

## **DAVID Bioinformatics Resources 6.7**

National Institute of Allergy and Infectious Diseases (NIAID), NIH

Help and Manual

## **Functional Annotation Chart**

Current Gene List: List\_1

**Current Background: Homo sapiens** 

417 DAVID IDs

**Options** 

## Rerun Using Options Create Sublist **<u> Download File</u>** 141 chart records RT Genes Count % P-Value Sublist Category Benjamini Term INTERPRO Steroid hormone receptor RT 24 5.8 5.5E-25 4.4E-22 INTERPRO Nuclear hormone receptor, ligand-binding, core RT 24 5.8 1.0E-24 4.1E-22 INTERPRO 1.0E-24 4.1E-22 Nuclear hormone receptor, ligand-binding RT 24 5.8 **INTERPRO** Zinc finger, nuclear hormone receptor-type RT 23 5.5 1.1E-23 3.1E-21 Protein kinase, ATP binding site INTERPRO 6.5E-23 1.3E-20 RT 56 13.4 INTERPRO Protein kinase, core RT \_\_\_\_ 56 13.4 5.7E-22 9.2E-20 INTERPRO Zinc finger, NHR/GATA-type RT 22 5.3 6.1F-21 8.2F-19 INTERPRO Tyrosine protein kinase, active site RT 23 5.5 1.6E-15 1.8E-13 INTERPRO Tyrosine protein kinase RT 24 5.8 1.2E-14 1.2F-12 **INTERPRO** Serine/threonine protein kinase, active site RT \_\_\_ 34 8.2 6.2E-11 5.5E-9 INTERPRO Serine/threonine protein kinase-related 33 7.9 3.8E-10 3.1E-8 RT INTERPRO SH2 motif RT 18 4.3 1.9E-9 1.4E-7 INTERPRO Vitamin D receptor RT 🚪 9 2.2 7.8E-9 5.2E-7 INTERPRO Src homology-3 domain 21 5.0 3.5E-7 2.2E-5 RT Serine/threonine protein kinase INTERPRO RT 23 5.5 5.2F-7 3.0F-5 DEATH-like INTERPRO RT = 5.4F-6 2.9F-4 11 2.6 INTERPRO PAS RT 🖥 7 1.7 1.4E-4 6.9E-3 INTERPRO Heat shock protein Hsp70 RT 5 1.2 1.6E-4 7.3E-3 **INTERPRO** Heat shock protein 70 5 1.2 1.6E-4 7.3E-3 RT = INTERPRO 7 1.6E-4 7.3E-3 Death RT 1.7 **INTERPRO** Armadillo-like helical RT = 12 2.9 3.4E-4 1.4E-2 INTERPRO PAC motif RT 🚪 6 1.4 3.9E-4 1.5E-2 INTERPRO Heat shock protein 70, conserved site 5 4.1E-4 1.5E-2 RT 🚪 1.2 INTERPRO SMAD domain-like 5 RT 1.2 4.1F-4 1.5F-2 INTERPRO 14-3-3 protein RT 4 1.0 4.9F-4 1.8F-2 INTERPRO eIF4-gamma/eIF5/eIF2-epsilon RT 🖥 4 1.0 4.9F-4 1.8F-2 **INTERPRO** MAD homology, MH1 RT 4 1.0 7.7E-4 2.6E-2 INTERPRO 7.7E-4 **Dwarfin** RT 4 1.0 2.6E-2 INTERPRO SMAD domain, Dwarfin-type RT I 4 1.0 7.7E-4 2.6E-2 INTERPRO 1.6E-3 MIF4G-like, type 3 RT I 4 1.0 5.2E-2 INTERPRO 4 1.6E-3 5.2E-2 Retinoid X receptor RT 1.0 INTERPRO MIF4-like, type 1/2/3 RT 4 1.0 1.6F-3 5.2F-2 1.8E-3 INTERPRO Peroxisome proliferator-activated receptor RT 3 0.7 5.6E-2 INTERPRO Cyclin-related RT 🔳 6 1.4 2.1E-3 6.1E-2 **INTERPRO** Actinin-type, actin-binding, conserved site RT 5 1.2 2.2E-3 6.5E-2 INTERPRO Peptidase C14, caspase non-catalytic subunit p10 4 1.0 2.8E-3 7.7E-2 RT INTERPRO MAD homology 1, Dwarfin-type RT 1.0 2.8E-3 7.7E-2 **INTERPRO** Peptidase C14, ICE, catalytic subunit p20, active site RT I 4 1.0 2.8E-3 7.7E-2 INTERPRO PAS fold 5 1.2 3.1E-3 8.2E-2 RT INTERPRO Janus kinase, JAK 3 0.7 3.5E-3 9.0E-2 RT INTERPRO Tyrosine-protein kinase, Jak/Tyk2 RT 3 0.7 3.5F-3 9.0F-2

