

>16

14

12

10 -

8 -

-log10(p-adj)

values above this threshold are capped

48

49

O- SCHE SCC SCHE KES KINS ** INFRANT HER COKUM* HE WE WE WE SCHED	4 -	33 34 35 37 36 37		9 12 19 19 24	2 10 7 13 21	3 4 5 8 13 20 2263	42 43 6 11 45 16 46 25			_e 1			45
	0 -	.4	C)				(h. C)	4	, &	As as		.Q	.0
		eo;n _{ir}	[®] O: _{CC}	id source				~			`	×	n,

id	source	term_id	term_name	term_size		p_value
1	CORUM	CORUM:5408	Neurotrophin-3-p75 complex	1		5.0e-02
2	GO:BP	GO:0048245	eosinophil chemotaxis	27		4.1e-04
3	GO:BP	GO:0070555	response to interleukin-1	132		6.2e-04
4	GO:BP	GO:0072677	eosinophil migration	31		6.3e-04
5	GO:BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	210		4.0e-03
6	GO:BP	GO:2000503	positive regulation of natural killer cell chemotaxis	6		4.9e-03
7	GO:BP	GO:0048247	lymphocyte chemotaxis	63		5.5e-03
8	GO:BP	GO:0071356	cellular response to tumor necrosis factor	229		5.6e-03
9	GO:BP	GO:0002548	monocyte chemotaxis	69		7.2e-03
10	GO:BP	GO:0034612	response to tumor necrosis factor	250		8.0e-03
11	GO:BP	GO:2000501	regulation of natural killer cell chemotaxis	8		9.2e-03
	GO:BP	GO:0006952	defense response	1769		9.5e-03
	GO:BP	GO:0035747	natural killer cell chemotaxis	10		1.5e-02
	GO:BP	GO:0070372	regulation of ERK1 and ERK2 cascade	298		1.6e-02
	GO:BP	GO:0070098	chemokine-mediated signaling pathway	90		1.6e-02
	GO:BP	GO:0070371	ERK1 and ERK2 cascade	321		2.1e-02
	GO:BP	GO:1990868	response to chemokine	99		2.1e-02 2.1e-02
			•			
	GO:BP	GO:1990869	cellular response to chemokine	99		2.1e-02
	GO:BP	GO:0030593	neutrophil chemotaxis	106		2.6e-02
	GO:BP	GO:0071347	cellular response to interleukin–1	106		2.6e-02
	GO:BP	GO:0043922	negative regulation by host of viral transcription	15		3.4e-02
	GO:BP	GO:0071346	cellular response to type II interferon	121		3.9e-02
	GO:BP	GO:0072676	lymphocyte migration	122		4.0e-02
24	GO:BP	GO:0006954	inflammatory response	824		4.6e-02
25	GO:BP	GO:1990266	neutrophil migration	128		4.6e-02
26	GO:BP	GO:0071621	granulocyte chemotaxis	130		4.8e-02
27	GO:CC	GO:0005576	extracellular region	4206		3.0e-04
28	GO:CC	GO:0005615	extracellular space	3284		1.4e-02
29	GO:CC	GO:0035580	specific granule lumen	61		3.7e-02
30	GO:CC	GO:0034774	secretory granule lumen	320		3.7e-02
31	GO:CC	GO:0060205	cytoplasmic vesicle lumen	323		3.8e-02
32	GO:CC	GO:0031983	vesicle lumen	324		3.8e-02
33	GO:MF	GO:0008009	chemokine activity	50		3.0e-04
34	GO:MF	GO:0048020	CCR chemokine receptor binding	50		3.0e-04
35	GO:MF	GO:0031726	CCR1 chemokine receptor binding	6		5.9e-04
36	GO:MF	GO:0031730	CCR5 chemokine receptor binding	7		8.3e-04
37	GO:MF	GO:0042379	chemokine receptor binding	76		1.1e-03
38	GO:MF	GO:0048018	receptor ligand activity	510		1.3e-02
39	GO:MF	GO:0030546	signaling receptor activator activity	519		1.4e-02
	GO:MF	GO:0030545	signaling receptor regulator activity	555		1.9e-02
	GO:MF	GO:0005125	cytokine activity	237		3.2e-02
	KEGG	KEGG:04060	Cytokine–cytokine receptor interaction	293		1.1e-03
	KEGG	KEGG:04061	Viral protein interaction with cytokine and cytokine receptor	98		1.6e-03
	KEGG	KEGG:04620	Toll–like receptor signaling pathway	102		1.8e-03
	KEGG	KEGG:04020	Chemokine signaling pathway	190		1.1e-02
	KEGG	KEGG:04002	Human cytomegalovirus infection	223		1.8e-02
	TF		· · ·	13		3.1e-02
47 40		TF:M05304_1	Factor: Zbtb5; motif: AGGRAGCTTC; match class: 1			
	WP	WP:WP4329	miRNA role in immune response in sepsis	65		5.2e-03
	WP	WP:WP5287	17q12 copy number variation syndrome	96		1.7e-02
	WP	WP:WP5095	Overview of proinflammatory and profibrotic mediators	127		3.8e-02
51	WP	WP:WP5092	Interactions of natural killer cells in pancreatic cancer	27	0.7	4.6e-02
			g:Profiler (I	biit.cs.ut.ee/g	hι(niiet)