Email	l.a.kelley@imperial.ac.uk
Description	P45472
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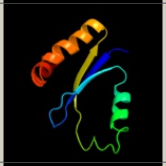
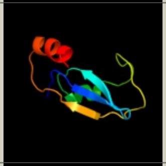
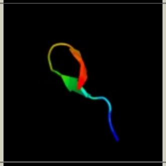
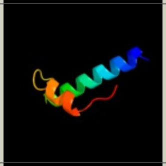
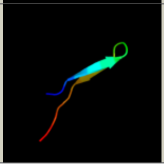
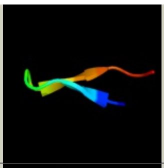
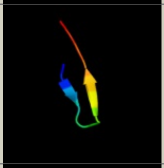
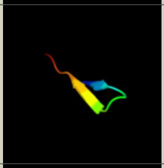
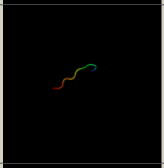
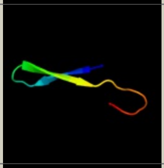
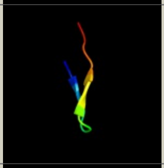
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zg2A_	Alignment		100.0	42	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0213 protein bh0048; **PDBTitle:** solution nmr structure of the upf0213 protein bh0048 from2 bacillus halodurans. northeast structural genomics target3 bhr2.
2	c1ywlA_	Alignment		100.0	34	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0213 protein ef2693; **PDBTitle:** solution nmr structure of the protein ef2693 from e.2 faecalis: northeast structural genomics consortium target3 efr36
3	c1yd6A_	Alignment		98.3	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrc; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease2 domain of uvrc from bacillus caldotenax
4	c1yd2A_	Alignment		97.8	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease domain of2 uvrc from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation
5	d1mk0a_	Alignment		97.5	21	**Fold:**GIY-YIG endonuclease **Superfamily:**GIY-YIG endonuclease **Family:**GIY-YIG endonuclease
6	c2wshC_	Alignment		89.9	6	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endonuclease ii; **PDBTitle:** structure of bacteriophage t4 endoii e118a mutant
7	c3h8tA_	Alignment		22.0	25	**PDB header:**heme-binding protein **Chain:** A: **PDB Molecule:**hmuy; **PDBTitle:** structure of porphyromonas gingivalis heme-binding protein hmuy in2 complex with heme
8	c1f0cB_	Alignment		21.0	53	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**ice inhibitor; **PDBTitle:** structure of the viral serpin crma
9	d1a6qa1	Alignment		17.2	15	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
10	c2yrvA_	Alignment		11.0	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**at-rich interactive domain-containing protein 4a; **PDBTitle:** solution structure of the rbb1nt domain of human2 rb(retinoblastoma)-binding protein 1
11	d1ylxa1	Alignment		10.4	22	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GK1464-like **Family:**GK1464-like

12	c2xk0A_	Alignment		9.4	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb protein pcl; **PDBTitle:** solution structure of the tudor domain from drosophila2 polycomblike (pcl)
13	d2z3ga1	Alignment		9.4	23	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
14	c3oj6C_	Alignment		9.3	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**blasticidin-s deaminase; **PDBTitle:** crystal structure of blasticidin s deaminase from coccidioides immitis
15	d1lkta_	Alignment		8.9	40	**Fold:**Head-binding domain of phage P22 tailspike protein **Superfamily:**Head-binding domain of phage P22 tailspike protein **Family:**Head-binding domain of phage P22 tailspike protein
16	d3orca_	Alignment		8.5	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
17	d2fr5a1	Alignment		8.3	23	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
18	c3b8fB_	Alignment		8.3	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative blasticidin s deaminase; **PDBTitle:** crystal structure of the cytidine deaminase from bacillus anthracis
19	c2eqjA_	Alignment		7.8	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metal-response element-binding transcription **PDBTitle:** solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
20	d1mq0a_	Alignment		7.8	15	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
21	d2d30a1	Alignment	not modelled	7.8	38	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
22	c3r2nC_	Alignment	not modelled	7.7	31	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from mycobacterium leprae
23	c3ijfX_	Alignment	not modelled	7.6	23	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from mycobacterium2 tuberculosis
24	c2diiA_	Alignment	not modelled	7.1	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
25	d1d0na5	Alignment	not modelled	7.1	11	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
26	d1yu0a1	Alignment	not modelled	6.7	23	**Fold:**Pseudo beta-prism **Superfamily:**Bacteriophage trimeric proteins domain **Family:**Mtd domain-like
27	d1uwza_	Alignment	not modelled	6.5	38	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
28	d2bj7a1	Alignment	not modelled	6.5	40	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like

29	c2dybA_	Alignment	not modelled	6.5	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 4; **PDBTitle:** the crystal structure of human p40(phox)
30	d2diia1	Alignment	not modelled	6.4	20	**Fold:**BSD domain-like **Superfamily:**BSD domain-like **Family:**BSD domain
31	d2hzab1	Alignment	not modelled	6.3	40	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
32	c2e5pA_	Alignment	not modelled	6.3	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
33	c3dmoD_	Alignment	not modelled	6.0	31	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytidine deaminase; **PDBTitle:** 1.6 a crystal structure of cytidine deaminase from2 burkholderia pseudomallei
34	c2vkyB_	Alignment	not modelled	5.6	40	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**tail protein, piigcn4; **PDBTitle:** headbinding domain of phage p22 tailspike c-terminally2 fused to isoleucine zipper piigcn4 (chimera i)
35	d1svya_	Alignment	not modelled	5.5	7	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like