

Table S1 GO analysis of LGALS1 coexpression genes.

Category	ID	Description	Count	pvalue	p.adjust
BP	GO:0030198	extracellular matrix organization	70	1.83E-46	7.03E-43
BP	GO:0043062	extracellular structure organization	70	6.01E-42	1.15E-38
BP	GO:0030199	collagen fibril organization	20	2.98E-21	3.82E-18
BP	GO:0001501	skeletal system development	48	1.54E-17	1.48E-14
BP	GO:0001503	ossification	42	1.17E-16	8.69E-14
BP	GO:0032963	collagen metabolic process	23	1.36E-16	6.69E-14
BP	GO:0061448	connective tissue development	33	3.30E-16	1.82E-13
BP	GO:0060348	bone development	28	6.54E-15	3.14E-12
BP	GO:0035987	endodermal cell differentiation	15	5.04E-14	2.15E-11
BP	GO:0071560	cellular response to transforming growth factor beta stimulus	29	2.15E-13	8.26E-11
BP	GO:0001706	endoderm formation	15	2.95E-13	1.03E-10
BP	GO:0071559	response to transforming growth factor beta	29	4.14E-13	1.33E-10
BP	GO:0051216	cartilage development	25	1.09E-12	3.23E-10
BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	33	1.28E-12	3.52E-10
BP	GO:0031589	cell-substrate adhesion	32	5.98E-12	1.53E-09
BP	GO:0007492	endoderm development	16	9.76E-12	2.22E-09
BP	GO:0002062	chondrocyte differentiation	18	9.82E-12	2.22E-09
BP	GO:0007179	transforming growth factor beta receptor signaling pathway	23	6.34E-11	1.36E-08
BP	GO:0034330	cell junction organization	28	8.78E-11	1.78E-08
BP	GO:0002063	chondrocyte development	10	2.67E-10	5.13E-08
BP	GO:0048762	mesenchymal cell differentiation	23	3.12E-10	5.71E-08
BP	GO:0060485	mesenchyme development	26	4.49E-10	7.85E-08
BP	GO:0090288	negative regulation of cellular response to growth factor stimulus	20	7.24E-10	1.21E-07
BP	GO:0007160	cell-matrix adhesion	23	1.32E-09	2.12E-07
BP	GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	23	1.45E-09	2.23E-07
BP	GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	17	1.51E-09	2.23E-07
BP	GO:0090287	regulation of cellular response to growth factor stimulus	26	1.92E-09	2.63E-07
BP	GO:0001704	formation of primary germ layer	17	1.98E-09	2.63E-07
BP	GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	17	1.98E-09	2.63E-07
BP	GO:0010810	regulation of cell-substrate adhesion	22	2.15E-09	2.76E-07
BP	GO:0048705	skeletal system morphogenesis	22	2.85E-09	3.53E-07
BP	GO:0022617	extracellular matrix disassembly	14	3.20E-09	3.72E-07
BP	GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	14	3.20E-09	3.72E-07
BP	GO:0091011	negative regulation of transmembrane receptor protein serine/threonine kinase signaling	17	3.36E-09	3.80E-07
BP	GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	14	4.51E-09	4.96E-07
BP	GO:0001837	epithelial to mesenchymal transition	18	4.94E-09	5.28E-07
BP	GO:0001649	osteoblast differentiation	22	1.37E-08	1.42E-06
BP	GO:0060349	bone morphogenesis	14	2.18E-08	2.21E-06
BP	GO:1903053	regulation of extracellular matrix organization	10	2.64E-08	2.60E-06
BP	GO:0032964	collagen biosynthetic process	11	3.25E-08	3.12E-06
BP	GO:0034329	cell junction assembly	21	3.48E-08	3.27E-06
BP	GO:0061035	regulation of cartilage development	12	3.70E-08	3.39E-06
BP	GO:0006909	phagocytosis	25	7.72E-08	6.90E-06
BP	GO:0030206	chondroitin sulfate biosynthetic process	8	9.22E-08	8.06E-06
BP	GO:0030574	collagen catabolic process	9	1.37E-07	1.17E-05
BP	GO:1901888	regulation of cell junction assembly	13	1.72E-07	1.44E-05
BP	GO:0085029	extracellular matrix assembly	8	1.76E-07	1.44E-05
BP	GO:0010717	regulation of epithelial to mesenchymal transition	13	1.96E-07	1.57E-05
BP	GO:0006024	glycosaminoglycan biosynthetic process	14	2.05E-07	1.61E-05
BP	GO:0007369	gastrulation	18	2.12E-07	1.63E-05
BP	GO:0006023	aminoglycan biosynthetic process	14	2.30E-07	1.74E-05
BP	GO:0050650	chondroitin sulfate proteoglycan biosynthetic process	8	2.38E-07	1.76E-05
BP	GO:0042476	odontogenesis	15	2.66E-07	1.93E-05
BP	GO:0002576	platelet degranulation	15	3.27E-07	2.33E-05
BP	GO:0006911	phagocytosis, engulfment	9	3.54E-07	2.48E-05
BP	GO:1903510	mucopolysaccharide metabolic process	14	3.64E-07	2.50E-05
BP	GO:0001952	regulation of cell-matrix adhesion	14	6.26E-07	4.22E-05
BP	GO:0002573	myeloid leukocyte differentiation	18	1.28E-06	8.51E-05
BP	GO:0045216	cell-cell junction organization	14	1.87E-06	0.000122031
BP	GO:0001654	eye development	24	1.95E-06	0.000125236
BP	GO:0030316	osteoclast differentiation	12	1.99E-06	0.000125236
BP	GO:0099024	plasma membrane invagination	9	2.10E-06	0.000130339
BP	GO:0071230	cellular response to amino acid stimulus	10	2.21E-06	0.000133926
BP	GO:0006029	proteoglycan metabolic process	11	2.23E-06	0.000133926
BP	GO:0150063	visual system development	24	2.39E-06	0.000141602
BP	GO:0007044	cell-substrate junction assembly	12	2.49E-06	0.000145153
BP	GO:1904888	cranial skeletal system development	10	2.55E-06	0.000146573
BP	GO:0030204	chondroitin sulfate metabolic process	8	2.78E-06	0.000157157
BP	GO:0048880	sensory system development	24	3.07E-06	0.000171044
BP	GO:0060541	respiratory system development	17	3.17E-06	0.00017403
BP	GO:0034332	adherens junction organization	14	3.24E-06	0.000175423
BP	GO:0030203	glycosaminoglycan metabolic process	15	4.44E-06	0.000237361
BP	GO:0050654	chondroitin sulfate proteoglycan metabolic process	8	5.01E-06	0.000264083
BP	GO:0006022	aminoglycan metabolic process	15	6.06E-06	0.000314856
BP	GO:1903055	positive regulation of extracellular matrix organization	6	6.45E-06	0.000330809
BP	GO:0061041	regulation of wound healing	14	6.96E-06	0.000352086
BP	GO:0010324	membrane invagination	9	7.57E-06	0.000375857
BP	GO:0070208	protein heterotrimerization	5	7.62E-06	0.000375857
BP	GO:0030282	bone mineralization	12	8.64E-06	0.000420353
BP	GO:0050673	epithelial cell proliferation	26	8.98E-06	0.00043163
BP	GO:0032330	regulation of chondrocyte differentiation	8	1.02E-05	0.000484739
BP	GO:0030324	lung development	15	1.09E-05	0.000512587
BP	GO:0033627	cell adhesion mediated by integrin	9	1.16E-05	0.000524031
BP	GO:0051893	regulation of focal adhesion assembly	9	1.16E-05	0.000524031
BP	GO:0090109	regulation of cell-substrate junction assembly	9	1.16E-05	0.000524031
BP	GO:0007229	integrin-mediated signaling pathway	11	1.24E-05	0.000555874
BP	GO:0030323	respiratory tube development	15	1.45E-05	0.000639916
BP	GO:0031214	biomineral tissue development	14	1.63E-05	0.000713264
BP	GO:0007045	cell-substrate adherens junction assembly	10	1.92E-05	0.000817952
BP	GO:0048041	focal adhesion assembly	10	1.92E-05	0.000817952
BP	GO:0010718	positive regulation of epithelial to mesenchymal transition	8	1.94E-05	0.000817952
BP	GO:0043010	camera-type eye development	20	2.31E-05	0.000964499
BP	GO:1903391	regulation of adherens junction organization	9	2.52E-05	0.001043188
BP	GO:0030166	proteoglycan biosynthetic process	8	3.01E-05	0.001229428
BP	GO:0048592	eye morphogenesis	13	3.78E-05	0.001528003
BP	GO:0097094	craniofacial suture morphogenesis	5	4.61E-05	0.001845129
BP	GO:0045785	positive regulation of cell adhesion	23	4.81E-05	0.001883174
BP	GO:0045667	regulation of osteoblast differentiation	12	4.82E-05	0.001883174

BP	GO:0034333	adherens junction assembly	10	4.85E-05	0.001883174
BP	GO:0001763	morphogenesis of a branching structure	15	4.92E-05	0.001891016
BP	GO:0060562	epithelial tube morphogenesis	20	5.33E-05	0.002030003
BP	GO:0001667	ameboidal-type cell migration	25	5.68E-05	0.002139978
BP	GO:1903034	regulation of response to wounding	14	5.96E-05	0.002224808
BP	GO:0009100	glycoprotein metabolic process	22	6.44E-05	0.002380758
BP	GO:0048701	embryonic cranial skeleton morphogenesis	7	6.71E-05	0.002457608
BP	GO:0045778	positive regulation of ossification	10	7.05E-05	0.002558058
BP	GO:0002064	epithelial cell development	15	7.40E-05	0.002635205
