

Category	Term	Count	%	P-value	Molecules	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
Day 1												
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	13	0.33121019	1.17E-15	CCL2, PPBP, CXCL13, IL19, CXCL2, CXCL9, JAK2, NGFR, CXCL11, IL10, CCL17, IL20, CXCL10	26	187	11368	30.3957219	3.22E-13	3.22E-13	1.60E-12
GOTERM_BP_DIRECT	GO:0070098~chemokine-mediated signaling pathway	8	0.20382166	9.77E-13	CCL2, PPBP, CXCL13, CXCL2, CXCL9, CXCL11, CCL17, CXCL10	26	37	11368	94.5363825	2.58E-10	1.29E-10	1.28E-09
GOTERM_BP_DIRECT	GO:0006955~immune response	11	0.28025478	5.33E-12	PPBP, CXCL13, IL19, CXCL2, CXCL9, NGFR, CXCL11, IL10, CCL17, IL20, CXCL10	26	198	11368	24.2905983	1.41E-09	4.69E-10	6.99E-09
GOTERM_BP_DIRECT	GO:0042127~regulation of cell proliferation	8	0.20382166	4.74E-09	PPBP, CXCL13, CXCL2, CXCL9, JAK2, NGFR, CXCL11, CXCL10	26	119	11368	29.3936652	1.25E-06	3.13E-07	6.21E-06
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	7	0.17834395	9.15E-09	PPBP, CXCL13, CXCL2, CXCL9, NGFR, CXCL11, CXCL10	26	73	11368	41.9262381	2.41E-06	4.83E-07	1.20E-05
GOTERM_BP_DIRECT	GO:0002690~positive regulation of leukocyte	5	0.12738854	1.28E-08	PPBP, CXCL13, CXCL9, CXCL11, CXCL10	26	13	11368	168.16568	3.39E-06	5.65E-07	1.68E-05
GOTERM_BP_DIRECT	GO:0046427~positive regulation of JAK-STAT cascade	4	0.10191083	1.12E-06	IL4, IL19, IL10, IL20	26	10	11368	174.892308	2.95E-04	4.21E-05	0.00146234
GOTERM_BP_DIRECT	GO:0048010~vascular endothelial growth factor receptor signaling	4	0.10191083	2.65E-06	VEGFB, NRP1, PGF, VEGFA	26	13	11368	134.532544	6.99E-04	8.74E-05	0.00347007
GOTERM_BP_DIRECT	GO:2001237~negative regulation of extrinsic apoptotic signaling pathway	4	0.10191083	2.65E-05	IL4, NRP1, LGALS3, IL19	26	27	11368	64.7749288	0.00698261	7.78E-04	0.03477005
GOTERM_BP_DIRECT	GO:0030816~positive regulation of cAMP metabolic	3	0.07643312	2.78E-05	CXCL9, CXCL11, CXCL10	26	4	11368	327.923077	0.00730833	7.33E-04	0.03639767
GOTERM_BP_DIRECT	GO:0060754~positive regulation of mast cell	3	0.07643312	6.93E-05	VEGFB, PGF, VEGFA	26	6	11368	218.615385	0.01812264	0.00166124	0.09072611
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	4	0.10191083	8.80E-05	CCL2, PPBP, LGALS3, CCL17	26	40	11368	43.7230769	0.022959	0.00193368	0.11520704
GOTERM_BP_DIRECT	GO:0043950~positive regulation of cAMP-mediated signaling	3	0.07643312	9.69E-05	CXCL9, CXCL11, CXCL10	26	7	11368	187.384615	0.02524609	0.00196501	0.1268241
GOTERM_BP_DIRECT	GO:0060326~cell chemotaxis	4	0.10191083	2.05E-04	CXCL2, CXCL11, CCL17, CXCL10	26	53	11368	32.9985486	0.0526111	0.00385296	0.26786786

GOTERM_BP_DIRECT	GO:0050930~induction of positive chemotaxis	3	0.07643312	2.07E-04	VEGFB, PGF, VEGFA	26	10	11368	131.169231	0.05311255	0.00363173	0.2704884
GOTERM_BP_DIRECT	GO:0051281~positive regulation of release of sequestered calcium ion into cytosol	3	0.07643312	6.19E-04	CXCL9, CXCL11, CXCL10	26	17	11368	77.158371	0.15076732	0.01016189	0.80778032
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	4	0.10191083	0.00110368	VEGFB, NRP1, PGF, VEGFA	26	94	11368	18.6055646	0.25288205	0.01700275	1.43645183
GOTERM_BP_DIRECT	GO:0007186~G-protein coupled receptor signaling pathway	8	0.20382166	0.00123718	CCL2, PPBP, CXCL13, CXCL2, CXCL9, CXCL11, CCL17, CXCL10	26	793	11368	4.41090309	0.27878462	0.01799269	1.60890525
GOTERM_BP_DIRECT	GO:0002548~monocyte chemotaxis	3	0.07643312	0.00124407	CCL2, LGALS3, CCL17	26	24	11368	54.6538462	0.28009788	0.01714811	1.61780467
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2	4	0.10191083	0.00151909	ICAM1, CCL2, NRP1, CCL17	26	105	11368	16.6564103	0.33058029	0.0198672	1.9721561
GOTERM_BP_DIRECT	GO:0001938~positive regulation of endothelial cell proliferation	3	0.07643312	0.00294993	VEGFB, PGF, VEGFA	26	37	11368	35.4511435	0.54156324	0.03645844	3.79683399
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	3	0.07643312	0.00642036	VEGFB, PGF, VEGFA	26	55	11368	23.848951	0.8173967	0.07438111	8.09295193
GOTERM_BP_DIRECT	GO:0010818~T cell chemotaxis	2	0.05095541	0.0087688	CXCL11, CXCL10	26	4	11368	218.615385	0.90223344	0.09615235	10.8988431
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	3	0.07643312	0.00913799	VEGFB, PGF, VEGFA	26	66	11368	19.8741259	0.91139069	0.09604883	11.3326753
GOTERM_BP_DIRECT	GO:0043524~negative regulation of neuron apoptotic process	3	0.07643312	0.0096786	CCL2, NRP1, NGF	26	68	11368	19.2895928	0.92328016	0.09760577	11.9644287
GOTERM_BP_DIRECT	GO:0045348~positive regulation of MHC class II biosynthetic process	2	0.05095541	0.01094944	IL4, IL10	26	5	11368	174.892308	0.9453384	0.10576983	13.4331889
GOTERM_BP_DIRECT	GO:0051045~negative regulation of membrane protein ectodomain proteolysis	2	0.05095541	0.01094944	IL10, TIMP1	26	5	11368	174.892308	0.9453384	0.10576983	13.4331889
GOTERM_BP_DIRECT	GO:0048246~macrophage chemotaxis	2	0.05095541	0.01312547	CCL2, LGALS3	26	6	11368	145.74359	0.96944009	0.12119095	15.8956629

GOTERM_BP_DIRECT	GO:0050918~positive chemotaxis	2	0.05095541	0.01746376	NRP1, VEGFA	26	8	11368	109.307692	0.99044953	0.1530495	20.613067
GOTERM_BP_DIRECT	GO:0090280~positive regulation of calcium ion import	2	0.05095541	0.01962603	CCL2, LGALS3	26	9	11368	97.1623932	0.9946614	0.16509812	22.8718911
GOTERM_BP_DIRECT	GO:0035729~cellular response to hepatocyte growth factor stimulus	2	0.05095541	0.01962603	NRP1, IL10	26	9	11368	97.1623932	0.9946614	0.16509812	22.8718911
GOTERM_BP_DIRECT	GO:0002042~cell migration involved in sprouting angiogenesis	2	0.05095541	0.02393688	NRP1, VEGFA	26	11	11368	79.4965035	0.99833211	0.19201079	27.1991104
GOTERM_BP_DIRECT	GO:0042832~defense response to protozoan	2	0.05095541	0.02393688	IL4, IL10	26	11	11368	79.4965035	0.99833211	0.19201079	27.1991104
GOTERM_BP_DIRECT	GO:1901741~positive regulation of myoblast fusion	2	0.05095541	0.03036904	IL4, CXCL9	26	14	11368	62.4615385	0.99970886	0.2309776	33.2402962
GOTERM_BP_DIRECT	GO:0090026~positive regulation of monocyte	2	0.05095541	0.03250404	CCL2, CXCL10	26	15	11368	58.2974359	0.9998373	0.23861282	35.1408238
GOTERM_BP_DIRECT	GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	2	0.05095541	0.03676051	IL6ST, JAK2	26	17	11368	51.438914	0.9999492	0.2589044	38.7815734
GOTERM_BP_DIRECT	GO:2000352~negative regulation of endothelial cell apoptotic process	2	0.05095541	0.03676051	IL4, ICAM1	26	17	11368	51.438914	0.9999492	0.2589044	38.7815734
GOTERM_BP_DIRECT	GO:0045662~negative regulation of myoblast differentiation	2	0.05095541	0.038882	CCL17, CXCL10	26	18	11368	48.5811966	0.99997162	0.2650357	40.5248054
GOTERM_BP_DIRECT	GO:0048247~lymphocyte chemotaxis	2	0.05095541	0.040999	CCL2, CCL17	26	19	11368	46.0242915	0.99998414	0.27077125	42.218545
GOTERM_BP_DIRECT	GO:0030155~regulation of cell	2	0.05095541	0.05151702	ICAM1, JAK2	26	24	11368	36.4358974	0.99999914	0.32149982	49.9925309
GOTERM_BP_DIRECT	GO:0051781~positive regulation of cell division	2	0.05095541	0.05151702	PPBP, VEGFA	26	24	11368	36.4358974	0.99999914	0.32149982	49.9925309

GOTERM_BP_DIRECT	GO:0010951~negative regulation of endopeptidase activity	2	0.05095541	0.05569315	TIMP1, NGF	26	26	11368	33.6331361	0.99999973	0.33560112	52.8017732
GOTERM_BP_DIRECT	GO:0071346~cellular response to interferon-gamma	2	0.05095541	0.05985162	CCL2, CCL17	26	28	11368	31.2307692	0.99999992	0.34869333	55.4536569
GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	2	0.05095541	0.06605638	CCL2, CCL17	26	31	11368	28.2084367	0.99999999	0.370358	59.1555262
GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	2	0.05095541	0.06605638	NRP1, VEGFA	26	31	11368	28.2084367	0.99999999	0.370358	59.1555262
GOTERM_BP_DIRECT	GO:0071356~cellular response to tumor necrosis factor	2	0.05095541	0.08645626	CCL2, CCL17	26	41	11368	21.3283302	1	0.44942856	69.4180384
GOTERM_BP_DIRECT	GO:0001934~positive regulation of protein	2	0.05095541	0.08645626	IL4, VEGFA	26	41	11368	21.3283302	1	0.44942856	69.4180384
GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	2	0.05095541	0.09849013	IL10, CXCL10	26	47	11368	18.6055646	1	0.487075	74.2953771
GOTERM_BP_DIRECT	GO:0016337~single organismal cell-cell adhesion	2	0.05095541	0.09849013	ICAM1, ICAM2	26	47	11368	18.6055646	1	0.487075	74.2953771
Day 7												
GOTERM_BP_DIRECT	GO:0051045~negative regulation of membrane protein ectodomain proteolysis	5	0.07338911	4.2252E-10	TIMP4, TIMP2, TIMP3, IL10, TIMP1	37	5	11368	307.243243	1.6352E-07	1.6352E-07	5.865E-07
GOTERM_BP_DIRECT	GO:0043086~negative regulation of catalytic activity	5	0.07338911	3.9581E-07	IL7, TIMP4, TIMP2, TIMP3, TIMP1	37	20	11368	76.8108108	0.00015316	7.6585E-05	0.00054941
GOTERM_BP_DIRECT	GO:0006955~immune response	8	0.11742257	2.3793E-06	PPBP, IL7, IL19, IL9, CCL5, CCL27, IL10, IL20	37	198	11368	12.4138684	0.00092037	0.00030688	0.00330266
GOTERM_BP_DIRECT	GO:0046427~positive regulation of JAK-STAT cascade	4	0.05871129	3.4472E-06	IL4, IL19, IL10, IL20	37	10	11368	122.897297	0.00133318	0.00033346	0.00478495
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	5	0.07338911	7.1369E-06	CCL2, PPBP, LGALS3, IFNG, CCL5	37	40	11368	38.4054054	0.00275817	0.00055224	0.00990623

GOTERM_BP_DIRECT	GO:0048010~vascular endothelial growth factor receptor signaling	4	0.05871129	8.1623E-06	VEGFB, NRP1, PGF, VEGFA	37	13	11368	94.5363825	0.00315384	0.00052633	0.01132949
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	7	0.10274475	2.3622E-05	CCL2, PPBP, IL19, JAK2, CCL5, IL10, IL20	37	187	11368	11.501084	0.00910031	0.00130514	0.0327852
GOTERM_BP_DIRECT	GO:2001237~negative regulation of extrinsic apoptotic signaling pathway	4	0.05871129	8.0972E-05	IL4, NRP1, LGALS3, IL19	37	27	11368	45.5175175	0.03085146	0.00390951	0.1123383
GOTERM_BP_DIRECT	GO:0045348~positive regulation of MHC class II biosynthetic process	3	0.04403347	9.6926E-05	IL4, IFNG, IL10	37	5	11368	184.345946	0.03681731	0.00415935	0.13445882
GOTERM_BP_DIRECT	GO:0060754~positive regulation of mast cell	3	0.04403347	0.0001451	VEGFB, PGF, VEGFA	37	6	11368	153.621622	0.05460974	0.00560001	0.20122381
GOTERM_BP_DIRECT	GO:0050930~induction of positive chemotaxis	3	0.04403347	0.00043184	VEGFB, PGF, VEGFA	37	10	11368	92.172973	0.15393393	0.01508129	0.59777069
GOTERM_BP_DIRECT	GO:0042832~defense response to protozoan	3	0.04403347	0.00052675	IL4, IFNG, IL10	37	11	11368	83.7936118	0.18446167	0.01684868	0.72870849
GOTERM_BP_DIRECT	GO:0043524~negative regulation of neuron apoptotic process	4	0.05871129	0.00126911	CCL2, CNTF, NRP1, GFRAL	37	68	11368	18.073132	0.38826524	0.03709868	1.74731859
GOTERM_BP_DIRECT	GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	3	0.04403347	0.00128704	CNTF, IL6ST, JAK2	37	17	11368	54.2193959	0.39250128	0.03497413	1.77180388
GOTERM_BP_DIRECT	GO:0002548~monocyte chemotaxis	3	0.04403347	0.00257581	CCL2, LGALS3, CCL5	37	24	11368	38.4054054	0.63142987	0.06437602	3.51676177
GOTERM_BP_DIRECT	GO:0030155~regulation of cell	3	0.04403347	0.00257581	ICAM1, JAG2, JAK2	37	24	11368	38.4054054	0.63142987	0.06437602	3.51676177
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	4	0.05871129	0.00320852	VEGFB, NRP1, PGF, VEGFA	37	94	11368	13.0741806	0.71168214	0.07478648	4.36285965
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2	4	0.05871129	0.00438158	ICAM1, CCL2, NRP1, CCL5	37	105	11368	11.7045045	0.81720654	0.09513056	5.91337706
GOTERM_BP_DIRECT	GO:0070098~chemokine-mediated signaling pathway	3	0.04403347	0.00605713	CCL2, PPBP, CCL5	37	37	11368	24.9116143	0.90474895	0.12245268	8.08763764

GOTERM_BP_DIRECT	GO:0042102~positive regulation of T cell proliferation	3	0.04403347	0.00605713	IL6ST, IFNG, CCL5	37	37	11368	24.9116143	0.90474895	0.12245268	8.08763764
GOTERM_BP_DIRECT	GO:0001938~positive regulation of endothelial cell proliferation	3	0.04403347	0.00605713	VEGFB, PGF, VEGFA	37	37	11368	24.9116143	0.90474895	0.12245268	8.08763764
GOTERM_BP_DIRECT	GO:0042127~regulation of cell proliferation	4	0.05871129	0.00620937	PPBP, JAG2, JAK2, JAG1	37	119	11368	10.327504	0.91023126	0.11915129	8.28285751
GOTERM_BP_DIRECT	GO:0003184~pulmonary valve morphogenesis	2	0.02935564	0.01260875	NOTCH2, JAG1	37	4	11368	153.621622	0.992632	0.21771054	16.1494849
GOTERM_BP_DIRECT	GO:0010033~response to organic substance	2	0.02935564	0.01260875	TIMP4, TIMP3	37	4	11368	153.621622	0.992632	0.21771054	16.1494849
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	3	0.04403347	0.01303292	VEGFB, PGF, VEGFA	37	55	11368	16.7587224	0.99376075	0.21475294	16.6481111
GOTERM_BP_DIRECT	GO:0043547~positive regulation of GTPase activity	3	0.04403347	0.01303292	F11R, CCL2, CCL5	37	55	11368	16.7587224	0.99376075	0.21475294	16.6481111
GOTERM_BP_DIRECT	GO:0007219~Notch signaling pathway	3	0.04403347	0.01489817	NOTCH2, JAG2, TIMP4	37	59	11368	15.6225378	0.99699949	0.23206041	18.8083039
GOTERM_BP_DIRECT	GO:0048304~positive regulation of isotype switching to IgG isotypes	2	0.02935564	0.0157367	IL4, IFNG	37	5	11368	122.897297	0.99784191	0.23424476	19.7623953
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	3	0.04403347	0.01842088	VEGFB, PGF, VEGFA	37	66	11368	13.965602	0.99924994	0.25903851	22.7469937
GOTERM_BP_DIRECT	GO:0045080~positive regulation of chemokine biosynthetic process	2	0.02935564	0.01885502	IL4, IFNG	37	6	11368	102.414414	0.99936796	0.2552171	23.2199325
GOTERM_BP_DIRECT	GO:0048246~macrophage chemotaxis	2	0.02935564	0.01885502	CCL2, LGALS3	37	6	11368	102.414414	0.99936796	0.2552171	23.2199325
GOTERM_BP_DIRECT	GO:0048245~eosinophil chemotaxis	2	0.02935564	0.01885502	LGALS3, CCL5	37	6	11368	102.414414	0.99936796	0.2552171	23.2199325
GOTERM_BP_DIRECT	GO:0010759~positive regulation of macrophage chemotaxis	2	0.02935564	0.02196374	CCL2, CCL5	37	7	11368	87.7837838	0.99981492	0.28148268	26.5287655
GOTERM_BP_DIRECT	GO:0050918~positive regulation of chemotaxis	2	0.02935564	0.02506288	NRP1, VEGFA	37	8	11368	76.8108108	0.99994581	0.30497881	29.6952775

GOTERM_BP_DIRECT	GO:0045582~positive regulation of T cell differentiation	2	0.02935564	0.02506288	IL4, IL7	37	8	11368	76.8108108	0.99994581	0.30497881	29.6952775
GOTERM_BP_DIRECT	GO:0035729~cellular response to hepatocyte growth factor stimulus	2	0.02935564	0.02815247	NRP1, IL10	37	9	11368	68.2762763	0.99998413	0.32611074	32.7255784
GOTERM_BP_DIRECT	GO:0044130~negative regulation of growth of symbiont in host	2	0.02935564	0.02815247	IFNG, IL10	37	9	11368	68.2762763	0.99998413	0.32611074	32.7255784
GOTERM_BP_DIRECT	GO:0090280~positive regulation of calcium ion import	2	0.02935564	0.02815247	CCL2, LGALS3	37	9	11368	68.2762763	0.99998413	0.32611074	32.7255784
GOTERM_BP_DIRECT	GO:0042511~positive regulation of tyrosine phosphorylation of Stat1 protein	2	0.02935564	0.03123254	IL6ST, IFNG	37	10	11368	61.4486486	0.99999536	0.34520975	35.6255161
GOTERM_BP_DIRECT	GO:0045672~positive regulation of osteoclast differentiation	2	0.02935564	0.03123254	IFNG, IL20	37	10	11368	61.4486486	0.99999536	0.34520975	35.6255161
GOTERM_BP_DIRECT	GO:0044344~cellular response to fibroblast growth factor stimulus	2	0.02935564	0.03123254	CCL2, CCL5	37	10	11368	61.4486486	0.99999536	0.34520975	35.6255161
GOTERM_BP_DIRECT	GO:0002042~cell migration involved in sprouting angiogenesis	2	0.02935564	0.03430311	NRP1, VEGFA	37	11	11368	55.8624079	0.99999864	0.36254913	38.4006883
GOTERM_BP_DIRECT	GO:0019221~cytokine-mediated signaling pathway	3	0.04403347	0.04417977	CCL2, IL1RN, JAK2	37	106	11368	8.69556349	0.99999997	0.4311219	46.5924538
GOTERM_BP_DIRECT	GO:0009725~response to hormone	2	0.02935564	0.04649108	TIMP2, TIMP1	37	15	11368	40.9657658	0.99999999	0.437712	48.3574858
GOTERM_BP_DIRECT	GO:0090026~positive regulation of monocyte	2	0.02935564	0.04649108	CCL2, CCL5	37	15	11368	40.9657658	0.99999999	0.437712	48.3574858
GOTERM_BP_DIRECT	GO:0050796~regulation of insulin secretion	2	0.02935564	0.04951463	IFNG, CCL5	37	16	11368	38.4054054	1	0.44873536	50.5847457

