

	Gene Set Category	Pathway	Set Size	%Up	Ntk Stat	Ntk q-value	Ntk Rank	NEK* Stat	NEK* q-value	NEK* Rank
1	GO:0004857	enzyme inhibitor activity	128	30	-4.25	<0.0001	14	-3.9	<0.0001	2
2	KEGG:01430	Cell Communication	53	28	-5.59	<0.0001	5	-3.04	<0.0001	15
3	KEGG:04510	Focal adhesion	135	33	-5.46	<0.0001	7	-2.96	<0.0001	19
4	KEGG:04512	ECM-receptor interaction	47	21	-5.95	<0.0001	3	-2.8	<0.0001	27
5	GO:0031497	chromatin assembly	54	20	-4.28	<0.0001	13	-2.97	<0.0001	18
6	KEGG:04210	Apoptosis	51	29	-4.24	<0.0001	15	-2.99	<0.0001	16
7	GO:0000785	chromatin	94	32	-4.34	<0.0001	12	-2.96	<0.0001	21
8	GO:0005604	basement membrane	23	17	-5.08	<0.0001	8	-2.81	<0.0001	26
9	GO:0006695	cholesterol biosynthesis	15	27	-3.52	<0.0001	32	-3.39	<0.0001	8
10	GO:0007059	chromosome segregation	25	12	-5.53	<0.0001	6	-2.7	<0.0001	38
11	GO:0043161	proteasomal ubiquitin-dependent protein catabolism	11	9	-3.36	<0.0001	38	-3.22	<0.0001	9
12	GO:0001501	skeletal development	47	23	-4.19	<0.0001	16	-2.73	<0.0001	32
13	GO:0006334	nucleosome assembly	52	19	-4.14	<0.0001	17	-2.65	<0.0001	40
14	BioCarta	Ceramide Signaling Pathway	14	21	-3.17	<0.0001	49	-3.06	<0.0001	13
15	GO:0043062	extracellular structure organization and biogenesis	11	9	-4.92	<0.0001	9	-2.37	<0.0001	56
16	GO:0030198	extracellular matrix organization and biogenesis	11	9	-4.92	<0.0001	9	-2.37	<0.0001	56
17	BioCarta	Caspase Cascade in Apoptosis	17	29	-3	<0.0001	63	-3.17	<0.0001	11
18	GO:0016126	sterol biosynthesis	22	32	-2.93	<0.0001	73	-3.18	<0.0001	10
19	KEGG:00220	Urea cycle and metabolism of amino groups	18	56	2.93	<0.0001	72	2.96	<0.0001	20
20	GO:0005201	extracellular matrix structural constituent	40	23	-7.39	<0.0001	1	-2.15	0.1692	116
21	GO:0005694	chromosome	190	35	-4.82	<0.0001	10	-2.31	0.1772	110
22	GO:0005581	collagen	15	13	-5.6	<0.0001	4	-2.05	0.2632	137
23	GO:0016810	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	38	61	2.33	0.1049	138.5	3.5	<0.0001	5
24	GO:0000786	nucleosome	39	18	-3.72	<0.0001	21	-2.05	0.2632	137
25	GO:0009064	glutamine family amino acid metabolism	23	65	2.33	0.1049	138.5	2.95	<0.0001	22
26	GO:0005605	basal lamina	14	14	-3.82	<0.0001	19	-2.01	0.2381	166
27	GO:0006928	cell motility	130	38	-3.86	<0.0001	18	-1.88	0.3154	176
28	GO:0040011	locomotion	130	38	-3.86	<0.0001	18	-1.88	0.3154	176
29	GO:0051674	localization of cell	130	38	-3.86	<0.0001	18	-1.88	0.3154	176
30	GO:0005578	extracellular matrix (sensu Metazoa)	102	24	-6.69	<0.0001	2	-1.75	0.3488	212.5
31	GO:0031012	extracellular matrix	102	24	-6.69	<0.0001	2	-1.75	0.3488	212.5
32	GO:0043065	positive regulation of apoptosis	110	55	2.05	0.1634	217.5	3.06	<0.0001	14
33	GO:0043068	positive regulation of programmed cell death	110	55	2.05	0.1634	217.5	3.06	<0.0001	14
34	GO:0006917	induction of apoptosis	99	54	1.88	0.2	264	2.99	<0.0001	17
35	GO:0012502	induction of programmed cell death	99	54	1.88	0.2	264	2.99	<0.0001	17

36	GO:0019079	viral genome replication	17	18	-1.55	0.3123	350	-3.95	<0.0001	1
37	GO:0007507	heart development	16	75	1.55	0.2995	363	3.61	<0.0001	4
38	GO:0019058	viral infectious cycle	24	25	-1.48	0.3229	394.5	-3.46	<0.0001	6
39	KEGG:00600	Glycosphingolipid metabolism	22	68	1.41	0.361	405.5	3.69	<0.0001	3
40	BioCarta	Segmentation Clock	10	30	-1.41	0.3416	420.5	-2.93	<0.0001	23
41	KEGG:04060	Cytokine-cytokine receptor interaction	79	33	-3.76	<0.0001	20	-1.23	0.5	426
42	GO:0006817	phosphate transport	30	33	-4.55	<0.0001	11	-1.17	0.5212	446.5
43	GO:0051248	negative regulation of protein metabolism	32	53	1.13	0.3968	583.5	3.44	<0.0001	7
44	GO:0004879	ligand-dependent nuclear receptor activity	20	50	0.31	0.6253	1103	3.12	<0.0001	12