Phyre2

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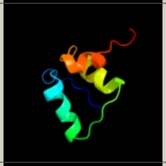
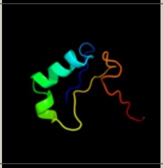
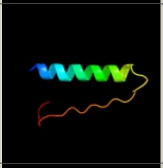
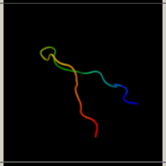
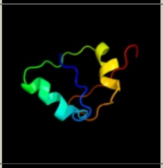
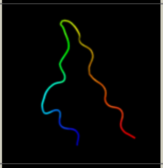
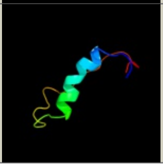
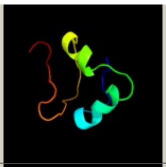
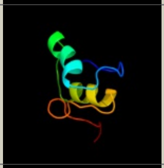
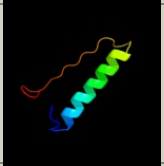
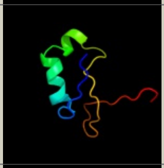
Description	P77433
Date	Thu Jan 5 12:29:16 GMT 2012
Unique Job ID	39c2cfbb9ccbcede

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2g40a1	Alignment		100.0	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**YkgG-like
2	c2g40A_	Alignment		100.0	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a duf162 family protein (dr_1909) from2 deinococcus radiodurans at 1.70 a resolution
3	d2g82a1	Alignment		37.6	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
4	d1a5ta2	Alignment		37.5	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
5	d2pkqo1	Alignment		33.9	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
6	d1d2na_	Alignment		33.1	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
7	c1a6cA_	Alignment		30.7	26	**PDB header:**virus **Chain:** A: **PDB Molecule:**tobacco ringspot virus capsid protein; **PDBTitle:** structure of tobacco ringspot virus
8	d1i32a1	Alignment		29.4	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
9	d1hdgo1	Alignment		29.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
10	c2y7uM_	Alignment		28.4	17	**PDB header:**virus **Chain:** M: **PDB Molecule:**coat protein; **PDBTitle:** x-ray structure of the grapevine fanleaf virus
11	c2qz4A_	Alignment		27.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp

12	d1vc2a1	Alignment		24.7	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
13	d1obfo1	Alignment		24.1	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
14	d3gpdg1	Alignment		23.6	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
15	d3cmco1	Alignment		21.7	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
16	c1nsfA_	Alignment		20.7	24	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
17	d1u8fo1	Alignment		20.7	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
18	d1gado1	Alignment		20.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
19	d1nbwa3	Alignment		18.2	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
20	c3co5B_	Alignment		17.9	8	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative two-component system transcriptional response **PDBTitle:** crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
21	c2ce7B_	Alignment	not modelled	17.8	22	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
22	d1j0xo1	Alignment	not modelled	17.4	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
23	d1rm4a1	Alignment	not modelled	17.1	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
24	c2z1dA_	Alignment	not modelled	16.5	36	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hypd; **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
25	c1fnnB_	Alignment	not modelled	16.4	14	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
26	d1q5za_	Alignment	not modelled	15.8	27	**Fold:**Invasion protein A (SipA) , C-terminal actin binding domain **Superfamily:**Invasion protein A (SipA) , C-terminal actin binding domain **Family:**Invasion protein A (SipA) , C-terminal actin binding domain
27	c1q5zA_	Alignment	not modelled	15.8	27	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**sipa; **PDBTitle:** crystal structure of the c-terminal actin binding domain of2 salmonella invasion protein a (sipa)
28	d1k3ta1	Alignment	not modelled	15.7	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

