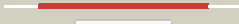



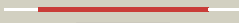



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2920c_(amt)_3231083_3232516
 Date Thu Aug 8 16:20:07 BST 2019
 Unique Job ID 5174152bd5320a4b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5aezA_	 Alignment		100.0	33	PDB header: membrane protein Chain: A: PDB Molecule: mep2; PDBTitle: crystal structure of candida albicans mep2
2	c5aexB_	 Alignment		100.0	35	PDB header: membrane protein Chain: B: PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
3	c2b2hA_	 Alignment		100.0	43	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: ammonium transporter amt-1 from a. fulgidus (as)
4	c2nuuF_	 Alignment		100.0	46	PDB header: transport protein/signaling protein Chain: F: PDB Molecule: ammonia channel; PDBTitle: regulating the escherichia coli ammonia channel: the crystal structure2 of the amtb-glnk complex
5	c6eu6A_	 Alignment		100.0	29	PDB header: membrane protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: sensor amt protein
6	c5aexJ_	 Alignment		100.0	34	PDB header: membrane protein Chain: J: PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
7	d1u7ga_	 Alignment		100.0	43	Fold: Ammonium transporter Superfamily: Ammonium transporter Family: Ammonium transporter
8	c3c1iA_	 Alignment		100.0	46	PDB header: transport protein Chain: A: PDB Molecule: ammonia channel; PDBTitle: substrate binding, deprotonation and selectivity at the periplasmic2 entrance of the e. coli ammonia channel amtb
9	c3hd6A_	 Alignment		100.0	18	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
10	c3b9yA_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
11	c4q2eA_	 Alignment		89.0	13	PDB header: transferase Chain: A: PDB Molecule: phosphatidate cytidyltransferase; PDBTitle: crystal structure of an intramembrane cdp-dag synthetase central for2 phospholipid biosynthesis (s200c/s258c, active mutant)

12	c5b57B_	Alignment		87.2	16	PDB header: metal transport Chain: B: PDB Molecule: putative hemin abc transport system, membrane protein; PDBTitle: inward-facing conformation of abc heme importer bhuv from2 burkholderia cenocepacia
13	c4ezdB_	Alignment		76.9	13	PDB header: transport protein Chain: B: PDB Molecule: urea transporter 1; PDBTitle: crystal structure of the ut-b urea transporter from bos taurus bound2 to selenourea
14	c4q2gA_	Alignment		63.3	12	PDB header: transferase Chain: A: PDB Molecule: phosphatidate cytidyltransferase; PDBTitle: crystal structure of an intramembrane cdp-dag synthetase central for2 phospholipid biosynthesis (s200c/s223c, inactive mutant)
15	c6gcsj_	Alignment		58.6	15	PDB header: oxidoreductase Chain: J: PDB Molecule: nujm subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
16	c4g1uB_	Alignment		57.2	16	PDB header: transport protein/hydrolase Chain: B: PDB Molecule: hemin transport system permease protein hmuu; PDBTitle: x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis
17	c4dbbB_	Alignment		56.6	17	PDB header: transport protein Chain: B: PDB Molecule: vitamin b12 import system permease protein btuc; PDBTitle: crystal structure of e159q mutant of btucdf
18	c3k3gA_	Alignment		39.7	20	PDB header: transport protein Chain: A: PDB Molecule: urea transporter; PDBTitle: crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
19	d2dexx1	Alignment		37.6	25	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Peptidylarginine deiminase Pad4, middle domain Family: Peptidylarginine deiminase Pad4, middle domain
20	c6mhhqE_	Alignment		28.5	21	PDB header: membrane protein Chain: E: PDB Molecule: gap junction alpha-3 protein, connexin-46; PDBTitle: structure of connexin-46 intercellular gap junction channel at 3.42 angstrom resolution by cryoem
21	c1vryA_	Alignment	not modelled	24.1	18	PDB header: membrane protein Chain: A: PDB Molecule: glycine receptor alpha-1 chain; PDBTitle: second and third transmembrane domains of the alpha-12 subunit of human glycine receptor
22	d1l7va_	Alignment	not modelled	21.1	14	Fold: ABC transporter involved in vitamin B12 uptake, BtuC Superfamily: ABC transporter involved in vitamin B12 uptake, BtuC Family: ABC transporter involved in vitamin B12 uptake, BtuC
23	c5x3xm_	Alignment	not modelled	20.5	15	PDB header: transport protein Chain: M: PDB Molecule: cobalt transport protein cbim; PDBTitle: 2.8a resolution structure of a cobalt energy-coupling factor2 transporter-cbimqo
24	c5gufA_	Alignment	not modelled	17.5	17	PDB header: transferase Chain: A: PDB Molecule: cdp-archaeol synthase; PDBTitle: structural insight into an intramembrane enzyme for archaeal membrane2 lipids biosynthesis
25	c6hwhX_	Alignment	not modelled	17.1	20	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
26	c6i1rA_	Alignment	not modelled	16.9	11	PDB header: membrane protein Chain: A: PDB Molecule: cmp-sialic acid transporter 1; PDBTitle: crystal structure of cmp bound cst in an outward facing conformation
27	c5i20C_	Alignment	not modelled	15.5	13	PDB header: membrane protein Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein
28	c4rngE_	Alignment	not modelled	14.8	25	PDB header: sugar binding protein Chain: E: PDB Molecule: mtn3/saliva family; PDBTitle: crystal structure of a bacterial homologue of sweet transporters
						PDB header: membrane protein Chain: C: PDB Molecule: full-length transmembrane domains of

