Phyre2

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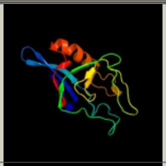
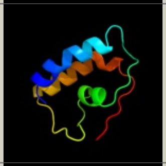
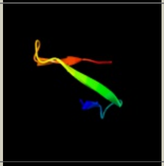
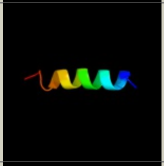
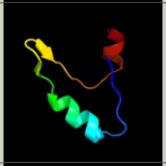
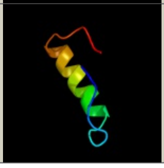
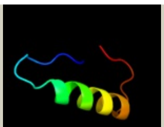
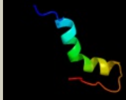
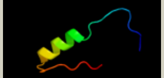
Description	P0AA99
Date	Thu Jan 5 11:12:18 GMT 2012
Unique Job ID	c838387958dd7907

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zata1	Alignment		99.6	19	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
2	d1y7ma1	Alignment		99.5	23	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
3	c1y7mB_	Alignment		99.4	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14040; **PDBTitle:** crystal structure of the b. subtilis ykud protein at 2 a2 resolution
4	c2hklB_	Alignment		99.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l,d-transpeptidase; **PDBTitle:** crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant
5	d2q3la1	Alignment		51.6	15	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Sfri0576-like
6	c2khfA_	Alignment		37.9	42	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plnj; **PDBTitle:** plantaricin j in dpc-micelles
7	c3qi7A_	Alignment		32.1	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
8	d1z8ga2	Alignment		29.7	22	**Fold:**SRCR-like **Superfamily:**SRCR-like **Family:**Hepsin, N-terminal domain
9	c2khgA_	Alignment		29.5	37	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plnj; **PDBTitle:** plantaricin j in tfe
10	c3p3dA_	Alignment		26.7	15	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleoporin 53; **PDBTitle:** crystal structure of the nup53 rrm domain from pichia guilliermondii
11	d1q5ma_	Alignment		22.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)

12	d1j96a_	Alignment		19.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
13	d2ooka1	Alignment		15.4	19	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Sfri0576-like
14	d1s1pa_	Alignment		14.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
15	c3l5aA_	Alignment		13.8	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh/flavin oxidoreductase/nadh oxidase; **PDBTitle:** crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
16	d1vyra_	Alignment		13.7	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
17	c2l4dA_	Alignment		13.6	10	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**sco1/senc family protein/cytochrome c; **PDBTitle:** cytochrome c domain of pp3183 protein from pseudomonas putida
18	d1hnga1	Alignment		13.2	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
19	d1d8ja_	Alignment		11.2	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**The central core domain of TFIIE beta
20	c3o12A_	Alignment		10.8	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yjl217w; **PDBTitle:** the crystal structure of a functionally unknown protein from2 saccharomyces cerevisiae.
21	c2zkr6_	Alignment	not modelled	10.3	15	**PDB header:**ribosomal protein/rna **Chain:** 6: **PDB Molecule:**60s ribosomal protein l30e; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
22	d2vzsa5	Alignment	not modelled	10.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
23	c3euhF_	Alignment	not modelled	10.0	33	**PDB header:**cell cycle **Chain:** F: **PDB Molecule:**muke; **PDBTitle:** crystal structure of the muke-mukf complex
24	c1ta9A_	Alignment	not modelled	9.8	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
25	d1afsa_	Alignment	not modelled	9.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
26	c2vd9A_	Alignment	not modelled	9.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** the crystal structure of alanine racemase from bacillus2 anthracis (ba0252) with bound l-ala-p
27	c3cpqB_	Alignment	not modelled	9.1	16	**PDB header:**ribosomal protein **Chain:** B: **PDB Molecule:**50s ribosomal protein l30e; **PDBTitle:** crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
28	c3canA_	Alignment	not modelled	9.1	8	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-

						activating2 enzyme from bacteroides vulgatus atcc 8482
29	d1q2ya_	Alignment	not modelled	8.2	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
30	c1vliA_	Alignment	not modelled	8.0	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
31	c3l7xA_	Alignment	not modelled	7.6	26	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative hit-like protein involved in cell-cycle **PDBTitle:** the crystal structure of smu.412c from streptococcus mutans ua159
32	c2bgsA_	Alignment	not modelled	7.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldose reductase; **PDBTitle:** holo aldose reductase from barley
33	d1vaza_	Alignment	not modelled	7.4	18	**Fold:**NSFL1 (p97 ATPase) cofactor p47, SEP domain **Superfamily:**NSFL1 (p97 ATPase) cofactor p47, SEP domain **Family:**NSFL1 (p97 ATPase) cofactor p47, SEP domain
34	d1f61a_	Alignment	not modelled	7.2	44	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
35	d1uera1	Alignment	not modelled	7.2	38	**Fold:**Long alpha-hairpin **Superfamily:**Fe,Mn superoxide dismutase (SOD), N-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), N-terminal domain
36	d1dqua_	Alignment	not modelled	7.0	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
37	c3up8B_	Alignment	not modelled	6.8	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative 2,5-diketo-d-gluconic acid reductase b; **PDBTitle:** crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b
38	c1x4rA_	Alignment	not modelled	6.6	17	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**parp14 protein; **PDBTitle:** solution structure of wwe domain in parp14 protein
39	c1zr6A_	Alignment	not modelled	6.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucooligosaccharide oxidase; **PDBTitle:** the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
40	d1frba_	Alignment	not modelled	6.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
41	d1igwa_	Alignment	not modelled	6.5	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
42	c2gq8A_	Alignment	not modelled	6.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, fmn-binding; **PDBTitle:** structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
43	c1ynpA_	Alignment	not modelled	6.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** aldo-keto reductase akr11c1 from bacillus halodurans (apo form)
44	c1wveB_	Alignment	not modelled	6.2	5	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-cresol dehydrogenase [hydroxylating] **PDBTitle:** p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
45	c3f7jB_	Alignment	not modelled	6.1	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**yvgn protein; **PDBTitle:** b.subtilis yvgn
46	c3b3dA_	Alignment	not modelled	6.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative morphine dehydrogenase; **PDBTitle:** b.subtilis ytbe
47	c2vxdA_	Alignment	not modelled	5.8	35	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleophosmin; **PDBTitle:** the structure of the c-terminal domain of nucleophosmin
48	d2cb5a_	Alignment	not modelled	5.8	23	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
49	c3e5bB_	Alignment	not modelled	5.7	56	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
50	c3h7uA_	Alignment	not modelled	5.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9
51	d2gdqa1	Alignment	not modelled	5.6	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
52	d1qnra_	Alignment	not modelled	5.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
53	c3o0kB_	Alignment	not modelled	5.4	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldo/keto reductase; **PDBTitle:** crystal structure of aldo/keto reductase from brucella melitensis
						PDB header:isomerase

54	c1o98A_	Alignment	not modelled	5.3	9	**Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
55	c2dsjA_	Alignment	not modelled	5.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
56	c2vldA_	Alignment	not modelled	5.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0286 protein pyrab01260; **PDBTitle:** crystal structure of a repair endonuclease from pyrococcus2 abyssi
57	d1cbya_	Alignment	not modelled	5.1	23	**Fold:**CytB endotoxin-like **Superfamily:**CytB endotoxin-like **Family:**CytB endotoxin-like
58	c1cbyA_	Alignment	not modelled	5.1	23	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-endotoxin cytb; **PDBTitle:** delta-endotoxin