913	-0.2276194	1.2071422	ISG20
ILMN_1700935	-0.5817646	1.2067223	HAS2
ILMN_2109489	-0.3629279	1.1954819	GZMB
ILMN_1719759	-0.4349685	1.1886253	TNC
ILMN_1715508	-0.4731118	1.1747693	NNMT
ILMN_1668039	-0.3205495	1.1702818	GYPC
ILMN_2061043	-0.5361143	1.1639661	CD48
ILMN_1801504	-0.523013	1.1615633	RUNX1
ILMN_3246766	-0.2767946	1.1546525	NPIPL3
ILMN_2366041	-0.6716672	1.1506507	ITM2C
ILMN_1718558	-0.4340115	1.1472871	PARP12
ILMN_2384544	-0.2476885	1.1429716	ADAM15

**Pathways**

Annotation Cluster	Enrichment Score	Count	P_Value	Benjamini	
Annotation Cluster 1	Enrichment Score: 7.58	SP_PIR_KEYWORDS	84	3.80E-13	1.20E-10
		UP_SEQ_FEATURE	84	5.40E-13	5.30E-10
		SP_PIR_KEYWORDS	68	1.90E-08	3.00E-06
		UP_SEQ_FEATURE	66	3.40E-08	1.70E-05
		SP_PIR_KEYWORDS	84	5.70E-07	3.10E-05
		SP_PIR_KEYWORDS	43	2.20E-06	8.90E-05
		GOTERM_CC_FAT	51	2.50E-05	2.00E-03
Annotation Cluster 2	Enrichment Score: 4.94	UP_SEQ_FEATURE	75	5.40E-05	1.70E-02
		GOTERM_BP_FAT	27	3.20E-06	1.90E-03
		GOTERM_BP_FAT	27	3.30E-06	1.40E-03
Annotation Cluster 3	Enrichment Score: 4.58	SP_PIR_KEYWORDS	16	1.40E-04	4.10E-03
		GOTERM_BP_FAT	27	2.80E-07	2.50E-04
		GOTERM_BP_FAT	20	1.20E-04	1.60E-02
Annotation Cluster 4	Enrichment Score: 3.74	GOTERM_BP_FAT	14	5.30E-04	3.10E-02
		SP_PIR_KEYWORDS	16	1.70E-07	1.80E-05
		SP_PIR_KEYWORDS	43	2.20E-06	8.90E-05
		GOTERM_CC_FAT	33	3.90E-06	9.50E-04
		GOTERM_CC_FAT	17	1.20E-05	1.40E-03
		GOTERM_CC_FAT	51	2.50E-05	2.00E-03
		GOTERM_CC_FAT	17	3.00E-05	1.80E-03
		GOTERM_CC_FAT	22	6.50E-04	1.40E-02
		KEGG_PATHWAY	6	1.80E-02	1.10E-01
		GOTERM_CC_FAT	5	2.40E-02	2.80E-01
Annotation Cluster 5	Enrichment Score: 3.62	GOTERM_CC_FAT	6	2.50E-02	2.80E-01
		SP_PIR_KEYWORDS	3	7.60E-02	4.10E-01
		GOTERM_BP_FAT	15	5.50E-05	9.50E-03
		GOTERM_BP_FAT	13	1.60E-04	1.80E-02
		GOTERM_BP_FAT	15	1.70E-04	1.70E-02
		GOTERM_BP_FAT	8	3.60E-04	2.70E-02
		GOTERM_BP_FAT	10	4.80E-04	3.20E-02
Annotation Cluster 6	Enrichment Score: 3.27	GOTERM_BP_FAT	8	6.60E-04	3.50E-02
		GOTERM_BP_FAT	14	2.20E-05	4.80E-03
		GOTERM_BP_FAT	13	1.10E-04	1.50E-02
		GOTERM_BP_FAT	10	1.70E-04	1.70E-02
		GOTERM_BP_FAT	8	3.00E-04	2.50E-02
		GOTERM_BP_FAT	7	3.80E-04	2.70E-02
		GOTERM_BP_FAT	9	5.10E-04	3.20E-02
		GOTERM_BP_FAT	7	6.40E-04	3.70E-02
		GOTERM_BP_FAT	7	6.40E-04	3.70E-02
		GOTERM_BP_FAT	7	9.50E-04	4.60E-02
GOTERM_BP_FAT	6	9.80E-04	4.50E-02		
GOTERM_BP_FAT	7	1.10E-03	5.10E-02		
GOTERM_BP_FAT	5	5.50E-03	1.50E-01		

ILMN_ID	Score	Gene	Annotation Cluster	Enrichment Score	Term	Count	P_Value	Benjamini			
ILMN_1805737	-0.4868437	1.1419221 PFKP	Annotation Cluster 7	Enrichment Score: 2.61	GOTERM_BP_FAT	<a href="#">immunoglobulin mediated immune response</a>	5	6.30E-03	1.50E-01		
ILMN_2114720	-0.2910049	1.1358421 SLPI			SP_PIR_KEYWORDS	<a href="#">immune response</a>	15	4.20E-07	3.30E-05		
ILMN_1695851	-0.2123577	1.1309191 PARVG			KEGG_PATHWAY	<a href="#">Cell adhesion molecules (CAMs)</a>	12	2.40E-05	2.40E-03		
ILMN_1762594	-0.2364039	1.1272446 NOD2			BIOCARTA	<a href="#">B Lymphocyte Cell Surface Molecules</a>	5	8.60E-05	2.80E-03		
ILMN_1758895	-0.5701722	1.1245126 CTSK			UP_SEQ_FEATURE	domain:Ig-like C1-type	6	1.00E-04	2.40E-02		
ILMN_1687301	-0.6841173	1.1204166 VCAN			SP_PIR_KEYWORDS	<a href="#">heterodimer</a>	8	2.10E-04	5.50E-03		
ILMN_1678827	-0.1769902	1.0991265 SPDYE7P			KEGG_PATHWAY	<a href="#">Allograft rejection</a>	6	4.40E-04	1.10E-02		
ILMN_1695404	-0.2068565	1.0963432 LY6E			BIOCARTA	<a href="#">Bystander B Cell Activation</a>	4	6.80E-04	1.30E-02		
ILMN_1680453	-0.6901841	1.0810174 ITM2C				<a href="#">Immunoglobulin/major histocompatibility complex, conserved site</a>	7	8.10E-04	1.90E-01		
ILMN_1747593	-0.5384941	1.079707 ISLR			GOTERM_BP_FAT	<a href="#">antigen processing and presentation</a>	7	9.50E-04	4.60E-02		
ILMN_2387496	-0.6742429	1.0743917 COAS3			UP_SEQ_FEATURE	region of interest:Connecting peptide	5	1.00E-03	1.50E-01		
ILMN_1749372	-0.2665476	1.0736879 GGT5			UP_SEQ_FEATURE	region of interest:Alpha-2	4	1.60E-03	2.00E-01		
ILMN_1767556	-0.3998735	1.0715685 C10orf10			UP_SEQ_FEATURE	region of interest:Alpha-1	4	1.60E-03	2.00E-01		
ILMN_1736178	-0.4081671	1.068581 AEBP1			INTERPRO	<a href="#">Immunoglobulin C1-set</a>	6	1.70E-03	2.50E-01		
ILMN_1772218	-0.4511487	1.0665296 HLA-DPA1			GOTERM_MF_FAT	<a href="#">MHC class II receptor activity</a>	4	1.90E-03	2.10E-01		
ILMN_2408987	-1.0307062	1.0658907 SMARCD3			KEGG_PATHWAY	<a href="#">Autoimmune thyroid disease</a>	6	2.20E-03	4.40E-02		
ILMN_2376205	-0.7288805	1.0646546 LTB			BIOCARTA	<a href="#">Antigen Dependent B Cell Activation</a>	4	2.50E-03	4.10E-02		
ILMN_2376204	-0.3408106	1.0642538 LTB			SMART	<a href="#">IGc1</a>	6	4.80E-03	4.90E-01		
ILMN_1750805	-0.318508	1.0515127 ARHGAP30			KEGG_PATHWAY	<a href="#">Graft-versus-host disease</a>	5	5.30E-03	7.40E-02		
ILMN_1752755	-0.7749436	1.049824 VWF			SP_PIR_KEYWORDS	<a href="#">mhc ii</a>	4	5.60E-03	8.10E-02		
ILMN_2400935	-0.4563044	1.0462416 TAGLN			GOTERM_BP_FAT	<a href="#">antigen processing and presentation of peptide antigen</a>	4	6.40E-03	1.50E-01		
ILMN_1799062	-0.4098382	1.0438011 NFKB2			KEGG_PATHWAY	<a href="#">Type I diabetes mellitus</a>	5	6.90E-03	8.50E-02		
ILMN_1769201	-0.4936057	1.0263821 ELF3			GOTERM_CC_FAT	<a href="#">MHC protein complex</a>	5	8.40E-03	1.30E-01		
ILMN_1708858	-0.7217799	1.0184444 CSNK1E			KEGG_PATHWAY	<a href="#">Systemic lupus erythematosus</a>	7	9.10E-03	9.90E-02		
ILMN_1798181	-0.4995381	1.0047315 IRF7			KEGG_PATHWAY	<a href="#">Viral myocarditis</a>	6	9.20E-03	9.00E-02		
ILMN_2353202	-0.5386101	1.0010649 PTK7		<a href="#">antigen processing and presentation of peptide or polysaccharide antigen via MHC class II</a>	4	1.00E-02	2.10E-01				
ILMN_1803686	-0.3430935	1.0008456 ADA	KEGG_PATHWAY	<a href="#">Intestinal immune network for IgA production</a>	5	1.20E-02	8.90E-02				
ILMN_1653652	-0.3883707	1.0007647 PTPRC	KEGG_PATHWAY	<a href="#">Asthma</a>	4	1.50E-02	1.10E-01				
ILMN_2413779	-0.4982294	0.9999508 SEZ6L2	KEGG_PATHWAY	<a href="#">Antigen processing and presentation</a>	6	1.70E-02	1.10E-01				
