

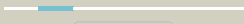


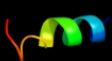






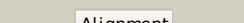




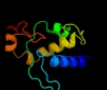

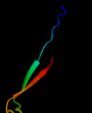










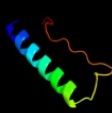


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jb0i_	 Alignment		40.2	28	Fold: Single transmembrane helix Superfamily: Subunit VIII of photosystem I reaction centre, PsaI Family: Subunit VIII of photosystem I reaction centre, PsaI
2	c3lw5l_	 Alignment		37.0	38	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: improved model of plant photosystem i
3	c2wse_	 Alignment		37.0	38	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: improved model of plant photosystem i
4	c2o01l_	 Alignment		30.9	38	PDB header: photosynthesis Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
5	d2nlva1	 Alignment		23.4	18	Fold: XisI-like Superfamily: XisI-like Family: XisI-like
6	d1n8ia_	 Alignment		21.4	36	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
7	c3d7qB_	 Alignment		19.2	24	PDB header: unknown function Chain: B: PDB Molecule: xisi protein-like; PDBTitle: crystal structure of a xisi-like protein (npun_ar114) from nostoc2 punctiforme pcc 73102 at 2.30 a resolution
8	d2czvc1	 Alignment		17.1	21	Fold: Ferredoxin-like Superfamily: Rnp2-like Family: Rpp14/Pop5-like
9	d2hxja1	 Alignment		11.5	16	Fold: FinO-like Superfamily: FinO-like Family: FinO-like
10	d1cf1a2	 Alignment		10.8	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
11	d2axth1	 Alignment		10.4	47	Fold: Single transmembrane helix Superfamily: Photosystem II 10 kDa phosphoprotein PsbH Family: PsbH-like

12	d2pgga1	Alignment		10.3	22	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
13	d1wi9a_	Alignment		10.2	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PCI domain (PINT motif)
14	c2v52M_	Alignment		10.0	75	PDB header: structural protein/contractile protein Chain: M: PDB Molecule: mkl/myocardin-like protein 1; PDBTitle: structure of mal-rpel2 complexed to g-actin
15	c3adyA_	Alignment		9.9	19	PDB header: proton transport Chain: A: PDB Molecule: dotd; PDBTitle: crystal structure of dotd from legionella
16	d2adza1	Alignment		9.6	20	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
17	d2ozbb1	Alignment		9.2	11	Fold: Nop domain Superfamily: Nop domain Family: Nop domain
18	d1li4a2	Alignment		8.7	15	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
19	d2efva1	Alignment		7.1	14	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: MJ0366-like
20	d1ew4a_	Alignment		6.4	18	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
21	c2p7vA_	Alignment	not modelled	6.3	15	PDB header: transcription Chain: A: PDB Molecule: regulator of sigma d; PDBTitle: crystal structure of the escherichia coli regulator of sigma 70, rsd, 2 in complex with sigma 70 domain 4
22	c2xi1A_	Alignment	not modelled	6.3	33	PDB header: viral protein Chain: A: PDB Molecule: nef; PDBTitle: crystal structure of the hiv-1 nef sequenced from a patient's sample
23	d1uuja_	Alignment	not modelled	6.0	30	Fold: Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain Superfamily: Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain Family: Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain
24	d2qw6a1	Alignment	not modelled	6.0	50	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
25	c2qw6A_	Alignment	not modelled	6.0	50	PDB header: hydrolase Chain: A: PDB Molecule: aaa atpase, central region; PDBTitle: crystal structure of the c-terminal domain of an aaa atpase from2 enterococcus faecium do
26	c2kw3C_	Alignment	not modelled	5.9	23	PDB header: dna binding protein Chain: C: PDB Molecule: regulatory factor x-associated protein; PDBTitle: heterotrimeric interaction between rfx5 and rfxap
27	c2r70A_	Alignment	not modelled	5.8	22	PDB header: transferase Chain: A: PDB Molecule: infectious bursal virus vp1 polymerase; PDBTitle: crystal structure of infectious bursal disease virus vp12 polymerase, cocrystallized with an oligopeptide mimicking3 the vp3 c-terminus.
28	c3ik5A_	Alignment	not modelled	5.6	25	PDB header: viral protein/signaling protein Chain: A: PDB Molecule: protein nef;

28	cstk2a	Alignment	not modelled	5.6	29	PDBTitle: sivmac239 nef in complex with tcr zeta itam 1 polypeptide2 (a63-r80)
29	dlayra2	Alignment	not modelled	5.5	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
30	d1efnb	Alignment	not modelled	5.4	25	Fold: Regulatory factor Nef Superfamily: Regulatory factor Nef Family: Regulatory factor Nef