INTERDO	Thursid have an exceptor	RT	2	0.7	2 55 2	9.0E-2
INTERPRO	Thyroid hormone receptor		3	0.7	3.5E-3	
INTERPRO	Tyrosine-protein kinase, ephrin receptor	RT	4	1.0	3.6E-3	8.8E-2
INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT =	7	1.7	3.9E-3	9.3E-2
INTERPRO	Peptidase C14, caspase precursor p45, core	RT	4	1.0	4.5E-3	1.0E-1
INTERPRO	Ephrin receptor, ligand binding	RT	4	1.0	4.5E-3	1.0E-1
INTERPRO	Receptor tyrosine kinase, class V, conserved site	RT	4	1.0	4.5E-3	1.0E-1
INTERPRO	Helicase, superfamily 1 and 2, ATP-binding	RT =	9	2.2	5.1E-3	1.1E-1
INTERPRO	DNA/RNA helicase, C-terminal	RT =	9	2.2	5.1E-3	1.1E-1
INTERPRO	Peptidase C14, caspase catalytic	RT	4	1.0	5.5E-3	1.2E-1
INTERPRO	Peptidase C14, ICE, catalytic subunit p20	RT	4	1.0	5.5E-3	1.2E-1
INTERPRO	DEAD-like helicase, N-terminal	RT =	9	2.2	5.7E-3	1.2E-1
INTERPRO	Spectrin/alpha-actinin	RT	5	1.2	6.8E-3	1.4E-1
INTERPRO	Calponin-like actin-binding	RT =	7	1.7	7.6E-3	1.5E-1
INTERPRO	<u>Chromo domain</u>	RT	5	1.2	7.7E-3	1.5E-1
INTERPRO	<u>Cullin protein, neddylation domain</u>	RT	3	0.7	8.6E-3	1.6E-1
INTERPRO	Initiation factor eIF-4 gamma, MA3	RT	3	0.7	8.6E-3	1.6E-1
INTERPRO	<u>EF-hand, Ca insensitive</u>	<u>RT</u>	3	0.7	8.6E-3	1.6E-1
INTERPRO	Phosphatidylinositol 3- and 4-kinase, catalytic	RT	4	1.0	9.3E-3	1.7E-1
INTERPRO	PAS fold-3	RT	4	1.0	9.3E-3	1.7E-1
INTERPRO	Phosphatidylinositol 3- and 4-kinase, conserved site	RT	4	1.0	9.3E-3	1.7E-1
INTERPRO	WW/Rsp5/WWP	RT	6	1.4	9.8E-3	1.7E-1
INTERPRO	Bromodomain, conserved site	RT	5	1.2	1.2E-2	2.0E-1
INTERPRO	Nuclear translocator	<u>RT</u>	3	0.7	1.2E-2	1.9E-1
INTERPRO	Peptidase C14, caspase precursor p45	RT	4	1.0	1.3E-2	2.0E-1
INTERPRO	<u>Armadillo</u>	RT	5	1.2	1.3E-2	2.0E-1
