

	Gene Set Category	Pathway	Set Size	Percent Up	Ntk Stat	Ntk q-value	Ntk Rank	NEK* Stat	NEK* q-value	NEK* Rank
1	KEGG:00330	Arginine and proline metabolism	38	68	3.49	<0.0001	11	4.07	<0.0001	2
2	GO:0016066	cellular defense response (sensu Vertebrata)	12	75	3.6	<0.0001	10	3.99	<0.0001	6
3	KEGG:04512	ECM-receptor interaction	47	19	-4.3	<0.0001	3	-3.38	<0.0001	16
4	GO:0042087	cell-mediated immune response	11	73	3.33	<0.0001	16	4.03	<0.0001	3
5	GO:0042088	T-helper 1 type immune response	11	73	3.33	<0.0001	16	4.03	<0.0001	3
6	BioCyc	fatty acid oxidation pathway	14	71	3.31	<0.0001	17	3.51	<0.0001	10
7	GO:0005604	basement membrane	23	4	-4.81	<0.0001	2	-3.1	<0.0001	28
8	KEGG:04510	Focal adhesion	135	38	-3.71	<0.0001	7	-3.13	<0.0001	25
9	GO:0016126	sterol biosynthesis	22	23	-2.99	<0.0001	30	-3.65	<0.0001	8
10	GO:0001817	regulation of cytokine production	16	75	3.25	<0.0001	20	3.12	<0.0001	26
11	GO:0019888	protein phosphatase regulator activity	32	22	-2.94	<0.0001	36	-3.47	<0.0001	12
12	GO:0050954	sensory perception of mechanical stimulus	39	38	-2.78	<0.0001	48	-4.02	<0.0001	4
13	GO:0007605	sensory perception of sound	39	38	-2.78	<0.0001	48	-4.02	<0.0001	4
14	GO:0019208	phosphatase regulator activity	33	24	-2.66	<0.0001	54	-3.52	<0.0001	9
15	GO:0001816	cytokine production	17	76	3.3	<0.0001	18	2.88	<0.0001	48
16	GO:0042089	cytokine biosynthesis	17	76	3.3	<0.0001	18	2.88	<0.0001	48
17	GO:0042995	cell projection	36	19	-2.8	<0.0001	47	-3.26	<0.0001	19
18	GO:0042157	lipoprotein metabolism	25	68	2.44	<0.0001	68	4	<0.0001	5
19	GO:0016836	hydro-lyase activity	29	76	3.95	<0.0001	6	2.5	<0.0001	77
20	KEGG:04662	B cell receptor signaling pathway	45	73	3.63	<0.0001	9	2.46	<0.0001	80
21	GO:0005201	extracellular matrix structural constituent	40	23	-4.15	<0.0001	4	-2.37	<0.0001	93
22	GO:0007588	Excretion	16	69	2.33	0.1711	96	3.77	<0.0001	7
23	GO:0042158	lipoprotein biosynthesis	16	75	2.33	0.1711	96	3.45	<0.0001	14
24	GO:0006497	protein amino acid lipidation	16	75	2.33	0.1711	96	3.45	<0.0001	14
25	GO:0007409	Axonogenesis	18	61	2.33	0.1711	96	3.38	<0.0001	15
26	GO:0050900	immune cell migration	10	60	2.33	0.1711	96	3.33	<0.0001	17
27	GO:0030595	immune cell chemotaxis	10	60	2.33	0.1711	96	3.33	<0.0001	17
28	GO:0048468	cell development	34	59	2.33	0.1711	96	3.26	<0.0001	18
29	GO:0006631	fatty acid metabolism	80	60	4.09	<0.0001	5	2.33	0.1257	124
30	GO:0005605	basal lamina	14	0	-3.41	<0.0001	12	-2.33	0.1257	124
31	GO:0005578	extracellular matrix (sensu Metazoa)	102	22	-5.07	<0.0001	1	-2.05	0.1963	179.5
32	GO:0031012	extracellular matrix	102	22	-5.07	<0.0001	1	-2.05	0.1963	179.5
33	GO:0043062	extracellular structure organization and biogenesis	11	18	-3.28	<0.0001	19	-2.2	0.1175	162
34	GO:0030198	extracellular matrix organization and biogenesis	11	18	-3.28	<0.0001	19	-2.2	0.1175	162
35	GO:0006695	cholesterol biosynthesis	15	33	-1.88	0.3431	170	-3.49	<0.0001	11
36	GO:0051247	positive regulation of	21	81	1.88	0.3076	188	3.47	<0.0001	13

		protein metabolism								
37	BioCarta	Keratinocyte Differentiation	17	29	-1.64	0.4202	239	-4.22	<0.0001	1
38	GO:0006730	one-carbon compound metabolism	24	63	3.36	<0.0001	15	1.88	0.2279	239.5
39	GO:0001503	Ossification	10	50	3.64	<0.0001	8	1.55	0.3217	351
40	GO:0031214	biomineral formation	10	50	3.64	<0.0001	8	1.55	0.3217	351
41	GO:0042098	T cell proliferation	10	50	1.34	0.4614	387	3.18	<0.0001	21
42	GO:0006092	main pathways of carbohydrate metabolism	75	65	3.4	<0.0001	13	1.34	0.4057	412
43	GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	57	68	3.38	<0.0001	14	1.13	0.4582	532
44	KEGG:00632	Benzoate degradation via CoA ligation	32	41	-0.88	0.5939	664	-3.24	<0.0001	20