



Functional Annotation Chart

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Current Gene List: List_1

Current Background: Homo sapiens

417 DAVID IDs

Options























Rerun Using Options



Create Sublist

135 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	mutagenesis site	RT		170	40.8	3.6E-58	5.9E-55
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:ATP	RT		61	14.6	1.0E-25	8.4E-23
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:NR C4-type	RT		23	5.5	4.0E-25	2.2E-22
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	RT		23	5.5	4.0E-25	2.2E-22
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase	RT		54	12.9	3.4E-23	1.4E-20
<input type="checkbox"/>	UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT		77	18.5	3.8E-23	1.3E-20
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Proton acceptor	RT		57	13.7	1.3E-18	3.6E-16
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Ligand-binding	RT		15	3.6	4.5E-16	1.0E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO)	RT		20	4.8	4.9E-14	1.0E-11
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Modulating	RT		8	1.9	6.6E-9	1.2E-6
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH3	RT		18	4.3	3.5E-7	5.7E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Nuclear localization signal	RT		24	5.8	8.0E-7	1.2E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Hinge	RT		7	1.7	5.7E-6	7.8E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2	RT		12	2.9	7.6E-6	9.6E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 5	RT		7	1.7	9.7E-5	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Death	RT		7	1.7	9.7E-5	1.1E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Poly-Gln	RT		13	3.1	1.2E-4	1.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)	RT		15	3.6	1.2E-4	1.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT		9	2.2	1.2E-4	1.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 7	RT		6	1.4	1.4E-4	1.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Steroid-binding	RT		4	1.0	1.9E-4	1.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2; atypical	RT		4	1.0	1.9E-4	1.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 4	RT		7	1.7	3.2E-4	2.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	RT		4	1.0	3.4E-4	2.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:W2	RT		4	1.0	3.4E-4	2.6E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 6	RT		6	1.4	4.3E-4	3.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MH2	RT		4	1.0	5.3E-4	3.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MH1	RT		4	1.0	5.3E-4	3.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 3	RT		7	1.7	7.3E-4	4.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 3	RT		4	1.0	7.8E-4	5.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MIF4G	RT		4	1.0	7.8E-4	5.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Actin-binding	RT		5	1.2	8.1E-4	5.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 4	RT		5	1.2	9.9E-4	5.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 3	RT		5	1.2	1.2E-3	6.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	RT		4	1.0	1.5E-3	8.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 2	RT		7	1.7	1.6E-3	8.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 1	RT		7	1.7	1.6E-3	8.3E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 7	RT		5	1.2	1.7E-3	8.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Poly-Ser	RT		22	5.3	1.8E-3	9.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 1	RT		5	1.2	2.3E-3	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PAC	RT		5	1.2	2.3E-3	1.1E-1

