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Description	P00895
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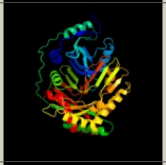
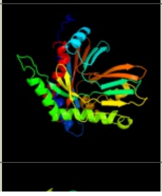
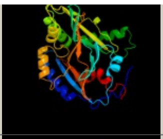
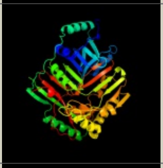
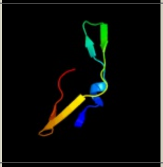
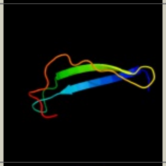
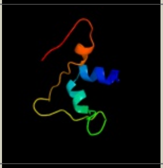
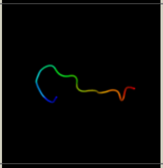
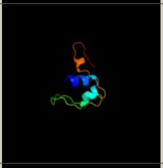
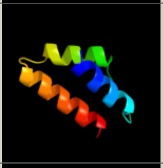
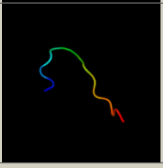
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i1qa_	Alignment		100.0	90	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
2	d1i7qa_	Alignment		100.0	72	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
3	d1qdla_	Alignment		100.0	35	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
4	d1k0ga_	Alignment		100.0	27	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
5	d2g5fa1	Alignment		100.0	24	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
6	c2i6yA_	Alignment		100.0	23	**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	26	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
8	c3h9mA_	Alignment		100.0	26	**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	d3bzna1	Alignment		100.0	21	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
10	c3os6A_	Alignment		100.0	27	**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.
11	c3hwoB_	Alignment		100.0	24	**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

12	c3r74B_	Alignment		100.0	25	**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		39.0	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
15	d1cvra1	Alignment		34.7	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Gingipain R (RgpB), C-terminal domain
16	d2qdya1	Alignment		27.7	14	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
17	c1wqkA_	Alignment		26.0	54	**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
18	d1ugpa_	Alignment		26.0	28	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
19	c2gutA_	Alignment		23.5	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	c1wxnA_	Alignment		22.3	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin apetx2; **PDBTitle:** solution structure of apetx2, a specific peptide inhibitor2 of asic3 proton-gated channels
21	c2qkdA_	Alignment	not modelled	21.8	9	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
22	d1rp3b_	Alignment	not modelled	18.2	22	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Anti-sigma factor FlgM **Family:**Anti-sigma factor FlgM
23	d1v29a_	Alignment	not modelled	15.2	21	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
24	c1t2bA_	Alignment	not modelled	14.7	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**p450cin; **PDBTitle:** crystal structure of cytochrome p450cin complexed with its2 substrate 1,8-cineole
25	d2fefa2	Alignment	not modelled	12.3	15	**Fold:**PA2201 C-terminal domain-like **Superfamily:**PA2201 C-terminal domain-like **Family:**PA2201 C-terminal domain-like
26	c2xt6B_	Alignment	not modelled	11.8	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
27	c3qyhG_	Alignment	not modelled	11.6	16	**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.
28	c2kztA_	Alignment	not modelled	10.9	14	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** structure of the tandem ma-3 region of pdcd4
29	c2npbA_	Alignment	not modelled	10.8	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**selenoprotein w; **PDBTitle:** nmr solution structure of mouse selw

30	c2crqA_	Alignment	not modelled	10.8	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**mitochondrial translational initiation factor 3; **PDBTitle:** solution structure of c-terminal domain of riken cdna2 2810012l14
31	c2km1A_	Alignment	not modelled	10.3	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein dre2; **PDBTitle:** solution structure of the n-terminal domain of the yeast protein dre2
32	c2jgdA_	Alignment	not modelled	10.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-oxoglutarate dehydrogenase e1 component; **PDBTitle:** e. coli 2-oxoglutarate dehydrogenase (e1o)
33	c2rg8A_	Alignment	not modelled	9.3	14	**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
34	d1e6va1	Alignment	not modelled	8.7	15	**Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Family:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
35	c2k27A_	Alignment	not modelled	8.7	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
36	d1tiga_	Alignment	not modelled	7.7	15	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
37	c1chmA_	Alignment	not modelled	7.1	15	**PDB header:**creatinase **Chain:** A: **PDB Molecule:**creatine amidinohydrolase; **PDBTitle:** enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
38	d2acfa1	Alignment	not modelled	7.1	18	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
39	d1chma1	Alignment	not modelled	7.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
40	c2vu4A_	Alignment	not modelled	6.7	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
41	c2kcdA_	Alignment	not modelled	6.7	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ssp0047; **PDBTitle:** solution nmr structure of ssp0047 from staphylococcus2 saprophyticus. northeast structural genomics consortium3 target syr6.
42	c3f8tA_	Alignment	not modelled	6.6	27	**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
43	c3rrrB_	Alignment	not modelled	6.6	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structure of the rsv f protein in the post-fusion conformation
44	c2z1tA_	Alignment	not modelled	6.5	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hydrogenase maturation protein hype
45	d1hxra_	Alignment	not modelled	6.4	11	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
46	d1a6ca2	Alignment	not modelled	6.2	22	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
47	d2af7a1	Alignment	not modelled	6.1	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
48	d1eyba_	Alignment	not modelled	6.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Homogentisate dioxygenase
49	c1ey2A_	Alignment	not modelled	6.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** human homogentisate dioxygenase with fe(ii)
50	d2fu5a1	Alignment	not modelled	5.9	11	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
51	c3dupB_	Alignment	not modelled	5.8	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
52	c3lf9A_	Alignment	not modelled	5.8	24	**PDB header:**immune system **Chain:** A: **PDB Molecule:**4e10_d0_1is1a_001_c (t161); **PDBTitle:** crystal structure of hiv epitope-scaffold 4e10_d0_1is1a_001_c
53	d1xe7a_	Alignment	not modelled	5.7	26	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YML079-like
54	d2ifea_	Alignment	not modelled	5.6	9	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
						PDB header:transferase

55	c3c66B_	Alignment	not modelled	5.6	26	**Chain:** B: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** yeast poly(a) polymerase in complex with fip1 residues 80-105
56	c2uvnB_	Alignment	not modelled	5.6	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome p450 130; **PDBTitle:** crystal structure of econazole-bound cyp130 from2 mycobacterium tuberculosis
57	c3nicA_	Alignment	not modelled	5.5	14	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**eco29kir; **PDBTitle:** dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
58	c3lk2B_	Alignment	not modelled	5.5	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**f-actin-capping protein subunit beta isoforms 1 and 2; **PDBTitle:** crystal structure of capz bound to the uncapping motif from carmil
59	d1zo0a1	Alignment	not modelled	5.4	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Ornithine decarboxylase antizyme-like
60	c2dyyG_	Alignment	not modelled	5.4	20	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**upf0076 protein ph0854; **PDBTitle:** crystal structure of putative translation initiation2 inhibitor ph0854 from pyrococcus horikoshii
61	d1ug3a1	Alignment	not modelled	5.4	13	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
62	c2yicC_	Alignment	not modelled	5.3	25	**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)
63	c3mgxB_	Alignment	not modelled	5.1	9	**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
64	c2hlwA_	Alignment	not modelled	5.0	21	**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