

- Running DAVID Trials - Differnet dimensions to GSEA
- All thresholds left to the default settings
- DAVID needs a background list of genes (like test vs training set) – the default (Homo sapiens) was used otherwise we could have run one tissue against all others

Functional Annotation Clustering (based on enrichment score) for blood

Functional Annotation Clustering

Current Gene List: List_4
Current Background: Homo sapiens
2825 DAVID IDs

☒ Options Classification Stringency: Medium ▼

[Rerun using options](#) [Create Sublist](#)

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307 Cluster(s)

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Number of Genes involved in GO term out of all our 2825

Pvalues are ranked



Annotation Cluster 1	Enrichment Score: 7.72	G	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/> GOTERM_BP_DIRECT	viral transcription	RT	45	4.4E-12	3.0E0	2.4E-8	8.4E-9
<input type="checkbox"/> GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT	39	4.6E-11	3.1E0	1.2E-7	8.7E-8
<input type="checkbox"/> GOTERM_BP_DIRECT	translational initiation	RT	49	5.8E-11	2.7E0	1.1E-7	1.1E-7
<input type="checkbox"/> UP_KEYWORDS	Ribosomal protein	RT	56	4.5E-10	2.4E0	8.4E-8	6.5E-7
<input type="checkbox"/> KEGG_PATHWAY	Ribosome	RT	48	2.5E-9	2.4E0	7.1E-7	3.3E-6
<input type="checkbox"/> UP_KEYWORDS	Ribonucleoprotein	RT	74	7.8E-9	2.0E0	8.7E-7	1.1E-5
<input type="checkbox"/> GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT	41	8.9E-9	2.6E0	1.2E-5	1.7E-5
<input type="checkbox"/> GOTERM_CC_DIRECT	ribosome	RT	49	4.2E-8	2.3E0	3.7E-5	6.5E-5
<input type="checkbox"/> GOTERM_MF_DIRECT	structural constituent of ribosome	RT	58	4.7E-7	2.0E0	4.2E-4	8.0E-4
<input type="checkbox"/> GOTERM_BP_DIRECT	rRNA processing	RT	55	1.5E-6	1.9E0	1.6E-3	2.8E-3
<input type="checkbox"/> GOTERM_BP_DIRECT	translation	RT	61	3.5E-6	1.8E0	3.2E-3	6.7E-3
<input type="checkbox"/> GOTERM_CC_DIRECT	cytosolic small ribosomal subunit	RT	19	1.6E-5	3.0E0	3.4E-3	2.4E-2
<input type="checkbox"/> GOTERM_CC_DIRECT	cytosolic large ribosomal subunit	RT	23	2.8E-5	2.6E0	5.0E-3	4.4E-2
Annotation Cluster 2	Enrichment Score: 2.27	G	Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/> GOTERM_MF_DIRECT	ligase activity	RT	54	2.1E-3	1.5E0	5.2E-1	3.4E0
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquitin protein ligase activity	RT	40	2.5E-3	1.6E0	5.3E-1	4.2E0
<input type="checkbox"/> GOTERM_MF_DIRECT	ubiquitin-protein transferase activity	RT	61	6.2E-3	1.4E0	7.1E-1	1.0E1


Functional Annotation Clustering based on enrichment score for blood

- With high clustering stringency

218 Cluster(s) [Download File](#)

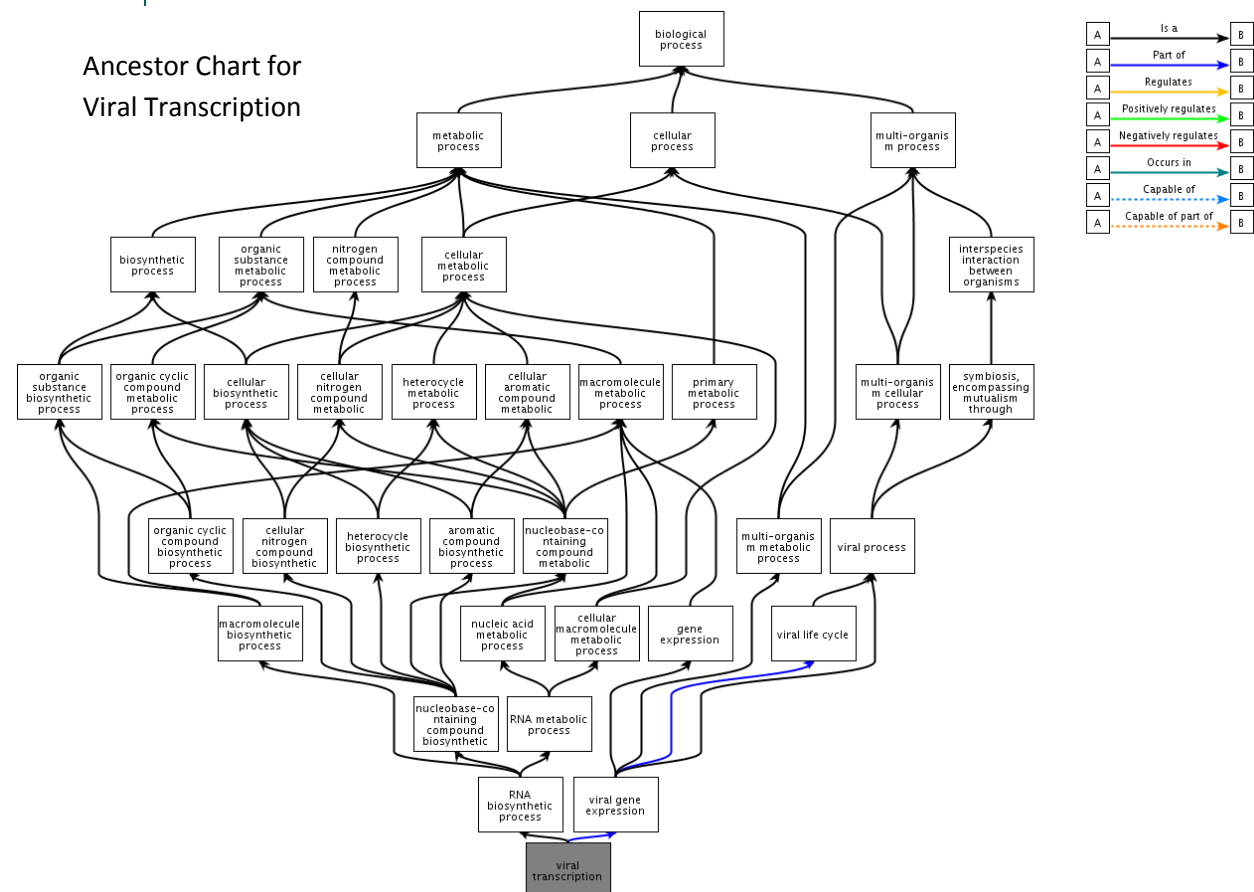
Annotation Cluster 1		Enrichment Score: 10	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT		45	4.4E-12	3.0E0	2.4E-8	8.4E-9
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT		39	4.6E-11	3.1E0	1.2E-7	8.7E-8
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT		49	5.8E-11	2.7E0	1.1E-7	1.1E-7
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT		41	8.9E-9	2.6E0	1.2E-5	1.7E-5
Annotation Cluster 2		Enrichment Score: 7.44	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT		56	4.5E-10	2.4E0	8.4E-8	6.5E-7
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		48	2.5E-9	2.4E0	7.1E-7	3.3E-6
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		58	4.7E-7	2.0E0	4.2E-4	8.0E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT		61	3.5E-6	1.8E0	3.2E-3	6.7E-3
Annotation Cluster 3		Enrichment Score: 2.31	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Tetratricopeptide repeat	RT		34	3.3E-4	1.9E0	6.4E-1	6.0E-1
<input type="checkbox"/>	INTERPRO	Tetratricopeptide repeat-containing domain	RT		31	1.5E-3	1.8E0	8.9E-1	2.6E0
<input type="checkbox"/>	UP_KEYWORDS	TPR repeat	RT		36	1.5E-3	1.7E0	6.8E-2	2.2E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 4	RT		24	3.3E-3	1.9E0	1.0E0	6.1E0
<input type="checkbox"/>	SMART	TPR	RT		30	3.7E-3	1.7E0	8.9E-1	5.3E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 3	RT		30	1.4E-2	1.6E0	1.0E0	2.4E1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 2	RT		32	1.6E-2	1.5E0	1.0E0	2.6E1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 1	RT		32	1.6E-2	1.5E0	1.0E0	2.6E1
<input type="checkbox"/>	INTERPRO	Tetratricopeptide-like helical	RT		38	5.4E-2	1.3E0	1.0E0	6.3E1

ID	 GO:0019083
Name	 viral transcription
Ontology	Biological Process
Definition	The process by which a viral genome, or part of a viral genome, is transcribed within the host cell.

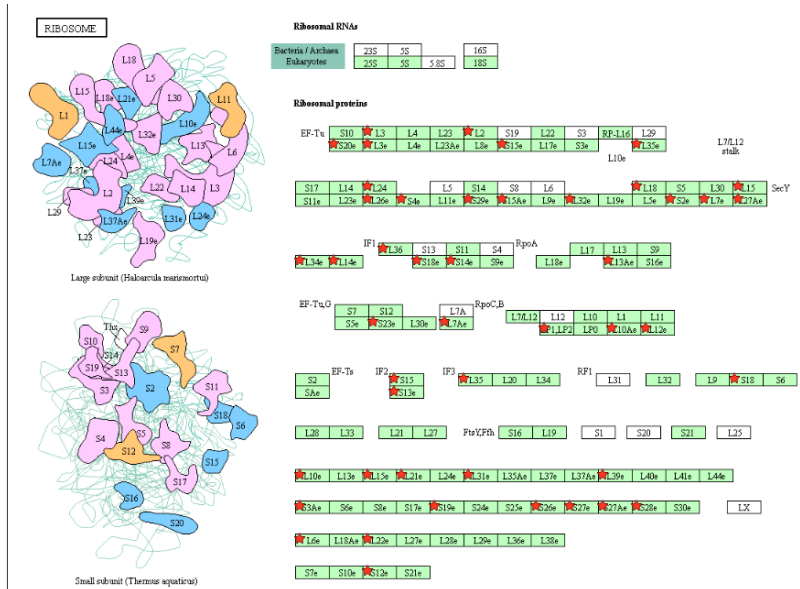
ID	 GO:0006614
Name	SRP-dependent cotranslational protein targeting to membrane
Ontology	Biological Process
Definition	The targeting of proteins to a membrane that occurs during translation and is dependent

