
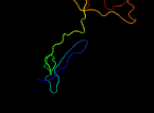





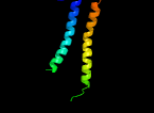

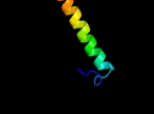
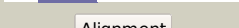
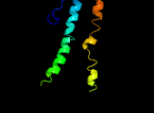
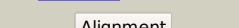

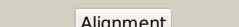

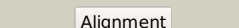
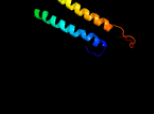
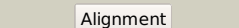
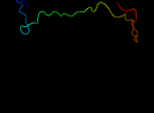








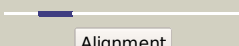
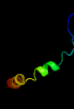
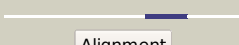
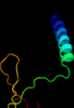
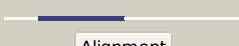

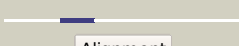
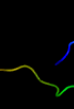

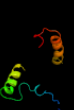

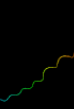


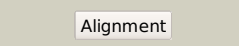

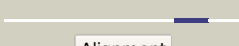
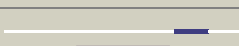



Phyre2

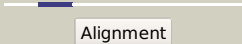

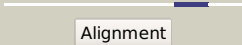
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Description	RVBD3695_(-)_4137384_4138316
Date	Fri Aug 9 18:20:38 BST 2019
Unique Job ID	5906940b7f9bb5a7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nl6C_	 Alignment		89.4	14	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
2	c6eznH_	 Alignment		22.3	20	PDB header: membrane protein Chain: H: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
3	c2dkdA_	 Alignment		18.4	25	PDB header: isomerase Chain: A: PDB Molecule: phosphoacetylglucosamine mutase; PDBTitle: crystal structure of n-acetylglucosamine-phosphate mutase,2 a member of the alpha-d-phosphohexomutase superfamily, in3 the product complex
4	c6hu9n_	 Alignment		14.4	16	PDB header: oxidoreductase/electron transport Chain: N: PDB Molecule: cytochrome b; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
5	c2zetD_	 Alignment		14.1	29	PDB header: signaling protein Chain: D: PDB Molecule: melanophilin; PDBTitle: crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin
6	c6hwhL_	 Alignment		13.9	15	PDB header: electron transport Chain: L: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
7	c6mizC_	 Alignment		13.7	13	PDB header: membrane protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: human trpm2 ion channel in an adpr-bound state
8	c4bjuB_	 Alignment		13.1	26	PDB header: isomerase Chain: B: PDB Molecule: n-acetylglucosamine-phosphate mutase; PDBTitle: genetic and structural validation of aspergillus fumigatus2 n-acetylphosphoglucosamine mutase as an antifungal target
9	c2yevB_	 Alignment		12.7	13	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase
10	c2kpyA_	 Alignment		12.4	23	PDB header: allergen Chain: A: PDB Molecule: major pollen allergen art v 1; PDBTitle: solution structure of the major allergen of artemisia vulgaris (art v2 1)
11	c2m76A_	 Alignment		12.0	20	PDB header: signaling protein Chain: A: PDB Molecule: carnitine o-palmitoyltransferase 1, brain isoform; PDBTitle: structure of the regulatory domain of human brain carnitine2 palmitoyltransferase 1

12	d1td4a_		Alignment		10.2	24	Fold: beta-clip Superfamily: Head decoration protein D (gpD, major capsid protein D) Family: Head decoration protein D (gpD, major capsid protein D)
13	d2f1la1		Alignment		9.8	20	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: RimM C-terminal domain-like
14	c6fkhe_		Alignment		9.7	23	PDB header: membrane protein Chain: E: PDB Molecule: atp synthase subunit alpha, chloroplastic; PDBTitle: chloroplast f1fo conformation 2
15	c2voyB_		Alignment		9.6	8	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
16	c4o7kA_		Alignment		8.3	12	PDB header: antitumor protein Chain: A: PDB Molecule: protein osa; PDBTitle: crystal structure of oncogenic suppression activity protein - a2 plasmid fertility inhibition factor
17	c4xtnj_		Alignment		8.0	6	PDB header: membrane protein Chain: J: PDB Molecule: sodium pumping rhodopsin; PDBTitle: crystal structure of the light-driven sodium pump kr2 in the2 pentameric red form, ph 4.9
18	d1c5ea_		Alignment		7.8	24	Fold: beta-clip Superfamily: Head decoration protein D (gpD, major capsid protein D) Family: Head decoration protein D (gpD, major capsid protein D)
19	c5wsnC_		Alignment		7.8	17	PDB header: virus Chain: C: PDB Molecule: e protein; PDBTitle: structure of japanese encephalitis virus
20	c2d3ff_		Alignment		7.7	35	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
21	c2d3fe_		Alignment	not modelled	7.7	35	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
22	c1x1kC_		Alignment	not modelled	7.7	35	PDB header: structural protein Chain: C: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
23	c2d3fD_		Alignment	not modelled	7.7	35	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
24	c1x1kA_		Alignment	not modelled	7.7	35	PDB header: structural protein Chain: A: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
25	c1x1kB_		Alignment	not modelled	7.7	35	PDB header: structural protein Chain: B: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
26	c1x1kD_		Alignment	not modelled	7.7	35	PDB header: structural protein Chain: D: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
							PDB header: structural protein Chain: A: PDB Molecule: collagen model peptides (pro-pro-gly)4-

27	c2d3fA_	Alignment	not modelled	7.3	36	pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4 PDB header: structural protein Chain: C: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4 PDB header: structural protein Chain: B: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4 PDB header: structural protein Chain: E: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4 PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4 PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
28	c2d3fC_	Alignment	not modelled	7.3	36	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
29	c2d3fB_	Alignment	not modelled	7.3	36	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4 PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4 PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
30	c1x1kE_	Alignment	not modelled	7.3	36	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
31	c3a19D_	Alignment	not modelled	7.0	38	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
32	c3a08F_	Alignment	not modelled	6.9	43	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
33	c2d3hF_	Alignment	not modelled	6.8	41	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4 PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4 PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
34	c2d3hD_	Alignment	not modelled	6.6	39	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
35	c3a19F_	Alignment	not modelled	6.6	39	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
36	c3a08D_	Alignment	not modelled	6.6	39	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
37	c1tmxA_	Alignment	not modelled	6.5	25	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyquinol 1,2-dioxygenase; PDBTitle: crystal structure of hydroxyquinol 1,2-dioxygenase from nocardiooides2 simplex 3e PDB header: membrane protein/calcium binding protein Chain: A: PDB Molecule: stra6; PDBTitle: structure of the stra6 receptor for retinol uptake in complex with2 calmodulin
38	c5sy1A_	Alignment	not modelled	6.3	11	PDB header: luminescent protein Chain: C: PDB Molecule: kaede; PDBTitle: crystal structure of stony coral fluorescent protein kaede, red form
39	c2gw4C_	Alignment	not modelled	6.3	47	PDB header: membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
40	c2hacA_	Alignment	not modelled	6.2	17	PDB header: membrane protein Chain: B: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
41	c2hacB_	Alignment	not modelled	6.2	17	PDB header: membrane protein Chain: B: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
42	c5fn2B_	Alignment	not modelled	6.2	17	PDB header: hydrolase Chain: B: PDB Molecule: presenilin-1; PDBTitle: cryo-em structure of gamma secretase in complex with a drug dapt
43	c6emkI_	Alignment	not modelled	5.9	42	PDB header: signaling protein Chain: I: PDB Molecule: target of rapamycin complex 2 subunit avo1; PDBTitle: cryo-em structure of saccharomyces cerevisiae target of rapamycin2 complex 2
44	c1x1kF_	Alignment	not modelled	5.7	30	PDB header: structural protein Chain: F: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4 PDB header: chaperone Chain: A: PDB Molecule: copc; PDBTitle: the crystal structure of copc from methylosinus trichosporium ob3b
45	c5icuA_	Alignment	not modelled	5.7	40	PDB header: membrane protein Chain: B: PDB Molecule: beta-type platelet-derived growth factor receptor; PDBTitle: pdgfr beta-tm
46	c2l6wB_	Alignment	not modelled	5.7	16	PDB header: membrane protein Chain: A: PDB Molecule: beta-type platelet-derived growth factor receptor; PDBTitle: pdgfr beta-tm
47	c2l6wA_	Alignment	not modelled	5.7	16	Fold: gpW/XkdW-like Superfamily: Head-to-tail joining protein W, gpW Family: Head-to-tail joining protein W, gpW
48	d1hywa_	Alignment	not modelled	5.6	17	PDB header: membrane protein Chain: C: PDB Molecule: acetylcholine receptor delta subunit; PDBTitle: gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
49	c4aq5C_	Alignment	not modelled	5.4	16	PDB header: ion channel/receptor Chain: C: PDB Molecule: acetylcholine receptor protein, delta chain; PDBTitle: refined structure of the nicotinic acetylcholine receptor2 at 4a resolution. PDB header: hydrolase
50	c2bg9C_	Alignment	not modelled	5.4	16	

51	c2rq7A_	 Alignment	not modelled	5.2	38	Chain: A; PDB Molecule: atp synthase epsilon chain; PDBTitle: solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1
52	c5n1tM_	 Alignment	not modelled	5.1	33	PDB header: oxidoreductase Chain: M; PDB Molecule: copc; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
53	c2cuoF_	 Alignment	not modelled	5.1	30	PDB header: structural protein Chain: F; PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9