Phyre²

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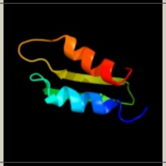
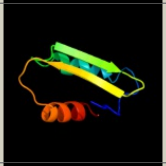
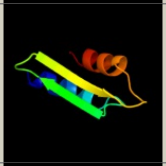
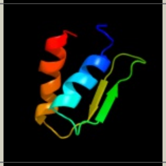
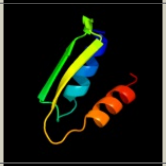
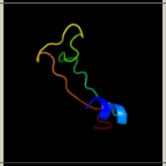
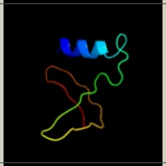
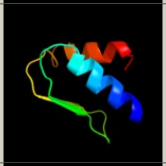
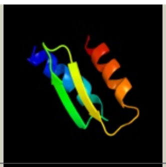
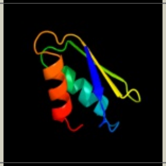
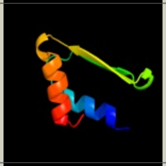
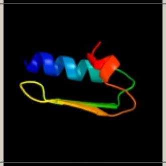
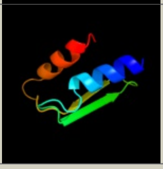
Description	P0AAY6
Date	Thu Jan 5 11:14:09 GMT 2012
Unique Job ID	c525ad8e43cf4f97

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sf4F_	Alignment		63.7	33	**PDB header:**signaling protein/protein binding **Chain:** F: **PDB Molecule:**protein inscuteable homolog; **PDBTitle:** crystal structure of the complex between the conserved cell polarity2 proteins inscuteable and lgn
2	c2gcfA_	Alignment		51.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
3	c3cxjB_	Alignment		43.4	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
4	d2ggpb1	Alignment		35.2	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
5	c1yg0A_	Alignment		35.1	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
6	d1sb6a_	Alignment		33.4	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
7	c2kt2A_	Alignment		33.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
8	d2hfva1	Alignment		29.6	15	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**RPA1041-like
9	d2a2ja1	Alignment		28.1	26	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
10	c2rogA_	Alignment		27.0	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
11	d1q8la_	Alignment		26.3	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain

12	d1mwza_	Alignment		26.2	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
13	d1cpza_	Alignment		24.9	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
14	c2k2pA_	Alignment		24.6	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
15	c1qupA_	Alignment		24.6	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
16	d1qupa2	Alignment		24.5	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
17	c2ga7A_	Alignment		24.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
18	c2aj1A_	Alignment		24.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
19	c1y3kA_	Alignment		24.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
20	c2crlA_	Alignment		23.0	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** the apo form of hma domain of copper chaperone for2 superoxide dismutase
21	c2kkhA_	Alignment	not modelled	22.5	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
22	c2hfvA_	Alignment	not modelled	22.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa1041; **PDBTitle:** solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
23	c1jk9D_	Alignment	not modelled	21.3	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
24	c2gloA_	Alignment	not modelled	21.2	15	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**brinker cg9653-pa; **PDBTitle:** solution structure of the brinker dna binding domain in2 complex with the omb enhancer
25	d1p6ta2	Alignment	not modelled	20.9	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
26	d1afia_	Alignment	not modelled	20.0	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
27	c2ldiA_	Alignment	not modelled	18.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
28	c2ofhX_	Alignment	not modelled	18.3	14	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form

