Phyre^2

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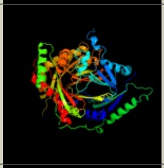
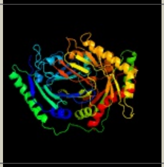
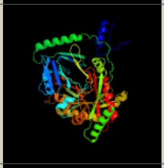
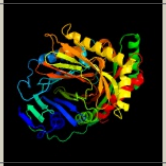
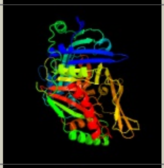
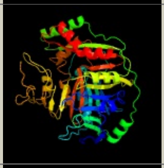
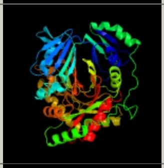
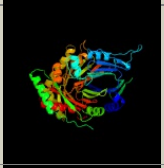
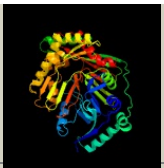
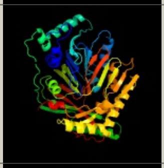
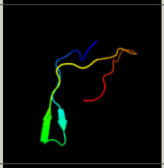
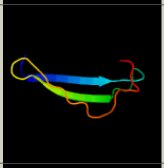
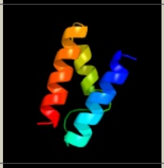
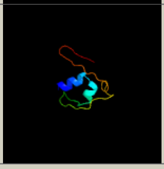
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4penA_	Alignment		100.0	100	**PDB header:**lyase **Chain:** A: **PDB Molecule:**anthranilate synthase component 1; **PDBTitle:** structure of anthranilate synthase component i (trpe) from2 mycobacterium tuberculosis with inhibitor bound
2	d1i1qa_	Alignment		100.0	41	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
3	d1i7qa_	Alignment		100.0	40	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
4	c5kckA_	Alignment		100.0	37	**PDB header:**lyase **Chain:** A: **PDB Molecule:**anthranilate synthase component i; **PDBTitle:** crystal structure of anthranilate synthase component i from2 streptococcus pneumoniae tigr4
5	d1qdla_	Alignment		100.0	39	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
6	c4grhA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminodeoxychorismate synthase; **PDBTitle:** crystal structure of pabb of stenotrophomonas maltophilia
7	d1k0ga_	Alignment		100.0	33	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
8	d2g5fa1	Alignment		100.0	26	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
9	c2i6yA_	Alignment		100.0	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**anthranilate synthase component i, putative; **PDBTitle:** structure and mechanism of mycobacterium tuberculosis salicylate2 synthase, mbti
10	d2fn0a1	Alignment		100.0	25	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
11	c3h9mA_	Alignment		100.0	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**p-aminobenzoate synthetase, component i; **PDBTitle:** crystal structure of para-aminobenzoate synthetase, component i from2 cytophaga hutchinsonii

12	d3bzna1	Alignment		100.0	21	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
13	c3hwoB_	Alignment		100.0	23	**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
14	c3os6A_	Alignment		100.0	26	**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.
15	c3gseA_	Alignment		100.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**menaquinone-specific isochorismate synthase; **PDBTitle:** crystal structure of menaquinone-specific isochorismate synthase from2 yersinia pestis co92
16	c3r74B_	Alignment		100.0	27	**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
17	c3nqkA_	Alignment		38.8	24	**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
18	d1cvra1	Alignment		34.6	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Gingipain R (RgpB), C-terminal domain
19	c2gutA_	Alignment		28.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arc/mediator, positive cofactor 2 glutamine/q- **PDBTitle:** solution structure of the trans-activation domain of the2 human co-activator arc105
20	d1ugpa_	Alignment		26.9	40	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
21	c1wqkA_	Alignment	not modelled	23.7	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
22	d2qdya1	Alignment	not modelled	23.6	16	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
23	c4aq2I_	Alignment	not modelled	20.8	12	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** resting state of homogentisate 1,2-dioxygenase
24	c1wxnA_	Alignment	not modelled	18.4	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin apetx2; **PDBTitle:** solution structure of apetx2, a specific peptide inhibitor2 of asic3 proton-gated channels
25	d1fe0a_	Alignment	not modelled	17.3	9	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
26	c4k6nA_	Alignment	not modelled	15.7	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aminodeoxychorismate lyase; **PDBTitle:** crystal structure of yeast 4-amino-4-deoxychorismate lyase
27	d2fefa2	Alignment	not modelled	15.6	15	**Fold:**PA2201 C-terminal domain-like **Superfamily:**PA2201 C-terminal domain-like **Family:**PA2201 C-terminal domain-like
28	c2km1A_	Alignment	not modelled	15.0	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein dre2; **PDBTitle:** solution structure of the n-terminal domain of the yeast protein dre2

29	c4gxtA_	Alignment	not modelled	13.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a conserved functionally unknown protein; **PDBTitle:** the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
30	c5h1nB_	Alignment	not modelled	12.9	26	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0253 protein yaep; **PDBTitle:** crystal structure of sf173 from shigella flexneri
31	d1v29a_	Alignment	not modelled	12.4	29	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
32	c2lt2A_	Alignment	not modelled	11.3	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** nmr structure of ba42 protein from the psychrophilic bacteria bizionia2 argentinensis sp. nov.
33	c5x49A_	Alignment	not modelled	11.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable xaa-pro aminopeptidase 3; **PDBTitle:** crystal structure of human mitochondrial x-prolyl aminopeptidase2 (xpnpep3)
34	c2xt6B_	Alignment	not modelled	10.7	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
35	c3j9oJ_	Alignment	not modelled	10.4	13	**PDB header:**structural protein **Chain:** J: **PDB Molecule:**intracellular growth locus protein b; **PDBTitle:** cryoem structure of a type vi secretion system
36	c2npbA_	Alignment	not modelled	10.3	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**selenoprotein w; **PDBTitle:** nmr solution structure of mouse selw
37	c5jnoB_	Alignment	not modelled	10.2	14	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**dna excision repair protein ercc-6-like; **PDBTitle:** crystal structure of the bd1-ntpr complex from bend3 and pich
38	c2edgA_	Alignment	not modelled	9.8	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** solution structure of the gcv_h domain from mouse glycine
39	c4zr0A_	Alignment	not modelled	9.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ceramide very long chain fatty acid hydroxylase scs7; **PDBTitle:** full length scs7p (only hydroxylase domain visible)
40	c6a2uA_	Alignment	not modelled	9.4	19	**PDB header:**signaling protein/oxidoreductase **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal; **PDBTitle:** crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase
41	c3qyhG_	Alignment	not modelled	9.2	30	**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.
42	c4as2D_	Alignment	not modelled	9.2	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**phosphorylcholine phosphatase; **PDBTitle:** pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
43	c4dapA_	Alignment	not modelled	9.2	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**sugar fermentation stimulation protein a; **PDBTitle:** the structure of escherichia coli sfsa
44	c3f8tA_	Alignment	not modelled	8.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted atpase involved in replication control, cdc46/mcm **PDBTitle:** crystal structure analysis of a full-length mcm homolog from2 methanopyrus kandleri
45	c1yx3A_	Alignment	not modelled	7.8	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
46	d2acfa1	Alignment	not modelled	7.7	15	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
47	c1ey2A_	Alignment	not modelled	7.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** human homogentisate dioxygenase with fe(ii)
48	d1eyba_	Alignment	not modelled	7.7	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Homogentisate dioxygenase
49	c3vf0A_	Alignment	not modelled	7.7	20	**PDB header:**cell adhesion/protein binding **Chain:** A: **PDB Molecule:**vinculin; **PDBTitle:** raver1 in complex with metavinculin l954 deletion mutant
50	c2ka7A_	Alignment	not modelled	7.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** nmr solution structure of tm0212 at 40 c
51	c5npxS_	Alignment	not modelled	7.3	35	**PDB header:**virus **Chain:** S: **PDB Molecule:**polyprotein; **PDBTitle:** atomic structure of the broad bean stain virus (bbsv) by cryo-em
52	c4davA_	Alignment	not modelled	7.2	24	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**sugar fermentation stimulation protein homolog; **PDBTitle:** the structure of pyrococcus furiosus sfsa in complex with dna
53	c2crqA_	Alignment	not modelled	6.8	10	**PDB header:**translation **Chain:** A: **PDB Molecule:**mitochondrial translational initiation factor 3; **PDBTitle:** solution structure of c-terminal domain of riken cdna2 2810012l14
54	c3luyA_	Alignment	not modelled	6.7	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium

						adolescentis
55	d1tiga_	Alignment	not modelled	6.7	8	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
56	d1chma1	Alignment	not modelled	6.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
57	d2af7a1	Alignment	not modelled	6.4	20	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
58	c5z2vB_	Alignment	not modelled	6.4	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recr from pseudomonas aeruginosa pao1
59	d1hxra_	Alignment	not modelled	6.1	22	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
60	d1ji8a_	Alignment	not modelled	6.0	31	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
61	c2z1tA_	Alignment	not modelled	6.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hydrogenase maturation protein hype
62	d2v4jc1	Alignment	not modelled	6.0	29	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
63	c2jgdA_	Alignment	not modelled	5.8	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-oxoglutarate dehydrogenase e1 component; **PDBTitle:** e. coli 2-oxoglutarate dehydrogenase (e1o)
64	c2rg8A_	Alignment	not modelled	5.8	7	**PDB header:**apoptosis, translation **Chain:** A: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** crystal structure of programmed for cell death 4 middle ma3 domain
65	d1onla_	Alignment	not modelled	5.8	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
66	d1yc5a1	Alignment	not modelled	5.7	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
67	d2fu5a1	Alignment	not modelled	5.6	22	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
68	c4ikaD_	Alignment	not modelled	5.6	75	**PDB header:**replication **Chain:** D: **PDB Molecule:**vpg; **PDBTitle:** crystal structure of ev71 3dpol-vpg
69	d1cc8a_	Alignment	not modelled	5.6	8	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
70	c5e37A_	Alignment	not modelled	5.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ef-hand domain-containing thioredoxin; **PDBTitle:** redox protein from chlamydomonas reinhardtii
71	d1k9xa_	Alignment	not modelled	5.5	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neurolysin-like
72	d2ifea_	Alignment	not modelled	5.4	16	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
73	c2k27A_	Alignment	not modelled	5.3	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
74	c3hq2A_	Alignment	not modelled	5.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bacillus subtilis m32 carboxypeptidase; **PDBTitle:** bsucp crystal structure
75	c2vu4A_	Alignment	not modelled	5.3	15	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**oxygen-evolving enhancer protein 2; **PDBTitle:** structure of psbp protein from spinacia oleracea at 1.98 a2 resolution
76	c4nm0B_	Alignment	not modelled	5.2	32	**PDB header:**transferase/peptide **Chain:** B: **PDB Molecule:**axin-1; **PDBTitle:** crystal structure of peptide inhibitor-free gsk-3/axin complex
77	d1ma3a_	Alignment	not modelled	5.1	29	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
78	c2kztA_	Alignment	not modelled	5.0	8	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** structure of the tandem ma-3 region of pdcd4
79	c5hycA_	Alignment	not modelled	5.0	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure based function annotation of a hypothetical protein2 mgg_01005 related to the development of rice blast fungus