Phyre2

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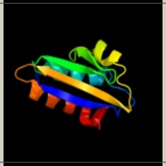
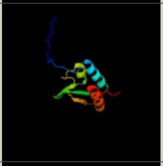
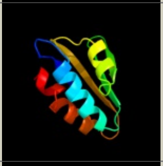
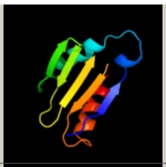
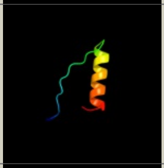
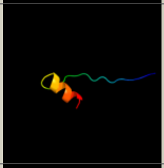
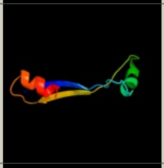
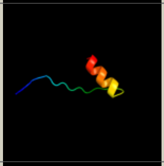
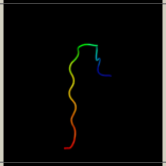
Description	P0A9N0
Date	Thu Jan 5 11:10:46 GMT 2012
Unique Job ID	6ff4da9c94952ee2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qr5a_	Alignment		100.0	28	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
2	d2hpra_	Alignment		100.0	33	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
3	d1ka5a_	Alignment		100.0	25	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
4	d1mo1a_	Alignment		100.0	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
5	c3le1B_	Alignment		100.0	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, hpr-related proteins; **PDBTitle:** crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis
6	d1pcha_	Alignment		100.0	24	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
7	c3ihsB_	Alignment		100.0	29	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphocarrier protein hpr; **PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
8	d1cm3a_	Alignment		99.9	27	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
9	d1ptfa_	Alignment		99.9	24	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
10	d2nzul1	Alignment		99.9	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
11	d1zvvj1	Alignment		99.9	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like

12	c2jpiA_	Alignment		67.9	13	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
13	d1vq3a_	Alignment		42.5	19	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
14	d1gtda_	Alignment		40.7	15	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
15	c2dgbA_	Alignment		37.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein purs; **PDBTitle:** structure of thermus thermophilus purs in the p21 form
16	c2zw2B_	Alignment		35.4	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
17	c3goeA_	Alignment		20.3	15	**PDB header:**recombination, replication **Chain:** A: **PDB Molecule:**dna repair protein rad60; **PDBTitle:** molecular mimicry of sumo promotes dna repair
18	c1ibaA_	Alignment		18.7	6	**PDB header:**phoshphotransferase **Chain:** A: **PDB Molecule:**glucose permease; **PDBTitle:** glucose permease (domain iib), nmr, 11 structures
19	d2vbua1	Alignment		16.7	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
20	d1r11a3	Alignment		16.1	14	**Fold:**MutS N-terminal domain-like **Superfamily:**tRNA-intron endonuclease N-terminal domain-like **Family:**tRNA-intron endonuclease N-terminal domain-like
21	d2cdqa3	Alignment	not modelled	15.8	24	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
22	c2yuiA_	Alignment	not modelled	12.6	13	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**anamorsin; **PDBTitle:** solution structure of the n-terminal domain in human2 cytokine-induced apoptosis inhibitor anamorsin
23	d1umdb2	Alignment	not modelled	12.0	22	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
24	c2etnA_	Alignment	not modelled	11.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
25	d1gtma1	Alignment	not modelled	11.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
26	d1aopa2	Alignment	not modelled	11.1	15	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
27	d1oqya2	Alignment	not modelled	10.8	56	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
28	d2etna2	Alignment	not modelled	10.1	12	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
29	c2l66B_	Alignment	not modelled	9.8	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family;

