
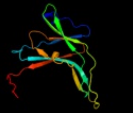

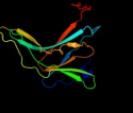



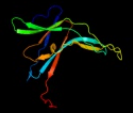



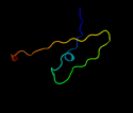






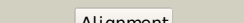








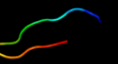
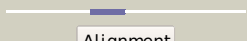
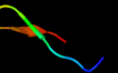
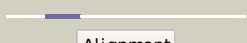

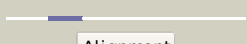


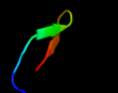


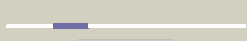
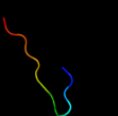
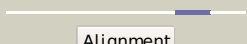
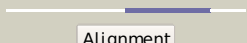
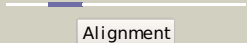
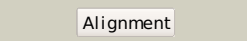
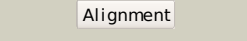
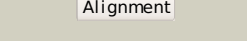
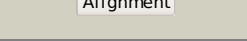
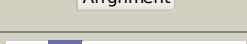



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xxfc_	 Alignment		100.0	96	Fold: Ecotin, trypsin inhibitor Superfamily: Ecotin, trypsin inhibitor Family: Ecotin, trypsin inhibitor
2	c2y6tE_	 Alignment		100.0	70	PDB header: hydrolase/inhibitor Chain: E: PDB Molecule: ecotin; PDBTitle: molecular recognition of chymotrypsin by the serine2 protease inhibitor ecotin from yersinia pestis
3	d1slua_	 Alignment		100.0	94	Fold: Ecotin, trypsin inhibitor Superfamily: Ecotin, trypsin inhibitor Family: Ecotin, trypsin inhibitor
4	d1ezsa_	 Alignment		100.0	98	Fold: Ecotin, trypsin inhibitor Superfamily: Ecotin, trypsin inhibitor Family: Ecotin, trypsin inhibitor
5	c1fi8E_	 Alignment		100.0	92	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: ecotin; PDBTitle: rat granzyme b [n66q] complexed to ecotin [81-84 iepd]
6	c1fi8F_	 Alignment		99.7	100	PDB header: hydrolase/hydrolase inhibitor Chain: F: PDB Molecule: ecotin; PDBTitle: rat granzyme b [n66q] complexed to ecotin [81-84 iepd]
7	c2la7A_	 Alignment		90.2	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein yp_557733.1 from burkholderia xenovorans
8	c2ktsA_	 Alignment		82.4	34	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hslj; PDBTitle: nmr structure of the protein np_415897.1
9	c1uw7A_	 Alignment		29.8	19	PDB header: replicase protein Chain: A: PDB Molecule: nsp9; PDBTitle: nsp9 protein from sars-coronavirus.
10	d2bhua1	 Alignment		25.5	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
11	d1qz8a_	 Alignment		22.2	19	Fold: Replicase NSP9 Superfamily: Replicase NSP9 Family: Replicase NSP9