<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:Spectrin 2	RT 	5	1.2	2.3E-3	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 6	RT 	5	1.2	2.3E-3	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CH 2	RT 	5	1.2	2.6E-3	1.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CH 1	RT 	5	1.2	2.6E-3	1.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Bromo	RT 	5	1.2	3.0E-3	1.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 5	RT 	5	1.2	3.4E-3	1.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase 1	RT 	4	1.0	3.8E-3	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Chromo	RT 	4	1.0	3.8E-3	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Protein kinase 2	RT 	4	1.0	3.8E-3	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 4	RT 	5	1.2	4.4E-3	1.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:MI	RT 	3	0.7	4.5E-3	1.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 4	RT 	3	0.7	4.5E-3	1.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:PDZ-binding	RT 	7	1.7	5.8E-3	2.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PI3K/PI4K	RT 	4	1.0	6.6E-3	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 9	RT 	4	1.0	6.6E-3	2.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 3	RT 	5	1.2	7.5E-3	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 2	RT 	9	2.2	7.6E-3	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PAS 2	RT 	4	1.0	7.7E-3	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 8	RT 	4	1.0	7.7E-3	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PAS 1	RT 	4	1.0	7.7E-3	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Fibronectin type-III 1	RT 	9	2.2	8.0E-3	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helicase C-terminal	RT 	8	1.9	8.1E-3	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 2	RT 	5	1.2	8.3E-3	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Arg/Lys-rich (basic)	RT 	5	1.2	9.1E-3	2.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in NEDD8)	RT 	3	0.7	9.2E-3	2.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO); alternate	RT 	3	0.7	9.2E-3	2.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT 	8	1.9	1.0E-2	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 8	RT 	4	1.0	1.2E-2	3.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Asp/Glu-rich (acidic)	RT 	8	1.9	1.2E-2	3.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	lipid moiety-binding region:N-myristoyl glycine	RT 	8	1.9	1.2E-2	3.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 5	RT 	12	2.9	1.3E-2	3.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2 2	RT 	3	0.7	1.9E-2	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:SH2 1	RT 	3	0.7	1.9E-2	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:FERM	RT 	5	1.2	2.0E-2	4.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Linker	RT 	4	1.0	2.0E-2	4.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 4	RT 	12	2.9	2.2E-2	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	sequence variant	RT 	282	67.6	2.2E-2	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:HECT	RT 	4	1.0	2.2E-2	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 2	RT 	4	1.0	2.5E-2	4.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:WW 1	RT 	4	1.0	2.5E-2	4.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 5	RT 	8	1.9	2.5E-2	4.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 6	RT 	10	2.4	2.5E-2	4.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ARM 1	RT 	4	1.0	2.9E-2	5.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 3	RT 	12	2.9	3.1E-2	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:DEAD box	RT 	4	1.0	3.4E-2	5.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 7	RT 	5	1.2	3.7E-2	6.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 1	RT 	12	2.9	3.8E-2	6.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:WD 2	RT 	12	2.9	3.8E-2	6.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	RT 	7	1.7	3.8E-2	6.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 9	RT	3	0.7	4.1E-2	6.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:HEAT 10	RT	3	0.7	4.1E-2	6.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:PAS	RT	3	0.7	4.1E-2	6.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:TAZ-type 2	RT	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Pocket; binds T and E1A	RT	2	0.5	4.3E-2	6.4E-1

<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:EIF4A-binding	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Cleavage; by calpain	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:KIX	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:Synthetic agonist	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Interaction with FANCD2	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Cleavage; by enterovirus/rhinovirus protease 2A	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Ku	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:eIF3/EIF4A-binding	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:PABPC1-binding	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	zinc finger region:TAZ-type 1	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Cleavage; by foot-and-mouth disease virus leader protease	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Cleavage (when cotranslationally processed)	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:CTAD	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Necessary but not sufficient for MKNK1- binding	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 35	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:GRR	RT 	2	0.5	4.3E-2	6.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Q motif	RT 	4	1.0	4.6E-2	6.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 6	RT 	6	1.4	5.0E-2	6.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:ANK 4	RT 	8	1.9	5.8E-2	7.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT 	8	1.9	6.3E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	short sequence motif:Nuclear export signal	RT 	4	1.0	6.3E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:4H	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 29	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	binding site:Phosphotyrosine	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 33	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Domain A	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:Domain B	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EGF-like 34	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand-like 1	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:EIF4E-binding	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	region of interest:NTAD	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:EF-hand-like 2	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:CBL N-terminal	RT 	2	0.5	6.4E-2	7.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region:Poly-Pro	RT 	15	3.6	6.9E-2	7.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	splice variant	RT 	178	42.7	7.5E-2	8.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of first active site	RT 	2	0.5	8.4E-2	8.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:LNR 3	RT 	2	0.5	8.4E-2	8.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of second active site	RT 	2	0.5	8.4E-2	8.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Guanylate kinase-like	RT 	3	0.7	8.9E-2	8.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:C2	RT 	5	1.2	9.7E-2	8.7E-1

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

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