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Description	P45848
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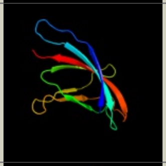
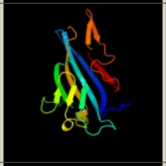
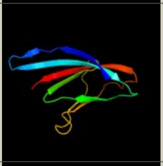
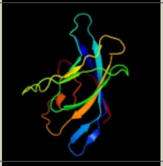
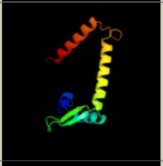
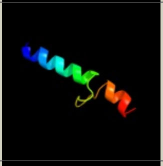
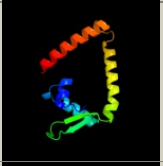
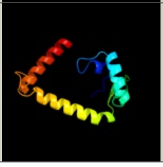
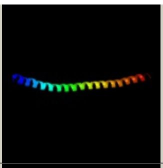
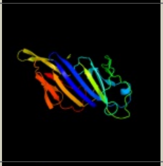
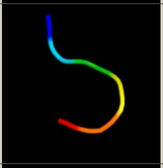
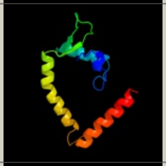
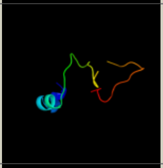
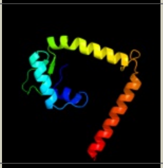
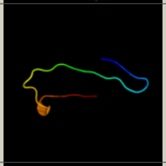
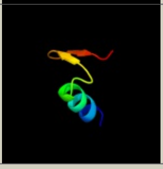
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kd4A_	Alignment		87.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative protease; **PDBTitle:** crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
2	d3b7sa2	Alignment		72.1	9	**Fold:**Leukotriene A4 hydrolase N-terminal domain **Superfamily:**Leukotriene A4 hydrolase N-terminal domain **Family:**Leukotriene A4 hydrolase N-terminal domain
3	c3ebhA_	Alignment		71.9	5	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**m1 family aminopeptidase; **PDBTitle:** structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
4	c3b7uX_	Alignment		61.6	10	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** leukotriene a4 hydrolase complexed with kelatorphan
5	c2gtqA_	Alignment		52.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
6	c3ciaA_	Alignment		51.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active aminopeptidase; **PDBTitle:** crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
7	c2xpyA_	Alignment		35.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leukotriene a-4 hydrolase; **PDBTitle:** structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae
8	d2etha1	Alignment		33.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
9	d1tkna_	Alignment		28.9	12	**Fold:**STAT-like **Superfamily:**CAPPD, an extracellular domain of amyloid beta A4 protein **Family:**CAPPD, an extracellular domain of amyloid beta A4 protein
10	d1lj9a_	Alignment		26.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
11	d2fbha1	Alignment		22.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators

12	c3hd7A_	Alignment		21.8	8	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
13	c3se6A_	Alignment		19.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 2; **PDBTitle:** crystal structure of the human endoplasmic reticulum aminopeptidase 2
14	c2i7uA_	Alignment		19.5	100	**PDB header:**de novo protein/ligand binding protein **Chain:** A: **PDB Molecule:**four-alpha-helix bundle; **PDBTitle:** structural and dynamical analysis of a four-alpha-helix2 bundle with designed anesthetic binding pockets
15	c3nrvC_	Alignment		18.3	13	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**putative transcriptional regulator (marr/emrr family); **PDBTitle:** crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
16	d2a61a1	Alignment		17.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
17	c2rngA_	Alignment		16.8	13	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**big defensin; **PDBTitle:** solution structure of big defensin
18	c3g3zA_	Alignment		15.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
19	c2rh0B_	Alignment		14.9	11	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**nudc domain-containing protein 2; **PDBTitle:** crystal structure of nudc domain-containing protein 22 (13542905) from mus musculus at 1.95 a resolution
20	d1xp8a2	Alignment		12.0	16	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
21	d1s3ja_	Alignment	not modelled	11.1	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
22	c3bj6B_	Alignment	not modelled	11.0	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
23	d1rw6a_	Alignment	not modelled	10.9	12	**Fold:**STAT-like **Superfamily:**CAPPD, an extracellular domain of amyloid beta A4 protein **Family:**CAPPD, an extracellular domain of amyloid beta A4 protein
24	c3k66A_	Alignment	not modelled	10.6	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**beta-amyloid-like protein; **PDBTitle:** x-ray crystal structure of the e2 domain of c. elegans apl-1
25	c3bogC_	Alignment	not modelled	10.3	87	**PDB header:**antifreeze protein **Chain:** C: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** snow flea antifreeze protein quasi-racemate
26	c3bogD_	Alignment	not modelled	10.3	87	**PDB header:**antifreeze protein **Chain:** D: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** snow flea antifreeze protein quasi-racemate
27	c1z5hB_	Alignment	not modelled	10.2	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tricorn protease interacting factor f3; **PDBTitle:** crystal structures of the tricorn interacting factor f32 from thermoplasma acidophilum
28	c3bjaA_	Alignment	not modelled	9.7	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a