12	c3ff6D_	 <div>Alignment</div>		19.0	29	PDB header: ligase Chain: D: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: human acc2 ct domain with cp-640186
13	c1od4C_	 <div>Alignment</div>		18.4	29	PDB header: ligase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
14	d1gl0i_	 <div>Alignment</div>		18.4	38	Fold: PMP inhibitors Superfamily: PMP inhibitors Family: PMP inhibitors
15	d1wo9a_	 <div>Alignment</div>		16.6	46	Fold: PMP inhibitors Superfamily: PMP inhibitors Family: PMP inhibitors
16	d2qyqa1	 <div>Alignment</div>		16.6	20	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
17	c2gzqa_	 <div>Alignment</div>		16.4	22	PDB header: lipid binding protein Chain: A: PDB Molecule: phosphatidylethanolamine-binding protein; PDBTitle: phosphatidylethanolamine-binding protein from plasmodium vivax
18	c2f91B_	 <div>Alignment</div>		16.3	46	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: serine protease inhibitor i/ii; PDBTitle: 1.2a resolution structure of a crayfish trypsin complexed2 with a peptide inhibitor, sgti
19	d1uyra2	 <div>Alignment</div>		15.7	29	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
20	c1wkpa_	 <div>Alignment</div>		15.2	36	PDB header: signaling protein Chain: A: PDB Molecule: flowering locus t protein; PDBTitle: flowering locus t (ft) from arabidopsis thaliana
21	c3h0ja_	 <div>Alignment</div>	not modelled	13.9	29	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the carboxyltransferase domain of2 acetyl-coenzyme a carboxylase in complex with compound 2
22	c3c5pF_	 <div>Alignment</div>	not modelled	13.7	17	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
23	c2jyzA_	 <div>Alignment</div>	not modelled	12.6	22	PDB header: unknown function Chain: A: PDB Molecule: cg7054-pa; PDBTitle: cg7054 solution structure
24	c2xu8B_	 <div>Alignment</div>	not modelled	12.1	30	PDB header: structural genomics Chain: B: PDB Molecule: pa1645; PDBTitle: structure of pa1645
25	d1igqa_	 <div>Alignment</div>	not modelled	11.7	28	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: Transcriptional repressor protein Korb
26	d1igub_	 <div>Alignment</div>	not modelled	11.6	28	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: Transcriptional repressor protein Korb
27	c2dreA_	 <div>Alignment</div>	not modelled	10.4	14	PDB header: plant protein Chain: A: PDB Molecule: water-soluble chlorophyll protein; PDBTitle: crystal structure of water-soluble chlorophyll protein from2 lepidium virginicum at 2.00 angstrom resolution
28	c1uytC_	 <div>Alignment</div>	not modelled	10.3	29	PDB header: transferase Chain: C: PDB Molecule: acetyl-coa carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
		 <div>Alignment</div>				Fold: PEBP-like

29	d1kn3a_	Alignment	not modelled	10.2	22	Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
30	d1qoua_	Alignment	not modelled	10.0	36	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
31	d1khua_	Alignment	not modelled	9.7	35	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
32	c2r77A_	Alignment	not modelled	9.6	17	PDB header: lipid binding protein Chain: A: PDB Molecule: phosphatidylethanolamine-binding protein, putative; PDBTitle: crystal structure of phosphatidylethanolamine-binding protein, 2 pfl0955c, from plasmodium falciparum
33	d1wpxb1	Alignment	not modelled	9.6	26	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
34	d1dd1a_	Alignment	not modelled	9.2	47	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
35	d1zxo2	Alignment	not modelled	9.1	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
36	d1a44a_	Alignment	not modelled	9.1	22	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
37	c4a1bB_	Alignment	not modelled	8.3	38	PDB header: ribosome Chain: B: PDB Molecule: rpl39; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rna and3 proteins of molecule 3.
38	c2l72A_	Alignment	not modelled	8.0	33	PDB header: protein binding Chain: A: PDB Molecule: actin depolymerizing factor, putative; PDBTitle: solution structure and dynamics of adf from toxoplasma gondii (tgadf)
39	d1o5ua_	Alignment	not modelled	7.6	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
40	d1ygsa_	Alignment	not modelled	7.6	47	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
41	d1zbsa1	Alignment	not modelled	7.5	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
42	d1xwva_	Alignment	not modelled	7.3	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: ML domain
43	d1u3em2	Alignment	not modelled	7.1	43	Fold: DNA-binding domain of intron-encoded endonucleases Superfamily: DNA-binding domain of intron-encoded endonucleases Family: DNA-binding domain of intron-encoded endonucleases
44	c3a9lB_	Alignment	not modelled	6.9	33	PDB header: hydrolase Chain: B: PDB Molecule: poly-gamma-glutamate hydrolase; PDBTitle: structure of bacteriophage poly-gamma-glutamate hydrolase
45	d1khxa_	Alignment	not modelled	6.9	41	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
46	c1khxA_	Alignment	not modelled	6.9	41	PDB header: transcription Chain: A: PDB Molecule: smad2; PDBTitle: crystal structure of a phosphorylated smad2
47	c2jv4A_	Alignment	not modelled	6.5	22	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis/trans isomerase; PDBTitle: structure characterisation of pina ww domain and comparison2 with other group iv ww domains, pin1 and ess1
48	d1jjcb3	Alignment	not modelled	6.3	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Myf domain
49	d2jnaa1	Alignment	not modelled	6.1	46	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
50	c3q1jA_	Alignment	not modelled	6.0	21	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 1 of human phd finger protein 20
51	c2zkr3_	Alignment	not modelled	5.8	83	PDB header: ribosomal protein/rna Chain: 3: PDB Molecule: 60s ribosomal protein l39e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
52	c2x24B_	Alignment	not modelled	5.3	24	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: bovine acc2 ct domain in complex with inhibitor