Phyre^2

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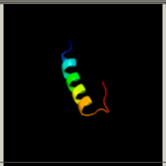
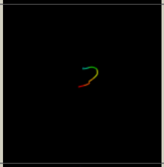
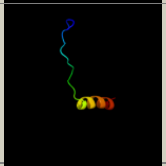
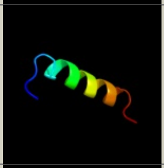
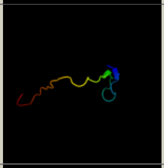
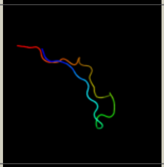
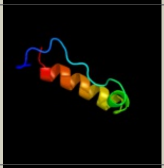
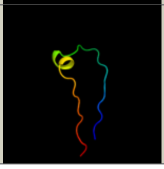
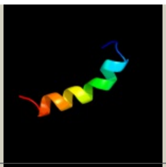
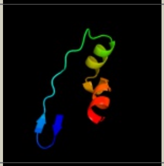
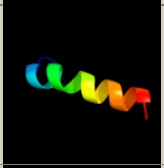
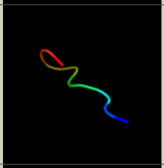
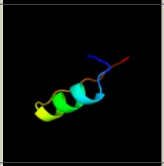
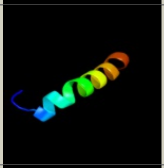
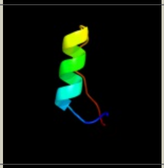
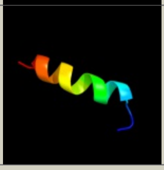
Description	P15069
Date	Thu Jan 5 11:34:32 GMT 2012
Unique Job ID	f64c5a298b28782e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1z6na1	Alignment		41.0	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
2	c3pwxB_	Alignment		36.0	11	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**putative flagellar hook-associated protein; **PDBTitle:** structure of putative flagellar hook-associated protein from vibrio2 parahaemolyticus
3	c2kujA_	Alignment		32.3	75	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**acanthaporin; **PDBTitle:** the solution structure of the dimeric acanthaporin
4	d2f8aa1	Alignment		28.7	0	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
5	d1mqsa_	Alignment		25.9	6	**Fold:**Sec1/munc18-like (SM) proteins **Superfamily:**Sec1/munc18-like (SM) proteins **Family:**Sec1/munc18-like (SM) proteins
6	c2he3A_	Alignment		21.4	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 2; **PDBTitle:** crystal structure of the selenocysteine to cysteine mutant of human2 glutathionine peroxidase 2 (gpx2)
7	d1fuia1	Alignment		21.3	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**FucI/AraA C-terminal domain-like **Family:**L-fucose isomerase, C-terminal domain
8	d1v9wa_	Alignment		19.7	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
9	d1udxa1	Alignment		19.7	28	**Fold:**Obg-fold **Superfamily:**Obg GTP-binding protein N-terminal domain **Family:**Obg GTP-binding protein N-terminal domain
10	c2ehhE_	Alignment		18.8	19	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
11	d1lnza1	Alignment		18.7	17	**Fold:**Obg-fold **Superfamily:**Obg GTP-binding protein N-terminal domain **Family:**Obg GTP-binding protein N-terminal domain

12	c3emxB_	Alignment		18.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
13	c2c49A_	Alignment		17.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sugar kinase mj0406; **PDBTitle:** crystal structure of methanocaldococcus jannaschii2 nucleoside kinase - an archaeal member of the ribokinase3 family
14	c2hyxA_	Alignment		17.7	5	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
15	d1m3va1	Alignment		17.5	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
16	d2j9ga2	Alignment		17.0	25	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
17	d2b5ea1	Alignment		16.0	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
18	d1ulza2	Alignment		15.8	21	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
19	d1w96a2	Alignment		15.7	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
20	d1woua_	Alignment		15.2	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
21	c3qdnA_	Alignment	not modelled	14.8	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
22	c3bf5A_	Alignment	not modelled	14.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribokinase related protein; **PDBTitle:** crystal structure of putative ribokinase (10640157) from thermoplasma2 acidophilum at 1.91 a resolution
23	c3b1qD_	Alignment	not modelled	14.1	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribokinase, putative; **PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
24	d1epua_	Alignment	not modelled	13.8	26	**Fold:**Sec1/munc18-like (SM) proteins **Superfamily:**Sec1/munc18-like (SM) proteins **Family:**Sec1/munc18-like (SM) proteins
25	d1o73a_	Alignment	not modelled	13.7	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
26	d1nhoa_	Alignment	not modelled	12.6	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
27	c3cynC_	Alignment	not modelled	12.5	5	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**probable glutathione peroxidase 8; **PDBTitle:** the structure of human gpx8
28	c3me5A_	Alignment	not modelled	12.4	63	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytosine-specific methyltransferase; **PDBTitle:** crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 301
						Fold: Four-helical up-and-down bundle

