

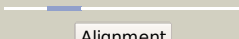

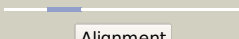






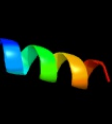





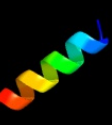







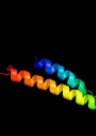

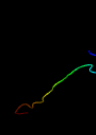
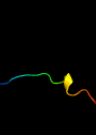
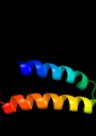



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0961 (-) _1074078_1074425
Date	Wed Jul 31 22:05:02 BST 2019
Unique Job ID	b3cfea48d5e35c0b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5gpdA_	 Alignment		39.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: sterol regulatory element-binding protein 1; PDBTitle: crystal structure of the binding domain of srebp from fission yeast
2	c3kdpG_	 Alignment		26.6	47	PDB header: hydrolase Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
3	c3kdpH_	 Alignment		26.6	47	PDB header: hydrolase Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
4	c2kvxA_	 Alignment		24.2	55	PDB header: plant protein Chain: A: PDB Molecule: kalata-b12; PDBTitle: solution structure of kalata b12
5	c4hqjG_	 Alignment		23.6	47	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
6	c6hraD_	 Alignment		23.1	50	PDB header: membrane protein Chain: D: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: cryo-em structure of the kdpfabc complex in an e1 outward-facing state2 (state 1)
7	c4hqjE_	 Alignment		22.0	47	PDB header: hydrolase/transport protein Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
8	c6hrbD_	 Alignment		18.1	44	PDB header: membrane protein Chain: D: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: cryo-em structure of the kdpfabc complex in an e2 inward-facing state2 (state 2)
9	c5mrwD_	 Alignment		18.1	44	PDB header: hydrolase Chain: D: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
10	c5mrwH_	 Alignment		18.1	44	PDB header: hydrolase Chain: H: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
11	c5mrwL_	 Alignment		18.1	44	PDB header: hydrolase Chain: L: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex

12	d1j5ja_	Alignment		15.5	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
13	c6gcs3_	Alignment		14.4	23	PDB header: oxidoreductase Chain: 3: PDB Molecule: nd3 subunit (nu3m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
14	c3ju6A_	Alignment		13.9	38	PDB header: transferase Chain: A: PDB Molecule: arginine kinase; PDBTitle: crystal structure of dimeric arginine kinase in complex with2 amppnp and arginine
15	c3rkoA_	Alignment		13.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-quinone oxidoreductase subunit a; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
16	c3rkoE_	Alignment		13.9	28	PDB header: oxidoreductase Chain: E: PDB Molecule: nadh-quinone oxidoreductase subunit a; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
17	d1m15a2	Alignment		12.8	37	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
18	c1wcoN_	Alignment		12.6	50	PDB header: peptide/antibiotic Chain: N: PDB Molecule: nisin z; PDBTitle: the solution structure of the nisin-lipid ii complex
19	c4he8B_	Alignment		12.4	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-quinone oxidoreductase subunit 7; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
20	d1qk1a2	Alignment		12.2	32	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
21	d1qh4a2	Alignment	not modelled	11.7	33	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
22	d1vrpa2	Alignment	not modelled	11.2	33	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
23	d1u6ra2	Alignment	not modelled	10.0	37	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
24	c2kr1A_	Alignment	not modelled	9.6	20	PDB header: ligase Chain: A: PDB Molecule: ubiquitin protein ligase e3a; PDBTitle: solution nmr structure of zinc binding n-terminal domain of ubiquitin-2 protein ligase e3a from homo sapiens. northeast structural genomics3 consortium (nesg) target hr3662
25	c3l2eB_	Alignment	not modelled	9.4	16	PDB header: transferase Chain: B: PDB Molecule: glycocyamine kinase beta chain; PDBTitle: glycocyamine kinase, alpha-beta heterodimer from marine worm2 namalycastis sp.
26	d1g0wa2	Alignment	not modelled	8.8	33	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
27	d1crka2	Alignment	not modelled	8.4	32	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
28	c1qk1H_	Alignment	not modelled	8.4	32	PDB header: transferase (creatine kinase) Chain: H: PDB Molecule: creatine kinase, ubiquitous mitochondrial; PDBTitle: crystal structure of human ubiquitous mitochondrial creatine kinase

29	c2m60A_	Alignment	not modelled	8.2	80	PDB header: antimicrobial protein Chain: A; PDB Molecule: enterocin jsb; PDBTitle: enterocin 7b
30	c6fh2A_	Alignment	not modelled	8.1	44	PDB header: signaling protein Chain: A; PDB Molecule: protein-arginine kinase; PDBTitle: protein arginine kinase mcsb in the amp-pn-bound state
31	d1xlyA_	Alignment	not modelled	8.0	86	Fold: RNA-binding protein She2p Superfamily: RNA-binding protein She2p Family: RNA-binding protein She2p
32	c4uoiB_	Alignment	not modelled	7.9	73	PDB header: viral protein Chain: B; PDB Molecule: genome polyprotein; PDBTitle: unexpected structure for the n-terminal domain of hepatitis c virus2 envelope glycoprotein e1
33	c1i0eD_	Alignment	not modelled	7.8	37	PDB header: transferase Chain: D; PDB Molecule: creatine kinase,m chain; PDBTitle: crystal structure of creatine kinase from human muscle
34	c1rl9A_	Alignment	not modelled	7.8	37	PDB header: transferase Chain: A; PDB Molecule: arginine kinase; PDBTitle: crystal structure of creatine- <i>adp</i> arginine kinase ternary2 complex
35	c1zecA_	Alignment	not modelled	7.2	86	PDB header: viral peptide Chain: A; PDB Molecule: nef1-25; PDBTitle: nmr solution structure of nef1-25, 20 structures
36	d2gw6a1	Alignment	not modelled	6.5	14	Fold: Restriction endonuclease-like Superfamily: tRNA-intron endonuclease catalytic domain-like Family: tRNA-intron endonuclease catalytic domain-like
37	d1ppjw_	Alignment	not modelled	6.0	22	Fold: Single transmembrane helix Superfamily: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
38	c6humC_	Alignment	not modelled	6.0	24	PDB header: proton transport Chain: C; PDB Molecule: nad(p)h-quinone oxidoreductase subunit 3; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
39	c4rf9A_	Alignment	not modelled	5.8	32	PDB header: transferase Chain: A; PDB Molecule: arginine kinase; PDBTitle: crystal structure of double-domain arginine kinase from anthopleura2 japonicas in complex with l-arginine and atpgs
40	d2glia5	Alignment	not modelled	5.4	36	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
41	d3cx5i1	Alignment	not modelled	5.4	30	Fold: Single transmembrane helix Superfamily: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
42	c4wo8A_	Alignment	not modelled	5.3	26	PDB header: transferase Chain: A; PDB Molecule: taurocyamine kinase; PDBTitle: the substrate-free duplicated taurocyamine kinase from schistosoma2 mansoni