						resolution
29	c3ju0A_	Alignment	not modelled	9.6	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7 integrase
30	c2zouB_	Alignment	not modelled	9.2	21	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**spondin-1; **PDBTitle:** crystal struture of human f-spondin reeler domain (fragment 2)
31	c2vn2B_	Alignment	not modelled	9.0	19	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
32	d2v9va2	Alignment	not modelled	7.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
33	c3cwcB_	Alignment	not modelled	7.8	35	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glycerate kinase 2; **PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
34	c3jtzA_	Alignment	not modelled	7.4	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structure of the arm-type binding domain of hpi integrase
35	c1cn3F_	Alignment	not modelled	7.1	88	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fragment of coat protein vp2; **PDBTitle:** interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of3 vp2 in viral entry
36	c2fl8N_	Alignment	not modelled	6.6	10	**PDB header:**virus/viral protein **Chain:** N: **PDB Molecule:**baseplate structural protein gp10; **PDBTitle:** fitting of the gp10 trimer structure into the cryoem map of the2 bacteriophage t4 baseplate in the hexagonal conformation.
37	c2pqnB_	Alignment	not modelled	6.6	27	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**mitochondrial division protein 1; **PDBTitle:** crystal structure of yeast fis1 complexed with a fragment of yeast2 mdv1
38	c3c5pF_	Alignment	not modelled	6.6	16	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**protein bas0735 of unknown function; **PDBTitle:** crystal structure of bas0735, a protein of unknown function from2 bacillus anthracis str. sterne
39	c3cooB_	Alignment	not modelled	6.4	21	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**spondin-1; **PDBTitle:** the crystal structure of reelin-n domain of f-spondin
40	c2oq0D_	Alignment	not modelled	6.3	16	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**gamma-interferon-inducible protein ifi-16; **PDBTitle:** crystal structure of the first hin-200 domain of interferon-inducible2 protein 16
41	c3pa8A_	Alignment	not modelled	6.2	9	**PDB header:**toxin/peptide inhibitor **Chain:** A: **PDB Molecule:**toxin b; **PDBTitle:** structure of the c. difficile tcdb cysteine protease domain in complex2 with a peptide inhibitor
42	c2l3nA_	Alignment	not modelled	6.2	53	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein rap1, telomere length regulator taz1; **PDBTitle:** solution structure of rap1-taz1 fusion protein
43	c2rddB_	Alignment	not modelled	6.0	7	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
44	c2khuA_	Alignment	not modelled	6.0	25	**PDB header:**transferase/protein binding **Chain:** A: **PDB Molecule:**immunoglobulin g-binding protein g, dna **PDBTitle:** solution structure of the ubiquitin-binding motif of human2 polymerase iota
45	c2l0gA_	Alignment	not modelled	5.9	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** solution nmr structure of ubiquitin-binding motif (ubm2) of human2 polymerase iota
46	c3pmrB_	Alignment	not modelled	5.9	27	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**amyloid-like protein 1; **PDBTitle:** crystal structure of e2 domain of human amyloid precursor-like protein2 1
47	d2hyma1	Alignment	not modelled	5.8	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
48	c2nnnB_	Alignment	not modelled	5.8	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
49	d1wfia_	Alignment	not modelled	5.6	7	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**Nuclear movement domain
50	c3n39D_	Alignment	not modelled	5.5	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein nrdi; **PDBTitle:** ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdi
51	c2x8kB_	Alignment	not modelled	5.3	12	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hypothetical protein 19.1; **PDBTitle:** crystal structure of spp1 dit (gp 19.1) protein, a paradigm2 of hub adsorption apparatus in gram-positive infecting3 phages.
52	c2o30A_	Alignment	not modelled	5.3	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nuclear movement protein; **PDBTitle:** nuclear movement protein from e. cuniculi gb-m1
53	c2kncA_	Alignment	not modelled	5.3	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex

54	c2jo1A_	Alignment	not modelled	5.3	23	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
55	c1kn7A_	Alignment	not modelled	5.2	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel protein kv1.4; **PDBTitle:** solution structure of the tandem inactivation domain2 (residues 1-75) of potassium channel rck4 (kv1.4)
56	d1ubea2	Alignment	not modelled	5.2	16	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
57	d1mo6a2	Alignment	not modelled	5.1	16	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
58	c2qwwB_	Alignment	not modelled	5.0	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution