Phyre2

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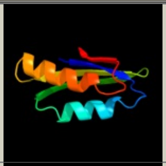
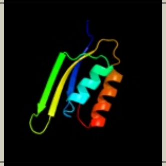
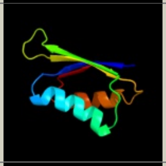
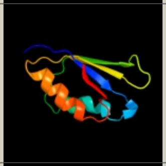
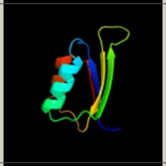
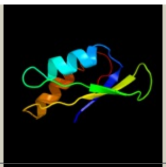
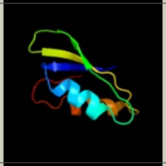
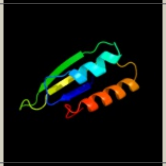
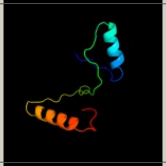
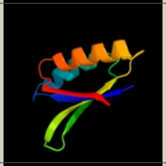
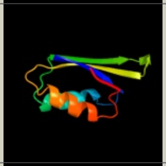
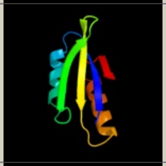
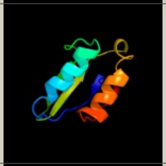
Description	P0AFV2
Date	Thu Jan 5 11:27:21 GMT 2012
Unique Job ID	12c51dc0d34b406d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ibwA_	Alignment		97.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
2	d1sc6a3	Alignment		95.6	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
3	d1u8sa2	Alignment		95.5	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
4	d1ygya3	Alignment		94.3	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
5	d2f1fa1	Alignment		94.0	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
6	d2fgca2	Alignment		93.3	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
7	d2pc6a2	Alignment		92.5	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
8	c2f1fA_	Alignment		92.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
9	c2fgcA_	Alignment		91.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
10	c1ygyA_	Alignment		90.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
11	c2pc6C_	Alignment		89.6	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea

12	c1rwuA_	Alignment		88.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed; **PDBTitle:** solution structure of conserved protein ybed from e. coli
13	d1rwua_	Alignment		88.5	16	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
14	d2joqa1	Alignment		80.6	12	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**HP0495-like
15	d1kona_	Alignment		74.9	13	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
16	c2e1cA_	Alignment		74.3	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
17	c1y7pB_	Alignment		73.7	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein af1403; **PDBTitle:** 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
18	d2cyya2	Alignment		68.6	12	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
19	c2phmA_	Alignment		65.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (phenylalanine-4-hydroxylase); **PDBTitle:** structure of phenylalanine hydroxylase dephosphorylated
20	c2jsxA_	Alignment		63.5	9	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein napd; **PDBTitle:** solution structure of the e. coli tat proofreading2 chaperone protein napd
21	d1lfpa_	Alignment	not modelled	62.1	13	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
22	c2ew9A_	Alignment	not modelled	56.3	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of apowln5-6
23	d1zpva1	Alignment	not modelled	55.9	5	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
24	d1mw7a_	Alignment	not modelled	55.7	16	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
25	c3k5pA_	Alignment	not modelled	54.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
26	c2djwF_	Alignment	not modelled	54.1	9	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
27	c2e1aD_	Alignment	not modelled	52.1	6	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
28	d1qupa2	Alignment	not modelled	52.0	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain

29	d1lk5a2	Alignment	not modelled	50.5	14	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
30	d1i1ga2	Alignment	not modelled	49.9	9	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
31	c1u8sB_	Alignment	not modelled	49.7	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
32	c2zbcH_	Alignment	not modelled	47.6	9	**PDB header:**transcription **Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc; **PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
33	d1u8sa1	Alignment	not modelled	46.6	5	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
34	c1i1gA_	Alignment	not modelled	40.7	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
35	c2qmxB_	Alignment	not modelled	39.2	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum tls
36	d3bpda1	Alignment	not modelled	38.8	16	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
37	d2f06a2	Alignment	not modelled	38.5	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
38	c1ybaC_	Alignment	not modelled	38.2	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
39	d1tdja2	Alignment	not modelled	36.5	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Allosteric threonine deaminase C-terminal domain
40	c2x3dC_	Alignment	not modelled	36.3	35	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**sso6206; **PDBTitle:** crystal structure of sso6206 from sulfolobus solfataricus p2
41	d1phza1	Alignment	not modelled	34.9	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
42	d2raqa1	Alignment	not modelled	34.0	24	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
43	c2crlA_	Alignment	not modelled	33.2	18	**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
44	c3mtjA_	Alignment	not modelled	32.0	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
45	c3mwbA_	Alignment	not modelled	31.5	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
46	d1m0sa2	Alignment	not modelled	30.5	13	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
47	d1o8ba2	Alignment	not modelled	28.1	10	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
48	d2cg4a2	Alignment	not modelled	27.8	21	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
49	d1p6ta1	Alignment	not modelled	26.3	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
50	c2e7xA_	Alignment	not modelled	26.3	7	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
51	c3hyjD_	Alignment	not modelled	26.1	12	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**protein duf199/whia; **PDBTitle:** crystal structure of the n-terminal laglidadg domain of duf199/whia
52	c2gqqB_	Alignment	not modelled	26.1	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**leucine-responsive regulatory protein; **PDBTitle:** crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
53	c3n0vD_	Alignment	not modelled	25.4	5	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
54	c3dxsX_	Alignment	not modelled	25.2	12	**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
55	d2nzca1	Alignment	not modelled	25.2	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**TM1266-like
56	c2l3mA_	Alignment	not modelled	25.0	14	**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
57	d2qmwa2	Alignment	not modelled	24.8	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
58	c2aj1A_	Alignment	not modelled	24.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
59	c3luyA_	Alignment	not modelled	24.3	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
60	c2ldiA_	Alignment	not modelled	24.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
61	d2qifa1	Alignment	not modelled	23.8	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
62	d1s6ua_	Alignment	not modelled	23.5	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
63	c2p6tH_	Alignment	not modelled	23.3	8	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
64	c2bj3D_	Alignment	not modelled	22.5	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
65	c2yy3B_	Alignment	not modelled	22.1	10	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 1-beta; **PDBTitle:** crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii
66	d1q8la_	Alignment	not modelled	21.4	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
67	d1uj4a2	Alignment	not modelled	21.2	15	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
68	d1cc8a_	Alignment	not modelled	20.9	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
69	d1p6ta2	Alignment	not modelled	20.5	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
70	c2cg4B_	Alignment	not modelled	18.8	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
71	c2ia0A_	Alignment	not modelled	17.3	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator pf0864; **PDBTitle:** transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
72	c2rogA_	Alignment	not modelled	17.0	19	**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
73	d1sb6a_	Alignment	not modelled	16.8	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
74	c1yjrA_	Alignment	not modelled	16.5	11	**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
75	d1osda_	Alignment	not modelled	16.1	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
76	c3i4pA_	Alignment	not modelled	16.0	4	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
77	c2gcfA_	Alignment	not modelled	15.8	9	**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
78	d1u0sa_	Alignment	not modelled	15.7	16	**Fold:**Ferredoxin-like **Superfamily:**CheY-binding domain of CheA **Family:**CheY-binding domain of CheA
79	c2vbzA_	Alignment	not modelled	15.3	15	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
80	d1afia_	Alignment	not modelled	14.2	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
						PDB header:isomerase

81	c1lk5C_	Alignment	not modelled	14.0	13	**Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
82	d2ggpb1	Alignment	not modelled	13.6	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
83	c1vi7A_	Alignment	not modelled	13.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yigz; **PDBTitle:** crystal structure of an hypothetical protein
84	d2f1fa2	Alignment	not modelled	13.1	6	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
85	c2ca9B_	Alignment	not modelled	12.9	16	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
86	d2i5nl1	Alignment	not modelled	12.7	21	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
87	c2ofhX_	Alignment	not modelled	12.5	15	**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
88	d2fmra_	Alignment	not modelled	12.4	13	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
89	c2k2pA_	Alignment	not modelled	12.0	5	**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
90	c2kt2A_	Alignment	not modelled	11.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
91	c2y3yC_	Alignment	not modelled	11.2	16	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** holo-ni(ii) hpnikr is a symmetric tetramer containing four2 canonic square-planar ni(ii) ions at physiological ph
92	c1yg0A_	Alignment	not modelled	11.2	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
93	d1q5ya_	Alignment	not modelled	11.1	6	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Nickel responsive regulator NikR, C-terminal domain
94	d2pc6a1	Alignment	not modelled	11.0	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
95	c2cveA_	Alignment	not modelled	10.9	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
96	c2w2mP_	Alignment	not modelled	10.6	29	**PDB header:**hydrolase/receptor **Chain:** P: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** wt pcsk9-deltac bound to wt egf-a of ldlr
97	c2pmwA_	Alignment	not modelled	10.6	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** the crystal structure of proprotein convertase subtilisin2 kexin type 9 (pcsk9)
98	c2p4eP_	Alignment	not modelled	10.6	29	**PDB header:**hydrolase **Chain:** P: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** crystal structure of pcsk9
99	d2cu6a1	Alignment	not modelled	10.3	13	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like