BP	GO:0030278	regulation of ossification	15	7.40E-05	0.002635205
BP	GO:0007162	negative regulation of cell adhesion	18	7.65E-05	0.002699233
BP	GO:0071675	regulation of mononuclear cell migration	7	7.79E-05	0.002722596
BP	GO:0061138	morphogenesis of a branching epithelium	14	8.11E-05	0.002810994
BP	GO:0014032	neural crest cell development	8	8.48E-05	0.002911426
BP	GO:1901201	regulation of extracellular matrix assembly	4	8.63E-05	0.002935516
BP	GO:0022612	gland morphogenesis	11	8.93E-05	0.003013111
BP	GO:0090596	sensory organ morphogenesis	17	9.04E-05	0.00302404
BP	GO:0048706	embryonic skeletal system development	11	9.66E-05	0.003200899
BP	GO:0009101	glycoprotein biosynthetic process	19	0.000100186	0.003292444
BP	GO:1903010	regulation of bone development	5	0.00010324	0.003364055
BP	GO:0030099	myeloid cell differentiation	23	0.000114728	0.00370696
BP	GO:0050900	leukocyte migration	25	0.000117799	0.003774489
BP	GO:0002685	regulation of leukocyte migration	14	0.000129769	0.004123638
BP	GO:0014031	mesenchymal cell development	8	0.000133969	0.004187884
BP	GO:0048864	stem cell development	8	0.000133969	0.004187884
BP	GO:0010712	regulation of collagen metabolic process	7	0.000136027	0.004217925
BP	GO:0051271	negative regulation of cellular component movement	21	0.00015452	0.004753046
BP	GO:0010812	negative regulation of cell-substrate adhesion	8	0.000166204	0.005031925
BP	GO:0045669	positive regulation of osteoblast differentiation	8	0.000166204	0.005031925
BP	GO:0048704	embryonic skeletal system morphogenesis	9	0.000167654	0.005036178
BP	GO:0016331	morphogenesis of embryonic epithelium	12	0.000171523	0.00504826
BP	GO:0048754	branching morphogenesis of an epithelial tube	12	0.000171523	0.00504826
BP	GO:1905521	regulation of macrophage migration	6	0.000171995	0.00504826
BP	GO:0002683	negative regulation of immune system process	24	0.000175731	0.00511884
BP	GO:0071674	mononuclear cell migration	8	0.000184566	0.005335772
BP	GO:0048771	tissue remodeling	13	0.000191627	0.005498542
BP	GO:0043200	response to amino acid	10	0.000193701	0.005516882
BP	GO:0060350	endochondral bone morphogenesis	7	0.000199445	0.00563871
BP	GO:2000146	negative regulation of cell motility	20	0.000215494	0.006047995
BP	GO:0000768	syncytium formation by plasma membrane fusion	7	0.000225221	0.006215279
BP	GO:0140253	cell-cell fusion	7	0.000225221	0.006215279
BP	GO:0014033	neural crest cell differentiation	8	0.000226304	0.006215279
BP	GO:0007517	muscle organ development	22	0.000228066	0.006219238
BP	GO:1903054	negative regulation of extracellular matrix organization	4	0.000247455	0.006700459
BP	GO:0042730	fibrinolysis	5	0.000249511	0.006708879
BP	GO:0071229	cellular response to acid chemical	14	0.000262569	0.007010964
BP	GO:0010631	epithelial cell migration	20	0.000279758	0.007418407
BP	GO:0030048	actin filament-based movement	11	0.000281725	0.007419411
BP	GO:0006949	syncytium formation	7	0.000284822	0.007449926
BP	GO:0060351	cartilage development involved in endochondral bone morphogenesis	5	0.000303017	0.007770827
BP	GO:0061037	negative regulation of cartilage development	5	0.000303017	0.007770827
BP	GO:0061045	negative regulation of wound healing	8	0.000303153	0.007770827
BP	GO:0090132	epithelium migration	20	0.000312075	0.007896324
BP	GO:0001101	response to acid chemical	19	0.000312156	0.007896324
BP	GO:0050651	dermatan sulfate proteoglycan biosynthetic process	4	0.000312126	0.008261957
BP	GO:0048010	vascular endothelial growth factor receptor signaling pathway	9	0.000332274	0.008261957
BP	GO:0030193	regulation of blood coagulation	8	0.000333057	0.008261957
BP	GO:0030336	negative regulation of cell migration	19	0.000336588	0.008296038
BP	GO:0060688	regulation of morphogenesis of a branching structure	7	0.000356475	0.00873022
