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Description	P0AFT8
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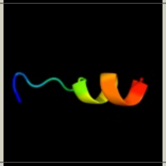
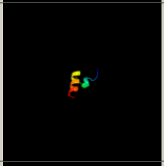
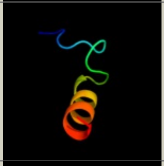
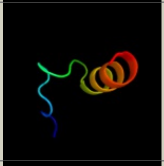
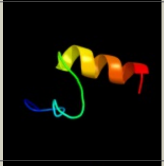
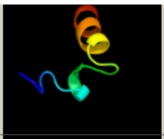
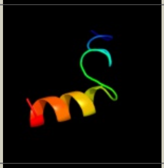
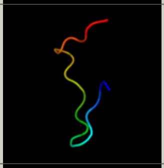
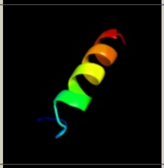
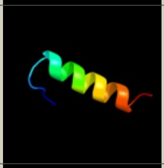
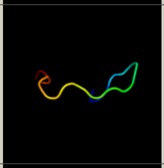
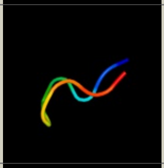
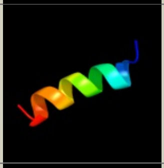
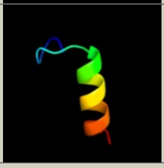
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hcuA_	Alignment		40.0	40	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
2	c3h5jA_	Alignment		38.3	40	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
3	c3q3wB_	Alignment		31.9	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** isopropylmalate isomerase small subunit from campylobacter jejuni.
4	d1v7la_	Alignment		25.9	40	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
5	c2pkpA_	Alignment		24.9	40	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
6	c3gseA_	Alignment		23.0	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**menaquinone-specific isochorismate synthase; **PDBTitle:** crystal structure of menaquinone-specific isochorismate synthase from2 yersinia pestis co92
7	c3h9mA_	Alignment		22.9	8	**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
8	c3os6A_	Alignment		22.9	20	**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.
9	d2fn0a1	Alignment		22.3	20	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
10	d2g5fa1	Alignment		22.1	12	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
11	d3bzna1	Alignment		20.0	28	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase

12	c2i6yA_	Alignment		19.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**anthranilate synthase component i, putative; **PDBTitle:** structure and mechanism of mycobacterium tuberculosis salicylate2 synthase, mbti
13	c3hwoB_	Alignment		19.1	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
14	c2crcA_	Alignment		17.8	42	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin conjugating enzyme 7 interacting **PDBTitle:** solution structure of the zf-ranbp domain of the protein2 hbv associated factor
15	d1lvaa4	Alignment		17.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
16	d1wgqa_	Alignment		15.8	9	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
17	c3b08H_	Alignment		15.6	47	**PDB header:**signaling protein/metal binding protein **Chain:** H: **PDB Molecule:**ranbp-type and c3hc4-type zinc finger-containing protein 1; **PDBTitle:** crystal structure of the mouse hoil1-l-nzf in complex with linear di-2 ubiquitin
18	d2dlqa2	Alignment		14.9	67	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
19	c2rrfA_	Alignment		14.7	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**zinc finger fyve domain-containing protein 21; **PDBTitle:** the solution structure of the c-terminal region of zinc finger fyve2 domain-containing protein 21
20	d2oz6a1	Alignment		14.5	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
21	c2kefA_	Alignment	not modelled	14.2	63	**PDB header:**antibiotic, hormone **Chain:** A: **PDB Molecule:**hepcidin; **PDBTitle:** solution nmr structures of human hepcidin at 325k
22	c3h0tC_	Alignment	not modelled	14.0	63	**PDB header:**immune system/antimicrobial protein **Chain:** C: **PDB Molecule:**hepcidin; **PDBTitle:** hepcidin-fab complex
23	c1m4eA_	Alignment	not modelled	13.1	63	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**hepcidin; **PDBTitle:** solution structure of hepcidin-20
24	c2bruC_	Alignment	not modelled	12.9	75	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p) transhydrogenase subunit beta; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
25	d1d4oa_	Alignment	not modelled	12.5	63	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
26	c1m4fA_	Alignment	not modelled	12.4	63	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**hepcidin; **PDBTitle:** solution structure of hepcidin-25
27	d1pnoa_	Alignment	not modelled	12.0	88	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
28	c3nsuA_	Alignment	not modelled	11.7	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**phosphatidylinositol 4,5-bisphosphate-binding protein slm1; **PDBTitle:** a systematic screen for protein-lipid interactions in saccharomyces2 cerevisiae
29	c1pt9B_	Alignment	not modelled	11.6	63	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of

