![NIH National Institutes of Health - DAVID Bioinformatics]

Functional Annotation Clustering

Current Gene List: new_converted_list
Current Background: new_converted_bg
37 DAVID IDs

Options   **Classification Stringency** Medium ⌄

[Rerun using options] [Create Sublist]

3 Cluster(s)   **Download File**

					Count	P_Value	Benjamini
Annotation Cluster 1		Enrichment Score: 0	G				
☐	UP_KW_CELLULAR_COMPONENT	Membrane	RT		12	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	TRANSMEM:Helical	RT		9	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	TOPO_DOM:Extracellular	RT		7	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	TOPO_DOM:Cytoplasmic	RT		8	1.0E0	1.0E0
Annotation Cluster 2		Enrichment Score: 0	G				
☐	UP_KW_DOMAIN	Signal	RT		12	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine	RT		8	1.0E0	1.0E0
☐	UP_KW_PTM	Glycoprotein	RT		9	1.0E0	1.0E0
☐	UP_KW_PTM	Disulfide bond	RT		13	1.0E0	1.0E0
Annotation Cluster 3		Enrichment Score: 0	G				
☐	INTERPRO	Chemokine_IL8-like_dom	RT		3	1.0E0	1.0E0
☐	INTERPRO	Interleukin_8-like_sf	RT		3	1.0E0	1.0E0
☐	INTERPRO	Chemokine_b/g/d	RT		3	1.0E0	1.0E0
☐	KEGG_PATHWAY	Chemokine signaling pathway	RT		5	1.0E0	1.0E0
☐	UP_SEQ_FEATURE	DOMAIN:Chemokine interleukin-8-like	RT		3	1.0E0	1.0E0
☐	GOTERM_BP_DIRECT	inflammatory response	RT		3	1.0E0	1.0E0
☐	GOTERM_BP_DIRECT	neutrophil chemotaxis	RT		3	1.0E0	1.0E0
☐	GOTERM_BP_DIRECT	antimicrobial humoral immune response mediated by antimicrobial peptide	RT		3	1.0E0	1.0E0
☐	UP_KW_BIOLOGICAL_PROCESS	Chemotaxis	RT		3	1.0E0	1.0E0
☐	UP_KW_BIOLOGICAL_PROCESS	Inflammatory response	RT		3	1.0E0	1.0E0
☐	BBID	109.Chemokine_families	RT		3	1.0E0	1.0E0
☐	GOTERM_BP_DIRECT	immune response	RT		5	1.0E0	1.0E0
☐	GOTERM_BP_DIRECT	chemokine-mediated signaling pathway	RT		4	1.0E0	1.0E0
☐	KEGG_PATHWAY	Cytokine-cytokine receptor interaction	RT		4	1.0E0	1.0E0
☐	KEGG_PATHWAY	Viral protein interaction with cytokine and cytokine receptor	RT		4	1.0E0	1.0E0
☐	SMART	SCY	RT		3	1.0E0	1.0E0

[15 terms] were not clustered.

Please cite DAVID within any publication that makes use of any methods inspired by **DAVID**.