Phyre2

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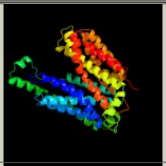
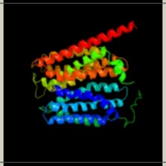
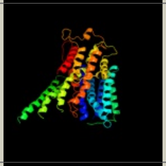
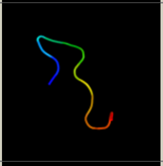
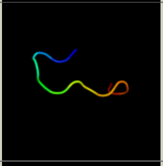
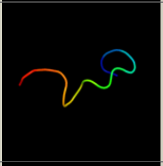
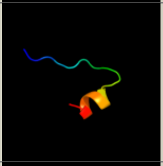
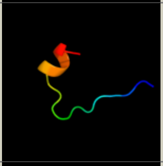
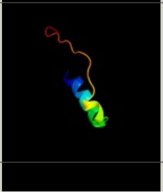
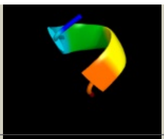
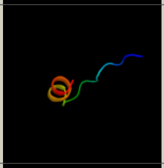
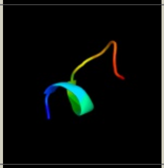
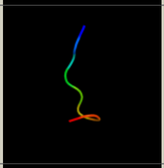
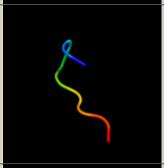
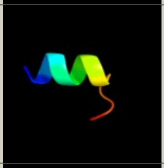
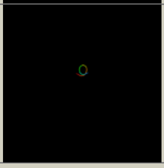
Description	A1A5C7
Date	Wed May 9 18:02:57 BST 2012
Unique Job ID	7e23fddf87cb6512

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3o7pA_	Alignment		100.0	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
2	d1pw4a_	Alignment		100.0	16	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
3	c2xutC_	Alignment		100.0	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
4	c2gfpA_	Alignment		99.9	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
5	d1pv7a_	Alignment		99.9	9	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
6	d1vhib_	Alignment		32.5	50	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
7	d1b3ta_	Alignment		28.7	50	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
8	c2jm2A_	Alignment		27.7	47	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**insulin-like growth factor-binding protein 6; **PDBTitle:** structure of the n-terminal subdomain of insulin-like2 growth factor (igf) binding protein-6 and its interactions3 with igfs
9	d1z8ga2	Alignment		26.4	28	**Fold:**SRCR-like **Superfamily:**SRCR-like **Family:**Hepsin, N-terminal domain
10	c2oyaA_	Alignment		22.2	28	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**macrophage receptor marco; **PDBTitle:** crystal structure analysis of the dimeric form of the srcr domain of2 mouse marco
11	c3rnvA_	Alignment		20.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helper component proteinase; **PDBTitle:** structure of the autocatalytic cysteine protease domain of potyvirus2 helper-component proteinase

12	c1r7gA_	Alignment		18.9	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 100mm dpc)
13	c1z8gA_	Alignment		18.0	28	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine protease hepsin; **PDBTitle:** crystal structure of the extracellular region of the transmembrane2 serine protease hepsin with covalently bound preferred substrate.
14	d1riea_	Alignment		16.5	33	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
15	d1tkla_	Alignment		15.8	18	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
16	c1s6xA_	Alignment		15.7	67	**PDB header:**toxin **Chain:** A: **PDB Molecule:**kvap channel; **PDBTitle:** solution structure of vstx
17	c2nvgA_	Alignment		15.6	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** soluble domain of rieske iron sulfur protein.
