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Description	P25736
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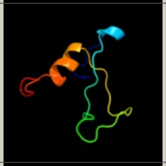
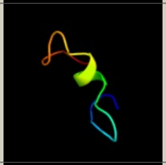
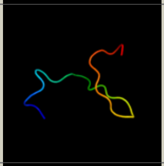
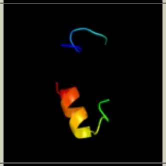
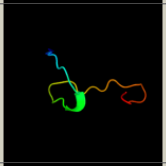
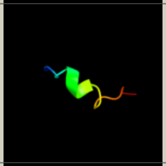
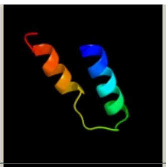
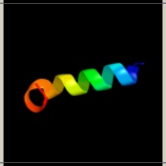
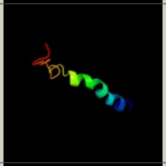
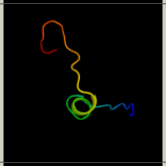
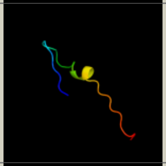
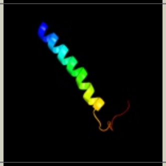
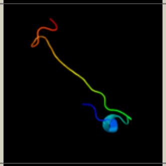
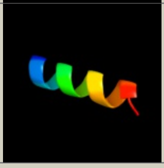
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ouoa_	Alignment		100.0	63	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**Endonuclease I
2	c2qgpA_	Alignment		93.5	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hnh endonuclease; **PDBTitle:** x-ray structure of the nhn endonuclease from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr87.
3	d2ebfx3	Alignment		29.5	47	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**PMT C-terminal domain like
4	c2e72A_	Alignment		29.2	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pogo transposable element with znf domain; **PDBTitle:** solution structure of the zinc finger domain of human2 kiaa0461
5	c3c4rC_	Alignment		23.4	24	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein encoded by2 cryptic prophage
6	d2ebfx1	Alignment		20.9	12	**Fold:**PMT central region-like **Superfamily:**PMT central region-like **Family:**PMT central region-like
7	c2lmdA_	Alignment		18.9	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prospero homeobox protein 1; **PDBTitle:** minimal constraints solution nmr structure of prospero homeobox2 protein 1 from homo sapiens, northeast structural genomics consortium3 target hr4660b
8	d1mija_	Alignment		15.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
9	c3gqeA_	Alignment		15.4	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of venezuelan equine encephalitis2 virus
10	d2evra1	Alignment		14.7	38	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**Spr N-terminal domain-like
11	c1tr8A_	Alignment		13.7	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)

12	c2ec5B_	Alignment		11.2	12	**PDB header:**toxin **Chain:** B: **PDB Molecule:**dermonecrotic toxin; **PDBTitle:** crystal structures reveal a thiol-protease like catalytic triad in the2 c-terminal region of pasteurella multocida toxin
13	d1em8b_	Alignment		11.1	21	**Fold:**DNA polymerase III psi subunit **Superfamily:**DNA polymerase III psi subunit **Family:**DNA polymerase III psi subunit
14	c1m8oB_	Alignment		10.6	26	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**platele integrin beta3 subunit: cytoplasmic **PDBTitle:** platelet integrin alfaiib-beta3 cytoplasmic domain
15	c3gpqA_	Alignment		10.6	21	**PDB header:**viral protein/rna **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of chikungunya virus in complex with2 rna
16	d1yc611	Alignment		9.7	28	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
17	c2bpbB_	Alignment		9.6	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
18	c3g9wC_	Alignment		9.1	20	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**integrin beta-1d; **PDBTitle:** crystal structure of talin2 f2-f3 in complex with the integrin beta1d2 cytoplasmic tail
19	d2bcgg3	Alignment		8.4	42	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GDI-like
20	c3t4aG_	Alignment		8.0	33	**PDB header:**immune system **Chain:** G: **PDB Molecule:**fibrinogen-binding protein; **PDBTitle:** structure of a truncated form of staphylococcal complement inhibitor b2 bound to human c3c at 3.4 angstrom resolution
21	d1js9c_	Alignment	not modelled	7.8	28	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