BP	GO:0051017	actin filament bundle assembly	11	0.000364656	0.008834356
BP	GO:1900046	regulation of hemostasis	8	0.000365322	0.008834356
BP	GO:0090130	tissue migration	20	0.000386628	0.009273925
BP	GO:0061572	actin filament bundle organization	11	0.000388323	0.009273925
BP	GO:0001953	negative regulation of cell-matrix adhesion	6	0.000411446	0.009765503
BP	GO:0050655	dermatan sulfate proteoglycan metabolic process	4	0.000433483	0.010225414
BP	GO:0048839	inner ear development	13	0.000436351	0.010230308
BP	GO:0050680	negative regulation of epithelial cell proliferation	12	0.000473497	0.011031371
BP	GO:0050678	regulation of epithelial cell proliferation	20	0.000476257	0.011031371
BP	GO:0043583	ear development	14	0.000498494	0.011477306
BP	GO:0002521	leukocyte differentiation	24	0.000506594	0.011594373
BP	GO:0006929	substrate-dependent cell migration	5	0.000516324	0.011747142
BP	GO:0050818	regulation of coagulation	8	0.000520831	0.011779961
BP	GO:0032965	regulation of collagen biosynthetic process	6	0.000532258	0.011968028
BP	GO:0010715	regulation of extracellular matrix disassembly	4	0.000556425	0.012366783
BP	GO:2000811	negative regulation of anoikis	4	0.000556425	0.012366783
BP	GO:0060840	artery development	9	0.000569236	0.012578801
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	9	0.000612244	0.013451884
BP	GO:0040013	negative regulation of locomotion	20	0.000623516	0.013621693
BP	GO:0033002	muscle cell proliferation	15	0.000644785	0.014006765
BP	GO:0030514	negative regulation of BMP signaling pathway	6	0.00067898	0.014461599
BP	GO:0031099	regeneration	13	0.000683688	0.014461599
BP	GO:0003158	endothelium development	10	0.000683814	0.014461599
BP	GO:0008360	regulation of cell shape	10	0.000683814	0.014461599
BP	GO:0097529	myeloid leukocyte migration	12	0.000689463	0.014461599
BP	GO:0051895	negative regulation of focal adhesion assembly	4	0.000702241	0.014461599
BP	GO:0071772	response to BMP	11	0.000704574	0.014461599
BP	GO:0071773	cellular response to BMP stimulus	11	0.000704574	0.014461599
BP	GO:0003382	epithelial cell morphogenesis	5	0.000710856	0.014461599
BP	GO:0030866	cortical actin cytoskeleton organization	5	0.000710856	0.014461599
BP	GO:0044319	wound healing, spreading of cells	5	0.000710856	0.014461599
BP	GO:0090505	epiboly involved in wound healing	5	0.000710856	0.014461599
BP	GO:0045670	regulation of osteoclast differentiation	7	0.000727924	0.01473089
BP	GO:0048568	embryonic organ development	21	0.0007939	0.015981923
BP	GO:0060317	cardiac epithelial to mesenchymal transition	5	0.000826457	0.016380034
BP	GO:0071295	cellular response to vitamin	5	0.000826457	0.016380034
BP	GO:0090504	epiboly	5	0.000826457	0.016380034
BP	GO:1990778	protein localization to cell periphery	16	0.000848043	0.01672167
BP	GO:0032331	negative regulation of chondrocyte differentiation	4	0.000873153	0.01704199
BP	GO:1903392	negative regulation of adherens junction organization	4	0.000873153	0.01704199
BP	GO:0034446	substrate adhesion-dependent cell spreading	8	0.000919081	0.017847814
BP	GO:0042554	superoxide anion generation	5	0.000955506	0.018461904
BP	GO:1903035	negative regulation of response to wounding	8	0.000991855	0.019068413

BP	GO:0060537	muscle tissue development	20	0.001007767	0.019277929
BP	GO:0048593	camera-type eye morphogenesis	9	0.001061106	0.019997583
BP	GO:1905517	macrophage migration	6	0.001064711	0.019997583
BP	GO:0070167	regulation of biomineral tissue development	8	0.001069167	0.019997583
BP	GO:0044331	cell-cell adhesion mediated by cadherin	4	0.001071392	0.019997583
BP	GO:1905523	positive regulation of macrophage migration	4	0.001071392	0.019997583
BP	GO:0048565	digestive tract development	10	0.001108772	0.020595305
BP	GO:0010811	positive regulation of cell-substrate adhesion	9	0.001132269	0.020930642