ILMN_1778668	-0.3758617	0.99820423 TAGLN	BIOCARTA	<a href="#">Antigen Processing and Presentation</a>	3	2.30E-02	1.90E-01				
ILMN_1744487	-0.5831665	0.9951158 C1QTNF5	INTERPRO	<a href="#">MHC class II, alpha/beta chain, N-terminal</a>	3	3.10E-02	6.40E-01				
ILMN_2261416	-0.3355521	0.99143887 CD3D	GOTERM_CC_FAT	<a href="#">MHC class II protein complex</a>	3	6.20E-02	5.10E-01				
ILMN_1765649	-0.2809076	0.9906851 IRF3	PIR_SUPERFAMILY	PIRSF001991:class II histocompatibility antigen	3	6.30E-02	8.20E-01				
ILMN_1745148	-0.4152842	0.9902657 ZNFX1	BIOCARTA	<a href="#">Th1/Th2 Differentiation</a>	3	8.30E-02	4.80E-01				
ILMN_2117508	-0.4875161	0.9897423 CTHRC1	Annotation Cluster 8	Enrichment Score: 2.53	SP_PIR_KEYWORDS	<a href="#">transmembrane protein</a>	25	5.70E-07	3.60E-05		
ILMN_2125747	-0.2444001	0.9888768 CORO1A			GOTERM_CC_FAT	<a href="#">integral to plasma membrane</a>	35	4.70E-05	2.30E-03		
ILMN_1785005	-0.3391531	0.98682004 NCF4			GOTERM_CC_FAT	<a href="#">plasma membrane part</a>	53	6.70E-05	2.70E-03		
ILMN_1717793	-0.4363792	0.9829914 C19orf33			GOTERM_CC_FAT	<a href="#">intrinsic to plasma membrane</a>	35	7.40E-05	2.60E-03		
ILMN_1676099	-0.1844222	0.98020583 SPON2			GOTERM_CC_FAT	<a href="#">plasma membrane</a>	75	5.70E-04	1.40E-02		
ILMN_1768311	-0.2497203	0.97880334 NPIPL3			UP_SEQ_FEATURE	topological domain:Extracellular	49	2.30E-03	2.20E-01		
ILMN_1775762	-0.2994535	0.975834 GNAI2			SP_PIR_KEYWORDS	<a href="#">membrane</a>	93	4.90E-03	7.50E-02		
ILMN_1689968	-0.412196	0.97220707 PLEKHO2			UP_SEQ_FEATURE	topological domain:Cytoplasmic	53	2.20E-02	6.80E-01		
ILMN_1687358	-0.2986337	0.9660672 Tmprss4			SP_PIR_KEYWORDS	<a href="#">transmembrane</a>	70	5.90E-02	3.60E-01		
ILMN_1704294	-0.2695893	0.96394974 CDH3			UP_SEQ_FEATURE	transmembrane region	69	7.00E-02	9.10E-01		
ILMN_1778319	-0.3999426	0.95954514 DMKN			SP_PIR_KEYWORDS	<a href="#">receptor</a>	26	7.70E-02	4.00E-01		
ILMN_1662799	-0.2291535	0.95948136 GPSM3			GOTERM_CC_FAT	<a href="#">integral to membrane</a>	77	4.40E-01	9.30E-01		
ILMN_1723978	-0.5471423	0.9585848 LGALS1			GOTERM_CC_FAT	<a href="#">intrinsic to membrane</a>	78	5.40E-01	9.50E-01		
ILMN_1673357	-0.334264	0.95752394 SLA2			Annotation Cluster 9	Enrichment Score: 2.17	SP_PIR_KEYWORDS	<a href="#">protein complex assembly</a>	17	1.60E-03	6.30E-02
ILMN_1730670	-0.4762125	0.95550716 FSTL3					GOTERM_BP_FAT	<a href="#">protein complex biogenesis</a>	17	1.60E-03	6.30E-02
ILMN_1691662	-0.2668986	0.95518255 LOC100101266					GOTERM_BP_FAT	<a href="#">macromolecular complex assembly</a>	18	9.70E-03	2.00E-01
ILMN_1778941	-0.400535	0.95327836 HNF1B					GOTERM_BP_FAT	<a href="#">macromolecular complex subunit organization</a>	18	1.80E-02	2.70E-01
ILMN_2309848	-0.6369321	0.949838 FXYD5					GOTERM_BP_FAT	<a href="#">protein oligomerization</a>	7	3.20E-02	4.00E-01
ILMN_2354334	-0.4306184	0.9450449 ATXN2L									
ILMN_1768595	-0.4287379	0.9405392 DLG4									
ILMN_2358652	-0.3726217	0.9391262 NXF1									

ILMN_ID	Correlation	Gene	Annotation Cluster 10	Enrichment Score: 2.15	Count	P_Value	Benjamini
ILMN_2206746	-0.3115692	0.9350952 BGN					
ILMN_1751161	-0.1818679	0.9343799 COL7A1	BIOCARTA	<a href="#">Lck and Fyn tyrosine kinases in initiation of TCR Activation</a>	6	2.70E-06	2.60E-04
ILMN_2375319	-0.2491265	0.9336667 RASGRP2	GOTERM_BP_FAT	<a href="#">T cell selection</a>	6	4.50E-06	1.60E-03
ILMN_2176063	-0.3155814	0.93324673 FCGR1C	GOTERM_BP_FAT	<a href="#">T cell activation</a>	11	8.80E-06	2.50E-03
ILMN_2367384	-0.5173004	0.93168837 EPHB2	GOTERM_BP_FAT	<a href="#">cell activation</a>	16	9.40E-06	2.30E-03
				<a href="#">Activation of Csk by cAMP-dependent Protein Kinase Inhibits</a>			
ILMN_1727271	-0.3755743	0.9295296 WARS	BIOCARTA	<a href="#">Signaling through the T Cell Receptor</a>	6	3.20E-05	1.60E-03
ILMN_1770454	-0.4362049	0.9271239 AGRN	KEGG_PATHWAY	<a href="#">Primary immunodeficiency</a>	7	3.40E-05	1.70E-03
ILMN_2208903	-0.2595646	0.9267303 CD52	GOTERM_BP_FAT	<a href="#">regulation of peptidyl-tyrosine phosphorylation</a>	8	3.80E-05	7.40E-03
ILMN_1685625	-0.5453749	0.92595446 UCP2	GOTERM_BP_FAT	<a href="#">lymphocyte activation</a>	12	9.20E-05	1.40E-02
ILMN_1711994	-0.4643634	0.9215085 TCIRG1	GOTERM_BP_FAT	<a href="#">positive regulation of immune system process</a>	13	1.10E-04	1.50E-02
ILMN_1791057	-0.2764992	0.920075 IFNAR2	GOTERM_BP_FAT	<a href="#">leukocyte activation</a>	13	1.20E-04	1.50E-02
ILMN_2085862	-0.5261843	0.9159903 SLC15A3	BIOCARTA	<a href="#">T Helper Cell Surface Molecules</a>	5	1.30E-04	3.10E-03
ILMN_2070052	-0.3671393	0.9148916 NPIPL3	GOTERM_BP_FAT	<a href="#">regulation of calcium-mediated signaling</a>	5	1.40E-04	1.60E-02
ILMN_1679880	-0.3090046	0.91471004 THOC6	GOTERM_BP_FAT	<a href="#">positive regulation of immune response</a>	10	1.70E-04	1.70E-02
ILMN_3243664	-0.4874971	0.91295207 NPIPL3	GOTERM_BP_FAT	<a href="#">hemopoietic or lymphoid organ development</a>	13	2.40E-04	2.20E-02
ILMN_2163723	-0.4142269	0.9102357 KRT7	GOTERM_BP_FAT	<a href="#">T cell differentiation</a>	7	2.60E-04	2.20E-02
ILMN_3243238	-0.2350038	0.90686095 TPSAB1	GOTERM_BP_FAT	<a href="#">activation of immune response</a>	8	3.00E-04	2.50E-02
ILMN_1781626	-0.6013486	0.90442723 C1S	GOTERM_CC_FAT	<a href="#">cell surface</a>	15	4.10E-04	1.20E-02
ILMN_1700541	-0.3621139	0.903176 FBLN1	GOTERM_BP_FAT	<a href="#">immune system development</a>	13	4.20E-04	2.90E-02
ILMN_2206098	-0.3154438	0.9030856 ATG10	GOTERM_BP_FAT	<a href="#">lymphocyte differentiation</a>	8	5.20E-04	3.20E-02
ILMN_2405009	-0.6482333	0.9002332 C1orf151	GOTERM_CC_FAT	<a href="#">T cell receptor complex</a>	4	5.50E-04	1.50E-02
ILMN_1675979	-0.2072399	0.8990485 RBMS3	GOTERM_BP_FAT	<a href="#">thymic T cell selection</a>	4	6.50E-04	3.60E-02
ILMN_2143685	-0.5237997	0.89562464 CLDN7	GOTERM_CC_FAT	<a href="#">external side of plasma membrane</a>	10	6.70E-04	1.40E-02
ILMN_3237946	-0.36541	0.8955296 PXDN	BIOCARTA	<a href="#">Bystander B Cell Activation</a>	4	6.80E-04	1.30E-02
				<a href="#">Severe combined immunodeficiency, T cell-negative, B-</a>			
