



Functional Annotation Chart

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Current Gene List: condition_specific_gene_list
Current Background: Homo sapiens
2052 DAVID IDs

Options

Rerun Using Options

Create Sublist

202 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2)	RT	<div><div></div></div>	325	15.8	4.9E-64	4.4E-60
<input type="checkbox"/>	UP_SEQ_FEATURE	CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2); alternate	RT	<div><div></div></div>	118	5.8	4.4E-35	2.0E-31
<input type="checkbox"/>	UP_SEQ_FEATURE	CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO1); alternate	RT	<div><div></div></div>	70	3.4	9.9E-25	2.9E-21
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:RRM	RT	<div><div></div></div>	67	3.3	2.0E-15	4.5E-12
<input type="checkbox"/>	UP_SEQ_FEATURE	COMPBIAS:Basic residues	RT	<div><div></div></div>	135	6.6	1.8E-14	3.3E-11
<input type="checkbox"/>	UP_SEQ_FEATURE	COMPBIAS:Acidic residues	RT	<div><div></div></div>	167	8.1	9.9E-13	1.5E-9
<input type="checkbox"/>	UP_SEQ_FEATURE	COMPBIAS:Basic and acidic residues	RT	<div><div></div></div>	678	33.0	1.7E-11	2.2E-8
<input type="checkbox"/>	UP_SEQ_FEATURE	CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)	RT	<div><div></div></div>	65	3.2	4.6E-10	5.1E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:Nuclear localization signal	RT	<div><div></div></div>	88	4.3	6.5E-10	6.4E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:RRM 1	RT	<div><div></div></div>	32	1.6	2.0E-8	1.6E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:RRM 2	RT	<div><div></div></div>	32	1.6	2.0E-8	1.6E-5
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Disordered	RT	<div><div></div></div>	1431	69.7	3.3E-7	2.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Immunoglobulin C1-set	RT	<div><div></div></div>	11	0.5	3.3E-7	2.3E-4
<input type="checkbox"/>	UP_SEQ_FEATURE	LIPID:S-geranylgeranyl cysteine	RT	<div><div></div></div>	29	1.4	2.1E-6	1.3E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO); alternate	RT	<div><div></div></div>	18	0.9	2.4E-6	1.4E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO1)	RT	<div><div></div></div>	23	1.1	4.8E-6	2.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	TOPO_DOM:Lumenal	RT	<div><div></div></div>	101	4.9	8.5E-6	4.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:Q motif	RT	<div><div></div></div>	15	0.7	9.0E-6	4.5E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Thioredoxin	RT	<div><div></div></div>	16	0.8	1.2E-5	5.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Ig-like C1-type	RT	<div><div></div></div>	15	0.7	1.3E-5	5.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:Effector region	RT	<div><div></div></div>	25	1.2	1.6E-5	6.7E-3
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Ubiquitin-like	RT	<div><div></div></div>	19	0.9	2.5E-5	1.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO)	RT	<div><div></div></div>	25	1.2	4.5E-5	1.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:DEAD box	RT	<div><div></div></div>	13	0.6	4.8E-5	1.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Alpha-2	RT	<div><div></div></div>	9	0.4	4.9E-5	1.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Alpha-1	RT	<div><div></div></div>	9	0.4	4.9E-5	1.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:PCI	RT	<div><div></div></div>	11	0.5	6.0E-5	2.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:RHD	RT	<div><div></div></div>	7	0.3	1.2E-4	3.9E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:DEAD-box RNA helicase Q	RT	<div><div></div></div>	12	0.6	1.3E-4	4.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Leucine-zipper	RT	<div><div></div></div>	26	1.3	1.4E-4	4.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	LIPID:Phosphatidylserine amidated glycine; alternate	RT	<div><div></div></div>	6	0.3	1.5E-4	4.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	LIPID:Phosphatidylethanolamine amidated glycine; alternate	RT	<div><div></div></div>	6	0.3	1.5E-4	4.2E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Connecting peptide	RT	<div><div></div></div>	13	0.6	1.6E-4	4.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:RRM 3	RT	<div><div></div></div>	15	0.7	2.5E-4	6.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:PHD-type	RT	<div><div></div></div>	19	0.9	2.8E-4	7.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:BZIP	RT	<div><div></div></div>	14	0.7	3.1E-4	7.5E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Helicase C-terminal	RT	<div><div></div></div>	24	1.2	3.1E-4	7.5E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:SAP	RT	<div><div></div></div>	10	0.5	3.6E-4	8.4E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DISULFID:Redox-active	RT	<div><div></div></div>	15	0.7	3.9E-4	9.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:1-4	RT	<div><div></div></div>	8	0.4	4.1E-4	9.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:RanBP2-type	RT	<div><div></div></div>	8	0.4	4.1E-4	9.0E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Self-association	RT	<div><div></div></div>	7	0.3	4.6E-4	9.7E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:RING-type	RT	<div><div></div></div>	37	1.8	5.3E-4	1.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:bZIP	RT	<div><div></div></div>	15	0.7	5.9E-4	1.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Serine/threonine specific protein phosphatases	RT	<div><div></div></div>	7	0.3	7.8E-4	1.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:C4-type	RT	<div><div></div></div>	16	0.8	8.2E-4	1.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:Prevents secretion from ER	RT	<div><div></div></div>	15	0.7	8.7E-4	1.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSIT:Mitochondrion	RT	<div><div></div></div>	78	3.8	9.6E-4	1.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:1-3	RT	<div><div></div></div>	8	0.4	9.7E-4	1.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Helicase ATP-binding	RT	<div><div></div></div>	24	1.2	9.9E-4	1.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 6	RT	<div><div></div></div>	42	2.0	1.0E-3	1.8E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:DUSP	RT	<div><div></div></div>	5	0.2	1.1E-3	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:MIT-interacting motif	RT	<div><div></div></div>	5	0.2	1.1E-3	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:C3H1-type	RT	<div><div></div></div>	15	0.7	1.5E-3	2.5E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD	RT	<div><div></div></div>	36	1.8	1.6E-3	2.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 5	RT	<div><div></div></div>	42	2.0	1.7E-3	2.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:1-2	RT	<div><div></div></div>	9	0.4	1.8E-3	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:ARID	RT	<div><div></div></div>	7	0.3	1.9E-3	2.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 4	RT	<div><div></div></div>	42	2.0	2.1E-3	3.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Basic motif	RT	<div><div></div></div>	14	0.7	2.3E-3	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:ADF-H	RT	<div><div></div></div>	6	0.3	2.4E-3	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	TOPO_DOM:Mitochondrial intermembrane	RT	<div><div></div></div>	26	1.3	2.4E-3	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:STAT transcription factor protein interaction	RT	<div><div></div></div>	5	0.2	2.4E-3	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	SITE:Cleavage; by ATG4B	RT	<div><div></div></div>	5	0.2	2.4E-3	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 3	RT	<div><div></div></div>	42	2.0	2.4E-3	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:1-1	RT	<div><div></div></div>	9	0.4	2.4E-3	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:PHD-type	RT	<div><div></div></div>	13	0.6	2.5E-3	3.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Interaction with Elongin BC complex	RT	<div><div></div></div>	4	0.2	3.4E-3	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Interaction with VTA1	RT	<div><div></div></div>	4	0.2	3.4E-3	4.4E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	COMPBIAS:Polar residues	RT	<div><div></div></div>	725	35.3	3.7E-3	4.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	CARBOHYD:(Microbial infection) N-beta-linked (GlcNAc) arginine	RT	<div><div></div></div>	6	0.3	3.8E-3	4.7E-1

Sublist	Category	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:TNFR-Cys	RT		7	0.3	4.0E-3	4.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:WD 1	RT		42	2.0	4.1E-3	5.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:WD 2	RT		42	2.0	4.1E-3	5.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE TOPO_DOM:Mitochondrial matrix	RT		19	0.9	4.7E-3	5.6E-1
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:TPR	RT		19	0.9	6.5E-3	7.7E-1
<input type="checkbox"/>	UP_SEQ_FEATURE MOTIF:Cx9C motif 1	RT		7	0.3	7.4E-3	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE ZN_FING:RanBP2-type	RT		7	0.3	7.4E-3	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE MOTIF:Cx9C motif 2	RT		7	0.3	7.4E-3	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:WD 7	RT		32	1.6	7.4E-3	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE MUTAGEN:K->R: No effect on sumoylation.	RT		5	0.2	7.4E-3	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE ZN_FING:PHD-type 2	RT		10	0.5	7.6E-3	8.2E-1
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:MHC class II alpha chain N-terminal	RT		4	0.2	7.8E-3	8.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:2-1	RT		8	0.4	8.0E-3	8.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:TNFR-Cys 2	RT		8	0.4	8.0E-3	8.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:TNFR-Cys 1	RT		8	0.4	8.0E-3	8.3E-1
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:C3H1-type	RT		12	0.6	8.6E-3	8.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE ZN_FING:PHD-type 1	RT		10	0.5	1.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE TRANSMEM:Helical; Anchor for type IV membrane protein	RT		14	0.7	1.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:Alpha-3	RT		5	0.2	1.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:CXXC-type	RT		5	0.2	1.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:Ribosomal protein eL8/eL30/eS12/Gadd45	RT		5	0.2	1.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE UNSURE:I or L	RT		5	0.2	1.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE ZN_FING:RING-type	RT		33	1.6	1.2E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:2-2	RT		8	0.4	1.2E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:Tudor-knot	RT		4	0.2	1.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:DDT	RT		4	0.2	1.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE SITE:Cleavage; by CASP8	RT		4	0.2	1.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:A20-type	RT		4	0.2	1.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:Bromo	RT		10	0.5	1.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE ZN_FING:CXXC-type	RT		5	0.2	1.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE MOTIF:Di-lysine motif	RT		6	0.3	2.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:TNFR-Cys 3	RT		7	0.3	2.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:CHCH	RT		7	0.3	2.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:v-SNARE coiled-coil homology	RT		5	0.2	2.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:V-SNARE coiled-coil homology	RT		5	0.2	2.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 15	RT		5	0.2	2.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:Membrane-binding amphipathic helix	RT		5	0.2	2.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 17	RT		5	0.2	2.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 16	RT		5	0.2	2.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:AN1-type	RT		4	0.2	2.4E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:KOW	RT		4	0.2	2.4E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE SITE:Contributes to redox potential value	RT		4	0.2	2.4E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:DED	RT		4	0.2	2.4E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:1-5	RT		4	0.2	2.4E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:TNFR-Cys	RT		6	0.3	2.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:Interaction with VPS4B	RT		3	0.1	2.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:Interaction with IST1	RT		3	0.1	2.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:CCHC NOA-type	RT		3	0.1	2.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:Interaction with MYO6	RT		3	0.1	2.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:MHC class I alpha chain C-terminal	RT		3	0.1	2.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:BAT2 N-terminal	RT		3	0.1	2.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE ZN_FING:CCHC NOA-type	RT		3	0.1	2.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE BINDING:in other chain	RT		10	0.5	2.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE LIPID:N-myristoyl glycine	RT		29	1.4	2.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:1	RT		35	1.7	2.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE PROPEP:Removed in mature form	RT		40	1.9	3.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:3	RT		32	1.6	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:SH2	RT		18	0.9	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 12	RT		5	0.2	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 10	RT		5	0.2	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE CROSSLNK:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	RT		5	0.2	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 14	RT		5	0.2	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 11	RT		5	0.2	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 13	RT		5	0.2	3.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 19	RT		4	0.2	3.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 18	RT		4	0.2	3.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:MRH	RT		4	0.2	3.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 20	RT		4	0.2	3.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE ACT_SITE:Proton acceptor	RT		102	5.0	3.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:CS	RT		6	0.3	3.8E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 9	RT		5	0.2	4.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 8	RT		5	0.2	4.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REPEAT:Spectrin 7	RT		5	0.2	4.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE ZN_FING:Matrin-type	RT		5	0.2	4.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:WW	RT		10	0.5	4.4E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:SH3	RT		30	1.5	4.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:MIT	RT		4	0.2	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:VHS	RT		4	0.2	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE MOTIF:PxVxL motif	RT		4	0.2	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:NTF2	RT		4	0.2	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:MRG	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:Interaction with RNA	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE CARBOHYD:(Microbial infection) O-alpha-linked (GlcNAc) threonine; by C.novyi toxin TcdA; alternate	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:Interaction with ESR1	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:VL9 epitope	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:Necessary for RNA-binding	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE LIPID:(Microbial infection) N6-stearoyl lysine	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:Interaction with NR1D1	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE TRANSMEM:Helical; Name=II	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE TRANSMEM:Helical; Name=I	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE ZN_FING:C2HC RNF-type	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE REGION:Necessary for transcriptional repression	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:RNA-binding S4	RT		3	0.1	4.9E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE DOMAIN:MHC class II beta chain N-terminal	RT		5	0.2	5.0E-2	1.0E0

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 6	RT		5	0.2	5.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Spectrin 5	RT		5	0.2	5.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:4	RT		27	1.3	5.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:2	RT		34	1.7	5.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ACT_SITE:Glycyl thioester intermediate	RT		13	0.6	5.2E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:MHC class I-like antigen recognition-like	RT		6	0.3	5.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Arf-GAP	RT		7	0.3	5.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:USP	RT		13	0.6	5.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:Bipartite nuclear localization signal	RT		10	0.5	6.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Cyclin-like	RT		7	0.3	6.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Cation-transporting P-type ATPase C-terminal	RT		4	0.2	6.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Tudor	RT		6	0.3	6.6E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	SITE:Important for catalytic activity	RT		8	0.4	7.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:7	RT		20	1.0	7.1E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:TPR 3	RT		21	1.0	7.2E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:PARP catalytic	RT		5	0.2	7.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:2-3	RT		5	0.2	7.5E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:PPIase cyclophilin-type	RT		6	0.3	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:Box 1 motif	RT		6	0.3	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Calcineurin-binding	RT		3	0.1	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:SKICH	RT		3	0.1	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Phosphoribosyltransferase	RT		3	0.1	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:HAT 8	RT		3	0.1	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Longin	RT		3	0.1	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:PABPC1-interacting motif-2 (PAM2)	RT		3	0.1	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	MUTAGEN:K->R: Loss of sumoylation.	RT		3	0.1	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	MUTAGEN:K->R: Complete loss of in vitro methylation by METTL21A.	RT		3	0.1	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:AN1-type	RT		3	0.1	7.7E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:RING-type; atypical	RT		8	0.4	7.8E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA_BIND:A.T hook 1	RT		4	0.2	8.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA_BIND:A.T hook 2	RT		4	0.2	8.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:PHD-type 3	RT		4	0.2	8.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:ITAM	RT		4	0.2	8.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:WWE	RT		4	0.2	8.3E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Catalytic	RT		6	0.3	8.8E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:MPN	RT		5	0.2	9.0E-2	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	ACT_SITE:Proton donor	RT		31	1.5	9.7E-2	1.0E0

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

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