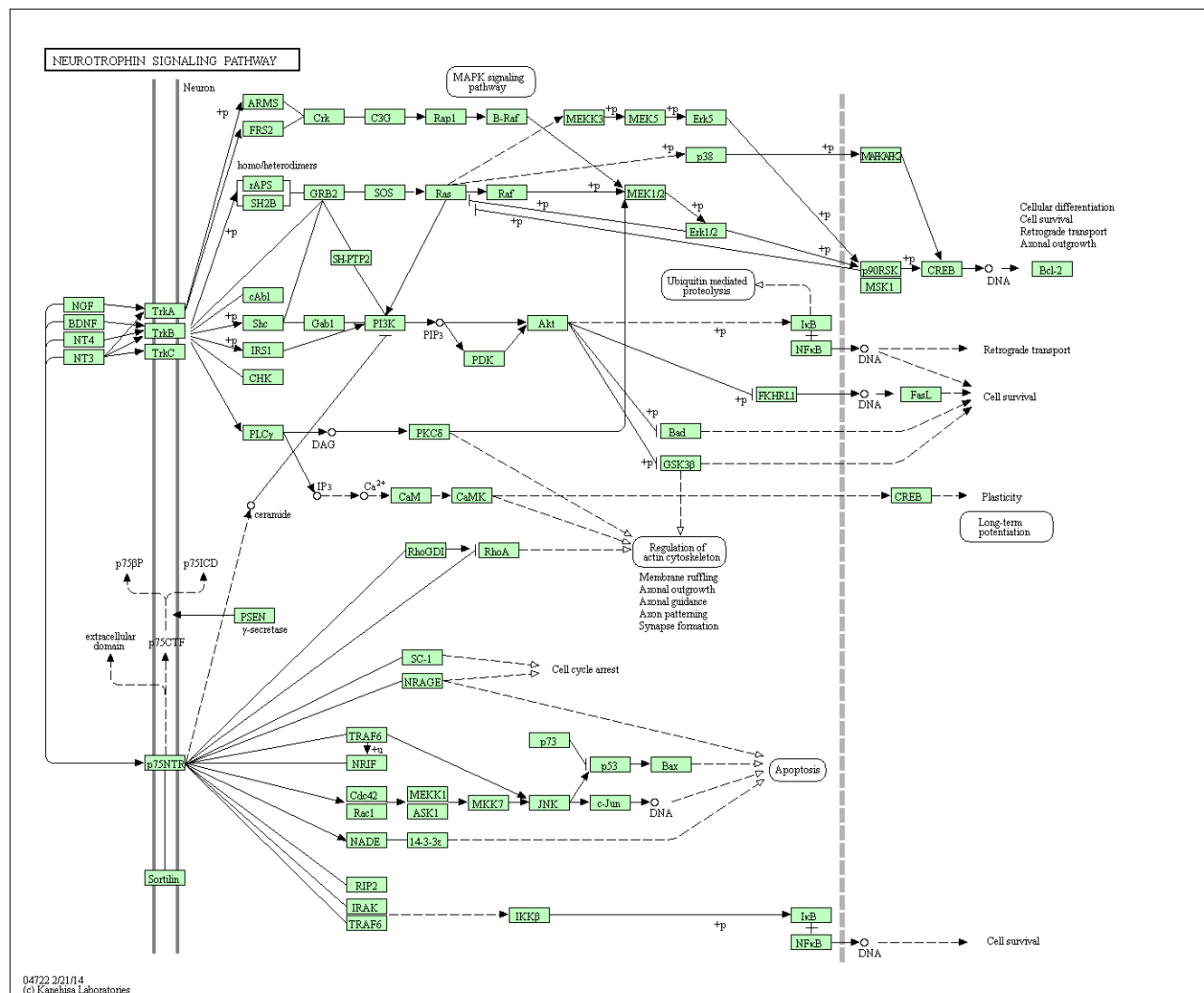
GO:0006440 GO:0006454

The nonsense-mediated decay pathway for nuclear-transcribed mRNAs degrades mRNAs in which an amino-acid codon has changed to a nonsense codon; this prevents the translation of such mRNAs into truncated, and potentially harmful, proteins.

