
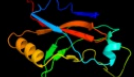









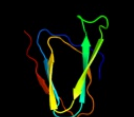







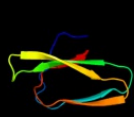


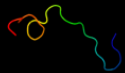


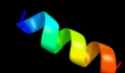
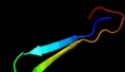


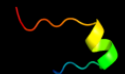



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1p6va_	 Alignment		100.0	50	Fold: Small protein B (SmpB) Superfamily: Small protein B (SmpB) Family: Small protein B (SmpB)
2	c1p6vC_	 Alignment		100.0	50	PDB header: rna binding protein/rna Chain: C: PDB Molecule: ssra-binding protein; PDBTitle: crystal structure of the trna domain of transfer-messenger2 rna in complex with smpb
3	c1j1hA_	 Alignment		100.0	46	PDB header: rna binding protein Chain: A: PDB Molecule: small protein b; PDBTitle: solution structure of a tmrna-binding protein, smpb, from2 thermus thermophilus
4	d1wjxa_	 Alignment		100.0	51	Fold: Small protein B (SmpB) Superfamily: Small protein B (SmpB) Family: Small protein B (SmpB)
5	d2ipqx1	 Alignment		37.1	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: STY4665 C-terminal domain-like
6	c2qnkA_	 Alignment		31.9	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyanthranilate 3,4-dioxygenase; PDBTitle: crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
7	c2agaA_	 Alignment		24.9	14	PDB header: transcription Chain: A: PDB Molecule: machado-joseph disease protein 1; PDBTitle: de-ubiquitinating function of ataxin-3: insights from the2 solution structure of the josephin domain
8	d1sdwa2	 Alignment		21.0	15	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: PHM/PNGase F Family: Peptidylglycine alpha-hydroxylating monooxygenase, PHM
9	d1zvfa1	 Alignment		19.7	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
10	d1yfua1	 Alignment		17.8	19	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
11	c1wqsA_	 Alignment		17.6	21	PDB header: hydrolase Chain: A: PDB Molecule: 3c-like protease; PDBTitle: crystal structure of norovirus 3c-like protease

12	dlg31a_	Alignment		15.1	36	Fold: GroES-like Superfamily: GroES-like Family: GroES
13	d2qfaa1	Alignment		14.1	27	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
14	c3jsbA_	Alignment		13.3	22	PDB header: rna binding protein Chain: A: PDB Molecule: rna-directed rna polymerase; PDBTitle: crystal structure of the n-terminal domain of the lymphocytic2 choriomeningitis virus I protein
15	c1hf9B_	Alignment		11.0	21	PDB header: atpase inhibitor Chain: B: PDB Molecule: atpase inhibitor (mitochondrial); PDBTitle: c-terminal coiled-coil domain from bovine if1
16	c2quoA_	Alignment		10.6	27	PDB header: toxin Chain: A: PDB Molecule: heat-labile enterotoxin b chain; PDBTitle: crystal structure of c terminal fragment of clostridium2 perfringens enterotoxin
17	d2raxa1	Alignment		10.1	27	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
18	d1m4ma_	Alignment		9.6	27	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
19	c2oa9B_	Alignment		9.5	10	PDB header: hydrolase Chain: B: PDB Molecule: r.mvai; PDBTitle: restriction endonuclease mvai in the absence of dna
20	c2w3zA_	Alignment		8.7	23	PDB header: hydrolase Chain: A: PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase
21	d1d1na_	Alignment	not modelled	8.3	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
22	d2c1ia1	Alignment	not modelled	8.1	24	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
23	d2nlya1	Alignment	not modelled	8.0	19	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Divergent polysaccharide deacetylase
24	d2cc0a1	Alignment	not modelled	7.9	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
25	c3mjda_	Alignment	not modelled	7.9	22	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
26	d1jd5a_	Alignment	not modelled	7.3	26	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
27	c2ylaA_	Alignment	not modelled	7.3	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
28	c3rpmA_	Alignment	not modelled	7.2	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetyl-hexosaminidase; PDBTitle: crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
29	c2z50A_	Alignment	not modelled	7.0	20	PDB header: protein transport Chain: A: PDB Molecule: protein adrm1;

29	c2z39A	Alignment	not modelled	7.0	29	PDBTitle: complex structures of mouse rpn13 (22-130aa) and ubiquitin
30	c2r2yA	Alignment	not modelled	7.0	29	PDB header: protein binding Chain: A: PDB Molecule: protein adrm1; PDBTitle: crystal structure of the proteasomal rpn13 pru-domain
31	d8ohma2	Alignment	not modelled	6.9	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
32	d2ieca1	Alignment	not modelled	6.8	71	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
33	d1kk1a1	Alignment	not modelled	6.6	36	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
34	d2i52a1	Alignment	not modelled	6.5	71	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
35	c2ogfD	Alignment	not modelled	6.1	57	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0408; PDBTitle: crystal structure of protein mj0408 from methanococcus jannaschii, 2 pfam duf372
36	d1jaka1	Alignment	not modelled	6.1	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
37	c2crvA	Alignment	not modelled	6.1	29	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: solution structure of c-terminal domain of mitochondrial2 translational initiationfactor 2
38	d1xb0b	Alignment	not modelled	6.0	27	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
39	d1yhta1	Alignment	not modelled	5.9	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
40	c2vm5A	Alignment	not modelled	5.9	27	PDB header: apoptosis Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1; PDBTitle: human bir2 domain of baculoviral inhibitor of apoptosis2 repeat-containing 1 (birc1)
41	d2gixa1	Alignment	not modelled	5.8	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
42	d1mkya3	Alignment	not modelled	5.8	9	Fold: Alpha-lytic protease prodomain-like Superfamily: Probable GTPase Der, C-terminal domain Family: Probable GTPase Der, C-terminal domain
43	c1oy7C	Alignment	not modelled	5.7	23	PDB header: apoptosis/peptide Chain: C: PDB Molecule: baculoviral iap repeat-containing protein 7; PDBTitle: structure and function analysis of peptide antagonists of melanoma2 inhibitor of apoptosis (ml-iap)
44	c2elvA	Alignment	not modelled	5.7	21	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 6th c2h2 zinc finger of human2 zinc finger protein 406
45	d1im3d	Alignment	not modelled	5.7	28	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytomegalovirus protein US2
46	d1gtda	Alignment	not modelled	5.6	23	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
47	c2odiA	Alignment	not modelled	5.6	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: r.bcni; PDBTitle: restriction endonuclease bcni-cognate dna substrate complex
48	d2i3ha1	Alignment	not modelled	5.5	23	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
49	d3d9ta1	Alignment	not modelled	5.5	26	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
50	d1q4qa	Alignment	not modelled	5.5	27	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
51	d1g73d	Alignment	not modelled	5.3	27	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
52	c3i7fA	Alignment	not modelled	5.3	25	PDB header: ligase Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: aspartyl trna synthetase from entamoeba histolytica
53	d1j5ua	Alignment	not modelled	5.1	16	Fold: MTH1598-like Superfamily: MTH1598-like Family: MTH1598-like