18	c2g9pA_	Alignment		15.5	21	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
19	d2nefa_	Alignment		14.9	27	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef
20	c2aexA_	Alignment		14.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coproporphyrinogen iii oxidase, mitochondrial; **PDBTitle:** the 1.58a crystal structure of human coproporphyrinogen oxidase2 reveals the structural basis of hereditary coproporphyria
21	c3rbbA_	Alignment	not modelled	14.2	30	**PDB header:**viral protein, protein binding **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** hiv-1 nef protein in complex with engineered hck sh3 domain
22	d1by2a_	Alignment	not modelled	13.8	39	**Fold:**SRCR-like **Superfamily:**SRCR-like **Family:**Scavenger receptor cysteine-rich (SRCR) domain
23	d1vjua_	Alignment	not modelled	13.2	36	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
24	d1efnb_	Alignment	not modelled	12.7	26	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef
25	c2ottY_	Alignment	not modelled	12.5	30	**PDB header:**immune system **Chain:** Y: **PDB Molecule:**t-cell surface glycoprotein cd5; **PDBTitle:** crystal structure of cd5_diii
26	d2fyuk1	Alignment	not modelled	12.5	17	**Fold:**Single transmembrane helix **Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
27	c3b9yA_	Alignment	not modelled	12.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
28	c3gceA_	Alignment	not modelled	10.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin component of carbazole 1,9a- **PDBTitle:** ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177
						Fold:SMAD/FHA domain

29	d1dd1a_	Alignment	not modelled	9.9	38	**Superfamily:**SMAD/FHA domain **Family:**SMAD domain
30	d1mjsa_	Alignment	not modelled	9.9	57	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**SMAD domain
31	d3cx5e1	Alignment	not modelled	9.9	33	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
32	d1khua_	Alignment	not modelled	9.7	43	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**SMAD domain
33	c2yvxD_	Alignment	not modelled	9.5	16	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
34	d1g2ha_	Alignment	not modelled	9.4	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
35	c3ik5A_	Alignment	not modelled	9.3	29	**PDB header:**viral protein/signaling protein **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** sivmac239 nef in complex with tcr zeta itam 1 polypeptide (a63-r80)
36	c2e76D_	Alignment	not modelled	9.2	25	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
37	d1fqta_	Alignment	not modelled	9.0	21	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
38	d1nyka_	Alignment	not modelled	9.0	36	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
39	d1ygsa_	Alignment	not modelled	8.9	38	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**SMAD domain
40	c2krhA_	Alignment	not modelled	8.9	27	**PDB header:**actin-binding protein **Chain:** A: **PDB Molecule:**actin-binding rho-activating protein; **PDBTitle:** structure of the c-terminal actin binding domain of abra
41	d1k1xa2	Alignment	not modelled	8.7	36	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**4-alpha-glucanotransferase, C-terminal domain
42	d1vm9a_	Alignment	not modelled	8.6	21	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
43	c3dinF_	Alignment	not modelled	8.4	15	**PDB header:**membrane protein, protein transport **Chain:** F: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
44	d1l0nk_	Alignment	not modelled	8.4	15	**Fold:**Single transmembrane helix **Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
45	c2i7fB_	Alignment	not modelled	8.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin component of dioxygenase; **PDBTitle:** sphingomonas yanoikuyae b1 ferredoxin
46	c2l7kA_	Alignment	not modelled	7.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cd1104.2 from clostridium difficile,2 northeast structural genomics consortium target cfr130
47	d1rfsa_	Alignment	not modelled	7.8	15	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
48	c1khxA_	Alignment	not modelled	7.8	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**smad2; **PDBTitle:** crystal structure of a phosphorylated smad2
49	d1khxa_	Alignment	not modelled	7.8	50	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**SMAD domain
50	c2de7E_	Alignment	not modelled	7.5	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ferredoxin component of carbazole; **PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
51	d1nvpd1	Alignment	not modelled	7.5	11	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
52	c3ljkA_	Alignment	not modelled	7.4	44	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** glucose-6-phosphate isomerase from francisella tularensis.
53	c2qpzA_	Alignment	not modelled	7.4	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase system ferredoxin **PDBTitle:** naphthalene 1,2-dioxygenase rieske ferredoxin
54	d1nh2d1	Alignment	not modelled	7.4	11	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
55	d2jo6a1	Alignment	not modelled	7.3	7	**Fold:**ISP domain **Superfamily:**ISP domain

						Family: NirD-like
56	c2jopA_	Alignment	not modelled	7.2	40	**PDB header:**immune system **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd5; **PDBTitle:** solution structure of the n-terminal extracellular domain2 of the lymphocyte receptor cd5 (cd5 domain 1)
57	d1vi7a2	Alignment	not modelled	7.2	18	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**YigZ C-terminal domain-like
58	d2raqa1	Alignment	not modelled	7.1	28	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
59	c2lafA_	Alignment	not modelled	7.1	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lipoprotein 34; **PDBTitle:** nmr solution structure of the n-terminal domain of the e. coli2 lipoprotein bamc
60	c1qdnA_	Alignment	not modelled	7.1	13	**PDB header:**fusion protein **Chain:** A: **PDB Molecule:**protein (n-ethylmaleimide sensitive fusion **PDBTitle:** amino terminal domain of the n-ethylmaleimide sensitive2 fusion protein (nsf)
61	d3bpda1	Alignment	not modelled	7.0	28	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
62	d2de6a1	Alignment	not modelled	6.9	36	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
63	c3cvfA_	Alignment	not modelled	6.9	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**homer protein homolog 3; **PDBTitle:** crystal structure of the carboxy terminus of homer3
64	c2vjjA_	Alignment	not modelled	6.9	43	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**tailspike protein; **PDBTitle:** tailspike protein of e.coli bacteriophage hk620 in complex2 with hexasaccharide
65	c3fmtF_	Alignment	not modelled	6.9	19	**PDB header:**replication inhibitor/dna **Chain:** F: **PDB Molecule:**protein seqa; **PDBTitle:** crystal structure of seqa bound to dna
66	c2x3dC_	Alignment	not modelled	6.8	22	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**sso6206; **PDBTitle:** crystal structure of sso6206 from sulfolobus solfataricus p2
67	c3d89A_	Alignment	not modelled	6.7	14	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rieske domain-containing protein; **PDBTitle:** crystal structure of a soluble rieske ferredoxin from mus musculus
68	c1nvpD_	Alignment	not modelled	6.6	11	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia gamma chain; **PDBTitle:** human tfiia/tbp/dna complex
69	d1xgsa1	Alignment	not modelled	6.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Methionine aminopeptidase, insert domain
70	c3j01A_	Alignment	not modelled	6.3	12	**PDB header:**ribosome/ribosomal protein **Chain:** A: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** structure of the ribosome-secye complex in the membrane environment
71	d2nsfa2	Alignment	not modelled	6.3	57	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Micothiol-dependent maleylpyruvate isomerase C-terminal domain-like
72	c2l2oA_	Alignment	not modelled	6.3	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**upf0727 protein c6orf115; **PDBTitle:** solution structure of human hspc280 protein
73	c3nuhB_	Alignment	not modelled	6.2	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
74	d3c0da1	Alignment	not modelled	6.1	7	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
75	c2eqfA_	Alignment	not modelled	6.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 3; **PDBTitle:** solution structure of the 7th a20-type zinc finger domain2 from human tumor necrosis factor, alpha-induced protein3
76	c1nh2D_	Alignment	not modelled	6.0	11	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia small chain; **PDBTitle:** crystal structure of a yeast tfiia/tbp/dna complex
77	d2z15a1	Alignment	not modelled	5.9	33	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
78	d2e74d1	Alignment	not modelled	5.9	23	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
79	d2bmoa1	Alignment	not modelled	5.9	33	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
80	c3chxG_	Alignment	not modelled	5.8	20	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**pmoc; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
81	d1z01a1	Alignment	not modelled	5.8	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain

82	c2kc7A_	Alignment	not modelled	5.8	21	**PDB header:** structural genomics, unknown function **Chain:** A: **PDB Molecule:** bfr218_protein; **PDBTitle:** solution nmr structure of bacteroides fragilis protein2 bf1650. northeast structural genomics consortium target3 bfr218
83	c1yewC_	Alignment	not modelled	5.7	17	**PDB header:** oxidoreductase, membrane protein **Chain:** C: **PDB Molecule:** particulate methane monooxygenase subunit c2; **PDBTitle:** crystal structure of particulate methane monooxygenase
84	d1qk7a_	Alignment	not modelled	5.7	44	**Fold:** Knottins (small inhibitors, toxins, lectins) **Superfamily:** omega toxin-like **Family:** Spider toxins
85	d1g8kb_	Alignment	not modelled	5.5	14	**Fold:** ISP domain **Superfamily:** ISP domain **Family:** Rieske iron-sulfur protein (ISP)
86	d1wgla_	Alignment	not modelled	5.5	14	**Fold:** RuvA C-terminal domain-like **Superfamily:** UBA-like **Family:** CUE domain
87	d1j97a_	Alignment	not modelled	5.4	19	**Fold:** HAD-like **Superfamily:** HAD-like **Family:** Phosphoserine phosphatase
88	d2b1xa1	Alignment	not modelled	5.4	25	**Fold:** ISP domain **Superfamily:** ISP domain **Family:** Ring hydroxylating alpha subunit ISP domain
89	d3e9va1	Alignment	not modelled	5.4	33	**Fold:** BTG domain-like **Superfamily:** BTG domain-like **Family:** BTG domain-like
90	c2w7zB_	Alignment	not modelled	5.4	39	**PDB header:** inhibitor **Chain:** B: **PDB Molecule:** pentapeptide repeat family protein; **PDBTitle:** structure of the pentapeptide repeat protein efsqnr, a dna2 gyrase inhibitor. free amines modified by cyclic3 pentylation with glutaraldehyde.
91	c3bu8B_	Alignment	not modelled	5.3	8	**PDB header:** dna binding protein **Chain:** B: **PDB Molecule:** telomeric repeat-binding factor 2; **PDBTitle:** crystal structure of trf2 trfh domain and tin2 peptide2 complex
92	d1j2ga2	Alignment	not modelled	5.2	44	**Fold:** T-fold **Superfamily:** Tetrahydrobiopterin biosynthesis enzymes-like **Family:** Urate oxidase (uricase)
93	c2x7aB_	Alignment	not modelled	5.2	16	**PDB header:** immune system **Chain:** B: **PDB Molecule:** bone marrow stromal antigen 2; **PDBTitle:** structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
94	d1q90c_	Alignment	not modelled	5.2	15	**Fold:** ISP domain **Superfamily:** ISP domain **Family:** Rieske iron-sulfur protein (ISP)
95	d2yzca2	Alignment	not modelled	5.1	44	**Fold:** T-fold **Superfamily:** Tetrahydrobiopterin biosynthesis enzymes-like **Family:** Urate oxidase (uricase)
96	d1mb6a_	Alignment	not modelled	5.1	43	**Fold:** Knottins (small inhibitors, toxins, lectins) **Superfamily:** omega toxin-like **Family:** Spider toxins
97	c2avpA_	Alignment	not modelled	5.0	4	**PDB header:** de novo protein **Chain:** A: **PDB Molecule:** synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix
98	c2k4fA_	Alignment	not modelled	5.0	25	**PDB header:** immune system, signaling protein **Chain:** A: **PDB Molecule:** t-cell surface glycoprotein cd3 epsilon chain; **PDBTitle:** mouse cd3epsilon cytoplasmic tail
99	d1a7ge_	Alignment	not modelled	5.0	21	**Fold:** Ferredoxin-like **Superfamily:** Viral DNA-binding domain **Family:** Viral DNA-binding domain