BP	GO:0048146	positive regulation of fibroblast proliferation	6	0.001183192	0.021767341
BP	GO:0030509	BMP signaling pathway	10	0.001243293	0.022764108
BP	GO:0030865	cortical cytoskeleton organization	5	0.001257738	0.022919444
BP	GO:0055093	response to hyperoxia	4	0.001299192	0.023452557
BP	GO:0071711	basement membrane organization	4	0.001299192	0.023452557
BP	GO:0060033	anatomical structure regression	3	0.001358374	0.024180311
BP	GO:0060346	bone trabecula formation	3	0.001358374	0.024180311
BP	GO:2000049	positive regulation of cell-cell adhesion mediated by cadherin	3	0.001358374	0.024180311
BP	GO:0001935	endothelial cell proliferation	12	0.001437375	0.025468697
BP	GO:0072659	protein localization to plasma membrane	14	0.001470417	0.025934651
BP	GO:0014706	striated muscle tissue development	19	0.001492416	0.026202459
BP	GO:0045165	cell fate commitment	14	0.001529836	0.026737367
BP	GO:0060390	regulation of SMAD protein signal transduction	4	0.00155878	0.027119955
BP	GO:0070206	protein trimerization	6	0.001599753	0.02765157
BP	GO:0001755	neural crest cell migration	5	0.001625294	0.02765157
BP	GO:0010955	negative regulation of protein processing	5	0.001625294	0.02765157
BP	GO:0034405	response to fluid shear stress	5	0.001625294	0.02765157
BP	GO:1903318	negative regulation of protein maturation	5	0.001625294	0.02765157
BP	GO:0050878	regulation of body fluid levels	23	0.001686804	0.028571632
BP	GO:0043491	protein kinase B signaling	15	0.001723631	0.028992046
BP	GO:0021675	nerve development	7	0.001726704	0.028992046
BP	GO:0002761	regulation of myeloid leukocyte differentiation	9	0.001745587	0.029181639
BP	GO:0001655	urogenital system development	17	0.0017534	0.029181639
BP	GO:0001885	endothelial cell development	6	0.001760765	0.029181639
BP	GO:0044272	sulfur compound biosynthetic process	12	0.001801263	0.029292945
BP	GO:0007015	actin filament organization	17	0.001811398	0.029292945
BP	GO:0003413	chondrocyte differentiation involved in endochondral bone morphogenesis	3	0.001835412	0.029292945
BP	GO:0016264	gap junction assembly	3	0.001835412	0.029292945
BP	GO:0032908	regulation of transforming growth factor beta1 production	3	0.001835412	0.029292945
BP	GO:0045217	cell-cell junction maintenance	3	0.001835412	0.029292945
BP	GO:2001241	positive regulation of extrinsic apoptotic signaling pathway in absence of ligand	3	0.001835412	0.029292945
BP	GO:0043277	apoptotic cell clearance	5	0.001836047	0.029292945
BP	GO:0097178	ruffle assembly	5	0.001836047	0.029292945
BP	GO:0031579	membrane raft organization	4	0.001852367	0.029418139
BP	GO:0001937	negative regulation of endothelial cell proliferation	7	0.001866847	0.029418139
BP	GO:0031100	animal organ regeneration	7	0.001866847	0.029418139
BP	GO:0055123	digestive system development	10	0.00202332	0.03175373
BP	GO:0007565	female pregnancy	12	0.002053747	0.032100238
BP	GO:0007043	cell-cell junction assembly	8	0.002138459	0.033208272
BP	GO:0042692	muscle cell differentiation	18	0.002141912	0.033208272
BP	GO:0060343	trabecula formation	4	0.00218214	0.033427609
BP	GO:1901889	negative regulation of cell junction assembly	4	0.00218214	0.033427609
BP	GO:2000209	regulation of anoikis	4	0.00218214	0.033427609
BP	GO:0007596	blood coagulation	17	0.002194327	0.033443993
BP	GO:0002687	positive regulation of leukocyte migration	9	0.002200606	0.033443993
BP	GO:0001822	kidney development	15	0.002290873	0.034542772
BP	GO:0048562	embryonic organ morphogenesis	15	0.002290873	0.034542772
BP	GO:0032233	positive regulation of actin filament bundle assembly	6	0.002318027	0.034748304
BP	GO:0003007	heart morphogenesis	14	0.002326416	0.034748304
BP	GO:0001570	vasculogenesis	7	0.002340653	0.034748304
BP	GO:0008589	regulation of smoothened signaling pathway	7	0.002340653	0.034748304
BP	GO:0001765	membrane raft assembly	3	0.002404878	0.035070203
BP	GO:0030208	dermatan sulfate biosynthetic process	3	0.002404878	0.035070203
BP	GO:0032905	transforming growth factor beta1 production	3	0.002404878	0.035070203
BP	GO:0090520	sphingolipid mediated signaling pathway	3	0.002404878	0.035070203
BP	GO:0048732	gland development	20	0.002407941	0.035070203
BP	GO:0030326	embryonic limb morphogenesis	9	0.002461053	0.035574246
BP	GO:0035113	embryonic appendage morphogenesis	9	0.002461053	0.035574246
BP	GO:0048660	regulation of smooth muscle cell proliferation	11	0.002499874	0.035907394
BP	GO:0022409	positive regulation of cell-cell adhesion	14	0.002502778	0.035907394
BP	GO:0120193	tight junction organization	6	0.002530421	0.03616903
BP	GO:0000038	very long-chain fatty acid metabolic process	4	0.00255026	0.036183583
BP	GO:0090025	regulation of monocyte chemotaxis	4	0.00255026	0.036183583
BP	GO:0007599	hemostasis	17	0.002563188	0.036232999
BP	GO:0044706	multi-multicellular organism process	13	0.002600377	0.036624364
BP	GO:0050817	coagulation	17	0.002642842	0.037086601
BP	GO:0048608	reproductive structure development	20	0.002682252	0.037502758
BP	GO:0048659	smooth muscle cell proliferation	11	0.002734355	0.038092732
BP	GO:0030510	regulation of BMP signaling pathway	7	0.002902133	0.03948567
BP	GO:0046849	bone remodeling	7	0.002902133	0.03948567
BP	GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	7	0.002902133	0.03948567
BP	GO:0061458	reproductive system development	20	0.002904825	0.03948567
BP	GO:0014812	muscle cell migration	8	0.002921022	0.03948567
BP	GO:0032526	response to retinoic acid	8	0.002921022	0.03948567
BP	GO:0007263	nitric oxide mediated signal transduction	4	0.00295885	0.03948567
BP	GO:0032967	positive regulation of collagen biosynthetic process	4	0.00295885	0.03948567
BP	GO:0045992	negative regulation of embryonic development	4	0.00295885	0.03948567
BP	GO:0098868	bone growth	4	0.00295885	0.03948567
BP	GO:1900027	regulation of ruffle assembly	4	0.00295885	0.03948567
BP	GO:1901652	response to peptide	22	0.002975611	0.03948567
BP	GO:0022604	regulation of cell morphogenesis	20	0.002982376	0.03948567
BP	GO:0032970	regulation of actin filament-based process	17	0.002982396	0.03948567
BP	GO:0050714	positive regulation of protein secretion	14	0.002992366	0.03948567
BP	GO:0042733	embryonic digit morphogenesis	6	0.002998652	0.03948567
BP	GO:0009312	oligosaccharide biosynthetic process	3	0.003072318	0.039641153
BP	GO:0030205	dermatan sulfate metabolic process	3	0.003072318	0.039641153
BP	GO:0032530	regulation of microvillus organization	3	0.003072318	0.039641153
BP	GO:0034331	cell junction maintenance	3	0.003072318	0.039641153
BP	GO:0051917	regulation of fibrinolysis	3	0.003072318	0.039641153
BP	GO:0061430	bone trabecula morphogenesis	3	0.003072318	0.039641153
BP	GO:0032102	negative regulation of response to external stimulus	17	0.003165312	0.040704429
BP	GO:0043616	keratinocyte proliferation	5	0.003200094	0.040878273
BP	GO:0097028	dendritic cell differentiation	5	0.003200094	0.040878273
BP	GO:0001958	endochondral ossification	4	0.003409992	0.04298826

BP	GO:0010714	positive regulation of collagen metabolic process	4	0.003409992	0.04298826
BP	GO:0036075	replacement ossification	4	0.003409992	0.04298826
BP	GO:0045671	negative regulation of osteoclast differentiation	4	0.003409992	0.04298826
BP	GO:0045600	positive regulation of fat cell differentiation	6	0.003528747	0.044219046
BP	GO:0030850	prostate gland development	5	0.003542124	0.044219046
BP	GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	5	0.003542124	0.044219046
BP	GO:0050921	positive regulation of chemotaxis	9	0.003570663	0.044431071
BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	10	0.003631417	0.04504129
BP	GO:0050867	positive regulation of cell activation	16	0.003684409	0.045530122