						transhydrogenase2 with a thio-nicotinamide nucleotide analogue
30	d1qdla_	Alignment	not modelled	11.1	24	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
31	d1acoa1	Alignment	not modelled	10.5	27	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
32	c1iclA_	Alignment	not modelled	9.9	46	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**th1ox; **PDBTitle:** solution structure of designed beta-sheet mini-protein th1ox
33	d1i5za1	Alignment	not modelled	9.7	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
34	d2gaua1	Alignment	not modelled	9.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
35	c3r74B_	Alignment	not modelled	9.0	12	**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
36	c2qdrA_	Alignment	not modelled	8.9	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative dioxygenase (npun_f5605) from nostoc2 punctiforme pcc 73102 at 2.60 a resolution
37	c1s6wA_	Alignment	not modelled	8.9	71	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**hepcidin; **PDBTitle:** solution structure of hybrid white striped bass hepcidin
38	c1wsuA_	Alignment	not modelled	8.5	25	**PDB header:**translation/rna **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** c-terminal domain of elongation factor selb complexed with2 secis rna
39	d1x1ga1	Alignment	not modelled	8.3	20	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
40	c2knnA_	Alignment	not modelled	8.3	57	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**cycloviolacin-o2; **PDBTitle:** solution structure of the cyclotide cycloviolacin o2 with2 glu6 methylated (cyo2me)
41	c3bl4B_	Alignment	not modelled	8.2	45	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function (arth_0117) from2 arthrobacter sp. fb24 at 2.20 a resolution
42	c2pjpA_	Alignment	not modelled	7.8	20	**PDB header:**translation/rna **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
43	d2b3ya1	Alignment	not modelled	7.6	33	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
44	d1v5ua_	Alignment	not modelled	7.2	14	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
45	c2rf4B_	Alignment	not modelled	7.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase i subunit rpa4; **PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43
46	d1k25a2	Alignment	not modelled	6.8	28	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
47	d1nekb2	Alignment	not modelled	6.5	50	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
48	d2coca1	Alignment	not modelled	6.4	19	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
49	c3gitA_	Alignment	not modelled	6.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase/acetyl-coa synthase subunit **PDBTitle:** crystal structure of a truncated acetyl-coa synthase
50	d1k0ga_	Alignment	not modelled	6.1	20	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
51	d1ft9a1	Alignment	not modelled	5.6	40	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
52	c2k2jA_	Alignment	not modelled	5.4	9	**PDB header:**hydrolase, signaling protein **Chain:** A: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate **PDBTitle:** nmr solution structure of the split ph domain from2 phospholipase c gamma 2
53	d1l5ja2	Alignment	not modelled	5.4	50	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
54	d1upqa_	Alignment	not modelled	5.4	14	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
55	d1k36a_	Alignment	not modelled	5.4	17	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin

						Family:EGF-type module
56	c3nggA_	Alignment	not modelled	5.1	42	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**omwaprin-a; **PDBTitle:** x-ray structure of omwaprin
57	d2h6ca1	Alignment	not modelled	5.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like