



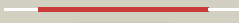

















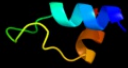







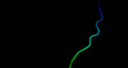


Phyre2

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Description	O08387
Date	Tue Jul 17 17:05:02 BST 2012
Unique Job ID	8394b0217ec82c09

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j01A_	 Alignment		100.0	41	PDB header: ribosome/ribosomal protein Chain: A; PDB Molecule: preprotein translocase secy subunit; PDBTitle: structure of the ribosome-secye complex in the membrane environment
2	c2zqpY_	 Alignment		100.0	38	PDB header: protein transport Chain: Y; PDB Molecule: preprotein translocase secy subunit; PDBTitle: crystal structure of secye translocon from thermus2 thermophilus
3	c3dl8H_	 Alignment		100.0	42	PDB header: protein transport Chain: H; PDB Molecule: preprotein translocase subunit secy; PDBTitle: structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
4	c3dinF_	 Alignment		100.0	39	PDB header: membrane protein, protein transport Chain: F; PDB Molecule: preprotein translocase subunit secy; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
5	c2wwbA_	 Alignment		100.0	21	PDB header: ribosome Chain: A; PDB Molecule: protein transport protein sec61 subunit alpha isoform 1; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
6	c2akiY_	 Alignment		100.0	42	PDB header: protein transport Chain: Y; PDB Molecule: preprotein translocase secy subunit; PDBTitle: normal mode-based flexible fitted coordinates of a2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
7	c2wwaA_	 Alignment		100.0	19	PDB header: ribosome Chain: A; PDB Molecule: sec sixty-one protein homolog; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
8	d1rh5a_	 Alignment		100.0	20	Fold: Preprotein translocase SecY subunit Superfamily: Preprotein translocase SecY subunit Family: Preprotein translocase SecY subunit
9	c3mp7A_	 Alignment		100.0	22	PDB header: protein transport Chain: A; PDB Molecule: preprotein translocase subunit secy; PDBTitle: lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
10	c2nscA_	 Alignment		71.6	28	PDB header: chaperone Chain: A; PDB Molecule: trigger factor; PDBTitle: structures of and interactions between domains of trigger factor from2 themotoga maritima
11	d1t11a2	 Alignment		66.4	16	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain

12	d1p9ya_	Alignment		65.2	13	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
13	d1w26a2	Alignment		56.7	13	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
14	c2d3o1_	Alignment		48.8	31	PDB header: ribosome Chain: 1: PDB Molecule: trigger factor; PDBTitle: structure of ribosome binding domain of the trigger factor2 on the 50s ribosomal subunit from d. radiodurans
15	c1w26B_	Alignment		45.3	25	PDB header: chaperone Chain: B: PDB Molecule: trigger factor; PDBTitle: trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
16	c1t11A_	Alignment		39.4	14	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: trigger factor
17	d1zl8a1	Alignment		19.8	32	Fold: L27 domain Superfamily: L27 domain Family: L27 domain
18	d1wmx_b	Alignment		18.0	33	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 30 carbohydrate binding module, CBM30 (PKD repeat)
19	d1y74a1	Alignment		16.3	27	Fold: L27 domain Superfamily: L27 domain Family: L27 domain
20	d1lebfa2	Alignment		11.5	29	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like
21	d1wpga4	Alignment	not modelled	10.9	13	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
22	c3ku7B_	Alignment	not modelled	10.7	25	PDB header: cell cycle factor; Chain: B: PDB Molecule: cell division topological specificity factor; PDBTitle: crystal structure of helicobacter pylori mine, a cell division2 topological specificity factor
23	c2i02B_	Alignment	not modelled	8.0	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
24	d1to9a_	Alignment	not modelled	7.9	19	Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: TENA/THI-4
25	c1to9A_	Alignment	not modelled	7.9	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: thi-4 protein; PDBTitle: crystal structure of thi-4 protein from bacillus subtilis
26	d2jdid1	Alignment	not modelled	7.5	12	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
27	c3kpaB_	Alignment	not modelled	7.5	21	PDB header: ligase Chain: B: PDB Molecule: probable ubiquitin fold modifier conjugating enzyme; PDBTitle: ubiquitin fold modifier conjugating enzyme from leishmania major2 (probable) PDB header: protein binding

28	c3okqA_	Alignment	not modelled	7.1	19	Chain: A; PDB Molecule: bud site selection protein 6; PDBTitle: crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
29	d1qd1a2	Alignment	not modelled	6.7	21	Fold: Ferredoxin-like Superfamily: Forminotransferase domain of forminotransferase-cyclodeaminase. Family: Forminotransferase domain of forminotransferase-cyclodeaminase.
30	c1mhsA_	Alignment	not modelled	6.6	13	PDB header: membrane protein, proton transport Chain: A; PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
31	d1jjcb1	Alignment	not modelled	6.5	23	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
32	d1iqoa_	Alignment	not modelled	6.4	21	Fold: Hypothetical protein MTH1880 Superfamily: Hypothetical protein MTH1880 Family: Hypothetical protein MTH1880
33	d2huec1	Alignment	not modelled	6.3	29	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
34	d1zqlc1	Alignment	not modelled	6.2	37	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like
35	d1uara1	Alignment	not modelled	6.1	10	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
36	d2gycf1	Alignment	not modelled	5.9	22	Fold: Ribosomal protein L9 C-domain Superfamily: Ribosomal protein L9 C-domain Family: Ribosomal protein L9 C-domain
37	c3qxlB_	Alignment	not modelled	5.9	27	PDB header: signaling protein Chain: B; PDB Molecule: ras-specific guanine nucleotide-releasing factor ralgs1; PDBTitle: crystal structure of the cdc25 domain from ral-specific guanine-2 nucleotide exchange factor ralgs1a
38	c2voyK_	Alignment	not modelled	5.8	22	PDB header: hydrolase Chain: K; PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
39	c4a01B_	Alignment	not modelled	5.8	14	PDB header: hydrolase Chain: B; PDB Molecule: proton pyrophosphatase; PDBTitle: crystal structure of the h-translocating pyrophosphatase
40	d1zrra1	Alignment	not modelled	5.7	14	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Acireductone dioxygenase
41	c3hlsE_	Alignment	not modelled	5.6	33	PDB header: signaling protein Chain: E; PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: crystal structure of the signaling helix coiled-coil doimain2 of the beta-1 subunit of the soluble guanylyl cyclase
42	c3mvuA_	Alignment	not modelled	5.5	8	PDB header: transcription regulator Chain: A; PDB Molecule: tena family transcriptional regulator; PDBTitle: crystal structure of a tena family transcription regulator2 (tm1040_3656) from silicibacter sp. tm1040 at 1.80 a resolution
43	c3gxxB_	Alignment	not modelled	5.5	29	PDB header: transcription Chain: B; PDB Molecule: transcription elongation factor spt6; PDBTitle: structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
44	d2fiqa1	Alignment	not modelled	5.4	25	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
45	c1uv7A_	Alignment	not modelled	5.1	21	PDB header: transport Chain: A; PDB Molecule: general secretion pathway protein m; PDBTitle: periplasmic domain of epsm from vibrio cholerae
46	d1uv7a_	Alignment	not modelled	5.1	21	Fold: RRF/tRNA synthetase additional domain-like Superfamily: General secretion pathway protein M, EpsM Family: General secretion pathway protein M, EpsM