				<a href="#">cell/natural killer-cell positive</a>			
ILMN_2059549	-0.3507316	0.89245695 SYK	OMIM_DISEASE	<a href="#">regulation of cellular protein metabolic process</a>	3	7.30E-04	1.10E-01
ILMN_1780663	-0.20952	0.890468 KLHL30	GOTERM_BP_FAT	<a href="#">negative regulation of immune system process</a>	17	8.00E-04	4.00E-02
ILMN_1786823	-0.4492833	0.88830346 ICAM2	GOTERM_BP_FAT	<a href="#">regulation of lymphocyte activation</a>	7	9.50E-04	4.60E-02
ILMN_1688780	-0.2806633	0.8874346 S100A4	GOTERM_BP_FAT	<a href="#">immune response-regulating signal transduction</a>	9	9.70E-04	4.60E-02
ILMN_1666819	-0.2121657	0.88143635 PHLDB1	GOTERM_BP_FAT	<a href="#">receptor complex</a>	6	9.80E-04	4.50E-02
ILMN_1711566	-0.6160435	0.87931806 TIMP1	GOTERM_CC_FAT	<a href="#">positive regulation of calcium-mediated signaling</a>	8	1.30E-03	2.30E-02
ILMN_1761788	-0.318937	0.8782567 MOXD1	GOTERM_BP_FAT	<a href="#">hemopoiesis</a>	4	1.50E-03	6.40E-02
ILMN_1815895	-0.3069491	0.8761135 HLA-DRB1	GOTERM_BP_FAT	<a href="#">regulation of leukocyte activation</a>	11	1.50E-03	6.50E-02
ILMN_1782057	-0.3002019	0.8751354 ATP8B2	GOTERM_BP_FAT	<a href="#">positive regulation of lymphocyte activation</a>	9	2.00E-03	7.70E-02
ILMN_1691290	-0.3353199	0.87388796 CELSR3	GOTERM_BP_FAT	<a href="#">leukocyte differentiation</a>	7	2.10E-03	7.90E-02
ILMN_2049536	-0.3740616	0.8712451 TRPV2	GOTERM_BP_FAT	<a href="#">regulation of protein modification process</a>	8	2.10E-03	7.80E-02
ILMN_1807972	-0.2756432	0.8699051 MICAL1	GOTERM_BP_FAT	<a href="#">Antigen Dependent B Cell Activation</a>	12	2.50E-03	8.80E-02
ILMN_1751034	-0.3884175	0.8682534 ITPRIPL2	BIOCARTA	<a href="#">T Cytotoxic Cell Surface Molecules</a>	4	2.50E-03	4.10E-02
ILMN_1659905	-0.4851455	0.86781186 FKBP10	BIOCARTA	<a href="#">immune response-regulating cell surface receptor signaling pathway</a>	4	2.50E-03	4.10E-02
				<a href="#">regulation of protein amino acid phosphorylation</a>			
ILMN_1782538	-0.4386903	0.8672385 VIM	GOTERM_BP_FAT	<a href="#">regulation of cell activation</a>	5	2.50E-03	8.80E-02
ILMN_1705783	-0.1545213	0.8622637 NXF1	GOTERM_BP_FAT	<a href="#">positive regulation of leukocyte activation</a>	9	2.60E-03	8.90E-02
ILMN_3203186	-0.2641656	0.8597576 AL543610	GOTERM_BP_FAT	<a href="#">positive thymic T cell selection</a>	9	2.80E-03	9.30E-02
ILMN_1765446	-0.342277	0.8553318 EMP3	GOTERM_BP_FAT	<a href="#">positive regulation of peptidyl-tyrosine phosphorylation</a>	7	3.30E-03	1.10E-01
ILMN_1800354	-0.76649	0.854432 CST3	GOTERM_BP_FAT	<a href="#">positive regulation of T cell activation</a>	3	3.70E-03	1.20E-01
ILMN_1703692	-0.318653	0.8499179 TUBB	GOTERM_BP_FAT	<a href="#">positive regulation of cell activation</a>	5	3.80E-03	1.20E-01
ILMN_1724994	-0.3724864	0.8418111 COL4A2	GOTERM_BP_FAT	<a href="#">Hematopoietic cell lineage</a>	7	4.20E-03	1.20E-01
ILMN_2366330	-0.2997862	0.83980304 FERMT3	GOTERM_BP_FAT	<a href="#">CTL mediated immune response against target cells</a>	7	4.60E-03	7.60E-02
ILMN_2169801	-0.2454689	0.83863986 TPSAB1	KEGG_PATHWAY	<a href="#">negative thymic T cell selection</a>	7	4.90E-03	6.80E-02
ILMN_2390299	-0.5079346	0.8307578 PSMB8	BIOCARTA	<a href="#">regulation of B cell activation</a>	4	4.90E-03	6.80E-02
ILMN_1799120	-0.2293101	0.83003724 WFDC2	GOTERM_BP_FAT	<a href="#">positive regulation of alpha-beta T cell activation</a>	3	4.90E-03	1.40E-01
ILMN_1670305	-1.0948417	0.8281291 SERPING1	GOTERM_BP_FAT	<a href="#">immune response-activating signal transduction</a>	5	5.10E-03	1.40E-01
ILMN_2226955	-0.2938926	0.8268525 VOPIP1	GOTERM_BP_FAT	<a href="#">regulation of lymphocyte proliferation</a>	4	5.20E-03	1.40E-01
ILMN_1778401	-0.4915565	0.82583493 HLA-B	GOTERM_BP_FAT	<a href="#">T cell differentiation in the thymus</a>	5	5.50E-03	1.50E-01
ILMN_3236021	-0.3892692	0.824837 ANKRD36	GOTERM_BP_FAT		6	5.60E-03	1.50E-01
ILMN_1716563	-0.2985041	0.8247995 PRKCB	GOTERM_BP_FAT		4	5.80E-03	1.50E-01

ILMN_1665943	-0.2437771	0.8244704	MAP4K1	GOTERM_BP_FAT	<a href="#">regulation of leukocyte proliferation</a>	6	5.90E-03	1.50E-01
ILMN_1779257	-0.3663034	0.8213204	CD40	GOTERM_BP_FAT	<a href="#">regulation of mononuclear cell proliferation</a>	6	5.90E-03	1.50E-01
ILMN_1684306	-0.4423175	0.8178873	S100A4	GOTERM_BP_FAT	<a href="#">positive T cell selection</a>	3	6.30E-03	1.50E-01
ILMN_1713901	-0.2925592	0.81592023	KDELR3	GOTERM_BP_FAT	<a href="#">negative T cell selection</a>	3	6.30E-03	1.50E-01
ILMN_1785061	-0.2745637	0.8151372	EPH82	GOTERM_BP_FAT	<a href="#">positive regulation of alpha-beta T cell proliferation</a>	3	6.30E-03	1.50E-01
ILMN_2111739	-0.4774336	0.8130309	MAN2C1	GOTERM_BP_FAT	<a href="#">positive regulation of lymphocyte proliferation</a>	5	6.70E-03	1.60E-01
ILMN_2408400	-0.2415248	0.81145334	NSUN5	GOTERM_BP_FAT	<a href="#">positive regulation of mononuclear cell proliferation</a>	5	7.10E-03	1.60E-01
ILMN_1666078	-0.2263312	0.80954427	HLA-H	GOTERM_BP_FAT	<a href="#">positive regulation of leukocyte proliferation</a>	5	7.10E-03	1.60E-01
ILMN_2058251	-0.3064233	0.80710375	VIM	GOTERM_BP_FAT	<a href="#">positive regulation of T cell differentiation</a>	4	9.30E-03	2.00E-01
ILMN_2062468	-0.5679551	0.8070511	IGFBP7	BIOCARTA	<a href="#">The Co-Stimulatory Signal During T-cell Activation</a>	4	9.80E-03	1.10E-01
ILMN_1794707	-0.354936	0.80371445	ATHL1	GOTERM_BP_FAT	<a href="#">positive regulation of B cell activation</a>	4	1.00E-02	2.10E-01
ILMN_1805750	-0.39717	0.79880387	IFITM3	GOTERM_BP_FAT	<a href="#">antigen receptor-mediated signaling pathway</a>	4	1.00E-02	2.10E-01
ILMN_1735148	-0.3728589	0.79594487	SEC24B	GOTERM_BP_FAT	<a href="#">regulation of humoral immune response</a>	3	1.10E-02	2.20E-01
ILMN_1808777	-0.3808807	0.79474026	EHD2	GOTERM_BP_FAT	<a href="#">positive regulation of cell proliferation</a>	13	1.20E-02	2.20E-01
ILMN_1689004	-0.4236876	0.7932473	TNFRSF12A	GOTERM_BP_FAT	<a href="#">regulation of phosphorylation</a>	14	1.20E-02	2.20E-01
ILMN_1785272	-0.4044341	0.79318005	COL1A2	GOTERM_BP_FAT	<a href="#">positive regulation of lymphocyte differentiation</a>	4	1.20E-02	2.20E-01
ILMN_1789599	-0.6776331	0.7889098	C1orf151	GOTERM_BP_FAT	<a href="#">regulation of cytokine production</a>	8	1.20E-02	2.20E-01
ILMN_2098126	-0.33206	0.7836308	CCL5	GOTERM_BP_FAT	<a href="#">regulation of alpha-beta T cell activation</a>	4	1.30E-02	2.30E-01
ILMN_1713636	-0.3276164	0.7820336	S100A6	GOTERM_BP_FAT	<a href="#">regulation of alpha-beta T cell proliferation</a>	3	1.30E-02	2.30E-01
ILMN_1720287	-0.2498446	0.7791793	E4F1	GOTERM_MF_FAT	<a href="#">protein kinase binding</a>	7	1.40E-02	3.50E-01
ILMN_1690125	-0.4682108	0.77619785	PDLM7	GOTERM_BP_FAT	<a href="#">positive regulation of protein modification process</a>	8	1.40E-02	2.50E-01
ILMN_1747195	-0.5296944	0.77611643	PSMB8	GOTERM_BP_FAT	<a href="#">positive regulation of cellular protein metabolic process</a>	9	1.50E-02	2.50E-01
ILMN_1712545	-0.3020494	0.7758006	S100A3	GOTERM_BP_FAT	<a href="#">regulation of phosphorus metabolic process</a>	14	1.60E-02	2.60E-01
ILMN_1730777	-0.3567672	0.77183926	KRT19	GOTERM_BP_FAT	<a href="#">regulation of phosphate metabolic process</a>	14	1.60E-02	2.60E-01
					<a href="#">immune response-activating cell surface receptor signaling pathway</a>	4	1.60E-02	2.60E-01
ILMN_1671295	-0.2948444	0.77169406	MST151	GOTERM_BP_FAT	<a href="#">acid</a>	3	1.70E-02	1.60E-01
ILMN_1653220	-0.2644714	0.7711403	PITPNM1	SP_PIR_KEYWORDS	<a href="#">regulation of MAPKKK cascade</a>	6	1.70E-02	2.70E-01
ILMN_1705750	-0.4122929	0.7699518	TGM2	GOTERM_BP_FAT	<a href="#">Antigen processing and presentation</a>	6	1.70E-02	1.10E-01
ILMN_3248247	-0.3075986	0.76758534	LOC349114	KEGG_PATHWAY	<a href="#">HIV Induced T Cell Apoptosis</a>	3	1.90E-02	1.70E-01
ILMN_1654246	-0.6002158	0.7673532	SIRT6	BIOCARTA	<a href="#">positive regulation of protein metabolic process</a>	9	1.90E-02	2.80E-01
ILMN_1815500	-0.3069432	0.7641663	ITPR3	GOTERM_BP_FAT	<a href="#">protein amino acid phosphorylation</a>	17	2.10E-02	3.10E-01
ILMN_1787109	-0.5007137	0.76132065	CLK2	GOTERM_BP_FAT	<a href="#">regulation of T cell activation</a>	6	2.20E-02	3.20E-01
ILMN_1719449	-0.3440301	0.754508	DCLK2	GOTERM_BP_FAT	<a href="#">IL 5 Signaling Pathway</a>	3	2.30E-02	1.90E-01
ILMN_1815057	-0.3384102	0.75351226	PDGFRB	BIOCARTA	<a href="#">activation of MAPK activity</a>	5	2.60E-02	3.50E-01
ILMN_2155719	-0.5270782	0.7532077	NBPFL	GOTERM_BP_FAT	<a href="#">positive regulation of cytokine biosynthetic process</a>	4	2.80E-02	3.60E-01
ILMN_1777342	-0.2784544	0.75301546	PREX1	GOTERM_BP_FAT	<a href="#">positive regulation of B cell proliferation</a>	3	3.00E-02	3.80E-01
ILMN_1811702	-0.4603844	0.7490145	GRN	GOTERM_BP_FAT	<a href="#">protein kinase cascade</a>	11	3.10E-02	3.90E-01
ILMN_1705602	-0.4110136	0.7484236	KLHL17	GOTERM_BP_FAT	<a href="#">kinase binding</a>	7	3.20E-02	4.80E-01
ILMN_1651767	-0.3164083	0.7468634	MKL1	GOTERM_MF_FAT	<a href="#">regulation of T cell differentiation</a>	4	3.20E-02	4.00E-01
ILMN_1895548	-0.2717167	0.7460645	AKO21726	GOTERM_BP_FAT	<a href="#">positive regulation of protein amino acid phosphorylation</a>	5	3.40E-02	4.10E-01
ILMN_1780806	-0.3624143	0.7455973	ANKRD36B	GOTERM_BP_FAT	<a href="#">positive regulation of protein kinase activity</a>	8	3.40E-02	4.00E-01
ILMN_3228688	-0.582792	0.74362123	HLA-DRB1	GOTERM_BP_FAT	<a href="#">cell proliferation</a>	12	3.70E-02	4.30E-01
ILMN_1738675	-0.2855184	0.7427395	PTPN6	GOTERM_BP_FAT	<a href="#">regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains</a>	4	3.90E-02	4.40E-01
ILMN_2090105	-0.9173182	0.7417683	TAGLN2	GOTERM_BP_FAT	<a href="#">positive regulation of kinase activity</a>	8	4.00E-02	4.40E-01
ILMN_1752526	-0.308724	0.73536175	RNF144B	GOTERM_BP_FAT	<a href="#">MAPKKK cascade</a>	7	4.10E-02	4.50E-01
ILMN_2101885	-0.3070515	0.73364246	TUBB	GOTERM_BP_FAT	<a href="#">regulation of adaptive immune response</a>	4	4.10E-02	4.40E-01
ILMN_1675709	-0.2769983	0.7305087	ARFGAP1	GOTERM_BP_FAT	<a href="#">regulation of B cell mediated immunity</a>	3	4.20E-02	4.50E-01
ILMN_1803988	-0.3516586	0.72845715	MCL1	GOTERM_BP_FAT	<a href="#">regulation of immunoglobulin mediated immune response</a>	3	4.20E-02	4.50E-01
ILMN_1708025	-0.3238424	0.7281853	RBPMS	GOTERM_BP_FAT	<a href="#">positive regulation of phosphorylation</a>	5	4.40E-02	4.60E-01
ILMN_3246005	-0.3095196	0.72722805	KDM5B	GOTERM_BP_FAT	<a href="#">positive regulation of transferase activity</a>	8	4.70E-02	4.70E-01
ILMN_1691717	-0.3052667	0.72658294	RHBDF2	GOTERM_BP_FAT	<a href="#">T cell receptor signaling pathway</a>	6	4.70E-02	2.10E-01
ILMN_1807493	-0.4520136	0.7222337	ACVRL1	KEGG_PATHWAY	<a href="#">positive regulation of phosphate metabolic process</a>	5	4.80E-02	4.80E-01
ILMN_1727043	-0.2914142	0.721914	GLT25D1	GOTERM_BP_FAT	<a href="#">positive regulation of phosphorus metabolic process</a>	5	4.80E-02	4.80E-01
ILMN_1814917	-0.3462726	0.72037286	TLE2	GOTERM_BP_FAT	<a href="#">IL 17 Signaling Pathway</a>	3	5.00E-02	3.40E-01
ILMN_1652631	-0.5696183	0.71945685	GLIPR2	BIOCARTA				

ILMN_1689655	-0.352833	0.7193123	HLA-DRA	GOTERM_BP_FAT	<a href="#">regulation of immune effector process</a>	5	5.00E-02	4.80E-01
ILMN_2157441	-0.3784043	0.7175189	HLA-DRA	GOTERM_BP_FAT	<a href="#">regulation of leukocyte mediated immunity</a>	4	5.10E-02	4.90E-01
ILMN_3229210	-0.3558461	0.71513367	FLJ45340	GOTERM_BP_FAT	<a href="#">positive regulation of MAP kinase activity</a>	5	5.10E-02	4.90E-01
ILMN_1779010	-0.3212784	0.71320313	MAP3K3	GOTERM_BP_FAT	<a href="#">negative regulation of cell communication</a>	8	5.40E-02	5.00E-01
ILMN_1765021	-0.4371012	0.7113927	TOP3B	GOTERM_BP_FAT	<a href="#">regulation of lymphocyte differentiation</a>	4	5.50E-02	5.00E-01
ILMN_2380237	-0.3958364	0.71032566	C1QTNF1	GOTERM_BP_FAT	<a href="#">regulation of B cell proliferation</a>	3	5.60E-02	5.00E-01
					<a href="#">positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains</a>	3	6.30E-02	5.40E-01
ILMN_2278729	-0.3459377	0.7091275	EIF3B	GOTERM_BP_FAT	<a href="#">positive regulation of adaptive immune response</a>	3	6.70E-02	5.50E-01
ILMN_2375992	-0.344336	0.7083419	SPINT1	GOTERM_BP_FAT	<a href="#">regulation of cytokine biosynthetic process</a>	4	8.10E-02	6.10E-01
ILMN_3230608	-0.4429316	0.7077526	NBPF14	GOTERM_BP_FAT	<a href="#">negative regulation of signal transduction</a>	7	8.30E-02	6.10E-01
ILMN_2371911	-0.9583868	0.7015006	MUC1	GOTERM_BP_FAT	<a href="#">B cell activation</a>	4	8.60E-02	6.20E-01
ILMN_1736567	-0.5390354	0.7010446	CD74	GOTERM_BP_FAT	<a href="#">enzyme binding</a>	12	8.80E-02	7.10E-01
ILMN_1668748	-0.3158949	0.70089024	MED15	GOTERM_MF_FAT	<a href="#">positive regulation of T cell proliferation</a>	3	9.90E-02	6.50E-01
ILMN_1811117	-0.3808893	0.69952255	DKFZp667P0924	GOTERM_BP_FAT	<a href="#">positive regulation of catalytic activity</a>	12	1.00E-01	6.50E-01
ILMN_1703593	-0.394547	0.6987069	BAIAP2L1	GOTERM_BP_FAT	<a href="#">regulation of protein kinase activity</a>	9	1.00E-01	6.50E-01
ILMN_1778111	-0.3320264	0.69664574	FLJ45340	GOTERM_BP_FAT	<a href="#">positive regulation of molecular function</a>	13	1.10E-01	6.70E-01
ILMN_2366634	-0.3590136	0.69484407	PKM2	GOTERM_BP_FAT	<a href="#">regulation of production of molecular mediator of immune response</a>	3	1.10E-01	6.70E-01
ILMN_2407434	-0.3631673	0.6850699	DCLK2	GOTERM_BP_FAT	<a href="#">regulation of kinase activity</a>	9	1.20E-01	6.80E-01
ILMN_2382431	-0.8878012	0.6826305	ANKRD36	GOTERM_BP_FAT	<a href="#">positive regulation of immune effector process</a>	3	1.20E-01	6.90E-01
ILMN_1699931	-0.4965842	0.6793603	HCST	GOTERM_BP_FAT	<a href="#">regulation of MAP kinase activity</a>	5	1.30E-01	7.00E-01
ILMN_2383489	-0.3749546	0.6792119	CDK5RAP3	GOTERM_BP_FAT	<a href="#">Cytokines and Inflammatory Response</a>	3	1.30E-01	6.30E-01
ILMN_1752592	-0.3833149	0.6780105	HLA-DRB4	BIOCARTA	<a href="#">regulation of transferase activity</a>	9	1.40E-01	7.20E-01
ILMN_2379644	-0.5249819	0.67535543	CD74	GOTERM_BP_FAT	<a href="#">negative regulation of response to stimulus</a>	4	1.60E-01	7.50E-01
ILMN_1701643	-0.3674708	0.6733213	GDPD5	GOTERM_BP_FAT	<a href="#">regulation of lymphocyte mediated immunity</a>	3	1.70E-01	7.70E-01
ILMN_1656920	-0.499193	0.67319584	CRIP1	GOTERM_BP_FAT	<a href="#">alternative initiation</a>	3	1.70E-01	6.20E-01
ILMN_1737157	-0.6897214	0.6702828	GRAMD1A	SP_PIR_KEYWORDS	<a href="#">regulation of T cell proliferation</a>	3	2.10E-01	8.20E-01
ILMN_1739794	-0.4857385	0.666808	CD3E	GOTERM_BP_FAT	<a href="#">regulation of secretion</a>	4	5.20E-01	9.80E-01
ILMN_1758315	-0.4451488	0.6659471	SLC9A9	GOTERM_BP_FAT	<a href="#">regulation of cellular localization</a>	3	8.60E-01	1.00E+00
ILMN_2175912	-0.4234652	0.6652375	ITGB2	GOTERM_BP_FAT				
ILMN_1683026	-0.388655	0.66396236	PSMB10	Annotation Cluster 11	Enrichment Score: 1.9	Count	P_Value	Benjamini
ILMN_1753584	-0.5324534	0.66179246	KRT8	GOTERM_BP_FAT	<a href="#">response to virus</a>	8	7.40E-04	3.80E-02
ILMN_1727402	-0.5068444	0.6616992	HCLS1	KEGG_PATHWAY	<a href="#">Toll-like receptor signaling pathway</a>	7	1.00E-02	8.90E-02
ILMN_2147133	-0.4381964	0.65923274	NBPF1	KEGG_PATHWAY	<a href="#">Cytosolic DNA-sensing pathway</a>	3	2.70E-01	6.80E-01
ILMN_1676256	-0.3549909	0.658206	TPSAB1	Annotation Cluster 12	Enrichment Score: 1.87	Count	P_Value	Benjamini
ILMN_1737205	-0.4199736	0.65487623	MCM4	GOTERM_BP_FAT	<a href="#">programmed cell death</a>	19	1.80E-03	7.10E-02
ILMN_1790637	-0.375038	0.65421516	C11orf80	GOTERM_BP_FAT	<a href="#">apoptosis</a>	17	8.50E-03	1.90E-01
ILMN_2161746	-0.4203926	0.6510027	TRIP10	GOTERM_BP_FAT	<a href="#">cell death</a>	19	9.70E-03	2.00E-01
ILMN_2410783	-0.6115214	0.6435011	GAA	GOTERM_BP_FAT	<a href="#">death</a>	19	1.00E-02	2.10E-01
ILMN_2064606	-0.4619445	0.64152145	TBC1D2B	SP_PIR_KEYWORDS	<a href="#">Apoptosis</a>	7	2.90E-01	7.40E-01
ILMN_1674874	-0.3659361	0.64023876	MFSD10	Annotation Cluster 13	Enrichment Score: 1.71	Count	P_Value	Benjamini
ILMN_1761138	-0.4229533	0.6345543	C9orf142	SP_PIR_KEYWORDS	<a href="#">collagen</a>	7	8.80E-04	1.70E-02
ILMN_1742330	-0.5733025	0.631179	PLXNB1	INTERPRO	<a href="#">Collagen triple helix repeat</a>	6	4.20E-03	3.10E-01
ILMN_1754842	-1.1469843	0.6292545	DLGAP4	SP_PIR_KEYWORDS	<a href="#">hydroxyproline</a>	4	9.20E-03	1.20E-01
ILMN_2395375	-0.43235	0.62881	GABBR1	SP_PIR_KEYWORDS	<a href="#">hydroxylation</a>	5	9.60E-03	1.20E-01
ILMN_3200362	-0.5219584	0.6270053	NBPF1	GOTERM_BP_FAT	<a href="#">extracellular structure organization</a>	7	2.50E-02	3.40E-01
ILMN_1761912	-0.5853727	0.61685646	MGAT1	GOTERM_CC_FAT	<a href="#">extracellular matrix part</a>	6	2.50E-02	2.80E-01
ILMN_2398847	-0.4906956	0.6160503	ARHGAP17	SP_PIR_KEYWORDS	<a href="#">hydroxylysine</a>	3	5.10E-02	3.30E-01
ILMN_1773885	-0.9395435	0.61211187	DMAP1	SP_PIR_KEYWORDS	<a href="#">triple helix</a>	3	5.10E-02	3.30E-01
ILMN_2066066	-0.4463386	0.6036648	HLA-DRB6	GOTERM_BP_FAT	<a href="#">extracellular matrix organization</a>	5	5.40E-02	4.90E-01
ILMN_1683576	-0.4752797	0.6011738	MAGED2	UP_SEQ_FEATURE	domain:Collagen-like	3	6.70E-02	9.10E-01
ILMN_2349658	-0.976337	0.5986835	TSPO	GOTERM_CC_FAT	<a href="#">collagen</a>	3	8.70E-02	6.00E-01
ILMN_1778360	-0.5825829	0.594741	PYGB	Annotation Cluster 14	Enrichment Score: 1.68	Count	P_Value	Benjamini
ILMN_1653828	-0.452502	0.5902511	CHFR	GOTERM_BP_FAT	<a href="#">regulation of protein kinase cascade</a>	13	1.60E-04	1.80E-02
ILMN_2410909	-0.4180519	0.585066	AKT1	GOTERM_BP_FAT	<a href="#">regulation of JNK cascade</a>	5	1.20E-02	2.20E-01
ILMN_2114422	-0.4646005	0.5784965	NOD1	GOTERM_BP_FAT	<a href="#">regulation of stress-activated protein kinase signaling pathway</a>	5	1.50E-02	2.50E-01

ILMN_1786197	-0.4536233	0.56482023	NR2F1
ILMN_1752340	-0.6061316	0.56157315	ARF5
ILMN_1761068	-0.5335256	0.56072944	DKFZp434K1323
ILMN_1728049	-0.517863	0.51490104	S100A16
ILMN_1772888	-0.6104952	0.44741943	AX746718
ILMN_3281563	-0.7814937	0.377732	RPL12

Annotation Cluster	Enrichment Score	Count	P_Value	Benjamini				
Annotation Cluster 15	Enrichment Score: 1.56	GOTERM_BP_FAT	<a href="#">regulation of MAPKKK cascade</a>	6	1.70E-02	2.70E-01		
		GOTERM_BP_FAT	<a href="#">regulation of cellular response to stress</a>	5	5.30E-02	4.90E-01		
		GOTERM_BP_FAT	<a href="#">positive regulation of molecular function</a>	13	1.10E-01	6.70E-01		
		GOTERM_BP_FAT	<a href="#">positive regulation of transport</a>	4	5.90E-01	9.90E-01		
		SP_PIR_KEYWORDS	<a href="#">protease inhibitor</a>	6	8.50E-03	1.10E-01		
		GOTERM_MF_FAT	<a href="#">endopeptidase inhibitor activity</a>	7	1.30E-02	3.60E-01		
		SP_PIR_KEYWORDS	<a href="#">Serine protease inhibitor</a>	5	1.40E-02	1.50E-01		
		GOTERM_MF_FAT	<a href="#">peptidase inhibitor activity</a>	7	1.60E-02	3.60E-01		
		GOTERM_MF_FAT	<a href="#">serine-type endopeptidase inhibitor activity</a>	5	3.40E-02	4.80E-01		
		UP_SEQ_FEATURE	site:Reactive bond	3	9.80E-02	9.30E-01		
GOTERM_MF_FAT	<a href="#">enzyme inhibitor activity</a>	7	1.50E-01	7.50E-01				
Annotation Cluster 16	Enrichment Score: 1.54	SP_PIR_KEYWORDS	<a href="#">zymogen</a>	10	7.40E-04	1.60E-02		
		UP_SEQ_FEATURE	propeptide:Activation peptide	6	1.70E-03	1.90E-01		
		UP_SEQ_FEATURE	domain:Peptidase S1	6	8.40E-03	5.30E-01		
		INTERPRO	<a href="#">Peptidase S1A_chymotrypsin</a>	6	1.00E-02	4.50E-01		
		INTERPRO	<a href="#">Peptidase S1/S6_chymotrypsin/Hap_active site</a>	6	1.10E-02	4.30E-01		
		INTERPRO	<a href="#">Peptidase S1 and S6_chymotrypsin/Hap</a>	6	1.60E-02	4.50E-01		
		PIR_SUPERFAMILY	PIRSF001135:trypsin	4	1.90E-02	7.10E-01		
		SP_PIR_KEYWORDS	<a href="#">Serine protease</a>	6	2.20E-02	2.00E-01		
		SP_PIR_KEYWORDS	<a href="#">serine proteinase</a>	4	2.50E-02	2.20E-01		
		GOTERM_MF_FAT	<a href="#">endopeptidase activity</a>	11	2.80E-02	4.50E-01		
		SP_PIR_KEYWORDS	<a href="#">Protease</a>	12	2.80E-02	2.30E-01		
		SMART	<a href="#">Tryp_SPc</a>	6	4.00E-02	8.50E-01		
		GOTERM_MF_FAT	<a href="#">serine-type endopeptidase activity</a>	6	5.40E-02	6.00E-01		
		GOTERM_MF_FAT	<a href="#">peptidase activity</a>	13	7.90E-02	7.20E-01		
		UP_SEQ_FEATURE	active site:Charge relay system	6	8.30E-02	9.30E-01		
		GOTERM_MF_FAT	<a href="#">serine-type peptidase activity</a>	6	8.80E-02	7.00E-01		
		GOTERM_MF_FAT	<a href="#">serine hydrolase activity</a>	6	9.10E-02	6.90E-01		
		GOTERM_MF_FAT	<a href="#">peptidase activity, acting on L-amino acid peptides</a>	12	1.10E-01	7.20E-01		
		GOTERM_BP_FAT	<a href="#">proteolysis</a>	18	2.70E-01	8.80E-01		
		SP_PIR_KEYWORDS	<a href="#">hydrolase</a>	22	2.80E-01	7.40E-01		
		Annotation Cluster 17	Enrichment Score: 1.51	UP_SEQ_FEATURE	region of interest:Coil 2	5	6.80E-03	4.90E-01
				UP_SEQ_FEATURE	region of interest:Linker 12	5	6.80E-03	4.90E-01
UP_SEQ_FEATURE	region of interest:Coil 1B			5	9.40E-03	5.30E-01		
UP_SEQ_FEATURE	region of interest:Linker 1			5	9.40E-03	5.30E-01		
UP_SEQ_FEATURE	region of interest:Coil 1A			5	9.40E-03	5.30E-01		
UP_SEQ_FEATURE	region of interest:Rod			5	9.80E-03	5.20E-01		
UP_SEQ_FEATURE	region of interest:Head			5	1.10E-02	5.30E-01		
INTERPRO	<a href="#">Filament</a>			5	1.30E-02	4.30E-01		
INTERPRO	<a href="#">Intermediate filament protein, conserved site</a>			5	1.30E-02	4.30E-01		
SP_PIR_KEYWORDS	<a href="#">Intermediate filament</a>			5	1.30E-02	1.40E-01		
INTERPRO	<a href="#">Intermediate filament protein</a>			5	1.40E-02	4.20E-01		
PIR_SUPERFAMILY	PIRSF002282:cytoskeletal keratin			5	1.60E-02	8.70E-01		
INTERPRO	<a href="#">Type II keratin</a>			3	4.80E-02	7.10E-01		
UP_SEQ_FEATURE	site:Stutter			3	5.70E-02	8.90E-01		
UP_SEQ_FEATURE	region of interest:Tail			4	5.90E-02	8.90E-01		
GOTERM_BP_FAT	<a href="#">cytoskeleton organization</a>			11	7.70E-02	6.00E-01		
GOTERM_CC_FAT	<a href="#">intermediate filament</a>			6	1.20E-01	6.90E-01		
GOTERM_CC_FAT	<a href="#">intermediate filament cytoskeleton</a>			6	1.20E-01	7.00E-01		
SP_PIR_KEYWORDS	<a href="#">keratin</a>			4	2.40E-01	7.00E-01		
GOTERM_CC_FAT	<a href="#">keratin filament</a>			3	3.50E-01	9.20E-01		
GOTERM_CC_FAT	<a href="#">cytoskeletal part</a>			14	5.90E-01	9.60E-01		
Annotation Cluster 18	Enrichment Score: 1.46			INTERPRO	<a href="#">Immunoglobulin-like fold</a>	20	7.70E-05	3.90E-02
		INTERPRO	<a href="#">Immunoglobulin/major histocompatibility complex, conserved site</a>	7	8.10E-04	1.90E-01		
		INTERPRO	<a href="#">Immunoglobulin-like</a>	16	1.70E-03	2.00E-01		



	SP_PIR_KEYWORDS	<a href="#">Immunoglobulin domain</a>	13	9.60E-03	1.10E-01
	INTERPRO	<a href="#">Immunoglobulin subtype</a>	9	5.80E-02	7.30E-01
	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	6	7.40E-02	9.20E-01
	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	6	7.60E-02	9.20E-01
	SMART	<a href="#">IG</a>	9	1.70E-01	9.60E-01
	UP_SEQ_FEATURE	domain:Ig-like C2-type 3	4	1.70E-01	9.80E-01
	UP_SEQ_FEATURE	domain:Ig-like V-type	4	1.80E-01	9.80E-01
	INTERPRO	<a href="#">Immunoglobulin subtype 2</a>	5	2.60E-01	9.60E-01
	SMART	<a href="#">IGc2</a>	5	4.30E-01	9.90E-01
	INTERPRO	<a href="#">Immunoglobulin</a>	4	4.70E-01	1.00E+00
<b>Annotation Cluster 19</b>	<b>Enrichment Score: 1.46</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	GOTERM_BP_FAT	<a href="#">in utero embryonic development</a>	8	1.10E-02	2.10E-01
	GOTERM_BP_FAT	<a href="#">blastocyst development</a>	4	2.10E-02	3.00E-01
	GOTERM_BP_FAT	<a href="#">blastocyst formation</a>	3	3.00E-02	3.80E-01
	GOTERM_BP_FAT	<a href="#">chordate embryonic development</a>	9	8.60E-02	6.20E-01
	GOTERM_BP_FAT	<a href="#">embryonic development ending in birth or egg hatching</a>	9	8.80E-02	6.20E-01
<b>Annotation Cluster 20</b>	<b>Enrichment Score: 1.44</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	GOTERM_CC_FAT	<a href="#">lysosome</a>	8	3.00E-02	3.00E-01
	GOTERM_CC_FAT	<a href="#">lytic vacuole</a>	8	3.00E-02	3.00E-01
	SP_PIR_KEYWORDS	<a href="#">lysosome</a>	6	3.10E-02	2.40E-01
	GOTERM_CC_FAT	<a href="#">vacuole</a>	8	6.60E-02	5.20E-01
<b>Annotation Cluster 21</b>	<b>Enrichment Score: 1.33</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	SP_PIR_KEYWORDS	<a href="#">calcium binding</a>	7	1.30E-03	2.30E-02
	INTERPRO	<a href="#">S100/CaBP-9k-type, calcium binding, subdomain</a>	4	4.60E-03	2.90E-01
	INTERPRO	<a href="#">S100/CaBP-9k-type, calcium binding</a>	4	5.10E-03	2.90E-01
	UP_SEQ_FEATURE	calcium-binding region:1; low affinity	3	1.90E-02	6.60E-01