29	c3sggA_	Alignment	not modelled	15.1	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical hydrolase; **PDBTitle:** crystal structure of a hypothetical hydrolase (bt_2193) from2 bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution
30	c2dhrC_	Alignment	not modelled	14.4	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
31	c2c9oC_	Alignment	not modelled	13.4	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
32	c3l7oB_	Alignment	not modelled	13.3	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
33	d1in4a2	Alignment	not modelled	12.8	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
34	c3b9pA_	Alignment	not modelled	12.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
35	c3u7jA_	Alignment	not modelled	12.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
36	c1xwiA_	Alignment	not modelled	12.5	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
37	d1sxje2	Alignment	not modelled	12.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
38	d2joya1	Alignment	not modelled	12.2	14	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L14e
39	d1v5wa_	Alignment	not modelled	12.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
40	c3u5cG_	Alignment	not modelled	12.1	22	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**40s ribosomal protein s6-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
41	d2b4ro1	Alignment	not modelled	11.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
42	c1jr3E_	Alignment	not modelled	11.2	29	**PDB header:**transferase **Chain:** E: **PDB Molecule:**dna polymerase iii, delta' subunit; **PDBTitle:** crystal structure of the processivity clamp loader gamma2 complex of e. coli dna polymerase iii
43	d1njfa_	Alignment	not modelled	11.1	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
44	d1ggaa1	Alignment	not modelled	11.1	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	c1w5sB_	Alignment	not modelled	11.0	13	**PDB header:**replication **Chain:** B: **PDB Molecule:**origin recognition complex subunit 2 orc2; **PDBTitle:** structure of the aeropyrum pernix orc2 protein (adp form)
46	d2pl1a1	Alignment	not modelled	10.8	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	c2xznY_	Alignment	not modelled	10.5	17	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rps6e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
48	c1ahuB_	Alignment	not modelled	10.4	15	**PDB header:**flavoenzyme **Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase; **PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
49	c1l6jA_	Alignment	not modelled	10.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
50	c2r65A_	Alignment	not modelled	9.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell division protease ftsh homolog; **PDBTitle:** crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
51	d1t9ka_	Alignment	not modelled	8.9	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
52	c2kyrA_	Alignment	not modelled	8.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
53	d2r48a1	Alignment	not modelled	8.7	8	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
						PDB header:dna binding protein

54	c3cnbC_	Alignment	not modelled	8.7	7	**Chain:** C: **PDB Molecule:**dna-binding response regulator, merr family; **PDBTitle:** crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h
55	d2a9sa1	Alignment	not modelled	8.4	11	**Fold:**Anticodon-binding domain-like **Superfamily:**CinA-like **Family:**CinA-like
56	c2zayA_	Alignment	not modelled	8.3	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
57	d1u0sy_	Alignment	not modelled	8.3	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
58	d1r7ra3	Alignment	not modelled	8.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
59	c3eulB_	Alignment	not modelled	8.1	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**possible nitrate/nitrite response transcriptional **PDBTitle:** structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
60	c3d8bB_	Alignment	not modelled	8.1	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
61	c2j17A_	Alignment	not modelled	7.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase yil113w; **PDBTitle:** ptyr bound form of sdp-1
62	c3q3qA_	Alignment	not modelled	7.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
63	c3s93B_	Alignment	not modelled	7.3	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tudor domain-containing protein 5; **PDBTitle:** crystal structure of conserved motif in tdrd5
64	d1biaa2	Alignment	not modelled	7.3	14	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Biotin repressor (BirA)
65	d1qvra3	Alignment	not modelled	7.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
66	d1izca_	Alignment	not modelled	7.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
67	c1izcA_	Alignment	not modelled	7.1	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
68	d1r6bx3	Alignment	not modelled	7.1	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
69	d1p2fa2	Alignment	not modelled	7.1	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	d1sp8a1	Alignment	not modelled	6.9	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
71	d1lv7a_	Alignment	not modelled	6.9	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
72	c1eakA_	Alignment	not modelled	6.7	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
73	d2ce7a2	Alignment	not modelled	6.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
74	c1nbwA_	Alignment	not modelled	6.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerol dehydratase reactivase alpha subunit; **PDBTitle:** glycerol dehydratase reactivase
75	c3eihB_	Alignment	not modelled	6.5	14	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of s.cerevisiae vps4 in the presence of atpgammas
76	d1fnna2	Alignment	not modelled	6.3	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
77	d1zesa1	Alignment	not modelled	6.2	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
78	d1sqia1	Alignment	not modelled	6.2	10	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
						PDB header:oxidoreductase

79	c3ecjC_	Alignment	not modelled	6.1	38	**Chain:** C: **PDB Molecule:**protein (homoprotocatechuate 2,3-dioxygenase); **PDBTitle:** structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution
80	c3b8iF_	Alignment	not modelled	6.1	21	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
81	c3iuyB_	Alignment	not modelled	6.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase ddx53; **PDBTitle:** crystal structure of ddx53 dead-box domain
82	d1e94e_	Alignment	not modelled	5.9	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
83	d1stza2	Alignment	not modelled	5.7	11	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**HrcA C-terminal domain-like
84	d2d0oa3	Alignment	not modelled	5.6	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
85	c4a1dE_	Alignment	not modelled	5.6	25	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**rpl6; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
86	c3izcG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**60s ribosomal protein rpl6 (l6e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
87	d1s8na_	Alignment	not modelled	5.3	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
88	c2yvkA_	Alignment	not modelled	5.2	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
89	d1g6oa_	Alignment	not modelled	5.2	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
90	c2f6rA_	Alignment	not modelled	5.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional coenzyme a synthase; **PDBTitle:** crystal structure of bifunctional coenzyme a synthase (coa synthase):2 (18044849) from mus musculus at 1.70 a resolution
91	d1sp8a2	Alignment	not modelled	5.1	11	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases