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Functional Annotation Clustering

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Current Gene List: [List_1](#)

Current Background: [Homo sapiens](#)

12 DAVID IDs

Options Classification Stringency

Kappa Similarity Similarity Term Overlap Similarity Threshold

Classification Initial Group Membership Final Group Membership Multiple Linkage Threshold

Enrichment Thresholds EASE

Display Fold Change Bonferroni Benjamini FDR LT,PH,PT

6 Cluster(s)

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Annotation Cluster	Enrichment Score	RT	Count	P_Value	Benjamini
Annotation Cluster 1	1.86	G			
<input type="checkbox"/> UP_KEYWORDS	Cell membrane	RT	7	2.8E-3	8.8E-2
<input type="checkbox"/> GOTERM_CC_DIRECT	plasma membrane	RT	8	4.0E-3	1.8E-1
<input type="checkbox"/> UP_KEYWORDS	Membrane	RT	9	1.5E-2	2.2E-1
<input type="checkbox"/> UP_SEQ_FEATURE	splice variant	RT	7	2.2E-1	9.2E-1
Annotation Cluster 2	1.64	G			
<input type="checkbox"/> UP_KEYWORDS	Cell adhesion	RT	4	1.8E-3	1.1E-1
<input type="checkbox"/> UP_KEYWORDS	Glycoprotein	RT	7	1.9E-2	2.3E-1
<input type="checkbox"/> GOTERM_BP_DIRECT	cell adhesion	RT	3	3.5E-2	9.9E-1
<input type="checkbox"/> UP_KEYWORDS	Signal	RT	6	5.2E-2	3.6E-1
<input type="checkbox"/> UP_SEQ_FEATURE	signal peptide	RT	5	9.6E-2	7.4E-1
Annotation Cluster 3	1.36	G			
<input type="checkbox"/> UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT	8	2.7E-3	2.0E-1
<input type="checkbox"/> UP_SEQ_FEATURE	signal peptide	RT	5	9.6E-2	7.4E-1
<input type="checkbox"/> UP_KEYWORDS	Alternative splicing	RT	8	3.1E-1	8.5E-1
Annotation Cluster 4	1.3	G			
<input type="checkbox"/> UP_KEYWORDS	Membrane	RT	9	1.5E-2	2.2E-1
<input type="checkbox"/> UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT	6	2.8E-2	5.4E-1
<input type="checkbox"/> UP_SEQ_FEATURE	transmembrane region	RT	7	3.6E-2	5.2E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	integral component of plasma membrane	RT	4	4.8E-2	7.1E-1
<input type="checkbox"/> UP_KEYWORDS	Transmembrane helix	RT	7	5.2E-2	3.9E-1
<input type="checkbox"/> UP_KEYWORDS	Transmembrane	RT	7	5.2E-2	3.3E-1
<input type="checkbox"/> UP_SEQ_FEATURE	topological domain:Extracellular	RT	5	5.5E-2	6.0E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	integral component of membrane	RT	5	3.9E-1	1.0E0
Annotation Cluster 5	1.08	G			
<input type="checkbox"/> UP_KEYWORDS	Membrane	RT	9	1.5E-2	2.2E-1
<input type="checkbox"/> UP_SEQ_FEATURE	sequence variant	RT	10	1.5E-1	8.4E-1
<input type="checkbox"/> UP_KEYWORDS	Polymorphism	RT	9	2.6E-1	8.7E-1
Annotation Cluster 6	1.07	G			
<input type="checkbox"/> UP_KEYWORDS	Ion transport	RT	3	4.4E-2	3.9E-1
<input type="checkbox"/> GOTERM_CC_DIRECT	integral component of plasma membrane	RT	4	4.8E-2	7.1E-1
<input type="checkbox"/> UP_KEYWORDS	Transport	RT	3	2.9E-1	8.4E-1

9 terms were not clustered.

Please cite [Nature Protocols 2009; 4\(1\):44](#) & [Genome Biology 2003; 4\(5\):P3](#) within any publication that makes use of any methods inspired by DAVID.



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