29	d1sgga_	Alignment	not modelled	18.0	32	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
30	d1p6ta1	Alignment	not modelled	17.6	24	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
31	d1fe0a_	Alignment	not modelled	16.1	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
32	d2aw0a_	Alignment	not modelled	15.6	13	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
33	c3dxsX_	Alignment	not modelled	15.4	21	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
34	c3senD_	Alignment	not modelled	15.2	18	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**caskin-1; **PDBTitle:** structure of caskin1 tandem sams
35	c1yjrA_	Alignment	not modelled	15.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
36	d1jx7a_	Alignment	not modelled	14.2	13	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
37	d1jvna2	Alignment	not modelled	14.1	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
38	d1osda_	Alignment	not modelled	13.7	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
39	c2l0eA_	Alignment	not modelled	13.6	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** structural and functional analysis of tm vi of the nhe1 isoform of the2 na+/h+ exchanger
40	d2qifa1	Alignment	not modelled	13.3	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
41	c2ew9A_	Alignment	not modelled	13.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of apowln5-6
42	d1x40a1	Alignment	not modelled	13.0	17	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
43	c1b0xA_	Alignment	not modelled	12.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (epha4 receptor tyrosine kinase); **PDBTitle:** the crystal structure of an eph receptor sam domain reveals2 a mechanism for modular dimerization.
44	d1b0xa_	Alignment	not modelled	12.8	16	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
45	c2ropA_	Alignment	not modelled	11.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of domains 3 and 4 of human atp7b
46	c3k1rB_	Alignment	not modelled	11.8	29	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**usher syndrome type-1g protein; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
47	c2embA_	Alignment	not modelled	11.8	63	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 342-2 372) of human zinc finger protein 473
48	d1kvja_	Alignment	not modelled	11.6	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
49	c2p57A_	Alignment	not modelled	11.5	40	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**gtpase-activating protein znf289; **PDBTitle:** gap domain of znf289, an id1-regulated zinc finger protein
50	c2qkqA_	Alignment	not modelled	11.5	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-b receptor 4; **PDBTitle:** structure of the sam domain of human ephrin type-b receptor2 4
51	d1cc8a_	Alignment	not modelled	11.4	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
52	d1bboa1	Alignment	not modelled	11.4	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
53	d2czra1	Alignment	not modelled	11.2	33	**Fold:**Restriction endonuclease-like **Superfamily:**TBP-interacting protein-like **Family:**TBP-interacting protein-like
54	c2a2jA_	Alignment	not modelled	11.1	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase; **PDBTitle:** crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
55	c3ed3A_	Alignment	not modelled	11.1	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase mpd1; **PDBTitle:** crystal structure of the yeast dithiol/disulfide2 oxidoreductase mpd1p

56	d1fnda2	Alignment	not modelled	10.6	14	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
57	d2d1pa1	Alignment	not modelled	10.6	25	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
58	d1v38a_	Alignment	not modelled	10.4	8	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
59	c3h8mB_	Alignment	not modelled	10.4	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 7; **PDBTitle:** sam domain of human ephrin type-a receptor 7 (epha7)
60	d2v0ea1	Alignment	not modelled	10.4	31	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
61	c3dwdB_	Alignment	not modelled	10.2	30	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**adp-ribosylation factor gtpase-activating protein 1; **PDBTitle:** crystal structure of the arfgap domain of human arfgap1
62	c2kyzA_	Alignment	not modelled	10.1	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
63	c2d9lA_	Alignment	not modelled	10.1	30	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoporin-like protein rip; **PDBTitle:** solution structure of the arfgap domain of human rip
64	c1vzhB_	Alignment	not modelled	10.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**desulfoferrodoxin; **PDBTitle:** structure of superoxide reductase bound to ferrocyanide and2 active site expansion upon x-ray induced photoreduction
65	d1g7ea_	Alignment	not modelled	10.0	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ERP29 N domain-like
66	d1ucva_	Alignment	not modelled	9.8	36	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
67	c2iqjB_	Alignment	not modelled	9.7	27	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**stromal membrane-associated protein 1-like; **PDBTitle:** crystal structure of the gap domain of smap1l (loc64744)2 stromal membrane-associated protein 1-like
68	d1iowa2	Alignment	not modelled	9.5	24	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
69	c2owaB_	Alignment	not modelled	9.5	40	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**arfgap-like finger domain containing protein; **PDBTitle:** crystal structure of putative gtpase activating protein for2 adp ribosylation factor from cryptosporidium parvum3 (cgd5_1040)
70	d1dcqa2	Alignment	not modelled	9.4	20	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**Pyk2-associated protein beta ARF-GAP domain
71	d1b4fa_	Alignment	not modelled	8.9	21	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
72	c1wwuA_	Alignment	not modelled	8.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein flj21935; **PDBTitle:** solution structure of the sam_pnt domain of human protein2 flj21935
73	d2ckca1	Alignment	not modelled	8.7	31	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
74	c2ckcA_	Alignment	not modelled	8.7	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 7; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
75	d1dpua_	Alignment	not modelled	8.6	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
76	c1dpuA_	Alignment	not modelled	8.6	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
77	c2e8nA_	Alignment	not modelled	8.6	29	**PDB header:**transferase, signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** solution structure of the c-terminal sam-domain of ephaa2:2 ephrin type-a receptor 2 precursor (ec 2.7.10.1)
78	c2l3mA_	Alignment	not modelled	8.4	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
79	c2w9kA_	Alignment	not modelled	8.3	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crithidia fasciculata cytochrome c
80	c2dl0A_	Alignment	not modelled	8.3	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sam-domain of the sam and sh32 domain containing protein 1