		Alignment				**PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
30	c3k6qB_	Alignment	not modelled	9.3	14	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein; **PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
31	d1hmja_	Alignment	not modelled	9.2	19	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
32	d1srva_	Alignment	not modelled	9.0	12	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
33	d1eika_	Alignment	not modelled	9.0	13	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
34	d2ayia1	Alignment	not modelled	9.0	15	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
35	d1t4aa_	Alignment	not modelled	8.8	15	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
36	d1zjca1	Alignment	not modelled	8.7	9	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
37	d1m2ka_	Alignment	not modelled	8.3	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
38	c2pmzV_	Alignment	not modelled	8.2	13	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
39	d1kr4a_	Alignment	not modelled	8.1	33	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
40	d2f23a2	Alignment	not modelled	7.9	12	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
41	d1we3a2	Alignment	not modelled	7.8	12	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
42	c2p73A_	Alignment	not modelled	7.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase (mannosyltransferase) involved **PDBTitle:** crystal structure of a glycosyltransferase involved in the2 glycosylation of the major capsid of pbcv-1
43	c1ztgD_	Alignment	not modelled	7.7	10	**PDB header:**dna, rna binding protein/dna **Chain:** D: **PDB Molecule:**poly(rc)-binding protein 1; **PDBTitle:** human alpha polyc binding protein kh1
44	d1o8bb1	Alignment	not modelled	7.6	9	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
45	d1sjpa2	Alignment	not modelled	7.5	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
46	d1dzfa2	Alignment	not modelled	7.5	13	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
47	d1udxa3	Alignment	not modelled	7.2	20	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
48	d1dk7a_	Alignment	not modelled	7.2	11	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
49	c2p4vA_	Alignment	not modelled	7.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
50	d1w85b2	Alignment	not modelled	6.9	28	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
51	c2pn0D_	Alignment	not modelled	6.6	23	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
52	c3bmbB_	Alignment	not modelled	6.6	20	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
53	c2k4yA_	Alignment	not modelled	6.4	21	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**feoa-like protein; **PDBTitle:** nmr structure of feoa-like protein from clostridium2 acetobutylicum: northeast structural genomics consortium3 target car178
54	d1grja2	Alignment	not modelled	6.4	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
						PDB header:ligase/protein binding

55	c2ekeC_	Alignment	not modelled	6.4	13	**Chain:** C: **PDB Molecule:**ubiquitin-like protein smt3; **PDBTitle:** structure of a sumo-binding-motif mimic bound to smt3p-2 ubc9p: conservation of a noncovalent ubiquitin-like3 protein-e2 complex as a platform for selective4 interactions within a sumo pathway
56	d1p88a_	Alignment	not modelled	6.4	17	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
57	d1xi3a_	Alignment	not modelled	6.3	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
58	c3e19D_	Alignment	not modelled	6.2	26	**PDB header:**transcription regulator, metal binding p **Chain:** D: **PDB Molecule:**feoa; **PDBTitle:** crystal structure of iron uptake regulatory protein (feoa) solved by2 sulfur sad in a monoclinic space group
59	d2fy9a1	Alignment	not modelled	6.2	35	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
60	d2bfdb2	Alignment	not modelled	6.2	16	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
61	d2j0wa3	Alignment	not modelled	6.1	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
62	c2ro5B_	Alignment	not modelled	6.1	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** rdc-refined solution structure of the n-terminal dna2 recognition domain of the bacillus subtilis transition-3 state regulator spovt
63	d1bgva1	Alignment	not modelled	6.0	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
64	d2gcxa1	Alignment	not modelled	5.9	32	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
65	d1o8ba1	Alignment	not modelled	5.9	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
66	d1yfba1	Alignment	not modelled	5.8	18	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
67	d1b26a1	Alignment	not modelled	5.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
68	c2k5fA_	Alignment	not modelled	5.6	26	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferrous iron transport protein a; **PDBTitle:** solution nmr structure of feoa protein from chlorobium2 tepidum. northeast structural genomics consortium target3 ctr121
69	c2w1tB_	Alignment	not modelled	5.5	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
70	d2hmfa2	Alignment	not modelled	5.5	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
71	d1v77a_	Alignment	not modelled	5.4	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**RNase P subunit p30
72	d1kida_	Alignment	not modelled	5.2	11	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
73	d1efpa1	Alignment	not modelled	5.2	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
74	c3lzkC_	Alignment	not modelled	5.2	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
75	c3u7jA_	Alignment	not modelled	5.1	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
76	d1yema_	Alignment	not modelled	5.1	19	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain