

Supplementary Table 2: Up-regulated gene ontology pathways in IBD patients harboring proximal neoplasia using DAVID webtool

Category	Term	Count	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Secreted	51	4.77	3.62E-20	3.62E-20	2.15E-19
UP_KEYWORDS	Disulfide bond	55	2.91	2.36E-12	1.18E-12	1.41E-11
GOTERM_CC_DIRECT	GO:0005576~extracellular region	38	4.16	5.21E-12	2.60E-12	3.97E-11
GOTERM_CC_DIRECT	GO:0005615~extracellular space	36	4.48	3.82E-12	3.82E-12	2.92E-11
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	16	15.01	2.46E-11	8.21E-12	1.88E-10
UP_SEQ_FEATURE	disulfide bond	50	3.04	4.26E-11	2.13E-11	1.13E-10
UP_KEYWORDS	Signal	54	2.73	6.78E-11	2.26E-11	4.03E-10
UP_SEQ_FEATURE	signal peptide	54	2.86	2.39E-11	2.39E-11	6.36E-11
UP_KEYWORDS	Extracellular matrix	15	10.39	3.63E-08	9.07E-09	2.16E-07
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	15	9.72	6.15E-08	1.54E-08	4.69E-07
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	9	26.16	3.56E-07	3.56E-07	2.00E-06
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	42	2.42	4.11E-06	8.23E-07	3.14E-05
UP_KEYWORDS	Glycoprotein	53	2.07	5.06E-06	1.01E-06	3.01E-05
GOTERM_BP_DIRECT	GO:0030198~extracellular matrix organization	15	7.42	1.35E-05	1.35E-05	1.95E-05
GOTERM_CC_DIRECT	GO:0005604~basement membrane	7	13.95	0.002	0.0003	0.01
UP_KEYWORDS	Proteoglycan	6	21.72	0.002	0.0003	0.01
GOTERM_BP_DIRECT	GO:0030307~positive regulation of cell growth	8	15.34	0.001	0.0005	0.001
GOTERM_MF_DIRECT	GO:0008201~heparin binding	9	9.00	0.002	0.001	0.01
UP_KEYWORDS	EGF-like domain	9	6.82	0.01	0.002	0.06
UP_KEYWORDS	Pyrrolidone carboxylic acid	6	13.82	0.02	0.002	0.09
KEGG_PATHWAY	hsa04510:Focal adhesion	10	6.08	0.00	0.003	0.03
KEGG_PATHWAY	hsa04512:ECM-receptor interaction	7	10.08	0.01	0.003	0.06
GOTERM_CC_DIRECT	GO:0009986~cell surface	13	3.82	0.02	0.003	0.17
UP_KEYWORDS	Inflammatory response	7	8.22	0.04	0.005	0.26
UP_KEYWORDS	S-nitrosylation	5	16.12	0.05	0.01	0.32
GOTERM_CC_DIRECT	GO:0005796~Golgi lumen	6	10.29	0.04	0.01	0.34
UP_KEYWORDS	Cell adhesion	11	4.07	0.07	0.01	0.45
UP_KEYWORDS	Muscle protein	5	14.30	0.08	0.01	0.51
SMART	SM00181:SM00181	9	5.17	0.02	0.01	0.31
UP_SEQ_FEATURE	glycosylation site:O-linked (Xyl...) (glycosaminoglycan)	4	50.73	0.03	0.01	0.09
INTERPRO	IPR001007: von Willebrand factor, type C	5	21.03	0.03	0.01	0.12
INTERPRO	IPR009030: Insulin-like growth factor binding protein, N-terminal	7	8.97	0.04	0.01	0.17
SMART	SM00214:SM00214	5	15.75	0.02	0.01	0.27
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	43	1.80	0.03	0.01	0.07
INTERPRO	IPR000742: Epidermal growth factor-like domain	9	6.42	0.02	0.01	0.10
SMART	SM00209:SM00209	6	11.34	0.01	0.01	0.17
SMART	SM00041:SM00041	4	22.34	0.05	0.01	0.71
INTERPRO	IPR000884: Thrombospondin, type 1 repeat	6	15.14	0.01	0.01	0.06
UP_SEQ_FEATURE	domain:VWFC	4	39.46	0.07	0.01	0.19
INTERPRO	IPR001134: Netrin domain	4	28.52	0.10	0.02	0.46
GOTERM_MF_DIRECT	GO:0050840~extracellular matrix binding	4	30.81	0.06	0.02	0.35
INTERPRO	IPR008993: Tissue inhibitor of metalloproteinases-like, OB-fold	4	26.24	0.12	0.02	0.59
INTERPRO	IPR006207: Cystine knot, C-terminal	4	26.24	0.12	0.02	0.59
UP_KEYWORDS	Heparin-binding	5	10.43	0.25	0.02	1.66
UP_SEQ_FEATURE	domain:NTR	4	32.28	0.12	0.02	0.35
INTERPRO	IPR016187: C-type lectin fold	6	8.95	0.14	0.02	0.72
UP_SEQ_FEATURE	domain:CTCK	4	28.41	0.18	0.03	0.52
UP_KEYWORDS	Collagen	5	9.54	0.32	0.03	2.31
GOTERM_BP_DIRECT	GO:0030199~collagen fibril organization	5	19.17	0.13	0.03	0.20
GOTERM_BP_DIRECT	GO:0043434~response to peptide hormone	5	17.04	0.20	0.04	0.32
UP_KEYWORDS	Antimicrobial	5	8.45	0.46	0.04	3.57
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	11	4.69	0.12	0.04	0.18
UP_KEYWORDS	Calcium	13	2.66	0.51	0.04	4.17
UP_KEYWORDS	Immunity	9	3.58	0.53	0.04	4.44
GOTERM_BP_DIRECT	GO:0042493~response to drug	10	4.69	0.26	0.04	0.43
UP_KEYWORDS	Sushi	4	12.67	0.56	0.04	4.70
UP_KEYWORDS	Innate immunity	7	4.83	0.50	0.04	4.02
GOTERM_BP_DIRECT	GO:0007229~integrin-mediated signaling pathway	6	11.09	0.20	0.04	0.32
INTERPRO	IPR013032: EGF-like, conserved site	7	5.83	0.30	0.04	1.65
GOTERM_MF_DIRECT	GO:0001968~fibronectin binding	4	21.25	0.17	0.05	1.07

GOTERM_BP_DIRECT	GO:0042346~positive regulation of NF-kappaB import into nucleus	4	27.89	0.34	0.05	0.59
UP_KEYWORDS	Protease inhibitor	5	7.21	0.66	0.05	6.20
UP_KEYWORDS	Acute phase	3	28.00	0.65	0.05	6.12
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	9	3.67	0.38	0.05	3.62
UP_KEYWORDS	Host-virus interaction	8	3.70	0.71	0.05	7.13
UP_SEQ_FEATURE	domain:EGF-like 4; calcium-binding	4	20.89	0.39	0.06	1.29
INTERPRO	IPR017891:Insulin-like growth factor binding protein, N-terminal, (3	44.73	0.43	0.06	2.52
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	13	2.93	0.28	0.06	1.84
UP_SEQ_FEATURE	domain:EGF-like 3; calcium-binding	4	18.69	0.49	0.07	1.79
UP_SEQ_FEATURE	domain:EGF-like 5; calcium-binding	4	18.69	0.49	0.07	1.79
GOTERM_MF_DIRECT	GO:0050786~RAGE receptor binding	3	42.01	0.39	0.08	2.74
GOTERM_MF_DIRECT	GO:0048407~platelet-derived growth factor binding	3	42.01	0.39	0.08	2.74
GOTERM_BP_DIRECT	GO:0072593~reactive oxygen species metabolic process	4	18.59	0.75	0.09	1.97
GOTERM_BP_DIRECT	GO:0048662~negative regulation of smooth muscle cell proliferati	4	18.59	0.75	0.09	1.97
GOTERM_BP_DIRECT	GO:0030308~negative regulation of cell growth	6	7.54	0.73	0.09	1.85
GOTERM_BP_DIRECT	GO:0022617~extracellular matrix disassembly	6	7.67	0.70	0.09	1.72
UP_SEQ_FEATURE	short sequence motif:Cell attachment site	5	9.76	0.60	0.09	2.44
GOTERM_BP_DIRECT	GO:0050832~defense response to fungus	4	21.91	0.57	0.09	1.21
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	7	6.03	0.69	0.09	1.66
INTERPRO	IPR016186:C-type lectin-like	5	8.04	0.63	0.09	4.43
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	10	3.68	0.81	0.09	2.40
INTERPRO	IPR001881:EGF-like calcium-binding	5	7.81	0.66	0.09	4.90
SMART	SM00032:SM00032	4	8.94	0.50	0.10	9.64
GOTERM_BP_DIRECT	GO:0043589~skin morphogenesis	3	51.13	0.80	0.10	2.29
UP_SEQ_FEATURE	domain:Sushi 2	4	15.78	0.67	0.10	2.91
UP_SEQ_FEATURE	domain:Sushi 1	4	15.78	0.67	0.10	2.91
GOTERM_BP_DIRECT	GO:0032355~response to estradiol	6	7.80	0.67	0.10	1.59
INTERPRO	IPR004827:Basic-leucine zipper domain	4	12.15	0.71	0.10	5.51
GOTERM_BP_DIRECT	GO:0050873~brown fat cell differentiation	4	20.45	0.65	0.10	1.49
SMART	SM00121:SM00121	3	20.48	0.48	0.10	8.95
INTERPRO	IPR000436:Sushi/SCR/CCP	4	11.51	0.76	0.10	6.38
SMART	SM00338:SM00338	4	9.45	0.45	0.11	8.31
UP_KEYWORDS	Hereditary hemolytic anemia	3	17.16	0.94	0.11	15.21
GOTERM_BP_DIRECT	GO:0006953~acute-phase response	4	14.96	0.93	0.12	3.67
INTERPRO	IPR000867:Insulin-like growth factor-binding protein, IGFBP	3	24.60	0.84	0.12	8.18
GOTERM_BP_DIRECT	GO:0030514~negative regulation of BMP signaling pathway	4	14.61	0.94	0.12	3.93
UP_KEYWORDS	Lectin	5	5.25	0.96	0.13	17.40
GOTERM_BP_DIRECT	GO:0071305~cellular response to vitamin D	3	41.83	0.91	0.13	3.45
UP_KEYWORDS	Hydroxylation	4	7.55	0.97	0.13	18.22
GOTERM_BP_DIRECT	GO:0006928~movement of cell or subcellular component	5	8.92	0.92	0.13	3.66
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	9	3.27	0.43	0.13	5.55
KEGG_PATHWAY	hsa05144:Malaria	4	10.23	0.52	0.14	7.12
GOTERM_BP_DIRECT	GO:0006898~receptor-mediated endocytosis	6	6.05	0.97	0.14	4.78
GOTERM_MF_DIRECT	GO:0005178~integrin binding	5	7.27	0.67	0.15	6.04