INTERPRO	Spectrin repeat	RT 📱	4	1.0	1.4E-2	2.2E-1
INTERPRO	Phosphoinositide 3-kinase, C2	RT 📱	3	0.7	1.5E-2	2.3E-1
INTERPRO	Bromodomain	RT 📱	5	1.2	1.7E-2	2.4E-1
INTERPRO	Cyclin	RT	5	1.2	1.7E-2	2.4E-1
INTERPRO	WD40/YVTN repeat-like	RT 🚃	15	3.6	1.7E-2	2.5E-1
INTERPRO	<u>Ubiquitin-conjugating enzyme, E2</u>	RT	5	1.2	1.8E-2	2.5E-1
INTERPRO	Cullin homology	RT	3	0.7	2.0E-2	2.6E-1
INTERPRO	Phosphatidylinositol Kinase	RT	3	0.7	2.4E-2	3.1E-1
INTERPRO	Cullin, N-terminal	RT	3	0.7	2.4E-2	3.1E-1
INTERPRO	<u>Cullin, conserved site</u>	RT	3	0.7	2.4E-2	3.1E-1
INTERPRO	<u>Cullin, N-terminal region</u>	RT	3	0.7	2.4E-2	3.1E-1
INTERPRO	Phosphoinositide 3-kinase accessory region PIK	RT	3	0.7	2.4E-2	3.1E-1
INTERPRO	WD40 repeat 2	RT 🔳	12	2.9	2.5E-2	3.2E-1
INTERPRO	<u>Ubiquitin</u>	RT	5	1.2	2.7E-2	3.2E-1
INTERPRO	FERM domain	RT 📱	5	1.2	2.9E-2	3.4E-1
INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT 📱	5	1.2	3.1E-2	3.5E-1
INTERPRO	HECT	RT 📱	4	1.0	3.1E-2	3.5E-1
INTERPRO	<u>Metallophosphoesterase</u>	RT 📱	4	1.0	3.1E-2	3.5E-1
INTERPRO	ATPase, AAA-type, core	RT 📱	5	1.2	3.3E-2	3.6E-1
INTERPRO	WD40 repeat	RT 🖀	13	3.1	3.3E-2	3.6E-1
INTERPRO	Band 4.1 domain	RT 📱	5	1.2	3.5E-2	3.7E-1
INTERPRO	FERM conserved site	RT 📱	5	1.2	3.5E-2	3.7E-1
INTERPRO	WD40 repeat, region	RT 🖀	12	2.9	3.5E-2	3.7E-1
INTERPRO	WD40 repeat, subgroup	RT 🖀	12	2.9	3.9E-2	3.9E-1
INTERPRO	Nucleotide-binding, alpha-beta plait	RT 🔳	11	2.6	3.9E-2	3.9E-1
INTERPRO	<u>Ubiquitin supergroup</u>	RT 📱	5	1.2	3.9E-2	3.9E-1
INTERPRO	Nucleic acid-binding, OB-fold	RT 📱	5	1.2	4.2E-2	4.0E-1
INTERPRO	Sterile alpha motif-type	RT 📱	6	1.4	4.2E-2	4.0E-1
INTERPRO	RNA helicase, ATP-dependent, DEAD-box, conserved site	RT 📱	4	1.0	4.4E-2	4.1E-1

