Phyre²

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Description	P65290
Date	Thu Jan 5 12:10:09 GMT 2012
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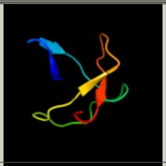
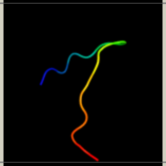
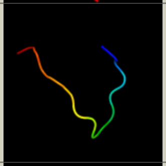
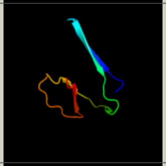
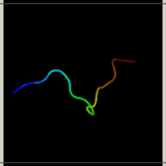
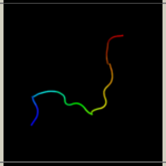
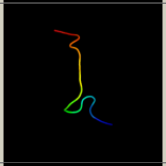
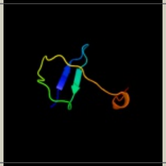
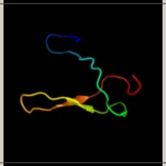
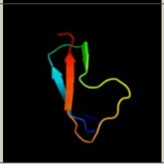
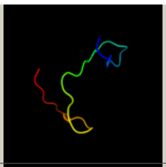
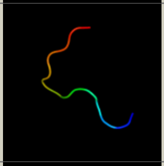
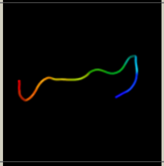
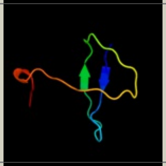
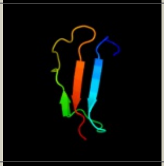
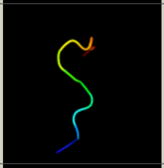
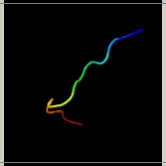
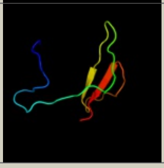
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cp0A_	Alignment		72.4	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein implicated in regulation of membrane **PDBTitle:** crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
2	c2kvqG_	Alignment		57.1	19	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
3	c2jvvA_	Alignment		57.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
4	c2lllA_	Alignment		54.1	8	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-b2; **PDBTitle:** solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a
5	d1nz9a_	Alignment		48.3	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
6	d2gnra1	Alignment		47.6	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
7	c2e6zA_	Alignment		46.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
8	d1nppa2	Alignment		45.5	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
9	d1h9ma1	Alignment		43.8	14	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
10	d1fdra1	Alignment		38.9	13	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
11	d1k25a1	Alignment		37.8	10	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain

12	d1q1ca1	Alignment		36.9	20	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
13	c2dxcG_	Alignment		36.7	29	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**thiocyanate hydrolase subunit alpha; **PDBTitle:** recombinant thiocyanate hydrolase, fully-matured form
14	d2do3a1	Alignment		35.7	25	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
15	d1oxxk1	Alignment		35.4	8	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
16	d1pyya1	Alignment		35.3	8	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
17	c3qz9D_	Alignment		34.0	29	**PDB header:**lyase **Chain:** D: **PDB Molecule:**co-type nitrile hydratase beta subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
18	c1h9mB_	Alignment		33.8	11	**PDB header:**binding protein **Chain:** B: **PDB Molecule:**molybdenum-binding-protein; **PDBTitle:** two crystal structures of the cytoplasmic molybdate-binding2 protein modg suggest a novel cooperative binding mechanism3 and provide insights into ligand-binding specificity.4 peg-grown form with molybdate bound
19	d1ugpb_	Alignment		33.2	21	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
20	d1ifra_	Alignment		33.2	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
21	d1h9ra1	Alignment	not modelled	33.0	14	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
22	d1v29b_	Alignment	not modelled	31.6	14	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
23	c3e0eA_	Alignment	not modelled	31.3	19	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein a; **PDBTitle:** crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
24	d1ivta_	Alignment	not modelled	30.7	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
25	c3jt0B_	Alignment	not modelled	28.1	15	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of the c-terminal fragment (426-558)2 lamin-b1 from homo sapiens, northeast structural genomics3 consortium target hr5546a
26	d2zjrm1	Alignment	not modelled	27.7	36	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
27	d2asba1	Alignment	not modelled	27.2	6	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
28	d1pkla3	Alignment	not modelled	27.1	37	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain

29	c2fhdA_	Alignment	not modelled	22.4	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
30	d2qdyb1	Alignment	not modelled	21.8	23	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
31	d1fr3a_	Alignment	not modelled	21.4	8	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
32	c2kppA_	Alignment	not modelled	20.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0431 protein; **PDBTitle:** solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
33	d1h9ra2	Alignment	not modelled	20.4	9	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
34	d1v43a2	Alignment	not modelled	19.5	9	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
35	c1m1gB_	Alignment	not modelled	18.9	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
36	d1yloa1	Alignment	not modelled	18.5	16	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
37	d1vhea1	Alignment	not modelled	18.2	23	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
38	d1kyaa2	Alignment	not modelled	17.9	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
39	c2k5hA_	Alignment	not modelled	16.6	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
40	c1h9sA_	Alignment	not modelled	16.2	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**molybdenum transport protein mode; **PDBTitle:** molybdate bound complex of dimop domain of mode from e.coli
41	d2ccwa1	Alignment	not modelled	15.8	7	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
42	d1g2914	Alignment	not modelled	15.5	15	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
43	d1te7a_	Alignment	not modelled	15.3	15	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**yqfB-like
44	d1ah9a_	Alignment	not modelled	15.2	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
45	d1qfja1	Alignment	not modelled	15.0	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
46	d1h9ma2	Alignment	not modelled	14.9	10	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
47	d2j01t1	Alignment	not modelled	14.6	36	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
48	c1rouA_	Alignment	not modelled	14.6	19	**PDB header:**rotamase (isomerase) **Chain:** A: **PDB Molecule:**fkbp59-i; **PDBTitle:** structure of fkbp59-i, the n-terminal domain of a 59 kda2 fk506-binding protein, nmr, 22 structures
49	c3p8bB_	Alignment	not modelled	14.1	12	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
50	d1y0ya1	Alignment	not modelled	13.8	10	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
51	d2cowa1	Alignment	not modelled	13.6	13	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
52	c3zv0D_	Alignment	not modelled	13.1	23	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1p-cbf5p complex
53	c2lbgA_	Alignment	not modelled	12.9	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**major prion protein; **PDBTitle:** structure of the chr of the prion protein in dpc micelles
54	d1hh2p1	Alignment	not modelled	12.8	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
						PDB header:lyase **Chain:** B: **PDB Molecule:**d-serine deaminase;