KEGG_PATHWAY	hsa05205:Proteoglycans in cancer	7	4.43	0.38	0.15	4.74
GOTERM_MF_DIRECT	GO:0005539~glycosaminoglycan binding	3	25.67	0.74	0.15	7.25
GOTERM_BP_DIRECT	GO:2000811~negative regulation of anoikis	3	27.07	1.00	0.15	8.12
UP_SEQ_FEATURE	domain:Leucine-zipper	5	7.86	0.87	0.16	5.28
GOTERM_BP_DIRECT	GO:0006936~muscle contraction	5	7.24	1.00	0.16	7.61
GOTERM_CC_DIRECT	GO:0043202~lysosomal lumen	4	7.87	0.89	0.16	15.65
GOTERM_BP_DIRECT	GO:0001649~osteoblast differentiation	5	7.10	1.00	0.16	8.11
GOTERM_BP_DIRECT	GO:0051591~response to cAMP	4	11.36	1.00	0.16	7.88
GOTERM_BP_DIRECT	GO:0050727~regulation of inflammatory response	4	11.36	1.00	0.16	7.88
GOTERM_BP_DIRECT	GO:0030207~chondroitin sulfate catabolic process	3	32.87	0.98	0.16	5.57
GOTERM_BP_DIRECT	GO:0007568~aging	6	5.48	0.99	0.16	7.23
GOTERM_BP_DIRECT	GO:0042542~response to hydrogen peroxide	4	11.58	1.00	0.16	7.49
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	7	4.63	0.99	0.16	6.13
GOTERM_BP_DIRECT	GO:0090303~positive regulation of wound healing	3	30.68	0.99	0.16	6.38
INTERPRO	IPR026823:Complement Clr-like EGF domain	3	20.50	0.93	0.16	11.50
GOTERM_BP_DIRECT	GO:0045087~innate immune response	14	2.43	0.99	0.16	6.94
GOTERM_CC_DIRECT	GO:0005584~collagen type I trimer	2	159.47	0.86	0.16	13.95
INTERPRO	IPR001751:S100/Calbindin-D9k, conserved site	3	19.68	0.94	0.16	12.39

GOTERM_BP_DIRECT	GO:0014002~astrocyte development	3	28.76	0.99	0.16	7.23
GOTERM_BP_DIRECT	GO:0070373~negative regulation of ERK1 and ERK2 cascade	4	12.03	0.99	0.16	6.75
UP_KEYWORDS	Polymorphism	79	1.17	0.99	0.16	24.30
GOTERM_BP_DIRECT	GO:0071230~cellular response to amino acid stimulus	4	12.52	0.99	0.17	6.05
GOTERM_CC_DIRECT	GO:0030133~transport vesicle	4	8.50	0.84	0.17	12.91
GOTERM_BP_DIRECT	GO:0007267~cell-cell signaling	7	4.26	1.00	0.17	9.00
GOTERM_MF_DIRECT	GO:0004601~peroxidase activity	3	23.11	0.81	0.17	8.86
INTERPRO	IPR013787:S100/CaBP-9k-type, calcium binding, subdomain	3	18.22	0.96	0.17	14.25
GOTERM_CC_DIRECT	GO:0031410~cytoplasmic vesicle	5	5.35	0.89	0.17	15.61
INTERPRO	IPR008160:Collagen triple helix repeat	4	8.63	0.96	0.17	13.62
GOTERM_BP_DIRECT	GO:0009612~response to mechanical stimulus	4	10.58	1.00	0.17	9.54
GOTERM_BP_DIRECT	GO:0007165~signal transduction	15	2.22	1.00	0.18	10.27
GOTERM_BP_DIRECT	GO:0031668~cellular response to extracellular stimulus	3	24.22	1.00	0.18	10.03
GOTERM_BP_DIRECT	GO:0030203~glycosaminoglycan metabolic process	5	6.50	1.00	0.18	10.90
BIOCARTA	h_slrpPathway:Small Leucine-rich Proteoglycan (SLRP) molecules	3	32.54	0.18	0.18	3.05
GOTERM_CC_DIRECT	GO:0042383~sarcolemma	4	6.93	0.96	0.19	21.28
UP_SEQ_FEATURE	calcium-binding region:1; low affinity	3	28.04	0.93	0.19	7.00
GOTERM_CC_DIRECT	GO:0005589~collagen type VI trimer	2	106.31	0.95	0.19	20.18
UP_SEQ_FEATURE	region of interest:Heparin-binding	3	26.63	0.95	0.19	7.72
UP_SEQ_FEATURE	domain:IGFBP N-terminal	3	26.63	0.95	0.19	7.72
UP_SEQ_FEATURE	domain:TSP type-1	3	25.37	0.96	0.20	8.47
UP_SEQ_FEATURE	calcium-binding region:2; high affinity	3	24.21	0.97	0.20	9.25
GOTERM_BP_DIRECT	GO:0007613~memory	4	9.44	1.00	0.21	12.86
UP_SEQ_FEATURE	region of interest:Triple-helical region	3	23.16	0.98	0.21	10.05
GOTERM_MF_DIRECT	GO:0001618~virus receptor activity	4	8.80	0.91	0.21	12.48
PIR_SUPERFAMILY	PIRSF000939:dual specificity protein phosphatase (MAP kinase ph	2	23.71	0.70	0.22	42.95
GOTERM_CC_DIRECT	GO:0031838~haptoglobin-hemoglobin complex	2	79.73	0.98	0.22	25.95
GOTERM_BP_DIRECT	GO:0008217~regulation of blood pressure	4	9.16	1.00	0.22	13.90
INTERPRO	IPR001304:C-type lectin	4	7.45	0.99	0.22	19.55
GOTERM_BP_DIRECT	GO:0001816~cytokine production	3	20.01	1.00	0.22	14.27
INTERPRO	IPR003410:Hyalin	2	109.34	0.99	0.22	21.45
INTERPRO	IPR016352:Small leucine-rich proteoglycan, class I, decorin/asporn	2	109.34	0.99	0.22	21.45
UP_KEYWORDS	Disease mutation	22	1.58	1.00	0.22	33.11
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	9	2.99	1.00	0.22	14.87
UP_KEYWORDS	Congenital generalized lipodystrophy	2	59.12	1.00	0.23	34.68
PIR_SUPERFAMILY	PIRSF001875:alpha-defensin	2	27.67	0.65	0.23	38.18
INTERPRO	IPR000566:Lipocalin/cytosolic fatty-acid binding protein domain	3	14.47	0.99	0.23	21.32
INTERPRO	IPR018097:EGF-like calcium-binding, conserved site	4	6.76	1.00	0.23	24.56
INTERPRO	IPR027465:Proteinase inhibitor I35, tissue inhibitor of metalloprot	2	82.00	1.00	0.24	27.53
INTERPRO	IPR001820:Proteinase inhibitor I35, tissue inhibitor of metalloprot	2	82.00	1.00	0.24	27.53
INTERPRO	IPR016468:CCAAT/enhancer-binding	2	82.00	1.00	0.24	27.53
INTERPRO	IPR000152:EGF-type aspartate/asparagine hydroxylation site	4	6.50	1.00	0.24	26.91
SMART	SM00034:SM00034	4	5.58	0.91	0.24	29.94
GOTERM_BP_DIRECT	GO:0010951~negative regulation of endopeptidase activity	5	5.72	1.00	0.24	16.39
INTERPRO	IPR012674:Calycin	3	13.30	1.00	0.24	24.56
UP_SEQ_FEATURE	domain:Anaphylatoxin-like 2	2	177.56	1.00	0.24	15.07
UP_SEQ_FEATURE	domain:Anaphylatoxin-like 1	2	177.56	1.00	0.24	15.07
UP_SEQ_FEATURE	domain:Anaphylatoxin-like 3	2	177.56	1.00	0.24	15.07
UP_SEQ_FEATURE	domain:EGF-like 6; calcium-binding	3	20.49	0.99	0.25	12.61
INTERPRO	IPR011038:Calycin-like	3	12.62	1.00	0.25	26.76
UP_SEQ_FEATURE	domain:C-type lectin	4	8.66	1.00	0.25	14.77
GOTERM_BP_DIRECT	GO:0000188~inactivation of MAPK activity	3	17.04	1.00	0.25	18.98
PIR_SUPERFAMILY	PIRSF036495:IGFBP-related protein, CNN type	2	33.20	0.58	0.25	33.01
GOTERM_BP_DIRECT	GO:0001558~regulation of cell growth	4	8.29	1.00	0.25	17.82
SMART	SM00206:SM00206	2	61.43	0.90	0.25	28.53
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	7	3.59	1.00	0.25	18.90
UP_SEQ_FEATURE	domain:EGF-like 7; calcium-binding	3	19.02	1.00	0.25	14.42
GOTERM_BP_DIRECT	GO:0046851~negative regulation of bone remodeling	2	153.38	1.00	0.25	18.74
GOTERM_BP_DIRECT	GO:0032602~chemokine production	2	153.38	1.00	0.25	18.74
GOTERM_BP_DIRECT	GO:2000041~negative regulation of planar cell polarity pathway ir	2	153.38	1.00	0.25	18.74
GOTERM_BP_DIRECT	GO:0070488~neutrophil aggregation	2	153.38	1.00	0.25	18.74
GOTERM_BP_DIRECT	GO:0042060~wound healing	4	8.18	1.00	0.25	18.42

GOTERM_BP_DIRECT	GO:0030574~collagen catabolic process	4	8.18	1.00	0.25	18.42
GOTERM_BP_DIRECT	GO:0044344~cellular response to fibroblast growth factor stimulu:	3	17.70	1.00	0.26	17.76
UP_SEQ_FEATURE	domain:EGF-like	4	8.88	1.00	0.26	13.87
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	9	2.83	1.00	0.26	19.87
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	6	4.18	1.00	0.26	20.28
GOTERM_BP_DIRECT	GO:0051384~response to glucocorticoid	4	7.77	1.00	0.26	20.88
GOTERM_CC_DIRECT	GO:0031093~platelet alpha granule lumen	3	9.97	1.00	0.26	35.60
GOTERM_BP_DIRECT	GO:0071260~cellular response to mechanical stimulus	4	7.67	1.00	0.26	21.52
GOTERM_CC_DIRECT	GO:0005788~endoplasmic reticulum lumen	5	4.13	0.99	0.26	32.74
INTERPRO	IPR012395:IGFBP-related, CNN	2	65.60	1.00	0.27	33.13
INTERPRO	IPR018378:C-type lectin, conserved site	3	11.18	1.00	0.27	32.37
GOTERM_CC_DIRECT	GO:0005829~cytosol	29	1.44	1.00	0.27	35.08
UP_SEQ_FEATURE	repeat:LRR 12	4	7.89	1.00	0.28	18.58
UP_SEQ_FEATURE	domain:Sushi 3	3	16.65	1.00	0.28	18.27
SMART	SM00179:SM00179	4	4.91	0.97	0.29	38.94
PIR_SUPERFAMILY	PIRSF005879:CCAAT/enhancer-binding protein	2	41.50	0.50	0.29	27.42
INTERPRO	IPR006081:Mammalian defensins	2	54.67	1.00	0.30	38.31
INTERPRO	IPR016327:Alpha-defensin	2	54.67	1.00	0.30	38.31
INTERPRO	IPR025155:WxxW domain	2	54.67	1.00	0.30	38.31
INTERPRO	IPR002366:Defensin propeptide	2	54.67	1.00	0.30	38.31
GOTERM_BP_DIRECT	GO:2001244~positive regulation of intrinsic apoptotic signaling pa	3	14.38	1.00	0.30	25.32
SMART	SM00104:SM00104	2	35.10	0.98	0.31	44.45
UP_KEYWORDS	Host cell receptor for virus entry	3	8.31	1.00	0.31	47.67
GOTERM_BP_DIRECT	GO:0044691~tooth eruption	2	102.26	1.00	0.32	26.75
GOTERM_CC_DIRECT	GO:0043005~neuron projection	5	3.62	1.00	0.32	45.02
GOTERM_BP_DIRECT	GO:0007517~muscle organ development	4	6.82	1.00	0.33	28.24
UP_KEYWORDS	Prostaglandin biosynthesis	2	35.47	1.00	0.33	50.83
UP_KEYWORDS	Metalloprotease inhibitor	2	35.47	1.00	0.33	50.83
GOTERM_MF_DIRECT	GO:0031720~haptoglobin binding	2	102.70	0.99	0.33	21.95
INTERPRO	IPR000020:Anaphylatoxin/fibulin	2	46.86	1.00	0.33	43.08
UP_SEQ_FEATURE	repeat:LRR 11	4	7.03	1.00	0.34	24.41
UP_KEYWORDS	Prostaglandin metabolism	2	32.25	1.00	0.35	54.20
UP_KEYWORDS	Metalloenzyme inhibitor	2	32.25	1.00	0.35	54.20
GOTERM_CC_DIRECT	GO:0072562~blood microparticle	4	4.52	1.00	0.35	51.15
GOTERM_BP_DIRECT	GO:0043407~negative regulation of MAP kinase activity	3	12.78	1.00	0.35	30.62
GOTERM_MF_DIRECT	GO:0005516~calmodulin binding	5	4.33	1.00	0.35	30.39
KEGG_PATHWAY	hsa04974:Protein digestion and absorption	4	5.76	0.97	0.35	29.50
UP_KEYWORDS	Actin-binding	5	3.32	1.00	0.35	56.05
GOTERM_MF_DIRECT	GO:0050544~arachidonic acid binding	2	61.62	1.00	0.35	33.84
UP_KEYWORDS	Complement alternate pathway	2	29.56	1.00	0.35	57.34
UP_KEYWORDS	Glycation	2	29.56	1.00	0.35	57.34
KEGG_PATHWAY	hsa05206:MicroRNAs in cancer	7	3.08	0.93	0.35	23.34
GOTERM_CC_DIRECT	GO:0005811~lipid particle	3	7.72	1.00	0.36	50.61
KEGG_PATHWAY	hsa05143:African trypanosomiasis	3	11.39	0.95	0.36	26.89
UP_KEYWORDS	Fungicide	2	27.29	1.00	0.36	60.26
UP_KEYWORDS	Oxygen transport	2	27.29	1.00	0.36	60.26
UP_KEYWORDS	Phosphoprotein	51	1.21	1.00	0.36	59.40
GOTERM_MF_DIRECT	GO:0004867~serine-type endopeptidase inhibitor activity	4	6.49	1.00	0.36	26.10
GOTERM_CC_DIRECT	GO:0005901~caveola	3	6.93	1.00	0.36	57.54
GOTERM_MF_DIRECT	GO:0005515~protein binding	67	1.19	1.00	0.36	33.26
GOTERM_MF_DIRECT	GO:0008307~structural constituent of muscle	3	11.55	1.00	0.36	29.81
INTERPRO	IPR002345:Lipocalin	2	41.00	1.00	0.36	47.48
GOTERM_CC_DIRECT	GO:0030666~endocytic vesicle membrane	3	7.25	1.00	0.36	54.63
GOTERM_MF_DIRECT	GO:0035662~Toll-like receptor 4 binding	2	77.02	1.00	0.36	28.14
GOTERM_CC_DIRECT	GO:0005833~hemoglobin complex	2	26.58	1.00	0.37	59.41
GOTERM_BP_DIRECT	GO:0010811~positive regulation of cell-substrate adhesion	3	12.11	1.00	0.37	33.30
GOTERM_BP_DIRECT	GO:0046426~negative regulation of JAK-STAT cascade	3	12.11	1.00	0.37	33.30
GOTERM_CC_DIRECT	GO:0005856~cytoskeleton	6	2.73	1.00	0.37	57.16
GOTERM_BP_DIRECT	GO:0005975~carbohydrate metabolic process	7	3.10	1.00	0.37	33.02
UP_KEYWORDS	Ehlers-Danlos syndrome	2	25.34	1.00	0.37	62.98
GOTERM_BP_DIRECT	GO:0070459~prolactin secretion	2	76.69	1.00	0.37	33.97
GOTERM_BP_DIRECT	GO:0045629~negative regulation of T-helper 2 cell differentiation	2	76.69	1.00	0.37	33.97

GOTERM_BP_DIRECT	GO:0032119~sequestering of zinc ion	2	76.69	1.00	0.37	33.97
GOTERM_BP_DIRECT	GO:0002793~positive regulation of peptide secretion	2	76.69	1.00	0.37	33.97
GOTERM_CC_DIRECT	GO:0030141~secretory granule	3	6.38	1.00	0.37	63.03
UP_KEYWORDS	Serine protease inhibitor	3	6.26	1.00	0.37	66.13
UP_KEYWORDS	Pyruvate	2	23.65	1.00	0.38	65.52
UP_SEQ_FEATURE	metal ion-binding site:Zinc; via amide nitrogen and carbonyl oxyge	2	88.78	1.00	0.38	27.86
UP_SEQ_FEATURE	region of interest:Involved in metalloproteinase-binding	2	88.78	1.00	0.38	27.86
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	38	1.26	1.00	0.38	62.18
UP_KEYWORDS	Apoptosis	7	2.32	1.00	0.38	65.28
SMART	SM00048:SM00048	2	24.57	1.00	0.38	56.83
GOTERM_MF_DIRECT	GO:0043184~vascular endothelial growth factor receptor 2 bindin	2	51.35	1.00	0.39	39.08
INTERPRO	IPR000837:Fos transforming protein	2	36.45	1.00	0.39	51.54
GOTERM_BP_DIRECT	GO:0032570~response to progesterone	3	11.50	1.00	0.39	35.99
SMART	SM00038:SM00038	2	22.34	1.00	0.39	60.31
UP_KEYWORDS	Growth factor binding	2	19.71	1.00	0.40	72.14
UP_KEYWORDS	Cytoplasm	34	1.27	1.00	0.40	71.48
PIR_SUPERFAMILY	PIRSF002490:class I small leucine-rich proteoglycan, decorin/aspo	2	55.33	0.40	0.40	21.36
UP_KEYWORDS	Deafness	4	3.68	1.00	0.41	71.31
INTERPRO	IPR006080:Beta defensin/Neutrophil defensin	2	32.80	1.00	0.41	55.29
INTERPRO	IPR008343:Mitogen-activated protein (MAP) kinase phosphatase	2	32.80	1.00	0.41	55.29
GOTERM_BP_DIRECT	GO:0032870~cellular response to hormone stimulus	3	10.96	1.00	0.41	38.68
UP_SEQ_FEATURE	domain:TSP type-1 1	3	11.84	1.00	0.42	32.06
UP_SEQ_FEATURE	site:Reactive bond	3	11.84	1.00	0.42	32.06
UP_SEQ_FEATURE	domain:TSP type-1 2	3	11.84	1.00	0.42	32.06
UP_SEQ_FEATURE	repeat:LRR 10	4	6.12	1.00	0.42	33.14
GOTERM_CC_DIRECT	GO:0071682~endocytic vesicle lumen	2	19.93	1.00	0.42	69.95
GOTERM_CC_DIRECT	GO:0032982~myosin filament	2	19.93	1.00	0.42	69.95
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	4	5.68	1.00	0.42	41.39
GOTERM_BP_DIRECT	GO:0060355~positive regulation of cell adhesion molecule produc	2	61.35	1.00	0.42	40.48
GOTERM_BP_DIRECT	GO:0019731~antibacterial humoral response	3	10.70	1.00	0.42	40.02
GOTERM_BP_DIRECT	GO:0007566~embryo implantation	3	10.70	1.00	0.42	40.02
GOTERM_BP_DIRECT	GO:0045429~positive regulation of nitric oxide biosynthetic proce:	3	10.46	1.00	0.42	41.36
GOTERM_BP_DIRECT	GO:0045600~positive regulation of fat cell differentiation	3	10.46	1.00	0.42	41.36
INTERPRO	IPR000885:Fibrillar collagen, C-terminal	2	29.82	1.00	0.43	58.75
UP_SEQ_FEATURE	domain:EGF-like 1	4	5.92	1.00	0.43	35.58
KEGG_PATHWAY	hsa05146:Amoebiasis	4	4.73	1.00	0.44	44.00
GOTERM_BP_DIRECT	GO:0035556~intracellular signal transduction	7	2.84	1.00	0.44	44.26
GOTERM_BP_DIRECT	GO:0009267~cellular response to starvation	3	10.00	1.00	0.44	44.01
INTERPRO	IPR022272:Lipocalin conserved site	2	27.33	1.00	0.45	61.94
GOTERM_BP_DIRECT	GO:0031394~positive regulation of prostaglandin biosynthetic pro	2	51.13	1.00	0.46	46.34
GOTERM_BP_DIRECT	GO:0019800~peptide cross-linking via chondroitin 4-sulfate glycos	2	51.13	1.00	0.46	46.34
GOTERM_BP_DIRECT	GO:0060056~mammary gland involution	2	51.13	1.00	0.46	46.34
GOTERM_BP_DIRECT	GO:0048553~negative regulation of metalloenzyme activity	2	51.13	1.00	0.46	46.34
GOTERM_BP_DIRECT	GO:0051045~negative regulation of membrane protein ectodoma	2	51.13	1.00	0.46	46.34
UP_SEQ_FEATURE	propeptide:N-terminal propeptide	2	59.19	1.00	0.46	38.73
GOTERM_BP_DIRECT	GO:0007596~blood coagulation	8	2.49	1.00	0.46	48.16
GOTERM_BP_DIRECT	GO:0050900~leukocyte migration	4	5.29	1.00	0.46	47.35
GOTERM_BP_DIRECT	GO:0071560~cellular response to transforming growth factor beta	3	9.39	1.00	0.46	47.91
GOTERM_BP_DIRECT	GO:0030204~chondroitin sulfate metabolic process	3	9.39	1.00	0.46	47.91
KEGG_PATHWAY	hsa04668:TNF signaling pathway	4	4.77	1.00	0.46	43.23
INTERPRO	IPR000971:Globin	2	25.23	1.00	0.47	64.89
INTERPRO	IPR009050:Globin-like	2	25.23	1.00	0.47	64.89
INTERPRO	IPR012292:Globin, structural domain	2	23.43	1.00	0.48	67.61
GOTERM_BP_DIRECT	GO:0014012~peripheral nervous system axon regeneration	2	43.82	1.00	0.48	51.63
GOTERM_BP_DIRECT	GO:0030213~hyaluronan biosynthetic process	2	43.82	1.00	0.48	51.63
GOTERM_BP_DIRECT	GO:0060452~positive regulation of cardiac muscle contraction	2	43.82	1.00	0.48	51.63
GOTERM_BP_DIRECT	GO:0071481~cellular response to X-ray	2	43.82	1.00	0.48	51.63
UP_SEQ_FEATURE	repeat:LRR 9	4	5.30	1.00	0.49	44.21
GOTERM_MF_DIRECT	GO:0016504~peptidase activator activity	2	30.81	1.00	0.49	56.23
UP_SEQ_FEATURE	sequence variant	80	1.14	1.00	0.49	42.46
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	7	2.70	1.00	0.49	51.53
UP_SEQ_FEATURE	site:Not glycosylated	2	50.73	1.00	0.49	43.54

GOTERM_BP_DIRECT	GO:0044281~small molecule metabolic process	18	1.62	1.00	0.49	53.13
UP_SEQ_FEATURE	domain:EGF-like 2; calcium-binding	3	9.18	1.00	0.50	46.26
GOTERM_MF_DIRECT	GO:0005518~collagen binding	3	7.34	1.00	0.50	55.99
UP_SEQ_FEATURE	propeptide:C-terminal propeptide	2	44.39	1.00	0.50	47.97
GOTERM_MF_DIRECT	GO:0008289~lipid binding	4	4.43	1.00	0.51	55.02
GOTERM_BP_DIRECT	GO:0071407~cellular response to organic cyclic compound	3	8.07	1.00	0.51	57.77
GOTERM_BP_DIRECT	GO:0030168~platelet activation	5	3.53	1.00	0.52	57.55
GOTERM_BP_DIRECT	GO:0006006~glucose metabolic process	4	4.76	1.00	0.52	56.78
GOTERM_BP_DIRECT	GO:0051092~positive regulation of NF-kappaB transcription factor	4	4.72	1.00	0.52	57.48
GOTERM_BP_DIRECT	GO:0050680~negative regulation of epithelial cell proliferation	3	8.22	1.00	0.52	56.59
GOTERM_BP_DIRECT	GO:0009611~response to wounding	3	7.93	1.00	0.52	58.93
INTERPRO	IPR015526:Frizzled/secreted frizzled-related protein	2	20.50	1.00	0.52	72.43
INTERPRO	IPR006208:Cystine knot	2	20.50	1.00	0.52	72.43
INTERPRO	IPR013111:EGF, extracellular	2	20.50	1.00	0.52	72.43
GOTERM_BP_DIRECT	GO:0002523~leukocyte migration involved in inflammatory respor	2	38.35	1.00	0.52	56.40
GOTERM_BP_DIRECT	GO:0031622~positive regulation of fever generation	2	38.35	1.00	0.52	56.40
GOTERM_BP_DIRECT	GO:0043569~negative regulation of insulin-like growth factor rece	2	38.35	1.00	0.52	56.40
GOTERM_BP_DIRECT	GO:0060346~bone trabecula formation	2	38.35	1.00	0.52	56.40
GOTERM_BP_DIRECT	GO:0090263~positive regulation of canonical Wnt signaling pathw	4	4.61	1.00	0.52	59.56
GOTERM_MF_DIRECT	GO:0001077~transcriptional activator activity, RNA polymerase II c	5	3.36	1.00	0.53	54.93
GOTERM_BP_DIRECT	GO:0007179~transforming growth factor beta receptor signaling p	4	4.54	1.00	0.53	60.92
GOTERM_BP_DIRECT	GO:0033689~negative regulation of osteoblast proliferation	2	34.09	1.00	0.53	60.70
GOTERM_BP_DIRECT	GO:0030728~ovulation	2	34.09	1.00	0.53	60.70
GOTERM_BP_DIRECT	GO:0090244~Wnt signaling pathway involved in somitogenesis	2	34.09	1.00	0.53	60.70
GOTERM_BP_DIRECT	GO:0050776~regulation of immune response	4	4.51	1.00	0.53	61.59
GOTERM_BP_DIRECT	GO:0051216~cartilage development	3	7.54	1.00	0.53	62.31
GOTERM_BP_DIRECT	GO:0045669~positive regulation of osteoblast differentiation	3	7.54	1.00	0.53	62.31
UP_SEQ_FEATURE	repeat:LRR 8	4	4.80	1.00	0.53	52.76
UP_SEQ_FEATURE	glycosylation site:O-linked (Gal...)	2	39.46	1.00	0.54	52.05
UP_SEQ_FEATURE	glycosylation site:N-linked (Glc) (glycation)	2	39.46	1.00	0.54	52.05
GOTERM_MF_DIRECT	GO:0008191~metalloendopeptidase inhibitor activity	2	22.01	1.00	0.55	68.55
GOTERM_MF_DIRECT	GO:0005344~oxygen transporter activity	2	22.01	1.00	0.55	68.55
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	4	3.85	1.00	0.55	67.57
GOTERM_MF_DIRECT	GO:0030674~protein binding, bridging	3	6.25	1.00	0.56	66.62
GOTERM_MF_DIRECT	GO:0048018~receptor agonist activity	2	20.54	1.00	0.56	71.05
GOTERM_MF_DIRECT	GO:0005504~fatty acid binding	2	20.54	1.00	0.56	71.05
GOTERM_MF_DIRECT	GO:0035259~glucocorticoid receptor binding	2	23.70	1.00	0.56	65.84
GOTERM_MF_DIRECT	GO:0017017~MAP kinase tyrosine/serine/threonine phosphatase	2	23.70	1.00	0.56	65.84
KEGG_PATHWAY	hsa04380:Osteoclast differentiation	4	3.86	1.00	0.58	61.75
UP_SEQ_FEATURE	domain:Fibrillar collagen NC1	2	32.28	1.00	0.58	59.28
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	3	6.97	1.00	0.58	67.56
GOTERM_BP_DIRECT	GO:0031100~organ regeneration	3	6.97	1.00	0.58	67.56
GOTERM_BP_DIRECT	GO:0035313~wound healing, spreading of epidermal cells	2	27.89	1.00	0.58	68.07
UP_SEQ_FEATURE	compositionally biased region:Cys-rich	4	4.47	1.00	0.59	59.19
UP_SEQ_FEATURE	DNA-binding region:Basic motif	4	4.36	1.00	0.59	61.44
GOTERM_BP_DIRECT	GO:0006869~lipid transport	3	6.67	1.00	0.60	70.47
GOTERM_BP_DIRECT	GO:0050732~negative regulation of peptidyl-tyrosine phosphoryla	2	25.56	1.00	0.61	71.22
GOTERM_BP_DIRECT	GO:0030208~dermatan sulfate biosynthetic process	2	25.56	1.00	0.61	71.22
GOTERM_BP_DIRECT	GO:0045820~negative regulation of glycolytic process	2	25.56	1.00	0.61	71.22
GOTERM_BP_DIRECT	GO:0090179~planar cell polarity pathway involved in neural tube c	2	25.56	1.00	0.61	71.22
GOTERM_BP_DIRECT	GO:0050729~positive regulation of inflammatory response	3	6.48	1.00	0.61	72.30
KEGG_PATHWAY	hsa03320:PPAR signaling pathway	3	5.61	1.00	0.61	68.37
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme distal ligand)	2	27.32	1.00	0.62	65.42
GOTERM_BP_DIRECT	GO:0010952~positive regulation of peptidase activity	2	23.60	1.00	0.63	74.06
GOTERM_BP_DIRECT	GO:0006957~complement activation, alternative pathway	2	23.60	1.00	0.63	74.06
UP_SEQ_FEATURE	repeat:LRR 7	4	4.04	1.00	0.63	68.32
UP_SEQ_FEATURE	glycosylation site:C-linked (Man)	2	25.37	1.00	0.64	68.13
GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	3	6.14	1.00	0.64	75.74
GOTERM_BP_DIRECT	GO:0090090~negative regulation of canonical Wnt signaling pathw	4	3.79	1.00	0.65	76.92
GOTERM_BP_DIRECT	GO:0030502~negative regulation of bone mineralization	2	21.91	1.00	0.65	76.61
GOTERM_BP_DIRECT	GO:0001706~endoderm formation	2	21.91	1.00	0.65	76.61
GOTERM_BP_DIRECT	GO:0043508~negative regulation of JUN kinase activity	2	21.91	1.00	0.65	76.61

GOTERM_BP_DIRECT	GO:0001516~prostaglandin biosynthetic process	2	21.91	1.00	0.65	76.61
GOTERM_BP_DIRECT	GO:0070208~protein heterotrimerization	2	21.91	1.00	0.65	76.61
GOTERM_BP_DIRECT	GO:0031640~killing of cells of other organism	2	21.91	1.00	0.65	76.61
GOTERM_BP_DIRECT	GO:0060347~heart trabecula formation	2	21.91	1.00	0.65	76.61
GOTERM_BP_DIRECT	GO:0019371~cyclooxygenase pathway	2	21.91	1.00	0.65	76.61
GOTERM_BP_DIRECT	GO:0031116~positive regulation of microtubule polymerization	2	21.91	1.00	0.65	76.61
GOTERM_BP_DIRECT	GO:0045892~negative regulation of transcription, DNA-templated	7	2.22	1.00	0.66	78.94
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polym	11	1.75	1.00	0.66	79.49
GOTERM_BP_DIRECT	GO:0030214~hyaluronan catabolic process	2	20.45	1.00	0.66	78.92
GOTERM_BP_DIRECT	GO:0015671~oxygen transport	2	20.45	1.00	0.66	78.92
GOTERM_BP_DIRECT	GO:0043409~negative regulation of MAPK cascade	2	20.45	1.00	0.66	78.92
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	8	2.05	1.00	0.66	78.78
GOTERM_BP_DIRECT	GO:0030949~positive regulation of vascular endothelial growth fa	2	19.17	1.00	0.67	81.00
GOTERM_BP_DIRECT	GO:0048546~digestive tract morphogenesis	2	19.17	1.00	0.67	81.00
UP_SEQ_FEATURE	domain:EGF-like 9; calcium-binding	2	22.19	1.00	0.67	72.93
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme proximal ligand)	2	22.19	1.00	0.67	72.93
GOTERM_BP_DIRECT	GO:0007584~response to nutrient	3	5.61	1.00	0.67	80.98
UP_SEQ_FEATURE	domain:EGF-like 2	3	5.99	1.00	0.68	74.10
OMIM_DISEASE	166220:Osteogenesis imperfecta, type IV	2	131.67	0.69	0.69	14.58
OMIM_DISEASE	166210:Osteogenesis imperfecta, type II	2	131.67	0.69	0.69	14.58
OMIM_DISEASE	259420:Osteogenesis imperfecta, type III	2	131.67	0.69	0.69	14.58