GOTERM_BP_DIRECT	GO:2000352~negative regulation of endothelial cell apoptotic process	2	0.02935564	0.05252885	IL4, ICAM1	37	17	11368	36.1462639	1	0.45891453	52.7161312
GOTERM_BP_DIRECT	GO:0031663~lipopolysaccharide-mediated signaling pathway	2	0.02935564	0.05553378	CCL2, CCL5	37	18	11368	34.1381381	1	0.46834146	54.7557616
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	3	0.04403347	0.05597185	NOTCH2, VEGFA, JAG2	37	121	11368	7.61760107	1	0.46162095	55.0461924
GOTERM_BP_DIRECT	GO:0048247~lymphocyte chemotaxis	2	0.02935564	0.05852945	CCL2, CCL5	37	19	11368	32.341394	1	0.46785171	56.7075792
GOTERM_BP_DIRECT	GO:2001240~negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	2	0.02935564	0.05852945	GFRAL, IL7	37	19	11368	32.341394	1	0.46785171	56.7075792
GOTERM_BP_DIRECT	GO:0034097~response to cytokine	2	0.02935564	0.06449309	TIMP2, TIMP1	37	21	11368	29.2612613	1	0.49284983	60.3627078
GOTERM_BP_DIRECT	GO:0030890~positive regulation of B cell proliferation	2	0.02935564	0.06746112	IL4, IL7	37	22	11368	27.9312039	1	0.49996223	62.073087
GOTERM_BP_DIRECT	GO:0045747~positive regulation of Notch signaling	2	0.02935564	0.06746112	JAG2, JAG1	37	22	11368	27.9312039	1	0.49996223	62.073087
GOTERM_BP_DIRECT	GO:0043491~protein kinase B signaling	2	0.02935564	0.07336974	CCL2, CCL5	37	24	11368	25.6036036	1	0.52156804	65.2760232
GOTERM_BP_DIRECT	GO:0097191~extrinsic apoptotic signaling pathway	2	0.02935564	0.07336974	TNFRSF12A, IFNG	37	24	11368	25.6036036	1	0.52156804	65.2760232
GOTERM_BP_DIRECT	GO:0071407~cellular response to organic cyclic	2	0.02935564	0.07336974	CCL2, CCL5	37	24	11368	25.6036036	1	0.52156804	65.2760232
GOTERM_BP_DIRECT	GO:0051781~positive regulation of cell division	2	0.02935564	0.07336974	PPBP, VEGFA	37	24	11368	25.6036036	1	0.52156804	65.2760232
GOTERM_BP_DIRECT	GO:0071346~cellular response to interferon-gamma	2	0.02935564	0.08507799	CCL2, CCL5	37	28	11368	21.9459459	1	0.5679805	70.8946332
GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	2	0.02935564	0.09376466	CCL2, CCL5	37	31	11368	19.8221447	1	0.59634876	74.5045302
GOTERM_BP_DIRECT	GO:0000165~MAPK cascade	2	0.02935564	0.09376466	CCL2, CCL5	37	31	11368	19.8221447	1	0.59634876	74.5045302

GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	2	0.02935564	0.09376466	NRP1, VEGFA	37	31	11368	19.8221447	1	0.59634876	74.5045302
GOTERM_BP_DIRECT	GO:0009887~organ morphogenesis	2	0.02935564	0.09664236	NRP1, IL7	37	32	11368	19.2027027	1	0.59937552	75.6056297
GOTERM_BP_DIRECT	GO:0045669~positive regulation of osteoblast differentiation	2	0.02935564	0.09951118	IL6ST, JAG1	37	33	11368	18.6208026	1	0.6022445	76.6592659
Day 14												
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	9	0.20896215	1.1284E-13	CXCL1, CCL1, CCL12, CCL2, LGALS3, CXCL2, TREM1, CCL5, CCL7	34	58	17535	80.0278905	6.8582E-11	6.8582E-11	1.669E-10
GOTERM_BP_DIRECT	GO:0070098~chemokine-mediated signaling pathway	7	0.16252612	9.3138E-10	CXCL1, CCL1, CCL12, CCL2, CXCL2, CCL5, CCL7	34	57	17535	63.3359133	5.6628E-07	2.8314E-07	1.3781E-06
GOTERM_BP_DIRECT	GO:0002548~monocyte chemotaxis	6	0.1393081	3.3393E-09	CCL1, CCL12, CCL2, LGALS3, CCL5, CCL7	34	32	17535	96.7003676	2.0303E-06	6.7676E-07	4.9408E-06
GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	7	0.16252612	2.559E-08	CCL1, ICAM1, CCL12, CCL2, CXCL2, CCL5, CCL7	34	98	17535	36.8382353	1.5559E-05	3.8897E-06	3.7863E-05
GOTERM_BP_DIRECT	GO:0048247~lymphocyte chemotaxis	5	0.11609009	7.4222E-08	CCL1, CCL12, CCL2, CCL5, CCL7	34	22	17535	117.212567	4.5126E-05	9.0254E-06	0.00010982
GOTERM_BP_DIRECT	GO:0071346~cellular response to interferon-gamma	6	0.1393081	9.4911E-08	CCL1, ICAM1, CCL12, CCL2, CCL5, CCL7	34	61	17535	50.7280617	5.7704E-05	9.6176E-06	0.00014043
GOTERM_BP_DIRECT	GO:0051045~negative regulation of membrane protein ectodomain proteolysis	4	0.09287207	2.1146E-07	TIMP4, TIMP2, TIMP3, TIMP1	34	7	17535	294.705882	0.00012856	1.8366E-05	0.00031287
GOTERM_BP_DIRECT	GO:0048245~eosinophil chemotaxis	4	0.09287207	7.222E-07	CCL12, LGALS3, CCL5, CCL7	34	10	17535	206.294118	0.000439	5.4886E-05	0.00106857
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	8	0.18574414	1.0912E-06	CXCL1, CCL1, CCL12, CCL2, CXCL2, CCL5, IL22, CCL7	34	297	17535	13.8918598	0.00066323	7.3714E-05	0.00161453
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2	7	0.16252612	1.1469E-06	CCL1, ICAM1, CCL12, CCL2, VEGFA, CCL5, CCL7	34	186	17535	19.4093928	0.00069708	6.973E-05	0.00169697
GOTERM_BP_DIRECT	GO:0051384~response to	6	0.1393081	4.6582E-06	CXCL1, CCL1, CCL2, CXCL2, CCL5, IL22	34	133	17535	23.2662539	0.00282821	0.00025744	0.00689213
GOTERM_BP_DIRECT	GO:0071356~cellular response to tumor necrosis factor	6	0.1393081	4.6582E-06	CCL1, ICAM1, CCL12, CCL2, CCL5, CCL7	34	133	17535	23.2662539	0.00282821	0.00025744	0.00689213
GOTERM_BP_DIRECT	GO:0007568~aging	7	0.16252612	2.3577E-05	CCL2, VEGFA, GFRA1, CCL5, TIMP2, TIMP3, TIMP1	34	315	17535	11.4607843	0.01423284	0.00119388	0.03487915

GOTERM_BP_DIRECT	GO:0042246~tissue regeneration	4	0.09287207	3.8147E-05	NOTCH3, NOTCH2, NOTCH1, TIMP3	34	35	17535	58.9411765	0.02292671	0.00178253	0.056427
GOTERM_BP_DIRECT	GO:0016337~single organismal cell-cell adhesion	5	0.11609009	4.3457E-05	ICAM1, ICAM4, ICAM5, ICAM2, TCAM1	34	105	17535	24.5588235	0.0260764	0.00188554	0.06427974
GOTERM_BP_DIRECT	GO:0043547~positive regulation of GTPase activity	7	0.16252612	8.676E-05	CCL1, ICAM1, CCL12, F11R, CCL2, CCL5, CCL7	34	398	17535	9.07072125	0.051385	0.00351064	0.12829313
GOTERM_BP_DIRECT	GO:0010332~response to gamma radiation	4	0.09287207	8.7235E-05	CXCL1, CCL2, CXCL2, CCL7	34	46	17535	44.8465473	0.05165931	0.0033096	0.12899605
GOTERM_BP_DIRECT	GO:0008360~regulation of cell shape	5	0.11609009	8.85E-05	ICAM1, CCL12, CCL2, VEGFA, CCL7	34	126	17535	20.4656863	0.05238803	0.0031603	0.13086433
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	6	0.1393081	0.00011865	ICAM1, F11R, ICAM4, ICAM5, ICAM2, TCAM1	34	261	17535	11.8559838	0.06960538	0.00400011	0.17541833
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	6	0.1393081	0.00016482	CXCL1, ICAM1, NOTCH1, CCL2, TIMP4, CCL5	34	280	17535	11.0514706	0.0953583	0.00526066	0.24358478
GOTERM_BP_DIRECT	GO:0050729~positive regulation of inflammatory response	4	0.09287207	0.00022329	CCL1, CCL12, CCL2, CCL7	34	63	17535	32.745098	0.12696177	0.0067658	0.32987291
GOTERM_BP_DIRECT	GO:0043086~negative regulation of catalytic activity	4	0.09287207	0.00028	NOTCH1, TIMP4, TIMP3, TIMP1	34	68	17535	30.3373702	0.15655669	0.00807496	0.41348615
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	7	0.16252612	0.00030981	NOTCH2, NOTCH1, CNTF, LGALS3, VEGFA, GAS1, TIMP1	34	503	17535	7.17723073	0.1717091	0.00852666	0.45741019
GOTERM_BP_DIRECT	GO:0042493~response to drug	7	0.16252612	0.00040143	ICAM1, CCL2, HAVCR1, LGALS1, TIMP4, CCL5, TIMP2	34	528	17535	6.83739973	0.21660678	0.01055781	0.5923195
GOTERM_BP_DIRECT	GO:0050679~positive regulation of epithelial cell proliferation	4	0.09287207	0.00040401	NOTCH1, VEGFA, GAS1, CCL5	34	77	17535	26.7914439	0.21783159	0.01018466	0.59610464
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	6	0.1393081	0.00060137	NOTCH3, NOTCH2, F11R, NOTCH1, LGALS3, VEGFA	34	371	17535	8.34073252	0.30631848	0.0145232	0.88610482
GOTERM_BP_DIRECT	GO:0034097~response to cytokine	4	0.09287207	0.00084223	TIMP4, CCL5, TIMP2, TIMP1	34	99	17535	20.8377897	0.40087746	0.01951058	1.23894484
GOTERM_BP_DIRECT	GO:0035924~cellular response to vascular endothelial growth factor stimulus	3	0.06965405	0.00084772	NOTCH1, VEGFA, GAS1	34	23	17535	67.269821	0.4028771	0.01891629	1.24697958

GOTERM_BP_DIRECT	GO:0046427~positive regulation of JAK-STAT cascade	3	0.06965405	0.0009237	NOTCH1, CNTF, IL22	34	24	17535	64.4669118	0.42985683	0.01986671	1.35803054
GOTERM_BP_DIRECT	GO:0007219~Notch signaling pathway	4	0.09287207	0.00094478	NOTCH3, NOTCH2, NOTCH1, TIMP4	34	103	17535	20.0285551	0.43712649	0.01962218	1.3888304
GOTERM_BP_DIRECT	GO:0050918~positive chemotaxis	3	0.06965405	0.00125912	LGALS3, VEGFA, CCL5	34	28	17535	55.2573529	0.53514526	0.0252111	1.84690856
GOTERM_BP_DIRECT	GO:0042060~wound healing	4	0.09287207	0.00168853	NOTCH2, VEGFA, CXCL2, TIMP1	34	126	17535	16.372549	0.6420973	0.0326017	2.46946074
GOTERM_BP_DIRECT	GO:0010951~negative regulation of endopeptidase activity	4	0.09287207	0.00267017	TIMP4, TIMP2, TIMP3, TIMP1	34	148	17535	13.9387917	0.80321315	0.04953227	3.87883926
GOTERM_BP_DIRECT	GO:0071310~cellular response to organic substance	3	0.06965405	0.00269001	ICAM1, TIMP2, TIMP3	34	41	17535	37.7367288	0.80557959	0.04841689	3.90713501
GOTERM_BP_DIRECT	GO:0044344~cellular response to fibroblast growth factor stimulus	3	0.06965405	0.0028212	CCL2, VEGFA, CCL5	34	42	17535	36.8382353	0.82052392	0.04926602	4.09398639
GOTERM_BP_DIRECT	GO:0001975~response to amphetamine	3	0.06965405	0.00337545	CXCL1, ICAM1, CXCL2	34	46	17535	33.6349105	0.87200223	0.05704385	4.87968506
GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	4	0.09287207	0.00375309	ICAM1, CCL2, CXCL2, CCL5	34	167	17535	12.3529412	0.8983452	0.06153038	5.41159302
GOTERM_BP_DIRECT	GO:0071403~cellular response to high density lipoprotein particle stimulus	2	0.04643603	0.00376047	CCL2, CCL5	34	2	17535	515.735294	0.89880168	0.0600326	5.42195221
GOTERM_BP_DIRECT	GO:1901215~negative regulation of neuron death	3	0.06965405	0.00496382	CNTF, VEGFA, CCL5	34	56	17535	27.6286765	0.95146721	0.07653173	7.09823936
GOTERM_BP_DIRECT	GO:0045785~positive regulation of cell adhesion	3	0.06965405	0.00513829	CCL2, VEGFA, CCL5	34	57	17535	27.1439628	0.9563754	0.07717082	7.33897149
GOTERM_BP_DIRECT	GO:0043200~response to amino acid	3	0.06965405	0.00531556	ICAM1, CCL2, TIMP3	34	58	17535	26.6759635	0.96085502	0.07781745	7.58297199
GOTERM_BP_DIRECT	GO:0071549~cellular response to dexamethasone stimulus	3	0.06965405	0.00549563	ICAM1, CCL2, VEGFA	34	59	17535	26.2238285	0.96493519	0.07847089	7.83019939
GOTERM_BP_DIRECT	GO:0072104~glomerular capillary formation	2	0.04643603	0.00563555	NOTCH3, NOTCH2	34	3	17535	343.823529	0.96781027	0.07855491	8.02188995

GOTERM_BP_DIRECT	GO:0007399~nervous system development	4	0.09287207	0.00611446	CNTF, VEGFA, GFRA1, GFRA2	34	199	17535	10.3665386	0.97598327	0.08306715	8.67516104
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	4	0.09287207	0.00663646	NOTCH1, VEGFA, CCL5, CCL7	34	205	17535	10.0631277	0.98255005	0.08790353	9.38228804
GOTERM_BP_DIRECT	GO:0045185~enhancement of protein location	2	0.04643603	0.00750722	LGALS3, LGALS1	34	4	17535	257.867647	0.98976158	0.09680202	10.5504981
GOTERM_BP_DIRECT	GO:0035860~glial cell-derived neurotrophic factor receptor signaling pathway	2	0.04643603	0.00750722	GFRA4, GFRA2	34	4	17535	257.867647	0.98976158	0.09680202	10.5504981
GOTERM_BP_DIRECT	GO:0046533~negative regulation of photoreceptor cell differentiation	2	0.04643603	0.00750722	NOTCH1, CNTF	34	4	17535	257.867647	0.98976158	0.09680202	10.5504981
GOTERM_BP_DIRECT	GO:0061419~positive regulation of transcription from RNA polymerase II promoter in response to hypoxia	2	0.04643603	0.00937547	NOTCH1, VEGFA	34	5	17535	206.294118	0.99674373	0.11706506	13.0097297
GOTERM_BP_DIRECT	GO:0030855~epithelial cell	3	0.06965405	0.0094332	F11R, LGALS3, VEGFA	34	78	17535	19.8359729	0.9968571	0.11539028	13.0847154
GOTERM_BP_DIRECT	GO:0009408~response to heat	3	0.06965405	0.0094332	CXCL1, CCL2, CXCL2	34	78	17535	19.8359729	0.9968571	0.11539028	13.0847154
GOTERM_BP_DIRECT	GO:0048661~positive regulation of smooth muscle cell proliferation	3	0.06965405	0.01062738	NOTCH3, VEGFA, CCL5	34	83	17535	18.6410347	0.99849057	0.12657573	14.6222221
GOTERM_BP_DIRECT	GO:2000503~positive regulation of natural killer cell	2	0.04643603	0.0112403	CCL5, CCL7	34	6	17535	171.911765	0.99896443	0.13086891	15.4014844
GOTERM_BP_DIRECT	GO:0072602~interleukin-4 secretion	2	0.04643603	0.0112403	NOTCH2, NOTCH1	34	6	17535	171.911765	0.99896443	0.13086891	15.4014844
GOTERM_BP_DIRECT	GO:0002693~positive regulation of cellular	2	0.04643603	0.0112403	ICAM1, CCL2	34	6	17535	171.911765	0.99896443	0.13086891	15.4014844
GOTERM_BP_DIRECT	GO:0071333~cellular response to glucose stimulus	3	0.06965405	0.01214398	ICAM1, CCL2, LGALS1	34	89	17535	17.3843358	0.99940606	0.13806446	16.5383096

GOTERM_BP_DIRECT	GO:2001200~positive regulation of dendritic cell differentiation	2	0.04643603	0.01310174	LGALS3, LGALS1	34	7	17535	147.352941	0.99967069	0.14548865	17.72761
GOTERM_BP_DIRECT	GO:0060754~positive regulation of mast cell	2	0.04643603	0.01310174	VEGFA, CCL5	34	7	17535	147.352941	0.99967069	0.14548865	17.72761
GOTERM_BP_DIRECT	GO:0006874~cellular calcium ion homeostasis	3	0.06965405	0.01430453	CCL12, CCL2, CCL5	34	97	17535	15.9505761	0.99984311	0.15503553	19.198799
GOTERM_BP_DIRECT	GO:0009725~response to hormone	3	0.06965405	0.01486887	TIMP4, TIMP2, TIMP3	34	99	17535	15.6283422	0.99988924	0.15789619	19.8805834
GOTERM_BP_DIRECT	GO:0035148~tube formation	2	0.04643603	0.01495977	NOTCH1, VEGFA	34	8	17535	128.933824	0.99989528	0.15608927	19.9899037
GOTERM_BP_DIRECT	GO:0007417~central nervous system development	3	0.06965405	0.01544274	TIMP4, TIMP2, TIMP3	34	101	17535	15.3188701	0.99992228	0.15805815	20.5683778
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	3	0.06965405	0.02036787	LGALS3, VEGFA, CCL5	34	117	17535	13.2239819	0.99999632	0.20022112	26.2489317
GOTERM_BP_DIRECT	GO:0003184~pulmonary valve morphogenesis	2	0.04643603	0.02051355	NOTCH2, NOTCH1	34	11	17535	93.7700535	0.99999663	0.1983528	26.4110371
GOTERM_BP_DIRECT	GO:0071407~cellular response to organic cyclic	3	0.06965405	0.02202513	CCL2, LGALS1, CCL5	34	122	17535	12.6820154	0.99999868	0.20821442	28.0735751
GOTERM_BP_DIRECT	GO:0048246~macrophage chemotaxis	2	0.04643603	0.02235805	CCL2, LGALS3	34	12	17535	85.9558824	0.99999893	0.20785936	28.4350132
GOTERM_BP_DIRECT	GO:0007010~cytoskeleton organization	3	0.06965405	0.02408543	CCL12, CCL2, CCL7	34	128	17535	12.087546	0.99999963	0.21890069	30.2832938
GOTERM_BP_DIRECT	GO:0070986~left/right axis	2	0.04643603	0.02419918	NOTCH2, NOTCH1	34	13	17535	79.3438914	0.99999966	0.21664147	30.4034332
GOTERM_BP_DIRECT	GO:0010812~negative regulation of cell-substrate	2	0.04643603	0.02419918	NOTCH1, LGALS1	34	13	17535	79.3438914	0.99999966	0.21664147	30.4034332
GOTERM_BP_DIRECT	GO:0002544~chronic inflammatory response	2	0.04643603	0.02419918	CCL2, CCL5	34	13	17535	79.3438914	0.99999966	0.21664147	30.4034332
GOTERM_BP_DIRECT	GO:0010759~positive regulation of macrophage chemotaxis	2	0.04643603	0.02603696	CCL2, CCL5	34	14	17535	73.6764706	0.99999989	0.22795544	32.3178189
GOTERM_BP_DIRECT	GO:0090557~establishment of endothelial	2	0.04643603	0.02603696	ICAM1, F11R	34	14	17535	73.6764706	0.99999989	0.22795544	32.3178189

GOTERM_BP_DIRECT	GO:0090026~positive regulation of monocyte	2	0.04643603	0.03335454	CCL2, CCL5	34	18	17535	57.3039216	1	0.27919638	39.4640251
GOTERM_BP_DIRECT	GO:0090280~positive regulation of calcium ion import	2	0.04643603	0.03335454	CCL2, LGALS3	34	18	17535	57.3039216	1	0.27919638	39.4640251
GOTERM_BP_DIRECT	GO:0051593~response to folic acid	2	0.04643603	0.03517558	VEGFA, TIMP3	34	19	17535	54.2879257	1	0.28836269	41.1296512
GOTERM_BP_DIRECT	GO:0043524~negative regulation of neuron apoptotic process	3	0.06965405	0.03549494	CCL2, CNTF, GFRAL	34	158	17535	9.79244229	1	0.28684031	41.4173135
GOTERM_BP_DIRECT	GO:0002437~inflammatory response to antigenic	2	0.04643603	0.03880771	NOTCH2, NOTCH1	34	21	17535	49.1176471	1	0.30554162	44.3249433
GOTERM_BP_DIRECT	GO:0048010~vascular endothelial growth factor receptor signaling	2	0.04643603	0.03880771	CCL2, VEGFA	34	21	17535	49.1176471	1	0.30554162	44.3249433
GOTERM_BP_DIRECT	GO:0002687~positive regulation of leukocyte migration	2	0.04643603	0.04061879	CCL12, CCL2	34	22	17535	46.8850267	1	0.31360054	45.8570819
GOTERM_BP_DIRECT	GO:0030279~negative regulation of ossification	2	0.04643603	0.04061879	NOTCH1, GFRA4	34	22	17535	46.8850267	1	0.31360054	45.8570819
GOTERM_BP_DIRECT	GO:0045672~positive regulation of osteoclast differentiation	2	0.04643603	0.04242657	NOTCH2, CCL5	34	23	17535	44.8465473	1	0.32133364	47.3471411
GOTERM_BP_DIRECT	GO:0048844~artery morphogenesis	2	0.04643603	0.04603221	NOTCH3, VEGFA	34	25	17535	41.2588235	1	0.33982458	50.2056033
GOTERM_BP_DIRECT	GO:0007159~leukocyte cell-cell	2	0.04643603	0.04603221	ICAM1, CCL5	34	25	17535	41.2588235	1	0.33982458	50.2056033
GOTERM_BP_DIRECT	GO:0090023~positive regulation of neutrophil	2	0.04643603	0.04603221	CXCL1, CXCL2	34	25	17535	41.2588235	1	0.33982458	50.2056033
GOTERM_BP_DIRECT	GO:0071361~cellular response to	2	0.04643603	0.0478301	CCL5, CCL7	34	26	17535	39.6719457	1	0.34668927	51.5762192
GOTERM_BP_DIRECT	GO:0002052~positive regulation of neuroblast proliferation	2	0.04643603	0.0478301	NOTCH1, VEGFA	34	26	17535	39.6719457	1	0.34668927	51.5762192
GOTERM_BP_DIRECT	GO:0071354~cellular response to interleukin-6	2	0.04643603	0.05141601	ICAM1, CCL2	34	28	17535	36.8382353	1	0.36365701	54.2055281

