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Description	P0A8U6
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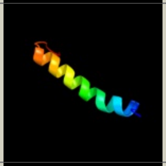
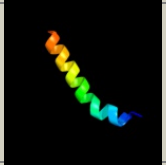
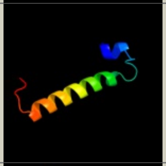
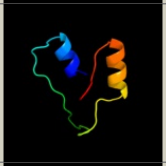
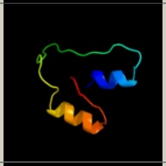
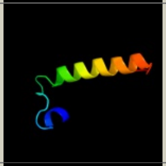
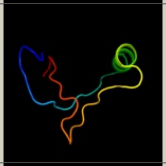
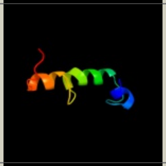
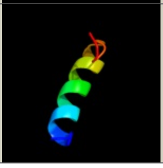
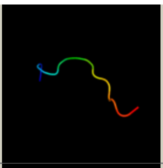
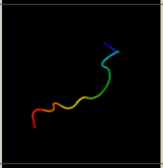
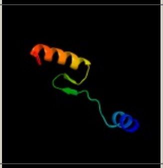
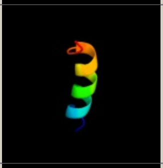
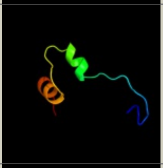
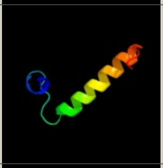
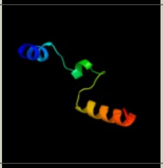
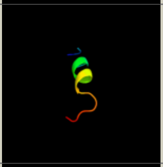
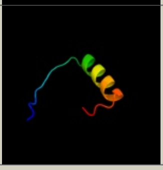
Unique Job ID	0ab10e7131344d3f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1cmca_	Alignment		100.0	100	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Met repressor, MetJ (MetR)
2	c1is7F_	Alignment		35.6	20	**PDB header:**hydrolase/protein binding **Chain:** F: **PDB Molecule:**gtp cyclohydrolase i; **PDBTitle:** crystal structure of rat gtpchi/gfrp stimulatory complex
3	d1wpla_	Alignment		35.6	20	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
4	d1n3la_	Alignment		27.2	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
5	d2pu9b1	Alignment		25.6	45	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
6	c2fekA_	Alignment		25.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** structure of a protein tyrosine phosphatase
7	c2wmyH_	Alignment		24.1	13	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**putative acid phosphatase wzb; **PDBTitle:** crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
8	c1q11A_	Alignment		18.3	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tyrosyl-trna2 synthetase with tyrosinol
9	d2if6a1	Alignment		17.9	32	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**YiiX-like
10	c2j5bA_	Alignment		16.1	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosynol
11	c2k29A_	Alignment		14.7	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb

12	d1txla_	Alignment		14.5	31	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Hypothetical protein YodA
13	c1txlA_	Alignment		14.5	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**metal-binding protein yoda; **PDBTitle:** crystal structure of metal-binding protein yoda from e.2 coli, pfam duf149
14	c2y69Q_	Alignment		14.5	18	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
15	d1q8da_	Alignment		13.5	29	**Fold:**GDNF receptor-like **Superfamily:**GDNF receptor-like **Family:**GDNF receptor-like
16	d2d5ra1	Alignment		13.5	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
17	c2dlcX_	Alignment		13.1	24	**PDB header:**ligase/trna **Chain:** X: **PDB Molecule:**tyrosyl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase
18	d1v54d_	Alignment		12.6	18	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
19	d1qcsa2	Alignment		11.2	17	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
20	d2bj7a1	Alignment		10.6	21	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
21	d1a8ra_	Alignment	not modelled	9.6	22	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
22	d1ioka2	Alignment	not modelled	9.2	44	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
23	c3idwA_	Alignment	not modelled	9.1	25	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
24	c2v5eA_	Alignment	not modelled	8.7	29	**PDB header:**receptor/glycoprotein complex **Chain:** A: **PDB Molecule:**gdnf family receptor alpha-1; **PDBTitle:** the structure of the gdnf\:coreceptor complex\: insights2 into ret signalling and heparin binding.
25	c3fubA_	Alignment	not modelled	8.6	29	**PDB header:**hormone **Chain:** A: **PDB Molecule:**gdnf family receptor alpha-1; **PDBTitle:** crystal structure of gdnf-gfralpha1 complex
26	d2hafa1	Alignment	not modelled	8.5	27	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
27	d2gf5a1	Alignment	not modelled	8.4	17	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
28	c1qdnA_	Alignment	not modelled	8.3	17	**PDB header:**fusion protein **Chain:** A: **PDB Molecule:**protein (n-ethylmaleimide sensitive fusion **PDBTitle:** amino terminal domain of the n-ethylmaleimide sensitive2 fusion protein (nsf)
						PDB header:ligase

29	c2cycB_	Alignment	not modelled	8.2	18	**Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
30	d1jf8a_	Alignment	not modelled	8.2	16	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
31	c2l18A_	Alignment	not modelled	7.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
32	d1sjpa2	Alignment	not modelled	7.8	44	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
33	d1h8ba_	Alignment	not modelled	7.7	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
34	d1sbxa_	Alignment	not modelled	7.7	50	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Dachshund-homology domain
35	d1wr6a1	Alignment	not modelled	7.6	26	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
36	c3fwcN_	Alignment	not modelled	7.3	23	**PDB header:**cell cycle, transcription **Chain:** N: **PDB Molecule:**nuclear mrna export protein sac3; **PDBTitle:** sac3:sus1:cdc31 complex
37	d1dk7a_	Alignment	not modelled	7.1	44	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
38	d1srva_	Alignment	not modelled	7.1	56	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
39	d1oela2	Alignment	not modelled	6.5	44	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
40	d1we3a2	Alignment	not modelled	6.4	56	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
41	d1np3a1	Alignment	not modelled	6.2	33	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI)
42	d1xrsb2	Alignment	not modelled	6.1	50	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
43	c2aj2A_	Alignment	not modelled	6.0	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0301 protein vc0467; **PDBTitle:** x-ray crystal structure of protein vc0467 from vibrio2 cholerae. northeast structural genomics consortium target3 vcr8.
44	c2p51A_	Alignment	not modelled	5.9	32	**PDB header:**hydrolase, gene regulation **Chain:** A: **PDB Molecule:**spcc18.06c protein; **PDBTitle:** crystal structure of the s. pombe pop2p deadenylation2 subunit
45	c1v91A_	Alignment	not modelled	5.7	71	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-palutoxin it2; **PDBTitle:** solution structure of insectidal toxin delta-paluit2-nh2
46	d2dofa1	Alignment	not modelled	5.7	13	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
47	d1wu2a2	Alignment	not modelled	5.6	36	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
48	c3t38B_	Alignment	not modelled	5.5	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
49	d2bnma1	Alignment	not modelled	5.4	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
50	c2cyaA_	Alignment	not modelled	5.4	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
51	d1sjpa3	Alignment	not modelled	5.3	0	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**GroEL-like chaperone, intermediate domain
52	d1wrda1	Alignment	not modelled	5.2	17	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
53	d2cyua1	Alignment	not modelled	5.2	11	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
54	d2nqra2	Alignment	not modelled	5.0	36	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like