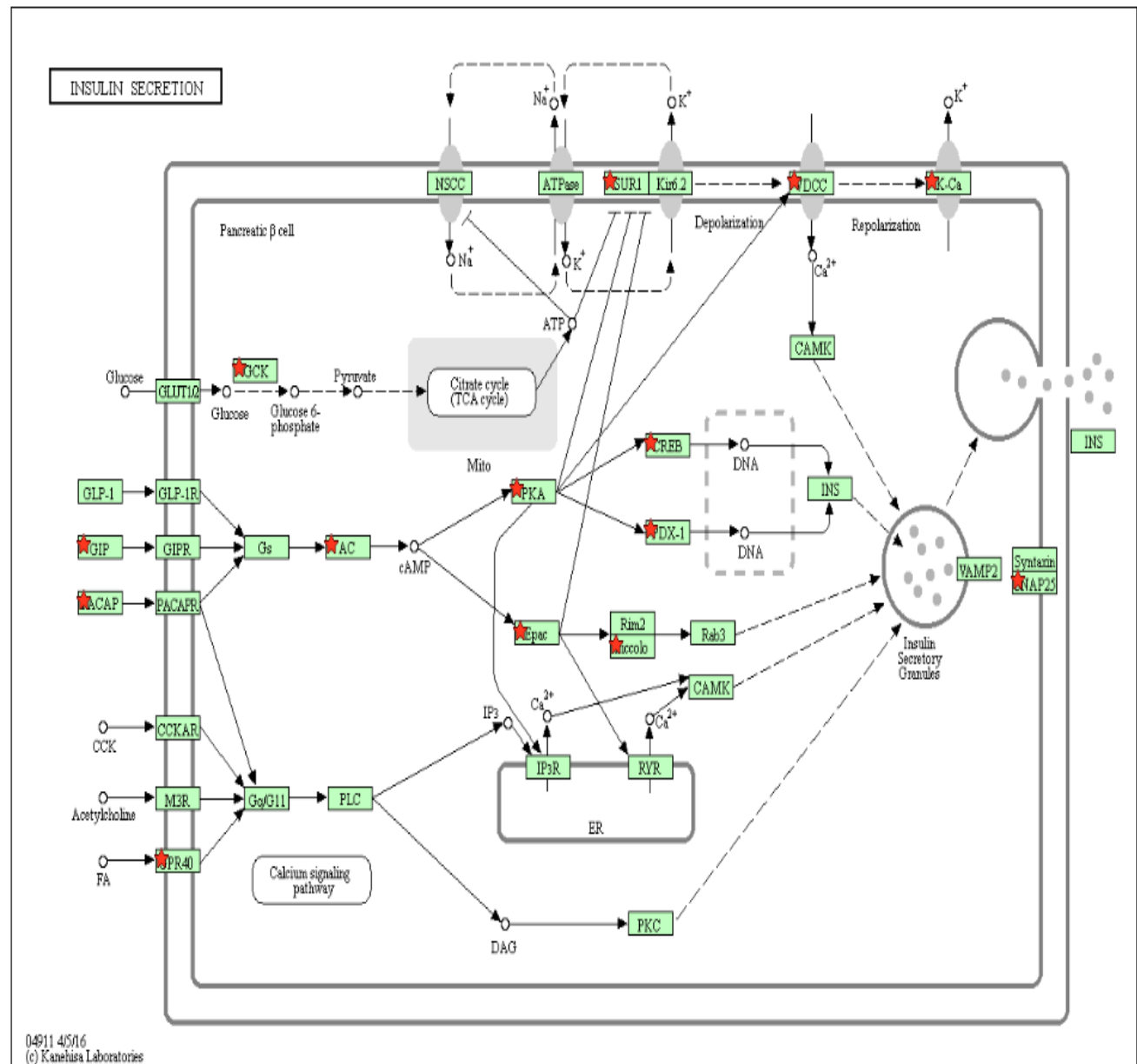


1. Ribosome Pathway





2. Neurotrophin signaling pathway






























3. Insulin secretion

COLON

Without low clustering Stringency

53 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 3.67			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT		13	4.4E-6	5.5E0	7.8E-3	7.5E-3
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		14	7.4E-6	4.7E0	1.5E-3	9.3E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT		12	1.4E-5	5.4E0	1.3E-2	2.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT		11	1.7E-5	5.9E0	1.0E-2	3.0E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		16	3.4E-5	3.7E0	1.9E-2	5.0E-2
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT		14	4.8E-5	4.0E0	8.3E-3	6.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT		12	9.3E-5	4.4E0	4.0E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT		16	1.7E-4	3.2E0	5.9E-2	2.9E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic small ribosomal subunit	RT		7	3.3E-4	7.4E0	5.5E-2	4.5E-1
<input type="checkbox"/>	UP_KEYWORDS	Ribonucleoprotein	RT		15	1.5E-3	2.7E0	1.6E-1	2.0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT		11	1.6E-3	3.4E0	1.7E-1	2.2E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA processing	RT		12	3.8E-3	2.8E0	6.2E-1	6.3E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	small ribosomal subunit	RT		4	1.5E-2	7.5E0	6.5E-1	1.9E1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic large ribosomal subunit	RT		5	4.4E-2	3.7E0	7.2E-1	4.6E1
Annotation Cluster 2		Enrichment Score: 1.17			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_CC_DIRECT	cell-cell adherens junction	RT		12	5.4E-2	1.9E0	7.7E-1	5.3E1
<input type="checkbox"/>	GOTERM_MF_DIRECT	cadherin binding involved in cell-cell adhesion	RT		11	6.1E-2	1.9E0	9.7E-1	6.0E1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell-cell adhesion	RT		10	9.3E-2	1.8E0	1.0E0	8.1E1
Annotation Cluster 3		Enrichment Score: 1.16			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	clathrin-mediated endocytosis	RT		4	6.9E-3	1.0E1	7.4E-1	1.1E1
<input type="checkbox"/>	GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class II	RT		7	1.0E-2	3.8E0	8.3E-1	1.6E1
<input type="checkbox"/>	GOTERM_MF_DIRECT	clathrin adaptor activity	RT		3	1.6E-2	1.5E1	9.5E-1	2.0E1
