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Description	P77393
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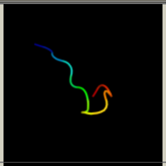
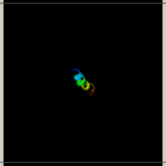
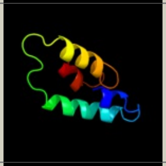
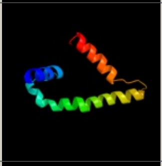
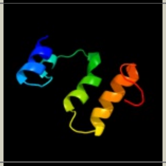
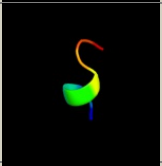
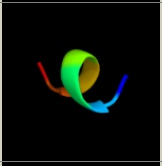
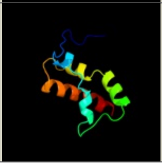
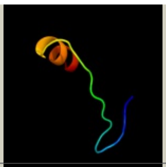
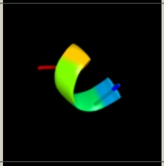
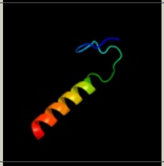
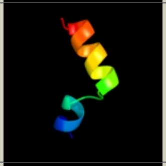
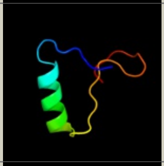
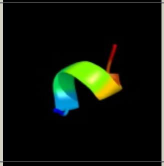
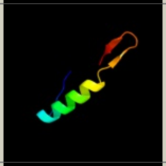
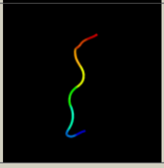
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1bcoa1	Alignment		29.0	38	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
2	d1hcia1	Alignment		24.9	30	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
3	c3nb2B_	Alignment		21.6	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of e. coli o157:h7 effector protein nleI
4	c2qzaA_	Alignment		21.2	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of salmonella effector protein sopa
5	c3r7wC_	Alignment		17.3	17	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**gtp-binding protein gtr1; **PDBTitle:** crystal structure of gtr1p-gtr2p complex
6	c3oa7A_	Alignment		16.8	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**head morphogenesis protein, chaotic nuclear migration **PDBTitle:** structure of the c-terminal domain of cnm67, a core component of the2 spindle pole body of saccharomyces cerevisiae
7	c3fd9C_	Alignment		16.5	18	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the transcriptional anti-activator exsd2 from pseudomonas aeruginosa
8	d1hssa_	Alignment		15.9	50	**Fold:**Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin **Superfamily:**Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin **Family:**Proteinase/alpha-amylase inhibitors
9	c1g3jB_	Alignment		13.3	86	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tcf3-cbd (catenin binding domain); **PDBTitle:** crystal structure of the xtcf3-cbd/beta-catenin armadillo2 repeat complex
10	d1ag9a_	Alignment		12.8	24	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
11	c1hm4A_	Alignment		9.6	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pentalenene synthase; **PDBTitle:** n219l pentalenene synthase

12	d1usma_	Alignment		9.2	20	**Fold:**DCoH-like **Superfamily:**PCD-like **Family:**PCD-like
13	c1jdhB_	Alignment		9.0	86	**PDB header:**transcription **Chain:** B: **PDB Molecule:**htcf-4; **PDBTitle:** crystal structure of beta-catenin and htcf-4
14	c2qb5B_	Alignment		8.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inositol-tetrakisphosphate 1-kinase; **PDBTitle:** crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+
15	d1ufza_	Alignment		8.8	43	**Fold:**RuvA C-terminal domain-like **Superfamily:**HBS1-like domain **Family:**HBS1-like domain
16	c3lr4A_	Alignment		8.6	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph
17	c3ouxB_	Alignment		8.5	100	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**lymphoid enhancer-binding factor 1; **PDBTitle:** structure of beta-catenin with phosphorylated lef-1
18	d1pvja_	Alignment		7.5	36	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
19	d2gjxa2	Alignment		7.4	16	**Fold:**Zincin-like **Superfamily:**beta-N-acetylhexosaminidase-like domain **Family:**beta-N-acetylhexosaminidase domain
20	d2cupa1	Alignment		7.3	75	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
21	d1dkia_	Alignment	not modelled	7.2	25	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
22	d2bv3a5	Alignment	not modelled	6.5	16	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
23	d1x63a1	Alignment	not modelled	6.3	75	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
24	d1go4a_	Alignment	not modelled	6.0	24	**Fold:**The spindle assembly checkpoint protein mad2 **Superfamily:**The spindle assembly checkpoint protein mad2 **Family:**The spindle assembly checkpoint protein mad2
25	d2bw3a1	Alignment	not modelled	5.9	20	**Fold:**Hermes dimerisation domain **Superfamily:**Hermes dimerisation domain **Family:**Hermes dimerisation domain
26	c2eefA_	Alignment	not modelled	5.7	60	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**protein phosphatase 1, regulatory (inhibitor) **PDBTitle:** solution structure of the cbm_21 domain from human protein2 phosphatase 1, regulatory (inhibitor) subunit 3b
27	c2z0lA_	Alignment	not modelled	5.7	31	**PDB header:**replication **Chain:** A: **PDB Molecule:**early antigen protein d; **PDBTitle:** crystal structure of ebv-dna polymerase accessory protein2 bmrf1
28	c1dipA_	Alignment	not modelled	5.5	75	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures

29	d1h2vc2	Alignment	not modelled	5.5	25	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
30	c1jpwD_	Alignment	not modelled	5.3	86	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**transcription factor 7-like 2; **PDBTitle:** crystal structure of a human tcf-4 / beta-catenin complex
31	c3bbaB_	Alignment	not modelled	5.2	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interpain a; **PDBTitle:** structure of active wild-type prevotella intermedia interpain a2 cysteine protease
32	d1ydla1	Alignment	not modelled	5.2	42	**Fold:**TFB5-like **Superfamily:**TFB5-like **Family:**TFB5-like
33	c2xxsA_	Alignment	not modelled	5.2	50	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein mxig; **PDBTitle:** solution structure of the n-terminal domain of the shigella2 type iii secretion protein mxig
34	c2gedB_	Alignment	not modelled	5.1	21	**PDB header:**protein transport, signaling protein **Chain:** B: **PDB Molecule:**signal recognition particle receptor beta **PDBTitle:** signal recognition particle receptor beta-subunit in2 nucleotide-free dimerized form
35	d1dvka_	Alignment	not modelled	5.1	28	**Fold:**Functional domain of the splicing factor Prp18 **Superfamily:**Functional domain of the splicing factor Prp18 **Family:**Functional domain of the splicing factor Prp18