


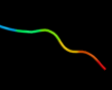



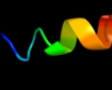


















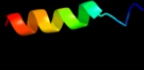






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hg5D_	 Alignment		26.3	19	PDB header: membrane protein Chain: D: PDB Molecule: kcsa channel; PDBTitle: cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
2	c2krxA_	 Alignment		26.1	57	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: asl3597 protein; PDBTitle: solution nmr structure of asl3597 from nostoc sp. pcc7120.2 northeast structural genomics consortium target id nsr244.
3	c1w8xP_	 Alignment		21.1	71	PDB header: virus Chain: P: PDB Molecule: protein p16; PDBTitle: structural analysis of prd1
4	c1rkCB_	 Alignment		17.7	54	PDB header: cell adhesion, structural protein Chain: B: PDB Molecule: talin; PDBTitle: human vinculin head (1-258) in complex with talin's2 vinculin binding site 3 (residues 1944-1969)
5	c1xwjB_	 Alignment		17.4	54	PDB header: cell adhesion/protein binding Chain: B: PDB Molecule: talin; PDBTitle: vinculin head (1-258) in complex with the talin vinculin2 binding site 3 (1945-1969)
6	d1xmeb2	 Alignment		15.7	47	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
7	d1smye_	 Alignment		14.2	29	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RNA polymerase omega subunit
8	d2gyc31	 Alignment		11.5	67	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
9	d1ynjk1	 Alignment		10.8	29	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RNA polymerase omega subunit
10	d2a5yb2	 Alignment		9.5	75	Fold: DEATH domain Superfamily: DEATH domain Family: Caspase recruitment domain, CARD
11	d1vkna2	 Alignment		9.5	36	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like

12	c1rqta	Alignment		9.2	67	PDB header: ribosome Chain: A: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: nmr structure of dimeric n-terminal domain of ribosomal protein l7 from e.coli
13	d1rqta	Alignment		9.2	67	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
14	c1rqtb	Alignment		9.2	67	PDB header: ribosome Chain: B: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: nmr structure of dimeric n-terminal domain of ribosomal protein l7 from e.coli
15	d2e74e1	Alignment		8.8	47	Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex
16	c2e74E	Alignment		8.8	47	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from m.laminosus
17	c2e75E	Alignment		8.8	47	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
18	c1vf5R	Alignment		8.8	47	PDB header: photosynthesis Chain: R: PDB Molecule: protein pet l; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
19	c1vf5E	Alignment		8.8	47	PDB header: photosynthesis Chain: E: PDB Molecule: protein pet l; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
20	c2e76E	Alignment		8.8	47	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmateillin (tds) from m.laminosus
21	d2q49a2	Alignment	not modelled	8.7	29	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
22	d2g17a2	Alignment	not modelled	8.2	27	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
23	d1whba	Alignment	not modelled	7.8	50	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
24	c3jycA	Alignment	not modelled	7.5	21	PDB header: metal transport Chain: A: PDB Molecule: inward-rectifier k+ channel kir2.2; PDBTitle: crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
25	c2kpeB	Alignment	not modelled	7.5	33	PDB header: membrane protein Chain: B: PDB Molecule: glycophorin-a; PDBTitle: refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
26	c2kpeA	Alignment	not modelled	7.5	33	PDB header: membrane protein Chain: A: PDB Molecule: glycophorin-a; PDBTitle: refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
27	d2gwfa1	Alignment	not modelled	7.2	50	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
28	d1ymka1	Alignment	not modelled	6.6	55	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
						PDB header: structural genomics, unknown function

29	c2ojlB_	Alignment	not modelled	6.6	50	Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
30	c2p0gB_	Alignment	not modelled	6.5	38	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: selenoprotein w-related protein; PDBTitle: crystal structure of selenoprotein w-related protein from2 vibrio cholerae. northeast structural genomics target vcr75
31	d1pgya_	Alignment	not modelled	6.4	47	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
32	d1pd0a4	Alignment	not modelled	6.1	27	Fold: Gelsolin-like Superfamily: C-terminal, gelsolin-like domain of Sec23/24 Family: C-terminal, gelsolin-like domain of Sec23/24
33	c2l0oA_	Alignment	not modelled	6.0	50	PDB header: membrane protein Chain: A: PDB Molecule: oxidoreductase that catalyzes reoxidation of dsba protein PDBTitle: dsbb3 peptide structure in 100% tfe
34	d2fa8a1	Alignment	not modelled	5.8	44	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
35	c3dexA_	Alignment	not modelled	5.5	56	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sav_2001; PDBTitle: crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.