81	c2dkzA_	Alignment	not modelled	8.2	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**hypothetical protein loc64762; **PDBTitle:** solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
82	c3hilB_	Alignment	not modelled	7.8	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** sam domain of human ephrin type-a receptor 1 (epha1)
83	c3fryB_	Alignment	not modelled	7.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable copper-exporting p-type atpase a; **PDBTitle:** crystal structure of the copa c-terminal metal binding domain
84	d2ca5a1	Alignment	not modelled	7.7	37	**Fold:**Long alpha-hairpin **Superfamily:**MxiH-like **Family:**MxiH-like
85	c1j9zB_	Alignment	not modelled	7.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
86	d1uv7a_	Alignment	not modelled	7.6	15	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**General secretion pathway protein M, EpsM **Family:**General secretion pathway protein M, EpsM
87	c1uv7A_	Alignment	not modelled	7.6	15	**PDB header:**transport **Chain:** A: **PDB Molecule:**general secretion pathway protein m; **PDBTitle:** periplasmic domain of epsm from vibrio cholerae
88	c3bq7A_	Alignment	not modelled	7.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase delta; **PDBTitle:** sam domain of diacylglycerol kinase delta1 (e35g)
89	d1ow5a_	Alignment	not modelled	7.5	14	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
90	c1ow5A_	Alignment	not modelled	7.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase ste11; **PDBTitle:** nmr structure of the saccharomyces cerevisiae sam (sterile2 alpha motif) domain
91	c3kkaD_	Alignment	not modelled	7.4	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** co-crystal structure of the sam domains of epha1 and epha2
92	c2ckaA_	Alignment	not modelled	7.3	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 8; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
93	d2ckaa1	Alignment	not modelled	7.3	31	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
94	c2eamA_	Alignment	not modelled	7.3	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative 47 kda protein; **PDBTitle:** solution structure of the n-terminal sam-domain of a human2 putative 47 kda protein
95	c2qs7D_	Alignment	not modelled	7.3	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative oxidoreductase of the dsre/dsrf-like2 family (sso1126) from sulfolobus solfataricus p2 at 2.09 a resolution
96	d2f3na1	Alignment	not modelled	7.3	12	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
97	c2fe9A_	Alignment	not modelled	7.3	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein vts1; **PDBTitle:** solution structure of the vts1 sam domain in the presence2 of rna
98	c2e8mA_	Alignment	not modelled	7.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**epidermal growth factor receptor kinase **PDBTitle:** solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
99	c3fehA_	Alignment	not modelled	7.1	27	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**centaurin-alpha-1; **PDBTitle:** crystal structure of full length centaurin alpha-1