<input type="checkbox"/>	KEGG_PATHWAY	Endocrine and other factor-regulated	RT		5	1.6E-2	5.1E0	9.1E-1	1.8E1

With High Clustering Stringency

Functional Annotation Clustering

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

431 DAVID IDs








Options **Classification Stringency** High ▼

Rerun using options

Create Sublist

36 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 4.28	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT		13	4.4E-6	5.5E0	7.8E-3	7.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT		12	1.4E-5	5.4E0	1.3E-2	2.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT		11	1.7E-5	5.9E0	1.0E-2	3.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT		12	9.3E-5	4.4E0	4.0E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA processing	RT		12	3.8E-3	2.8E0	6.2E-1	6.3E0
Annotation Cluster 2		Enrichment Score: 4.1	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		14	7.4E-6	4.7E0	1.5E-3	9.3E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		16	3.4E-5	3.7E0	1.9E-2	5.0E-2
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT		14	4.8E-5	4.0E0	8.3E-3	6.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT		16	1.7E-4	3.2E0	5.9E-2	2.9E-1
<input type="checkbox"/>	UP_KEYWORDS	Ribonucleoprotein	RT		15	1.5E-3	2.7E0	1.6E-1	2.0E0
Annotation Cluster 3		Enrichment Score: 1.32	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	ZnF_C2H2	RT		23	1.9E-2	1.7E0	9.6E-1	2.1E1
<input type="checkbox"/>	INTERPRO	Zinc finger, C2H2-like	RT		23	3.7E-2	1.6E0	1.0E0	4.4E1
<input type="checkbox"/>	INTERPRO	Zinc finger, C2H2	RT		23	5.4E-2	1.5E0	1.0E0	5.8E1
<input type="checkbox"/>	INTERPRO	Zinc finger C2H2-type/integrase DNA-binding domain	RT		19	1.4E-1	1.4E0	1.0E0	9.0E1
Annotation Cluster 4		Enrichment Score: 1.21	G		Count	P_Value	Fold Change	Benjamini	FDR

ID

 GO:0000184

Name

[nuclear-transcribed mRNA catabolic process, nonsense-mediated decay](#)


Ontology

Biological Process

Definition

The nonsense-mediated decay pathway for nuclear-transcribed mRNAs degrades mRNAs in which an amino-acid codon has changed to a nonsense codon; this prevents the translation of such mRNAs into truncated, and potentially harmful, proteins.

ID

 GO:0006364

Name

[rRNA processing](#)

Ontology

Biological Process

Definition

Any process involved in the conversion of a primary ribosomal RNA (rRNA) transcript into