55	c3gwqB_	Alignment	not modelled	12.7	7	**PDBTitle:** crystal structure of a putative d-serine deaminase (bxe_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
56	d1guta_	Alignment	not modelled	12.7	7	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
57	d3d31a1	Alignment	not modelled	12.3	5	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
58	c2egcA_	Alignment	not modelled	12.3	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a; **PDBTitle:** solution structure of the fifth sh3 domain from human2 kiaa0418 protein
59	c2k14A_	Alignment	not modelled	12.2	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**yuaf protein; **PDBTitle:** solution structure of the soluble domain of the nfed2 protein yuaf from bacillus subtilis
60	c2xhcA_	Alignment	not modelled	11.9	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
61	d1v10a2	Alignment	not modelled	11.0	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
62	d2hqha1	Alignment	not modelled	10.8	11	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
63	d2cp5a1	Alignment	not modelled	10.5	13	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
64	d2awna1	Alignment	not modelled	10.5	4	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
65	d2grea1	Alignment	not modelled	10.4	13	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
66	c3dm3A_	Alignment	not modelled	9.8	16	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication factor a; **PDBTitle:** crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e
67	c1piwA_	Alignment	not modelled	9.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical zinc-type alcohol dehydrogenase- **PDBTitle:** apo and holo structures of an nadp(h)-dependent cinnamyl2 alcohol dehydrogenase from saccharomyces cerevisiae
68	d2q07a1	Alignment	not modelled	9.6	10	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
69	c2d6fA_	Alignment	not modelled	9.4	14	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
70	d2e3ia1	Alignment	not modelled	9.3	18	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
71	d2gycn1	Alignment	not modelled	9.3	23	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
72	c1nwxN_	Alignment	not modelled	9.1	36	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**ribosomal protein l19; **PDBTitle:** complex of the large ribosomal subunit from deinococcus2 radiodurans with abt-773
73	d2vv5a1	Alignment	not modelled	9.1	15	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
74	d2zjrr1	Alignment	not modelled	8.8	17	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
75	c3m9qA_	Alignment	not modelled	8.8	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein male-specific lethal-3; **PDBTitle:** drosophila msl3 chromodomain
76	d1q7ha1	Alignment	not modelled	8.7	9	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
77	d1whma_	Alignment	not modelled	8.7	5	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
78	c3fp9E_	Alignment	not modelled	8.6	8	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
79	d1k3ra1	Alignment	not modelled	8.6	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
80	c2piaA_	Alignment	not modelled	8.2	11	**PDB header:**reductase **Chain:** A: **PDB Molecule:**phthalate dioxygenase reductase; **PDBTitle:** phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]

81	c1krhA_	Alignment	not modelled	8.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
82	c3es4B_	Alignment	not modelled	8.0	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein duf861 with a rmlc-like cupin fold; **PDBTitle:** crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
83	d1piwa1	Alignment	not modelled	7.8	9	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
84	d2cp2a1	Alignment	not modelled	7.8	13	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
85	d2cp0a1	Alignment	not modelled	7.6	17	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
86	d2jnaa1	Alignment	not modelled	7.6	20	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
87	d1tova_	Alignment	not modelled	7.6	17	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
88	c3i4oA_	Alignment	not modelled	7.5	6	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
89	c3jxoB_	Alignment	not modelled	7.4	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trka-n domain protein; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
90	d1iq8a3	Alignment	not modelled	7.4	11	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
91	d1hfua2	Alignment	not modelled	7.4	27	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
92	d1uufa1	Alignment	not modelled	7.3	10	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
93	d1m1ha1	Alignment	not modelled	7.1	15	**Fold:**N-utilization substance G protein NusG, insert domain **Superfamily:**N-utilization substance G protein NusG, insert domain **Family:**N-utilization substance G protein NusG, insert domain
94	c2asbA_	Alignment	not modelled	7.0	6	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** structure of a mycobacterium tuberculosis nusa-rna complex
95	c3zvkG_	Alignment	not modelled	7.0	18	**PDB header:**antitoxin/toxin/dna **Chain:** G: **PDB Molecule:**antitoxin of toxin-antitoxin system vapb; **PDBTitle:** crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
96	c1yqxB_	Alignment	not modelled	6.9	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sinapyl alcohol dehydrogenase; **PDBTitle:** sinapyl alcohol dehydrogenase at 2.5 angstrom resolution
97	c2e4hA_	Alignment	not modelled	6.8	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**restin; **PDBTitle:** solution structure of cytoskeletal protein in complex with2 tubulin tail
98	c2yyzA_	Alignment	not modelled	6.7	6	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar abc transporter, atp-binding protein; **PDBTitle:** crystal structure of sugar abc transporter, atp-binding protein
99	d2apoa1	Alignment	not modelled	6.7	18	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain