Phyre^2

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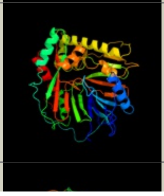
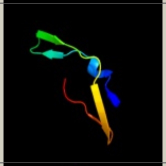
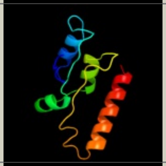
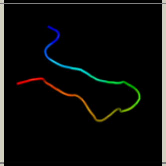
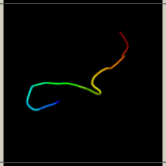
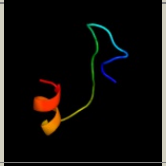
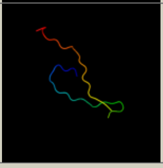
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hwoB_	Alignment		100.0	100	**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
2	c3os6A_	Alignment		100.0	38	**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.
3	d3bzna1	Alignment		100.0	27	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
4	d1qdla_	Alignment		100.0	25	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
5	d2fn0a1	Alignment		100.0	22	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
6	c3gseA_	Alignment		100.0	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**menaquinone-specific isochorismate synthase; **PDBTitle:** crystal structure of menaquinone-specific isochorismate synthase from2 yersinia pestis co92
7	d2g5fa1	Alignment		100.0	21	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
8	d1i1qa_	Alignment		100.0	22	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
9	d1i7qa_	Alignment		100.0	22	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
10	c3h9mA_	Alignment		100.0	17	**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
11	c2i6yA_	Alignment		100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**anthranilate synthase component i, putative; **PDBTitle:** structure and mechanism of mycobacterium tuberculosis salicylate2 synthase, mbti

12	c3r74B_	Alignment		100.0	21	**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	d1k0ga_	Alignment		100.0	22	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
14	c3nqkA_	Alignment		41.9	16	**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	d2ffca1	Alignment		23.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
16	d1hxra_	Alignment		19.4	22	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
17	d2fu5a1	Alignment		19.1	22	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
18	d1qusa_	Alignment		15.2	35	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
19	c2km1A_	Alignment		13.8	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein dre2; **PDBTitle:** solution structure of the n-terminal domain of the yeast protein dre2
20	d1a6ca2	Alignment		12.4	11	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
21	d1cvra1	Alignment	not modelled	9.6	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Gingipain R (RgpB), C-terminal domain
22	c2z1tA_	Alignment	not modelled	9.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hydrogenase maturation protein hype
23	c3fiuD_	Alignment	not modelled	8.7	12	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
24	c3fuyC_	Alignment	not modelled	8.6	30	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative integron gene cassette protein; **PDBTitle:** structure from the mobile metagenome of cole harbour salt2 marsh: integron cassette protein hfx_cass1
25	c1ey2A_	Alignment	not modelled	8.5	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** human homogentisate dioxygenase with fe(ii)
26	d1eyba_	Alignment	not modelled	8.5	28	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Homogentisate dioxygenase
27	d1d5ta2	Alignment	not modelled	8.1	21	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GDI-like
28	c1tzsA_	Alignment	not modelled	7.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cathepsin e; **PDBTitle:** crystal structure of an activation intermediate of2 cathepsin e
29	d2af7a1	Alignment	not modelled	7.0	17	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like

30	d3cmsa_	Alignment	not modelled	6.3	15	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Pepsin-like
31	c3c66B_	Alignment	not modelled	6.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** yeast poly(a) polymerase in complex with fip1 residues 80-105
32	d2c1wa1	Alignment	not modelled	6.0	25	**Fold:**EndoU-like **Superfamily:**EndoU-like **Family:**Eukaryotic EndoU ribonuclease
33	c3rrrB_	Alignment	not modelled	6.0	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structure of the rsv f protein in the post-fusion conformation
34	d1rd5a_	Alignment	not modelled	6.0	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
35	c1wxnA_	Alignment	not modelled	5.8	31	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin apetx2; **PDBTitle:** solution structure of apetx2, a specific peptide inhibitor2 of asic3 proton-gated channels
36	c3rpdB_	Alignment	not modelled	5.5	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methionine synthase (b12-independent); **PDBTitle:** the structure of a b12-independent methionine synthase from shewanella2 sp. w3-18-1 in complex with selenomethionine.