**Secondary
IDs**

one or more mature rRNA molecules.
GO:0006365

TONSIL

Medium Clustering Stringency

Current Gene List: List_1

Current Background: Homo sapiens

232 DAVID IDs


























☒ Options Classification Stringency Medium ▼

Rerun using options

Create Sublist

26 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 1.99			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT		9	1.2E-4	6.1E0	1.1E-1	1.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT		7	1.8E-3	5.5E0	6.0E-1	2.8E0
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		7	2.6E-3	4.9E0	2.8E-1	3.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT		6	3.4E-3	5.9E0	6.9E-1	5.3E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT		9	6.0E-3	3.3E0	7.9E-1	9.1E0
<input type="checkbox"/>	INTERPRO	Ribosomal protein, zinc-binding domain	RT		3	7.0E-3	2.3E1	9.7E-1	9.5E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT		6	7.1E-3	5.0E0	7.7E-1	1.1E1
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT		7	8.0E-3	4.0E0	7.9E-1	9.5E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		8	1.1E-2	3.3E0	9.8E-1	1.4E1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:C4-type	RT		5	1.1E-2	5.7E0	1.0E0	1.6E1
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT		7	1.2E-2	3.7E0	9.6E-1	1.5E1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic small ribosomal subunit	RT		4	1.4E-2	8.0E0	5.9E-1	1.6E1
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA processing	RT		7	2.8E-2	3.0E0	9.7E-1	3.6E1
<input type="checkbox"/>	UP_KEYWORDS	Ribonucleoprotein	RT		7	8.6E-2	2.3E0	9.2E-1	6.9E1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic large ribosomal subunit	RT		3	1.6E-1	4.2E0	9.8E-1	8.8E1
<input type="checkbox"/>	GOTERM_MF_DIRECT	poly(A) RNA binding	RT		14	4.7E-1	1.1E0	1.0E0	1.0E2
Annotation Cluster 2		Enrichment Score: 1.15			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Chloride	RT		4	4.0E-2	5.3E0	9.2E-1	4.1E1
<input type="checkbox"/>	GOTERM_BP_DIRECT	chloride transmembrane transport	RT		4	7.8E-2	4.0E0	9.9E-1	7.3E1
<input type="checkbox"/>	GOTERM_MF_DIRECT	chloride channel activity	RT		3	1.2E-1	5.0E0	1.0E0	8.2E1
Annotation Cluster 3		Enrichment Score: 1.07			Count	P_Value	Fold Change	Benjamini	FDR



























High Clustering Stringency

Current Gene List: List_1
 Current Background: Homo sapiens
 232 DAVID IDs

☒ Options Classification Stringency High ▾

20 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 2.07			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT		7	1.8E-3	5.5E0	6.0E-1	2.8E0
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		7	2.6E-3	4.9E0	2.8E-1	3.0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT		6	3.4E-3	5.9E0	6.9E-1	5.3E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT		9	6.0E-3	3.3E0	7.9E-1	9.1E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT		6	7.1E-3	5.0E0	7.7E-1	1.1E1
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT		7	8.0E-3	4.0E0	7.9E-1	9.5E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		8	1.1E-2	3.3E0	9.8E-1	1.4E1
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT		7	1.2E-2	3.7E0	9.6E-1	1.5E1
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA processing	RT		7	2.8E-2	3.0E0	9.7E-1	3.6E1
<input type="checkbox"/>	UP_KEYWORDS	Ribonucleoprotein	RT		7	8.6E-2	2.3E0	9.2E-1	6.9E1
Annotation Cluster 2		Enrichment Score: 1			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 4	RT		3	7.3E-2	6.7E0	1.0E0	6.8E1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 3	RT		3	9.5E-2	5.8E0	1.0E0	7.8E1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 1	RT		3	1.2E-1	5.0E0	1.0E0	8.6E1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 2	RT		3	1.2E-1	5.0E0	1.0E0	8.6E1
Annotation Cluster 3		Enrichment Score: 0.72			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	negative regulation of angiogenesis	RT		3	1.4E-1	4.5E0	1.0E0	9.1E1
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of endothelial cell proliferation	RT		3	1.7E-1	4.0E0	1.0E0	9.5E1
<input type="checkbox"/>	GOTERM_BP_DIRECT	response to hypoxia	RT		4	2.8E-1	2.2E0	1.0E0	9.9E1
Annotation Cluster 4		Enrichment Score: 0.7			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Initiation factor	RT		3	1.2E-1	5.0E0	9.0E-1	8.1E1

ALN

Medium Clustering Stringency

Functional Annotation Clustering

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

1777 DAVID IDs

☒ Options Classification Stringency Medium ▼

[Rerun using options](#)

[Create Sublist](#)

200 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 4.83	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT		38	1.1E-7	2.6E0	2.9E-5	1.7E-4
<input type="checkbox"/>	UP_KEYWORDS	Ribonucleoprotein	RT		50	5.5E-7	2.1E0	9.3E-5	8.0E-4
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		31	5.6E-7	2.7E0	1.6E-4	7.4E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT		26	3.2E-6	2.8E0	1.3E-2	5.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT		29	5.2E-6	2.6E0	1.1E-2	9.8E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT		23	5.4E-6	3.0E0	7.3E-3	1.0E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT		31	2.6E-5	2.3E0	1.8E-2	3.9E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		37	6.6E-5	2.0E0	8.1E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT		24	8.8E-5	2.5E0	8.6E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT		40	9.4E-5	1.9E0	7.4E-2	1.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic large ribosomal subunit	RT		15	9.7E-4	2.7E0	2.0E-1	1.4E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA processing	RT		31	2.7E-3	1.8E0	7.9E-1	4.8E0
Annotation Cluster 2		Enrichment Score: 2.38	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Translation protein SH3-like domain	RT		8	4.7E-5	7.0E0	9.8E-2	8.1E-2
<input type="checkbox"/>	INTERPRO	KOW	RT		5	3.9E-3	6.8E0	9.9E-1	6.6E0
<input type="checkbox"/>	SMART	KOW	RT		4	8.4E-3	8.3E0	8.3E-1	1.1E1
<input type="checkbox"/>	INTERPRO	Ribosomal protein L24/L26 conserved site	RT		2	1.9E-2	1.2E1	9.9E-1	2.9E1