29	d1st6a4	Alignment	not modelled	12.1	12	**Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
30	d2gs4a1	Alignment	not modelled	11.5	14	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**YciF-like
31	c2l5lA_	Alignment	not modelled	11.2	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides vulgatus
32	c3ia1A_	Alignment	not modelled	10.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thio-disulfide isomerase/thioredoxin; **PDBTitle:** crystal structure of thio-disulfide isomerase from thermus2 thermophilus
33	d1vl6a2	Alignment	not modelled	10.7	26	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
34	d1j08a2	Alignment	not modelled	10.5	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
35	d2fy6a1	Alignment	not modelled	10.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
36	c3fkfC_	Alignment	not modelled	10.2	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
37	c2l57A_	Alignment	not modelled	10.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
38	c3fvwA_	Alignment	not modelled	10.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad(p)h-dependent fmn reductase; **PDBTitle:** crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
39	c2vimA_	Alignment	not modelled	10.1	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
40	c1ylaB_	Alignment	not modelled	10.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ubiquitin-conjugating enzyme e2-25 kda; **PDBTitle:** ubiquitin-conjugating enzyme e2-25 kda (huntington interacting protein2 2)
41	c3go6B_	Alignment	not modelled	10.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribokinase rbsk; **PDBTitle:** crystal structure of m. tuberculosis ribokinase (rv2436) in2 complex with ribose and amp-pnp
42	d2dcna1	Alignment	not modelled	9.9	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
43	c3dwvB_	Alignment	not modelled	9.9	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase-like protein; **PDBTitle:** glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
44	d1xwaa_	Alignment	not modelled	9.8	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
45	c2h2yA_	Alignment	not modelled	9.7	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquitin-conjugating enzyme; **PDBTitle:** crystal structure of ubiquitin conjugating enzyme e2 from2 plasmodium falciparum
46	c3lhxA_	Alignment	not modelled	9.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ketodeoxygluconokinase; **PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri
47	c3kp8A_	Alignment	not modelled	9.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
48	d1dn1a_	Alignment	not modelled	9.5	17	**Fold:**Sec1/munc18-like (SM) proteins **Superfamily:**Sec1/munc18-like (SM) proteins **Family:**Sec1/munc18-like (SM) proteins
49	c3lwaA_	Alignment	not modelled	9.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**secreted thiol-disulfide isomerase; **PDBTitle:** the crystal structure of a secreted thiol-disulfide2 isomerase from corynebacterium glutamicum to 1.75a
50	c2dmlA_	Alignment	not modelled	9.3	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a6; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a6
51	d2djja1	Alignment	not modelled	9.1	5	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
52	c2p31B_	Alignment	not modelled	9.1	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase 7; **PDBTitle:** crystal structure of human glutathione peroxidase 7
53	c2ywiA_	Alignment	not modelled	9.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
54	c2e0qA_	Alignment	not modelled	8.9	8	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
						Fold: Thioredoxin fold

55	d1i5ga_	Alignment	not modelled	8.8	9	**Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
56	d1t6ex_	Alignment	not modelled	8.8	19	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
57	d1y76a1	Alignment	not modelled	8.8	22	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
58	d2akja4	Alignment	not modelled	8.7	24	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
59	c3ha9A_	Alignment	not modelled	8.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized thioredoxin-like protein; **PDBTitle:** the 1.7a crystal structure of a thioredoxin-like protein from2 aeropyrum pernix
60	c1s6xA_	Alignment	not modelled	8.5	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**kvap channel; **PDBTitle:** solution structure of vstx
61	c2wx4C_	Alignment	not modelled	8.4	17	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**decapping protein 1; **PDBTitle:** asymmetric trimer of the drosophila melanogaster dcp1 c-2 terminal domain
62	d1beta_	Alignment	not modelled	8.2	38	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Neurotrophin
63	c3hypB_	Alignment	not modelled	8.2	9	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
64	c3h8qB_	Alignment	not modelled	8.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 3; **PDBTitle:** crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
65	d1jb0j_	Alignment	not modelled	8.0	19	**Fold:**Single transmembrane helix **Superfamily:**Subunit IX of photosystem I reaction centre, PsaJ **Family:**Subunit IX of photosystem I reaction centre, PsaJ
66	c3fxaA_	Alignment	not modelled	8.0	23	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
67	c3pp5A_	Alignment	not modelled	8.0	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**brk1; **PDBTitle:** high-resolution structure of the trimeric scar/wave complex precursor2 brk1
68	d1uj4a1	Alignment	not modelled	7.9	24	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
69	d1qgva_	Alignment	not modelled	7.9	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**spliceosomal protein U5-15Kd
70	c3s5oA_	Alignment	not modelled	7.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial; **PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
71	c3r74B_	Alignment	not modelled	7.8	18	**PDB header:**lyase, biosynthetic protein **Chain:** B: **PDB Molecule:**anthranilate/para-aminobenzoate synthases component i; **PDBTitle:** crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
72	d1lk5a1	Alignment	not modelled	7.8	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
73	c2dj0A_	Alignment	not modelled	7.8	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thioredoxin-related transmembrane protein 2; **PDBTitle:** the solution structure of the thioredoxin domain of human2 thioredoxin-related transmembrane protein 2
74	c3hz4A_	Alignment	not modelled	7.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
75	c3ij2B_	Alignment	not modelled	7.6	38	**PDB header:**hormone/protein binding **Chain:** B: **PDB Molecule:**beta-nerve growth factor; **PDBTitle:** ligand-receptor structure
76	d1m0sa1	Alignment	not modelled	7.5	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
77	d1rpua_	Alignment	not modelled	7.5	44	**Fold:**Tombusvirus P19 core protein, VP19 **Superfamily:**Tombusvirus P19 core protein, VP19 **Family:**Tombusvirus P19 core protein, VP19
78	c1rpuA_	Alignment	not modelled	7.5	44	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**19 kda protein; **PDBTitle:** crystal structure of cirv p19 bound to sirna
79	d1o8xa_	Alignment	not modelled	7.5	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
80	d1fp1d1	Alignment	not modelled	7.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Plant O-methyltransferase, N-terminal domain
						PDB header:transcription, cell cycle

81	c1xbsA_	Alignment	not modelled	7.4	27	**Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
82	c2nwhA_	Alignment	not modelled	7.4	21	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens
83	c1v98A_	Alignment	not modelled	7.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
84	c2vc6A_	Alignment	not modelled	7.3	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
85	c2diyA_	Alignment	not modelled	7.2	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**thioredoxin-like protein 2; **PDBTitle:** the solution structure of the thioredoxin domain of human2 thioredoxin-like protein 2
86	d2elba1	Alignment	not modelled	7.2	11	**Fold:**BAR/IMD domain-like **Superfamily:**BAR/IMD domain-like **Family:**BAR domain
87	c1lnzA_	Alignment	not modelled	7.0	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**spo0b-associated gtp-binding protein; **PDBTitle:** structure of the obg gtp-binding protein
88	c2vocA_	Alignment	not modelled	7.0	9	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** thioredoxin a active site mutants form mixed disulfide2 dimers that resemble enzyme-substrate reaction3 intermediate
89	d2gyqa1	Alignment	not modelled	7.0	15	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**YciF-like
90	c3etnD_	Alignment	not modelled	6.8	4	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative phosphosugar isomerase involved in capsule **PDBTitle:** crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
91	c3dxbE_	Alignment	not modelled	6.8	14	**PDB header:**splicing, transcription **Chain:** E: **PDB Molecule:**thioredoxin n-terminally fused to puf60(uhm); **PDBTitle:** structure of the uhm domain of puf60 fused to thioredoxin
92	d1bndb_	Alignment	not modelled	6.7	38	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Neurotrophin
93	d2ucza_	Alignment	not modelled	6.7	19	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
94	d2b5xa1	Alignment	not modelled	6.6	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
95	c2e7pC_	Alignment	not modelled	6.5	19	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
96	c2j6pF_	Alignment	not modelled	6.5	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**sb(v)-as(v) reductase; **PDBTitle:** structure of as-sb reductase from leishmania major
97	d1zmaa1	Alignment	not modelled	6.5	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
98	c1t00A_	Alignment	not modelled	6.5	9	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor
99	d2ifqa1	Alignment	not modelled	6.4	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase