Phyre^2

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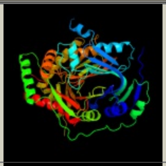
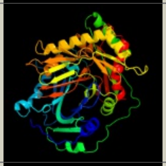
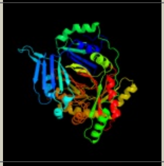
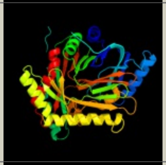
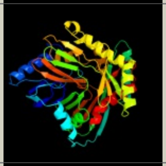
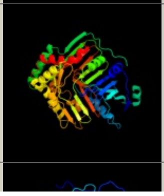
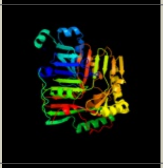
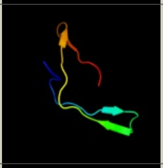
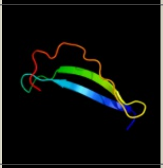
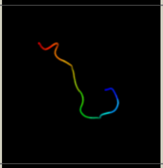
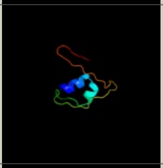
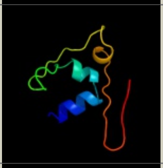
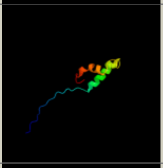
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i1qa_	Alignment		100.0	27	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
2	d1i7qa_	Alignment		100.0	28	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
3	d1k0ga_	Alignment		100.0	100	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
4	d1qdla_	Alignment		100.0	32	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
5	d2g5fa1	Alignment		100.0	20	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
6	c2i6yA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**anthranilate synthase component i, putative; **PDBTitle:** structure and mechanism of mycobacterium tuberculosis salicylate2 synthase, mbti
7	d2fn0a1	Alignment		100.0	20	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
8	c3h9mA_	Alignment		100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**p-aminobenzoate synthetase, component i; **PDBTitle:** crystal structure of para-aminobenzoate synthetase,2 component i from cytophaga hutchinsonii
9	c3os6A_	Alignment		100.0	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isochorismate synthase dhbc; **PDBTitle:** crystal structure of putative 2,3-dihydroxybenzoate-specific2 isochorismate synthase, dhbc from bacillus anthracis.
10	c3hwoB_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**isochorismate synthase entc; **PDBTitle:** crystal structure of escherichia coli enterobactin-specific2 isochorismate synthase entc in complex with isochorismate
11	d3bzna1	Alignment		100.0	19	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase

12	c3r74B_	Alignment		100.0	17	**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
13	c3gseA_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**menaquinone-specific isochorismate synthase; **PDBTitle:** crystal structure of menaquinone-specific isochorismate synthase from2 yersinia pestis co92
14	c3nqkA_	Alignment		35.2	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a structural genomics, unknown function2 (bacova_03322) from bacteroides ovatus at 2.61 a resolution
15	d1cvra1	Alignment		34.2	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Gingipain R (RgpB), C-terminal domain
16	c1wqkA_	Alignment		32.5	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin apetx1; **PDBTitle:** solution structure of apetx1, a specific peptide inhibitor2 of human ether-a-go-go-related gene potassium channels3 from the venom of the sea anemone anthopleura4 elegantissima: a new fold for an herg toxin
17	d1ugpa_	Alignment		22.1	23	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
18	d2qdya1	Alignment		19.7	12	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
19	c2k27A_	Alignment		16.7	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
20	c2npbA_	Alignment		14.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**selenoprotein w; **PDBTitle:** nmr solution structure of mouse selw
21	c3c8lB_	Alignment	not modelled	12.9	23	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ftsz-like protein of unknown function; **PDBTitle:** crystal structure of a ftsz-like protein of unknown function2 (npun_r1471) from nostoc punctiforme pcc 73102 at 1.22 a resolution
22	c2xt6B_	Alignment	not modelled	12.8	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
23	d1rp3b_	Alignment	not modelled	12.5	12	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Anti-sigma factor FlgM **Family:**Anti-sigma factor FlgM
24	c2jo8B_	Alignment	not modelled	10.5	35	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase 4; **PDBTitle:** solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
25	d1v29a_	Alignment	not modelled	10.4	24	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
26	d1qusa_	Alignment	not modelled	8.8	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
27	c1t2bA_	Alignment	not modelled	8.8	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**p450cin; **PDBTitle:** crystal structure of cytochrome p450cin complexed with its2 substrate 1,8-cineole
28	c2kztA_	Alignment	not modelled	8.4	20	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** structure of the tandem ma-3 region of pdcd4
						PDB header:transcription **Chain:** A: **PDB Molecule:**arc/mediator, positive cofactor 2

29	c2gutA_	Alignment	not modelled	8.1	17	glutamine/q- **PDBTitle:** solution structure of the trans-activation domain of the2 human co-activator arc105
30	c2km1A_	Alignment	not modelled	8.0	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein dre2; **PDBTitle:** solution structure of the n-terminal domain of the yeast protein dre2
31	c2jgdA_	Alignment	not modelled	7.6	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-oxoglutarate dehydrogenase e1 component; **PDBTitle:** e. coli 2-oxoglutarate dehydrogenase (e1o)
32	c3qyhG_	Alignment	not modelled	7.2	21	**PDB header:**lyase **Chain:** G: **PDB Molecule:**co-type nitrile hydratase alpha subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-h71l from2 pseudomonas putida.
33	d1eyba_	Alignment	not modelled	7.1	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Homogentisate dioxygenase
34	c1ey2A_	Alignment	not modelled	7.1	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** human homogentisate dioxygenase with fe(ii)
35	c2crqA_	Alignment	not modelled	7.0	24	**PDB header:**translation **Chain:** A: **PDB Molecule:**mitochondrial translational initiation factor 3; **PDBTitle:** solution structure of c-terminal domain of riken cdna2 2810012l14
36	c2qkdA_	Alignment	not modelled	6.7	20	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
37	c2rg8A_	Alignment	not modelled	6.6	20	**PDB header:**apoptosis, translation **Chain:** A: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** crystal structure of programmed for cell death 4 middle ma32 domain
38	c3mgxB_	Alignment	not modelled	6.2	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative p450 monooxygenase; **PDBTitle:** crystal structure of p450 oxyd that is involved in the biosynthesis of2 vancomycin-type antibiotics
39	c3rrrB_	Alignment	not modelled	5.9	33	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structure of the rsv f protein in the post-fusion conformation
40	c1wxnA_	Alignment	not modelled	5.9	38	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin apetx2; **PDBTitle:** solution structure of apetx2, a specific peptide inhibitor2 of asic3 proton-gated channels
41	c3f8tA_	Alignment	not modelled	5.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted atpase involved in replication control, **PDBTitle:** crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
42	c3dupB_	Alignment	not modelled	5.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
43	d1tiga_	Alignment	not modelled	5.4	15	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
44	c2yicC_	Alignment	not modelled	5.2	31	**PDB header:**lyase **Chain:** C: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (triclinic form)
45	c2zp2B_	Alignment	not modelled	5.1	11	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
46	c2hlwA_	Alignment	not modelled	5.1	15	**PDB header:**ligase, signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-conjugating enzyme e2 variant 1; **PDBTitle:** solution structure of the human ubiquitin-conjugating2 enzyme variant uev1a