BP	GO:0014902	myotube differentiation	8	0.003694512	0.045530122
BP	GO:0045598	regulation of fat cell differentiation	9	0.0037569	0.045890122
BP	GO:0072001	renal system development	15	0.003772027	0.045890122
BP	GO:0051047	positive regulation of secretion	19	0.003801134	0.045890122
BP	GO:0014910	regulation of smooth muscle cell migration	7	0.003804655	0.045890122
BP	GO:0031532	actin cytoskeleton reorganization	7	0.003804655	0.045890122
BP	GO:0042475	odontogenesis of dentin-containing tooth	7	0.003804655	0.045890122
BP	GO:0051146	striated muscle cell differentiation	14	0.003807269	0.045890122
BP	GO:0010935	regulation of macrophage cytokine production	3	0.003842735	0.046029027
BP	GO:0030213	hyaluronan biosynthetic process	3	0.003842735	0.046029027
BP	GO:0003180	aortic valve morphogenesis	4	0.003905722	0.046253802
BP	GO:0036296	response to increased oxygen levels	4	0.003905722	0.046253802
BP	GO:0032570	response to progesterone	5	0.003909619	0.046253802
BP	GO:0033628	regulation of cell adhesion mediated by integrin	5	0.003909619	0.046253802
BP	GO:1903532	positive regulation of secretion by cell	18	0.004020201	0.04741617
BP	GO:0048145	regulation of fibroblast proliferation	7	0.004060338	0.047743121
BP	GO:0006801	superoxide metabolic process	6	0.004125492	0.048361333
CC	GO:0031012	extracellular matrix	78	6.05E-43	2.24E-40
CC	GO:0062023	collagen-containing extracellular matrix	71	5.20E-41	9.62E-39
CC	GO:0005788	endoplasmic reticulum lumen	45	1.41E-22	1.74E-20
CC	GO:0005581	collagen trimer	26	8.85E-22	8.19E-20
CC	GO:0044420	extracellular matrix component	18	1.39E-17	1.03E-15
CC	GO:0098644	complex of collagen trimers	12	5.68E-16	3.50E-14
CC	GO:0005583	fibrillar collagen trimer	9	1.39E-13	6.41E-12
CC	GO:0098643	banded collagen fibril	9	1.39E-13	6.41E-12
CC	GO:0005925	focal adhesion	35	4.53E-11	1.85E-09
CC	GO:0005924	cell-substrate adherens junction	35	5.21E-11	1.85E-09
CC	GO:0005604	basement membrane	17	5.51E-11	1.85E-09
CC	GO:0030055	cell-substrate junction	35	7.35E-11	2.27E-09
CC	GO:0005912	adherens junction	39	1.07E-10	3.05E-09
CC	GO:0031091	platelet alpha granule	12	1.95E-06	5.16E-05
CC	GO:0031252	cell leading edge	26	2.59E-06	6.39E-05
CC	GO:0031093	platelet alpha granule lumen	10	4.50E-06	0.000104156
CC	GO:0045121	membrane raft	22	6.94E-06	0.00014359
CC	GO:0098857	membrane microdomain	22	7.30E-06	0.00014359
CC	GO:0015629	actin cytoskeleton	27	7.37E-06	0.00014359
CC	GO:0098589	membrane region	22	1.26E-05	0.00023391
CC	GO:0042641	actomyosin	9	3.24E-05	0.000570761
CC	GO:0001725	stress fiber	8	5.67E-05	0.000912218
CC	GO:0097517	contractile actin filament bundle	8	5.67E-05	0.000912218
CC	GO:0001726	ruffle	14	6.10E-05	0.000940818
CC	GO:0032432	actin filament bundle	8	8.31E-05	0.001229727
CC	GO:0005911	cell-cell junction	23	0.000204322	0.002907653
CC	GO:0045177	apical part of cell	21	0.000239375	0.003280319
CC	GO:0031253	cell projection membrane	19	0.000281625	0.003721473
CC	GO:0009897	external side of plasma membrane	14	0.000362637	0.004626754
CC	GO:0016324	apical plasma membrane	18	0.00039926	0.004711324
CC	GO:0005884	actin filament	8	0.000411832	0.004711324
CC	GO:0031985	Golgi cisterna	9	0.00041908	0.004711324
CC	GO:0043296	apical junction complex	11	0.000420199	0.004711324
CC	GO:0071437	invadopodium	4	0.000488774	0.005319009
CC	GO:0005902	microvillus	8	0.00069839	0.007363046
CC	GO:0030139	endocytic vesicle	17	0.000716404	0.007363046
CC	GO:0030667	secretory granule membrane	17	0.000834445	0.008344447
CC	GO:0005795	Golgi stack	10	0.000872473	0.008495128
CC	GO:0016459	myosin complex	7	0.000962888	0.00913509
CC	GO:0001527	microfibril	3	0.001488222	0.013766052
CC	GO:0032580	Golgi cisterna membrane	7	0.001763313	0.015912823
CC	GO:0031528	microvillus membrane	4	0.002079805	0.018322088
CC	GO:0034774	secretory granule lumen	17	0.002222562	0.01912437