GOTERM_BP_DIRECT	GO:0045861~negative regulation of proteolysis	2	0.04643603	0.05141601	TIMP2, TIMP3	34	28	17535	36.8382353	1	0.36365701	54.2055281
GOTERM_BP_DIRECT	GO:0016477~cell migration	3	0.06965405	0.05281298	VEGFA, GFRA1, TREM1	34	197	17535	7.85383697	1	0.36756936	55.1933116
GOTERM_BP_DIRECT	GO:0040007~growth	2	0.04643603	0.05320406	CNTF, VEGFA	34	29	17535	35.5679513	1	0.36577261	55.4662573
GOTERM_BP_DIRECT	GO:0032355~response to estradiol	3	0.06965405	0.05473185	CXCL1, VEGFA, CXCL2	34	201	17535	7.6975417	1	0.37026942	56.5177734
GOTERM_BP_DIRECT	GO:0031663~lipopolysaccharide-mediated signaling pathway	2	0.04643603	0.05677034	CCL2, CCL5	34	31	17535	33.2732448	1	0.37736704	57.8847487
GOTERM_BP_DIRECT	GO:0048663~neural fate commitment	2	0.04643603	0.05677034	NOTCH3, NOTCH1	34	31	17535	33.2732448	1	0.37736704	57.8847487
GOTERM_BP_DIRECT	GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	2	0.04643603	0.05677034	CNTF, VEGFA	34	31	17535	33.2732448	1	0.37736704	57.8847487
GOTERM_BP_DIRECT	GO:0045930~negative regulation of mitotic cell cycle	2	0.04643603	0.0585486	GAS1, TIMP2	34	32	17535	32.2334559	1	0.38286063	59.0443845
GOTERM_BP_DIRECT	GO:0006959~humoral immune	2	0.04643603	0.06209536	NOTCH2, NOTCH1	34	34	17535	30.3373702	1	0.3972155	61.2689297
GOTERM_BP_DIRECT	GO:0034612~response to tumor necrosis factor	2	0.04643603	0.06386388	CCL2, CCL5	34	35	17535	29.4705882	1	0.40215142	62.3355632
GOTERM_BP_DIRECT	GO:0048754~branching morphogenesis of an epithelial tube	2	0.04643603	0.06562916	NOTCH1, VEGFA	34	36	17535	28.6519608	1	0.40692398	63.3728806
GOTERM_BP_DIRECT	GO:2001240~negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	2	0.04643603	0.06562916	GFRAL, GAS1	34	36	17535	28.6519608	1	0.40692398	63.3728806
GOTERM_BP_DIRECT	GO:0030513~positive regulation of BMP signaling	2	0.04643603	0.06562916	NOTCH2, NOTCH1	34	36	17535	28.6519608	1	0.40692398	63.3728806
GOTERM_BP_DIRECT	GO:0002053~positive regulation of mesenchymal cell proliferation	2	0.04643603	0.06562916	VEGFA, GAS1	34	36	17535	28.6519608	1	0.40692398	63.3728806
GOTERM_BP_DIRECT	GO:0043491~protein kinase B signaling	2	0.04643603	0.06739122	CCL2, CCL5	34	37	17535	27.8775835	1	0.41154102	64.3816861

GOTERM_BP_DIRECT	GO:0042127~regulation of cell proliferation	3	0.06965405	0.07146402	CXCL1, NOTCH1, CXCL2	34	234	17535	6.61199095	1	0.42681903	66.6151308
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	4	0.09287207	0.07243989	LGALS3, VEGFA, GAS1, TIMP1	34	517	17535	3.99021504	1	0.42739734	67.1305281
GOTERM_BP_DIRECT	GO:0046677~response to antibiotic	2	0.04643603	0.0848355	CCL2, HAVCR1	34	47	17535	21.9461827	1	0.47764015	73.0635035
GOTERM_BP_DIRECT	GO:0006955~immune response	3	0.06965405	0.08963474	CXCL1, CXCL2, IL22	34	267	17535	5.79477859	1	0.49324369	75.0796269
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	3	0.06965405	0.0913501	ICAM1, CCL2, VEGFA	34	270	17535	5.73039216	1	0.49602011	75.7654333
GOTERM_BP_DIRECT	GO:0014070~response to organic cyclic compound	3	0.06965405	0.09249916	ICAM1, CCL5, TIMP3	34	272	17535	5.68825692	1	0.49651292	76.2149479
GOTERM_BP_DIRECT	GO:0001701~in utero embryonic development	3	0.06965405	0.09713839	NOTCH2, NOTCH1, VEGFA	34	280	17535	5.52573529	1	0.51038082	77.9519356