	INTERPRO	<a href="#">EF-HAND 1</a>	8	2.00E-02	5.10E-01
	UP_SEQ_FEATURE	domain:EF-hand 1	7	2.10E-02	6.80E-01
	UP_SEQ_FEATURE	domain:EF-hand 2	7	2.10E-02	6.80E-01
	UP_SEQ_FEATURE	calcium-binding region:2; high affinity	3	2.50E-02	7.10E-01
	SP_PIR_KEYWORDS	<a href="#">EF hand</a>	4	3.30E-02	2.40E-01
	PIRS_SUPERFAMILY	PIRSF002353:S-100 protein	3	3.60E-02	7.90E-01
	INTERPRO	<a href="#">EF-HAND 2</a>	7	5.50E-02	7.30E-01
	INTERPRO	<a href="#">EF-Hand type</a>	7	7.90E-02	7.60E-01
	UP_SEQ_FEATURE	calcium-binding region:2	3	3.90E-01	1.00E+00
	UP_SEQ_FEATURE	calcium-binding region:1	3	4.40E-01	1.00E+00
	INTERPRO	<a href="#">EF hand</a>	3	4.90E-01	1.00E+00
	INTERPRO	<a href="#">Calcium-binding EF-hand</a>	3	5.40E-01	1.00E+00
	SMART	<a href="#">EFh</a>	3	6.80E-01	1.00E+00
<b>Annotation Cluster 22</b>	<b>Enrichment Score: 1.31</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	GOTERM_BP_FAT	<a href="#">cell migration</a>	11	4.70E-03	1.40E-01
	GOTERM_BP_FAT	<a href="#">cell motion</a>	15	5.70E-03	1.50E-01
	GOTERM_BP_FAT	<a href="#">cell motility</a>	11	9.70E-03	2.10E-01
	GOTERM_BP_FAT	<a href="#">localization of cell</a>	11	9.70E-03	2.10E-01
	SP_PIR_KEYWORDS	<a href="#">inflammatory response</a>	5	1.30E-02	1.40E-01
	GOTERM_BP_FAT	<a href="#">cell chemotaxis</a>	4	1.60E-02	2.60E-01
	KEGG_PATHWAY	<a href="#">Cytokine-cytokine receptor interaction</a>	11	2.10E-02	1.10E-01
	GOTERM_BP_FAT	<a href="#">taxis</a>	7	2.30E-02	3.20E-01
	GOTERM_BP_FAT	<a href="#">chemotaxis</a>	7	2.30E-02	3.20E-01
	INTERPRO	<a href="#">Small chemokine, C-C group, conserved site</a>	3	3.90E-02	6.70E-01
	PIRS_SUPERFAMILY	PIRSF001950:small inducible chemokine, C/CC types	3	5.10E-02	8.10E-01
	GOTERM_BP_FAT	<a href="#">locomotory behavior</a>	8	8.20E-02	6.10E-01
	GOTERM_BP_FAT	<a href="#">leukocyte chemotaxis</a>	3	9.10E-02	6.30E-01
	INTERPRO	<a href="#">Small chemokine, interleukin-8-like</a>	3	9.40E-02	8.00E-01
	GOTERM_BP_FAT	<a href="#">behavior</a>	11	1.10E-01	6.70E-01
	GOTERM_MF_FAT	<a href="#">chemokine activity</a>	3	1.20E-01	7.30E-01
	GOTERM_MF_FAT	<a href="#">chemokine receptor binding</a>	3	1.40E-01	7.60E-01
	SMART	<a href="#">SCY</a>	3	1.40E-01	9.50E-01
	SP_PIR_KEYWORDS	<a href="#">cytokine</a>	5	1.60E-01	6.10E-01
	GOTERM_BP_FAT	<a href="#">leukocyte migration</a>	3	1.80E-01	7.90E-01

	BBID	<a href="#">109.Chemokine_families</a>	3	2.00E-01	9.60E-01
	SP_PIR_KEYWORDS	<a href="#">chemotaxis</a>	3	2.10E-01	6.70E-01
	GOTERM_MF_FAT	<a href="#">cytokine activity</a>	5	2.60E-01	8.70E-01
<b>Annotation Cluster 23</b>	<b>Enrichment Score: 1.31</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	GOTERM_BP_FAT	<a href="#">virus-host interaction</a>	3	3.00E-02	3.80E-01
	GOTERM_BP_FAT	<a href="#">viral reproductive process</a>	4	5.30E-02	4.90E-01
	GOTERM_BP_FAT	<a href="#">viral reproduction</a>	4	7.30E-02	5.80E-01
<b>Annotation Cluster 24</b>	<b>Enrichment Score: 1.31</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	GOTERM_BP_FAT	<a href="#">negative regulation of immune system process</a>	7	9.50E-04	4.60E-02
	GOTERM_BP_FAT	<a href="#">negative regulation of lymphocyte activation</a>	3	1.70E-01	7.70E-01
	GOTERM_BP_FAT	<a href="#">negative regulation of leukocyte activation</a>	3	1.80E-01	7.90E-01
	GOTERM_BP_FAT	<a href="#">negative regulation of cell activation</a>	3	2.00E-01	8.10E-01
<b>Annotation Cluster 25</b>	<b>Enrichment Score: 1.29</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	SP_PIR_KEYWORDS	<a href="#">sushi</a>	4	2.80E-02	2.30E-01
	INTERPRO	<a href="#">Sushi/SCR/CCP</a>	4	3.40E-02	6.50E-01
	INTERPRO	<a href="#">Complement control module</a>	4	3.50E-02	6.50E-01
	SMART	<a href="#">CCP</a>	4	6.20E-02	8.90E-01
	UP_SEQ_FEATURE	domain:Sushi 2	3	9.50E-02	9.30E-01
	UP_SEQ_FEATURE	domain:Sushi 1	3	9.50E-02	9.30E-01
<b>Annotation Cluster 26</b>	<b>Enrichment Score: 1.26</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	GOTERM_BP_FAT	<a href="#">cellular calcium ion homeostasis</a>	8	1.30E-02	2.30E-01
	GOTERM_BP_FAT	<a href="#">calcium ion homeostasis</a>	8	1.50E-02	2.50E-01
	GOTERM_BP_FAT	<a href="#">cellular metal ion homeostasis</a>	8	1.80E-02	2.80E-01
	GOTERM_BP_FAT	<a href="#">metal ion homeostasis</a>	8	2.30E-02	3.20E-01
	GOTERM_BP_FAT	<a href="#">cellular di-, tri-valent inorganic cation homeostasis</a>	8	3.70E-02	4.20E-01
	GOTERM_BP_FAT	<a href="#">cation homeostasis</a>	9	4.30E-02	4.50E-01
	GOTERM_BP_FAT	<a href="#">di-, tri-valent inorganic cation homeostasis</a>	8	4.60E-02	4.70E-01
	GOTERM_BP_FAT	<a href="#">homeostatic process</a>	17	5.20E-02	4.90E-01
	GOTERM_BP_FAT	<a href="#">cellular cation homeostasis</a>	8	6.00E-02	5.20E-01
	GOTERM_BP_FAT	<a href="#">elevation of cytosolic calcium ion concentration</a>	5	6.40E-02	5.40E-01
	GOTERM_BP_FAT	<a href="#">cytosolic calcium ion homeostasis</a>	5	7.90E-02	6.00E-01
	GOTERM_BP_FAT	<a href="#">cellular homeostasis</a>	11	1.10E-01	6.70E-01
	GOTERM_BP_FAT	<a href="#">ion homeostasis</a>	10	1.10E-01	6.70E-01
	GOTERM_BP_FAT	<a href="#">cellular ion homeostasis</a>	9	1.40E-01	7.20E-01
	GOTERM_BP_FAT	<a href="#">cellular chemical homeostasis</a>	9	1.50E-01	7.40E-01
	GOTERM_BP_FAT	<a href="#">chemical homeostasis</a>	10	2.70E-01	8.80E-01
<b>Annotation Cluster 27</b>	<b>Enrichment Score: 1.2</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	UP_SEQ_FEATURE	domain:SH3	7	1.90E-02	6.80E-01
	SP_PIR_KEYWORDS	<a href="#">sh3 domain</a>	7	3.70E-02	2.60E-01
	INTERPRO	<a href="#">Src homology-3 domain</a>	7	5.30E-02	7.30E-01
	SMART	<a href="#">SH3</a>	7	1.30E-01	9.80E-01
	INTERPRO	<a href="#">Variant SH3</a>	3	2.00E-01	9.20E-01
<b>Annotation Cluster 28</b>	<b>Enrichment Score: 1.16</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	INTERPRO	<a href="#">Calponin-like actin-binding</a>	5	1.20E-02	4.30E-01
	SMART	<a href="#">CH</a>	5	2.70E-02	8.50E-01
	UP_SEQ_FEATURE	domain:CH	3	8.70E-02	9.30E-01
	SP_PIR_KEYWORDS	<a href="#">cytoskeleton</a>	6	8.70E-01	1.00E+00
<b>Annotation Cluster 29</b>	<b>Enrichment Score: 1.14</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	KEGG_PATHWAY	<a href="#">Toll-like receptor signaling pathway</a>	7	1.00E-02	8.90E-02
	GOTERM_BP_FAT	<a href="#">response to lipopolysaccharide</a>	4	8.90E-02	6.20E-01
	GOTERM_BP_FAT	<a href="#">response to molecule of bacterial origin</a>	4	1.10E-01	6.80E-01
	GOTERM_BP_FAT	<a href="#">response to bacterium</a>	5	2.70E-01	8.80E-01
<b>Annotation Cluster 30</b>	<b>Enrichment Score: 1.1</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	SP_PIR_KEYWORDS	<a href="#">phosphotransferase</a>	7	3.10E-02	2.40E-01
	SP_PIR_KEYWORDS	<a href="#">autophosphorylation</a>	3	1.10E-01	5.20E-01
	SP_PIR_KEYWORDS	<a href="#">ATP</a>	6	1.40E-01	5.90E-01
<b>Annotation Cluster 31</b>	<b>Enrichment Score: 1.09</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	GOTERM_BP_FAT	<a href="#">muscle organ development</a>	8	2.60E-02	3.40E-01
	GOTERM_BP_FAT	<a href="#">muscle tissue development</a>	5	9.20E-02	6.30E-01
	GOTERM_BP_FAT	<a href="#">striated muscle tissue development</a>	4	2.20E-01	8.40E-01



Annotation Cluster	Enrichment Score		Count	P_Value	Benjamini	
Annotation Cluster 32	Enrichment Score: 1.09	GOTERM_CC_FAT	<a href="#">platelet alpha granule</a>	5	7.90E-03	1.30E-01
		GOTERM_CC_FAT	<a href="#">platelet alpha granule lumen</a>	4	2.00E-02	2.60E-01
		GOTERM_CC_FAT	<a href="#">cytoplasmic membrane-bounded vesicle lumen</a>	4	2.40E-02	2.90E-01
		GOTERM_CC_FAT	<a href="#">vesicle lumen</a>	4	2.70E-02	2.80E-01
		GOTERM_CC_FAT	<a href="#">secretory granule</a>	6	1.10E-01	6.80E-01
		GOTERM_CC_FAT	<a href="#">cytoplasmic vesicle part</a>	6	1.20E-01	7.00E-01
		GOTERM_CC_FAT	<a href="#">cytoplasmic membrane-bounded vesicle</a>	11	2.50E-01	8.70E-01
		GOTERM_CC_FAT	<a href="#">membrane-bounded vesicle</a>	11	2.80E-01	8.90E-01
		GOTERM_CC_FAT	<a href="#">vesicle</a>	12	3.40E-01	9.20E-01
		GOTERM_CC_FAT	<a href="#">cytoplasmic vesicle</a>	11	4.20E-01	9.40E-01
Annotation Cluster 33	Enrichment Score: 1.06	SP_PIR_KEYWORDS	<a href="#">laminin egf-like domain</a>	3	4.80E-02	3.20E-01
		INTERPRO	<a href="#">EGF-like_laminin</a>	3	9.40E-02	8.00E-01
		SMART	<a href="#">EGF_Lam</a>	3	1.40E-01	9.50E-01
Annotation Cluster 34	Enrichment Score: 1.06	GOTERM_MF_FAT	<a href="#">glycosaminoglycan binding</a>	8	2.60E-03	2.20E-01
		GOTERM_MF_FAT	<a href="#">polysaccharide binding</a>	8	4.40E-03	2.90E-01
		GOTERM_MF_FAT	<a href="#">pattern binding</a>	8	4.40E-03	2.90E-01
		GOTERM_MF_FAT	<a href="#">peptidoglycan binding</a>	3	5.90E-03	2.80E-01
		GOTERM_MF_FAT	<a href="#">carbohydrate binding</a>	12	7.50E-03	3.00E-01
		GOTERM_BP_FAT	<a href="#">positive regulation of tumor necrosis factor production</a>	3	1.70E-02	2.70E-01
		GOTERM_BP_FAT	<a href="#">regulation of tumor necrosis factor production</a>	3	6.70E-02	5.50E-01
		GOTERM_BP_FAT	<a href="#">positive regulation of cytokine production</a>	4	1.30E-01	7.00E-01
		GOTERM_BP_FAT	<a href="#">positive regulation of MAPKKK cascade</a>	3	1.40E-01	7.20E-01
		UP_SEQ_FEATURE	repeat:LRR 4	6	1.80E-01	9.80E-01
		UP_SEQ_FEATURE	repeat:LRR 6	5	2.30E-01	9.90E-01
		GOTERM_BP_FAT	<a href="#">response to bacterium</a>	5	2.70E-01	8.80E-01
		UP_SEQ_FEATURE	repeat:LRR 3	6	2.80E-01	1.00E+00
		INTERPRO	<a href="#">Leucine-rich repeat</a>	5	2.80E-01	9.70E-01
		UP_SEQ_FEATURE	repeat:LRR 5	5	2.90E-01	1.00E+00
		UP_SEQ_FEATURE	repeat:LRR 1	6	3.20E-01	1.00E+00
		SP_PIR_KEYWORDS	<a href="#">leucine-rich repeat</a>	6	3.30E-01	7.80E-01
		UP_SEQ_FEATURE	repeat:LRR 2	6	3.30E-01	1.00E+00
		UP_SEQ_FEATURE	repeat:LRR 9	3	4.70E-01	1.00E+00
		UP_SEQ_FEATURE	repeat:LRR 8	3	5.30E-01	1.00E+00
UP_SEQ_FEATURE	repeat:LRR 7	3	6.20E-01	1.00E+00		
Annotation Cluster 35	Enrichment Score: 1.06	INTERPRO	<a href="#">EGF-like region, conserved site</a>	11	4.10E-03	3.50E-01
		SP_PIR_KEYWORDS	<a href="#">egf-like domain</a>	7	5.40E-02	3.40E-01
		INTERPRO	<a href="#">EGF</a>	5	7.70E-02	7.80E-01
		INTERPRO	<a href="#">EGF-like, type 3</a>	6	9.90E-02	8.10E-01
		INTERPRO	<a href="#">EGF-like</a>	6	1.10E-01	8.30E-01
		INTERPRO	<a href="#">EGF-type aspartate/asparagine hydroxylation conserved site</a>	4	1.20E-01	8.50E-01
		UP_SEQ_FEATURE	domain:EGF-like 2; calcium-binding	3	1.40E-01	9.80E-01
		SMART	<a href="#">EGF</a>	6	2.30E-01	9.50E-01
		UP_SEQ_FEATURE	domain:EGF-like 1	3	4.10E-01	1.00E+00
Annotation Cluster 36	Enrichment Score: 1.04	GOTERM_MF_FAT	<a href="#">identical protein binding</a>	15	4.50E-02	5.50E-01
		GOTERM_MF_FAT	<a href="#">protein dimerization activity</a>	12	1.10E-01	7.20E-01
		GOTERM_MF_FAT	<a href="#">protein homodimerization activity</a>	8	1.60E-01	7.60E-01
Annotation Cluster 37	Enrichment Score: 1.04	GOTERM_BP_FAT	<a href="#">activation of immune response</a>	8	3.00E-04	2.50E-02
		GOTERM_BP_FAT	<a href="#">innate immune response</a>	6	4.10E-02	4.50E-01
		SP_PIR_KEYWORDS	<a href="#">innate immunity</a>	4	6.30E-02	3.70E-01
		GOTERM_BP_FAT	<a href="#">humoral immune response</a>	4	9.40E-02	6.40E-01
		GOTERM_BP_FAT	<a href="#">complement activation</a>	3	1.10E-01	6.80E-01
		GOTERM_BP_FAT	<a href="#">activation of plasma proteins involved in acute inflammatory response</a>	3	1.20E-01	6.80E-01
		KEGG_PATHWAY	<a href="#">Complement and coagulation cascades</a>	4	1.30E-01	4.40E-01

	GOTERM_BP_FAT	<a href="#">protein maturation by peptide bond cleavage</a>	3	3.30E-01	9.20E-01
	GOTERM_BP_FAT	<a href="#">acute inflammatory response</a>	3	3.90E-01	9.50E-01
	GOTERM_BP_FAT	<a href="#">protein processing</a>	3	4.50E-01	9.70E-01
	GOTERM_BP_FAT	<a href="#">protein maturation</a>	3	5.00E-01	9.80E-01
<b>Annotation Cluster 38</b>	<b>Enrichment Score: 1.01</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	INTERPRO	<a href="#">von Willebrand factor, type A</a>	4	7.80E-02	7.70E-01
	UP_SEQ_FEATURE	short sequence motif:Cell attachment site	4	8.60E-02	9.30E-01
	SMART	<a href="#">VWA</a>	4	1.40E-01	9.70E-01
<b>Annotation Cluster 39</b>	<b>Enrichment Score: 0.98</b>		<b>Count</b>	<b>P_Value</b>	<b>Benjamini</b>
	UP_SEQ_FEATURE	domain:CUB 1	3	6.70E-02	9.10E-01
	UP_SEQ_FEATURE	domain:CUB 2	3	6.70E-02	9.10E-01
	INTERPRO	<a href="#">CUB</a>	3	1.40E-01	8.60E-01
	SMART	<a href="#">CUB</a>	3	2.00E-01	9.40E-01