CC	GO:0005901	caveola	7	0.003004188	0.02526249
CC	GO:0001931	uropod	3	0.003360268	0.027028246
CC	GO:0031254	cell trailing edge	3	0.003360268	0.027028246
CC	GO:0098858	actin-based cell projection	12	0.003563977	0.028056844
CC	GO:0060205	cytoplasmic vesicle lumen	17	0.003766388	0.029032574
CC	GO:0031983	vesicle lumen	17	0.003879521	0.029294342
CC	GO:0005938	cell cortex	13	0.003962324	0.029321196
CC	GO:0031256	leading edge membrane	10	0.004140987	0.030042456
CC	GO:0044853	plasma membrane raft	8	0.004222479	0.030044565
CC	GO:0008305	integrin complex	4	0.005633906	0.03933104
CC	GO:0032587	ruffle membrane	7	0.006558784	0.044920188
CC	GO:0055037	recycling endosome	10	0.006707017	0.044920188
CC	GO:0098552	side of membrane	17	0.006798731	0.044920188
CC	GO:0030027	lamellipodium	11	0.006962984	0.045198317
CC	GO:0030426	growth cone	10	0.007283307	0.046462479
CC	GO:0098636	protein complex involved in cell adhesion	4	0.007947492	0.049840201
MF	GO:0005201	extracellular matrix structural constituent	45	3.39E-35	1.69E-32
MF	GO:0030020	extracellular matrix structural constituent conferring tensile strength	19	3.26E-20	8.14E-18
MF	GO:0005518	collagen binding	19	2.51E-16	4.17E-14
MF	GO:0005178	integrin binding	19	4.34E-11	5.42E-09
MF	GO:0019838	growth factor binding	17	7.99E-09	7.97E-07
MF	GO:0048407	platelet-derived growth factor binding	6	9.49E-08	7.89E-06
MF	GO:0050839	cell adhesion molecule binding	31	2.47E-07	1.76E-05
MF	GO:0005539	glycosaminoglycan binding	19	5.85E-07	3.65E-05
MF	GO:0003779	actin binding	26	1.32E-06	7.33E-05
MF	GO:0031418	L-ascorbic acid binding	6	6.58E-06	0.000328453
MF	GO:0051015	actin filament binding	14	1.34E-05	0.000609186
MF	GO:0030169	low-density lipoprotein particle binding	5	2.27E-05	0.000944111
MF	GO:0004222	metalloendopeptidase activity	10	7.17E-05	0.002753392
MF	GO:0008201	heparin binding	13	8.45E-05	0.003012734
MF	GO:0048029	monosaccharide binding	8	0.000142876	0.004753005
MF	GO:0043394	proteoglycan binding	6	0.000236182	0.007365913
MF	GO:0001968	fibronectin binding	5	0.000267132	0.007470707

MF	GO:0048037	cofactor binding	24	0.000269484	0.007470707
MF	GO:0030246	carbohydrate binding	16	0.000595208	0.015632041
MF	GO:0005506	iron ion binding	11	0.000956853	0.023873474
MF	GO:0008376	acetylgalactosaminyltransferase activity	5	0.001074824	0.025539858
MF	GO:0020037	heme binding	9	0.001307682	0.027754388
MF	GO:1901681	sulfur compound binding	14	0.001313126	0.027754388
MF	GO:0071813	lipoprotein particle binding	5	0.001425896	0.027754388
MF	GO:0071814	protein-lipid complex binding	5	0.001425896	0.027754388
MF	GO:0031406	carboxylic acid binding	12	0.001537735	0.027754388
MF	GO:0008237	metallopeptidase activity	11	0.001565558	0.027754388
MF	GO:0030021	extracellular matrix structural constituent conferring compression resistance	4	0.00161298	0.027754388
MF	GO:0050431	transforming growth factor beta binding	4	0.00161298	0.027754388
MF	GO:0043177	organic acid binding	12	0.001692306	0.028148684
MF	GO:0000146	microfilament motor activity	4	0.001933103	0.030488108
MF	GO:0016757	transferase activity, transferring glycosyl groups	15	0.002016248	0.030488108
MF	GO:0050662	coenzyme binding	15	0.002016248	0.030488108
MF	GO:0005172	vascular endothelial growth factor receptor binding	3	0.002171499	0.030959373
MF	GO:0097493	structural molecule activity conferring elasticity	3	0.002171499	0.030959373
MF	GO:0046906	tetrapyrrole binding	9	0.002444592	0.033884757
MF	GO:0008417	fucosyltransferase activity	3	0.002842232	0.03833172
MF	GO:0004175	endopeptidase activity	17	0.003008987	0.039512753
MF	GO:0005516	calmodulin binding	11	0.003258417	0.041691031
MF	GO:0019955	cytokine binding	8	0.003472894	0.043324354
MF	GO:0050840	extracellular matrix binding	5	0.00410946	0.049446725
MF	GO:0003774	motor activity	8	0.004161849	0.049446725