High Clustering Stringency

Functional Annotation Clustering

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

1777 DAVID IDs




















☒ Options Classification Stringency High ▼

[Rerun using options](#)

[Create Sublist](#)

134 Cluster(s)

 [Download File](#)

Annotation Cluster 1		Enrichment Score: 5.49	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT		38	1.1E-7	2.6E0	2.9E-5	1.7E-4
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		31	5.6E-7	2.7E0	1.6E-4	7.4E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT		31	2.6E-5	2.3E0	1.8E-2	3.9E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		37	6.6E-5	2.0E0	8.1E-2	1.1E-1
Annotation Cluster 2		Enrichment Score: 2.06	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	TPR repeat	RT		25	3.0E-3	1.9E0	1.3E-1	4.2E0
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 2	RT		24	5.8E-3	1.8E0	1.0E0	1.0E1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 1	RT		24	5.8E-3	1.8E0	1.0E0	1.0E1
<input type="checkbox"/>	SMART	TPR	RT		20	7.8E-3	1.9E0	9.6E-1	1.0E1
<input type="checkbox"/>	INTERPRO	Tetratricopeptide repeat	RT		21	7.9E-3	1.9E0	1.0E0	1.3E1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 3	RT		22	8.3E-3	1.8E0	1.0E0	1.4E1
<input type="checkbox"/>	INTERPRO	Tetratricopeptide repeat-containing domain	RT		19	2.0E-2	1.8E0	9.9E-1	3.0E1
<input type="checkbox"/>	INTERPRO	Tetratricopeptide-like helical	RT		27	3.0E-2	1.5E0	1.0E0	4.2E1
Annotation Cluster 3		Enrichment Score: 1.96	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Domain of unknown function DUF1605	RT		6	9.4E-3	4.3E0	9.9E-1	1.5E1
<input type="checkbox"/>	SMART	SM00847	RT		6	1.1E-2	4.2E0	8.0E-1	1.5E1
<input type="checkbox"/>	INTERPRO	Helicase-associated domain	RT		6	1.2E-2	4.1E0	9.9E-1	1.9E1
Annotation Cluster 4		Enrichment Score: 1.64	G		Count	P_Value	Fold Change	Benjamini	FDR

MLN

Medium Clustering Stringency

Functional Annotation Clustering

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

1450 DAVID IDs


















☒ Options Classification Stringency Medium ▼

Rerun using options

Create Sublist

162 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 5.21			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT		24	4.9E-8	3.8E0	1.8E-4	9.0E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT		29	1.2E-7	3.1E0	2.2E-4	2.1E-4
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT		33	2.4E-7	2.8E0	3.7E-5	3.4E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT		25	3.7E-7	3.3E0	4.6E-4	6.8E-4
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		28	7.9E-7	2.9E0	2.1E-4	1.0E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT		30	1.4E-6	2.7E0	8.7E-4	2.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		36	2.2E-6	2.4E0	2.6E-3	3.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT		24	4.2E-6	3.0E0	3.9E-3	7.7E-3
<input type="checkbox"/>	UP_KEYWORDS	Ribonucleoprotein	RT		40	1.4E-5	2.1E0	1.3E-3	2.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT		37	1.8E-5	2.2E0	1.4E-2	3.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA processing	RT		31	1.2E-4	2.1E0	7.1E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic large ribosomal subunit	RT		14	4.5E-4	3.1E0	9.1E-2	6.7E-1
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic small ribosomal subunit	RT		11	1.0E-3	3.5E0	1.2E-1	1.5E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	small ribosomal subunit	RT		8	1.5E-3	4.5E0	1.5E-1	2.2E0
Annotation Cluster 2		Enrichment Score: 1.89			Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein polyubiquitination	RT		25	1.5E-3	2.0E0	4.7E-1	2.7E0
<input type="checkbox"/>	UP_KEYWORDS	Ligase	RT		36	5.1E-3	1.6E0	2.0E-1	7.1E0

High Clustering Stringency

Functional Annotation Clustering

[Help and Manual](#)

Current Gene List: List_1

















Current Background: Homo sapiens

1450 DAVID IDs

☒ Options Classification Stringency High ▼

113 Cluster(s)

 [Download File](#)