22	d1i5za1	Alignment	not modelled	7.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
23	d1qbaa2	Alignment	not modelled	7.7	18	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Bacterial chitobiase, n-terminal domain
24	d2dk1a1	Alignment	not modelled	7.6	18	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
25	c2a45L_	Alignment	not modelled	7.5	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** L: **PDB Molecule:**fibrinogen gamma chain; **PDBTitle:** crystal structure of the complex between thrombin and the central "e"2 region of fibrin
26	c3gnzP_	Alignment	not modelled	7.5	50	**PDB header:**toxin **Chain:** P: **PDB Molecule:**25 kda protein elicitor; **PDBTitle:** toxin fold for microbial attack and plant defense
27	c3bunB_	Alignment	not modelled	7.3	24	**PDB header:**ligase/signaling protein **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase cbl; **PDBTitle:** crystal structure of c-cbl-tkb domain complexed with its2 binding motif in sprouty4
28	c2cblA_	Alignment	not modelled	7.0	24	**PDB header:**complex (proto-oncogene/peptide) **Chain:** A: **PDB Molecule:**proto-oncogene cbl; **PDBTitle:** n-terminal domain of cbl in complex with its binding site2 on zap-70
						Fold: Knottins (small inhibitors, toxins, lectins)

29	d1yy9a4	Alignment	not modelled	6.9	30	**Superfamily:**Growth factor receptor domain **Family:**Growth factor receptor domain
30	c2qffA_	Alignment	not modelled	6.8	27	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of staphylococcal complement inhibitor
31	d1cwpa_	Alignment	not modelled	6.7	56	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
32	c3st1A_	Alignment	not modelled	6.3	40	**PDB header:**toxin **Chain:** A: **PDB Molecule:**necrosis-and ethylene-inducing protein; **PDBTitle:** crystal structure of necrosis and ethylene inducing protein 2 from the2 causal agent of cocoa's witches broom disease
33	c3nzqB_	Alignment	not modelled	6.2	32	**PDB header:**lyase **Chain:** B: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
34	c2kncB_	Alignment	not modelled	6.1	27	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
35	c2y69S_	Alignment	not modelled	6.0	43	**PDB header:**electron transport **Chain:** S: **PDB Molecule:**cytochrome c oxidase subunit 5b; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
36	d1d5ta2	Alignment	not modelled	6.0	35	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GDI-like
37	d3buxb2	Alignment	not modelled	6.0	17	**Fold:**N-cbl like **Superfamily:**N-terminal domain of cbl (N-cbl) **Family:**N-terminal domain of cbl (N-cbl)
38	d2gaua1	Alignment	not modelled	5.9	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
39	c2yqfA_	Alignment	not modelled	5.9	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** solution structure of the death domain of ankyrin-1
40	d1cwva5	Alignment	not modelled	5.8	22	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Invasin/intimin cell-adhesion fragment, C-terminal domain
41	c1cwpB_	Alignment	not modelled	5.7	56	**PDB header:**virus/rna **Chain:** B: **PDB Molecule:**coat protein; **PDBTitle:** structures of the native and swollen forms of cowpea2 chlorotic mottle virus determined by x-ray crystallography3 and cryo-electron microscopy
42	c1hp9A_	Alignment	not modelled	5.7	60	**PDB header:**toxin **Chain:** A: **PDB Molecule:**kappa-hefutoxin 1; **PDBTitle:** kappa-hefutoxins: a novel class of potassium channel toxins2 from scorpion venom
43	d1pbya1	Alignment	not modelled	5.3	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
44	c3rnvA_	Alignment	not modelled	5.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helper component proteinase; **PDBTitle:** structure of the autocatalytic cysteine protease domain of potyvirus2 helper-component proteinase
45	c2q4pA_	Alignment	not modelled	5.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein rs21-c6; **PDBTitle:** ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898