INTERPRO	<u>HEAT</u>	<u>RT</u>	5	1.2	4.7E-2	4.3E-1
INTERPRO	Beta-catenin	RT	2	0.5	4.9E-2	4.4E-1
INTERPRO	DNA helicase, ATP-dependent, Ku type	RT	2	0.5	4.9E-2	4.4E-1
INTERPRO	ERK1/2 MAP kinase	RT	2	0.5	4.9E-2	4.4E-1
INTERPRO	Zinc finger, TAZ-type	RT	2	0.5	4.9E-2	4.4E-1
INTERPRO	Nuclear receptor coactivator, CREB-bp-like, interlocking	RT	2	0.5	4.9E-2	4.4E-1
INTERPRO	HIF-1 alpha, transactivation domain, C-terminal	RT	2	0.5	4.9E-2	4.4E-1
INTERPRO	Ku70/Ku80, N-terminal alpha/beta	RT	2	0.5	4.9E-2	4.4E-1
INTERPRO	Protein of unknown function DUF902, CREBbp	RT 🖥	2	0.5	4.9E-2	4.4E-1
INTERPRO	Coactivator CBP, KIX	RT 🖥	2	0.5	4.9E-2	4.4E-1
INTERPRO	Ku70/Ku80 C-terminal arm	RT 📱	2	0.5	4.9E-2	4.4E-1
INTERPRO	<u>Transcriptional coactivation</u>	RT 📱	2	0.5	4.9E-2	4.4E-1
INTERPRO	Fibronectin, type III subdomain	RT 📱	4	1.0	5.1E-2	4.5E-1
INTERPRO	RNA helicase, DEAD-box type, Q motif	RT 📱	4	1.0	6.3E-2	5.1E-1
INTERPRO	Basic helix-loop-helix dimerisation region bHLH	<u>rt</u>	7	1.7	6.4E-2	5.1E-1
INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	<u>rt</u>	3	0.7	6.5E-2	5.2E-1
INTERPRO	Furin-like repeat	<u>rt</u>	3	0.7	7.2E-2	5.5E-1
INTERPRO	Protein of unknown function DUF1518	RT 📱	2	0.5	7.2E-2	5.5E-1
INTERPRO	Retinoblastoma-associated protein, A-box	<u>rt</u>	2	0.5	7.2E-2	5.5E-1
INTERPRO	Adaptor protein Cbl, N-terminal helical	<u>rt</u>	2	0.5	7.2E-2	5.5E-1
INTERPRO	Retinoblastoma-associated protein, B-box	<u>rt</u>	2	0.5	7.2E-2	5.5E-1
INTERPRO	Nuclear receptor coactivator, Ncoa-type, interlocking	RT 🖥	2	0.5	7.2E-2	5.5E-1
INTERPRO	Adaptor protein Cbl, EF hand-like	RT	2	0.5	7.2E-2	5.5E-1
INTERPRO	Adaptor protein Cbl, SH2-like	RT	2	0.5	7.2E-2	5.5E-1
INTERPRO	Steroid receptor coactivator	RT	2	0.5	7.2E-2	5.5E-1
INTERPRO	Nuclear receptor coactivator	RT 🖥	2	0.5	7.2E-2	5.5E-1
INTERPRO	Rac serine/threonine kinase	RT 📱	2	0.5	7.2E-2	5.5E-1
INTERPRO	Notch, NOD region	RT 📱	2	0.5	7.2E-2	5.5E-1
INTERPRO	<u>Like-Sm ribonucleoprotein, core</u>	RT 📱	3	0.7	7.9E-2	5.8E-1
INTERPRO	WD40 repeat, conserved site	RT 🔳	12	2.9	8.3E-2	5.9E-1
INTERPRO	Fibronectin, type III-like fold	<u>RT</u>	9	2.2	8.7E-2	6.0E-1
INTERPRO	Winged helix repressor DNA-binding	<u>RT</u>	9	2.2	9.3E-2	6.2E-1
INTERPRO	Membrane-associated quanylate kinase (MAGUK) scaffold protein	RT 🖥	2	0.5	9.5E-2	6.3E-1
INTERPRO	Calcium/calmodulin dependent protein kinase II, association-domain	RT 🖥	2	0.5	9.5E-2	6.3E-1
INTERPRO	Membrane-associated quanylate kinase (MAGUK), PEST domain, N-terminal	RT	2	0.5	9.5E-2	6.3E-1
INTERPRO	Histone deacetylase	RT	2	0.5	9.5E-2	6.3E-1
INTERPRO	c-SKI Smad4 binding	RT	2	0.5	9.5E-2	6.3E-1
INTERPRO	SKP1 component, POZ	RT 📱	2	0.5	9.5E-2	6.3E-1
INTERPRO	SKP1 component	<u>RT</u>	2	0.5	9.5E-2	6.3E-1
INTERPRO	Notch, NODP region	<u>RT</u>	2	0.5	9.5E-2	6.3E-1
INTERPRO	Protein disulphide isomerase	<u>RT</u>	2	0.5	9.5E-2	6.3E-1
INTERPRO	Tyrosine protein kinase, receptor-type, EGF/ERB/XmrK	RT	2	0.5	9.5E-2	6.3E-1
INTERPRO	Vinculin, conserved site	RT	2	0.5	9.5E-2	6.3E-1
INTERPRO	Calcium/calmodulin-dependent protein kinase II isoform	RT I	2	0.5	9.5E-2	6.3E-1
INTERPRO	PDZ-associated domain of NMDA receptors	<u>RT</u>	2	0.5	9.5E-2	6.3E-1
INTERPRO	Fibronectin, type III	RT 🖥	9	2.2	9.9E-2	6.4E-1

152 gene(s) from your list are not in the output.















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