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GOTERM_BP_DIRECT	GO:0051045~negative regulation of cell proliferation	4	0.08766163	2.3337E-07	TIMP4, TIMP2, TIMP3, TIMP1	30	6	12321	273.8	8.75E-05	8.75E-05	3.22E-04
GOTERM_BP_DIRECT	GO:0043086~negative regulation of cell proliferation	4	0.08766163	3.3005E-06	TIMP4, TIMP2, TIMP3, TIMP1	30	13	12321	126.369231	1.24E-03	6.19E-04	4.56E-03
GOTERM_BP_DIRECT	GO:0007219~Notch signaling	5	0.10957703	1.5173E-05	NOTCH3, NOTCH2, NOTCH1, JAG2, TIMP4	30	65	12321	31.5923077	5.67E-03	1.89E-03	2.10E-02
GOTERM_BP_DIRECT	GO:0003184~pulmonary artery morphogenesis	3	0.06574622	3.2002E-05	NOTCH2, NOTCH1, JAG1	30	4	12321	308.025	1.19E-02	3.00E-03	4.42E-02
GOTERM_BP_DIRECT	GO:0043524~negative regulation of cell proliferation	5	0.10957703	4.8134E-05	HRAS, NRP1, CNTF, GFRAL, GDNF	30	87	12321	23.6034483	1.79E-02	3.60E-03	6.65E-02
GOTERM_BP_DIRECT	GO:0035924~cellular morphogenesis	3	0.06574622	0.00029037	NOTCH1, VEGFA, GAS1	30	11	12321	112.009091	1.03E-01	1.80E-02	4.00E-01
GOTERM_BP_DIRECT	GO:0016337~single organ morphogenesis	4	0.08766163	0.00034882	ICAM1, ICAM4, ICAM5, ICAM2	30	59	12321	27.8440678	1.23E-01	1.85E-02	4.81E-01
GOTERM_BP_DIRECT	GO:0048010~vasculature morphogenesis	3	0.06574622	0.00041059	VEGFB, NRP1, VEGFA	30	13	12321	94.7769231	1.43E-01	1.91E-02	5.66E-01
GOTERM_BP_DIRECT	GO:0045747~positive regulation of cell proliferation	3	0.06574622	0.00223376	NOTCH1, JAG2, JAG1	30	30	12321	41.07	5.68E-01	8.90E-02	3.04E+00
GOTERM_BP_DIRECT	GO:0050679~positive regulation of cell proliferation	3	0.06574622	0.0030332	NOTCH1, HRAS, CCL5	30	35	12321	35.2028571	6.80E-01	1.08E-01	4.11E+00
GOTERM_BP_DIRECT	GO:0070374~positive regulation of cell proliferation	4	0.08766163	0.00321314	ICAM1, HRAS, NRP1, CCL5	30	127	12321	12.9354331	7.01E-01	1.04E-01	4.35E+00
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	4	0.08766163	0.00431153	ICAM1, ICAM4, ICAM5, ICAM2	30	141	12321	11.6510638	8.02E-01	1.26E-01	5.80E+00
GOTERM_BP_DIRECT	GO:0050793~regulation of cell proliferation	2	0.04383081	0.00470206	NOTCH2, NOTCH1	30	2	12321	410.7	0.82922892	0.12711919	6.30465038
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	3	0.06574622	0.00564258	LGALS3, TREM1, CCL5	30	48	12321	25.66875	0.88020355	0.14064112	7.52061283
GOTERM_BP_DIRECT	GO:0009912~auditory perception	2	0.04383081	0.00704508	NOTCH1, JAG2	30	3	12321	273.8	0.92943738	0.16201101	9.30667376
GOTERM_BP_DIRECT	GO:0072017~distal limb morphogenesis	2	0.04383081	0.00704508	NOTCH1, JAG1	30	3	12321	273.8	0.92943738	0.16201101	9.30667376
GOTERM_BP_DIRECT	GO:0046533~negative regulation of cell proliferation	2	0.04383081	0.00938277	NOTCH1, CNTF	30	4	12321	205.35	0.97084562	0.19824073	12.2127439
GOTERM_BP_DIRECT	GO:0060754~positive regulation of cell proliferation	2	0.04383081	0.01171515	VEGFB, VEGFA	30	5	12321	164.28	0.98795514	0.22890837	15.0259203
GOTERM_BP_DIRECT	GO:0060982~coronary artery morphogenesis	2	0.04383081	0.01171515	NOTCH1, NRP1	30	5	12321	164.28	0.98795514	0.22890837	15.0259203
GOTERM_BP_DIRECT	GO:2000737~negative regulation of cell proliferation	2	0.04383081	0.01404222	NOTCH1, JAG1	30	6	12321	136.9	0.99502413	0.25518527	17.7491651
GOTERM_BP_DIRECT	GO:0010033~response to hypoxia	2	0.04383081	0.01404222	TIMP4, TIMP3	30	6	12321	136.9	0.99502413	0.25518527	17.7491651
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	4	0.08766163	0.01457755	CNTF, VEGFA, GDNF, TIMP1	30	220	12321	7.46727273	0.995941	0.25161112	18.3640661
GOTERM_BP_DIRECT	GO:0035767~endothelial cell proliferation	2	0.04383081	0.01636401	NRP1, VEGFA	30	7	12321	117.342857	0.99794456	0.26608594	20.3853463
GOTERM_BP_DIRECT	GO:0035148~tube morphogenesis	2	0.04383081	0.01868051	NOTCH1, VEGFA	30	8	12321	102.675	0.999151	0.28590244	22.9372407
GOTERM_BP_DIRECT	GO:0010951~negative regulation of cell proliferation	2	0.04383081	0.01868051	TIMP2, TIMP1	30	8	12321	102.675	0.999151	0.28590244	22.9372407

GOTERM_BP_DIRECT GO:0048245~eosino 2	0.04383081	0.01868051	LGALS3, CCL5	30	8	12321	102.675	0.999151	0.28590244	22.9372407
GOTERM_BP_DIRECT GO:0032495~respon 2	0.04383081	0.02099175	NOTCH1, JAG1	30	9	12321	91.2666667	0.99964934	0.30345502	25.4075367
GOTERM_BP_DIRECT GO:0097193~intrins 2	0.04383081	0.02559847	HRAS, LGALS12	30	11	12321	74.6727273	0.9999402	0.34479116	30.1136617
GOTERM_BP_DIRECT GO:0048485~sympa 2	0.04383081	0.02559847	GDNF, GFRA3	30	11	12321	74.6727273	0.9999402	0.34479116	30.1136617
GOTERM_BP_DIRECT GO:0002042~cell m 2	0.04383081	0.02559847	NRP1, VEGFA	30	11	12321	74.6727273	0.9999402	0.34479116	30.1136617
GOTERM_BP_DIRECT GO:0050930~induct 2	0.04383081	0.02789397	VEGFB, VEGFA	30	12	12321	68.45	0.9999753	0.35727445	32.3544506
GOTERM_BP_DIRECT GO:0050918~positiv 2	0.04383081	0.02789397	NRP1, VEGFA	30	12	12321	68.45	0.9999753	0.35727445	32.3544506
GOTERM_BP_DIRECT GO:0009725~respon 2	0.04383081	0.03018425	TIMP2, TIMP1	30	13	12321	63.1846154	0.9999898	0.36855072	34.5235659
GOTERM_BP_DIRECT GO:0045944~positiv 5	0.10957703	0.03207347	NOTCH3, HRAS, VEGFA, JAG1, GDNF	30	519	12321	3.9566474	0.99999509	0.37510973	36.2640786
GOTERM_BP_DIRECT GO:0030154~cell di 3	0.06574622	0.04261254	NOTCH2, NOTCH1, LGALS3	30	140	12321	8.80071429	0.99999992	0.45382775	45.2115406
GOTERM_BP_DIRECT GO:0097150~neuror 2	0.04383081	0.04381693	NOTCH1, JAG1	30	19	12321	43.2315789	0.99999995	0.45123161	46.1562152
GOTERM_BP_DIRECT GO:0048661~positiv 2	0.04383081	0.04607098	NOTCH3, CCL5	30	20	12321	41.07	0.99999998	0.45659766	47.8837322
GOTERM_BP_DIRECT GO:2001240~negati 2	0.04383081	0.05726448	GFRAL, GDNF	30	25	12321	32.856	1	0.52150945	55.726419
GOTERM_BP_DIRECT GO:0034097~respon 2	0.04383081	0.06170629	TIMP2, TIMP1	30	27	12321	30.4222222	1	0.53720485	58.5232123
GOTERM_BP_DIRECT GO:0002548~monoc 2	0.04383081	0.0639196	LGALS3, CCL5	30	28	12321	29.3357143	1	0.53886723	59.854801
GOTERM_BP_DIRECT GO:0030155~regula 2	0.04383081	0.0639196	ICAM1, JAG2	30	28	12321	29.3357143	1	0.53886723	59.854801
GOTERM_BP_DIRECT GO:0030900~forebr 2	0.04383081	0.0639196	NOTCH3, NOTCH1	30	28	12321	29.3357143	1	0.53886723	59.854801
GOTERM_BP_DIRECT GO:2001237~negati 2	0.04383081	0.06612788	NRP1, LGALS3	30	29	12321	28.3241379	1	0.54042442	61.1437431
GOTERM_BP_DIRECT GO:0043406~positiv 2	0.04383081	0.07709402	HRAS, VEGFA	30	34	12321	24.1588235	1	0.58723082	66.9949515
GOTERM_BP_DIRECT GO:0045665~negati 2	0.04383081	0.09652056	NOTCH3, JAG1	30	43	12321	19.1023256	1	0.66294885	75.4007129