Annotation Cluster 1		Enrichment Score: 6.43	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT		24	4.9E-8	3.8E0	1.8E-4	9.0E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT		29	1.2E-7	3.1E0	2.2E-4	2.1E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT		25	3.7E-7	3.3E0	4.6E-4	6.8E-4
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		28	7.9E-7	2.9E0	2.1E-4	1.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT		24	4.2E-6	3.0E0	3.9E-3	7.7E-3
Annotation Cluster 2		Enrichment Score: 5.64	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT		33	2.4E-7	2.8E0	3.7E-5	3.4E-4
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		28	7.9E-7	2.9E0	2.1E-4	1.0E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT		30	1.4E-6	2.7E0	8.7E-4	2.0E-3
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		36	2.2E-6	2.4E0	2.6E-3	3.6E-3
<input type="checkbox"/>	UP_KEYWORDS	Ribonucleoprotein	RT		40	1.4E-5	2.1E0	1.3E-3	2.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT		37	1.8E-5	2.2E0	1.4E-2	3.4E-2
Annotation Cluster 3		Enrichment Score: 1.27	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	SMART	TPR	RT		16	1.9E-2	1.9E0	1.0E0	2.4E1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:TPR 4	RT		13	2.8E-2	2.0E0	1.0E0	4.0E1

Top 300 from each tissue – all combined

- * we could look at common terms that appear in all tissues – I have provided the annotations for some of the terms that were more common. I like the viral transcription one 😊





Medium Clustering Stringency

Current Gene List: List_1
 Current Background: Homo sapiens
 1288 DAVID IDs

☒ Options Classification Stringency Medium ▾

148 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 5.07				Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT			28	5.6E-8	3.3E0	1.5E-5	7.3E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT			26	6.2E-7	3.1E0	2.1E-3	1.1E-3
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT			30	6.7E-7	2.8E0	1.0E-4	9.6E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT			20	2.8E-6	3.5E0	4.8E-3	5.1E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT			27	4.9E-6	2.7E0	2.8E-3	7.2E-3
<input type="checkbox"/>	UP_KEYWORDS	Ribonucleoprotein	RT			38	6.0E-6	2.3E0	7.1E-4	8.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT			34	2.5E-5	2.2E0	2.8E-2	4.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT			21	2.8E-5	2.9E0	2.4E-2	5.2E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT			31	3.0E-5	2.3E0	3.5E-2	4.9E-2
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytosolic large ribosomal subunit	RT			15	3.6E-5	3.7E0	6.8E-3	5.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT			20	3.9E-5	3.0E0	2.6E-2	7.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA processing	RT			25	2.6E-3	1.9E0	6.7E-1	4.6E0
Annotation Cluster 2		Enrichment Score: 2.02				Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Translation protein SH3-like domain	RT			7	8.5E-5	8.4E0	1.4E-1	1.4E-1
<input type="checkbox"/>	INTERPRO	Ribosomal protein L24/L26, conserved site	RT			3	1.0E-2	1.7E1	1.0E0	1.6E1
<input type="checkbox"/>	INTERPRO	KOW	RT			4	1.3E-2	7.5E0	1.0E0	2.0E1
<input type="checkbox"/>	GOTERM_BP_DIRECT	cytoplasmic translation	RT			6	1.5E-2	4.0E0	9.9E-1	2.5E1
<input type="checkbox"/>	INTERPRO	Ribosomal protein L2 domain 2	RT			5	1.6E-2	5.0E0	1.0E0	2.4E1

High Clustering Stringency

Current Gene List: List_1

Current Background: Homo sapiens

1288 DAVID IDs



















Options Classification Stringency High ▼

Rerun using options

Create Sublist

98 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 5.57	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT		28	5.6E-8	3.3E0	1.5E-5	7.3E-5
<input type="checkbox"/>	UP_KEYWORDS	Ribosomal protein	RT		30	6.7E-7	2.8E0	1.0E-4	9.6E-4
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT		27	4.9E-6	2.7E0	2.8E-3	7.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	translation	RT		34	2.5E-5	2.2E0	2.8E-2	4.6E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT		31	3.0E-5	2.3E0	3.5E-2	4.9E-2
Annotation Cluster 2		Enrichment Score: 4.66	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational initiation	RT		26	6.2E-7	3.1E0	2.1E-3	1.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT		20	2.8E-6	3.5E0	4.8E-3	5.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT		21	2.8E-5	2.9E0	2.4E-2	5.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	viral transcription	RT		20	3.9E-5	3.0E0	2.6E-2	7.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA processing	RT		25	2.6E-3	1.9E0	6.7E-1	4.6E0
Annotation Cluster 3		Enrichment Score: 1.75	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	INTERPRO	Ribosomal protein L24/L26, conserved site	RT		3	1.0E-2	1.7E1	1.0E0	1.6E1
<input type="checkbox"/>	INTERPRO	KOW	RT		4	1.3E-2	7.5E0	1.0E0	2.0E1
<input type="checkbox"/>	SMART	KOW	RT		3	4.3E-2	8.6E0	1.0E0	4.5E1
Annotation Cluster 4		Enrichment Score: 1.63	G		Count	P_Value	Fold Change	Benjamini	FDR
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SOCS box	RT		7	2.1E-2	3.2E0	1.0E0	3.2E1
<input type="checkbox"/>	SMART								