29	c2m6iC	Alignment	not modelled	14.6	13	human glycine receptor PDBTitle: putative pentameric open-channel structure of full-length2 transmembrane domains of human glycine receptor alpha1 subunit
30	c5edlA	Alignment	not modelled	14.0	15	PDB header: transport protein Chain: A: PDB Molecule: putative hmp/thiamine permease protein ykoe; PDBTitle: crystal structure of an s-component of ecf transporter
31	c4apsB	Alignment	not modelled	12.4	10	PDB header: transport protein Chain: B: PDB Molecule: di-or tripeptide h+ symporter; PDBTitle: crystal structure of a pot family peptide transporter in an inward2 open conformation.
32	d2c42a2	Alignment	not modelled	11.2	36	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
33	c4qncA	Alignment	not modelled	11.0	21	PDB header: membrane protein Chain: A: PDB Molecule: chemical transport protein; PDBTitle: crystal structure of a semisweet in an occluded state
34	c5v2sA	Alignment	not modelled	11.0	33	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
35	c6rtfA	Alignment	not modelled	9.4	16	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 26 member 9,solute carrier family 26 PDBTitle: structure of murine solute carrier 26 family member a9 (slc26a9) anion2 transporter in an intermediate state
36	c5cthB	Alignment	not modelled	9.2	23	PDB header: transport protein Chain: B: PDB Molecule: bidirectional sugar transporter sweet2b; PDBTitle: the 3.7 a resolution structure of a eukaryotic sweet transporter
37	c6bm8A	Alignment	not modelled	8.7	42	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
38	c1f3kA	Alignment	not modelled	7.6	24	PDB header: toxin Chain: A: PDB Molecule: omega-conotoxin txvii; PDBTitle: three-dimensional solution structure of omega-conotoxin2 txvii, an l-type calcium channel blocker
39	c4x5mB	Alignment	not modelled	7.4	14	PDB header: transport protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of semisweet in the inward-open conformation
40	c4n2gA	Alignment	not modelled	7.4	33	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-2; PDBTitle: crystal structure of protein arginine deiminase 2 (d169a, 10 mm ca2+)
41	d1u1ha2	Alignment	not modelled	7.2	40	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Cobalamin-independent methionine synthase
42	c6exsA	Alignment	not modelled	7.1	12	PDB header: membrane protein Chain: A: PDB Molecule: peptide abc transporter permease; PDBTitle: crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
43	c6gcsG	Alignment	not modelled	6.8	24	PDB header: oxidoreductase Chain: G: PDB Molecule: 30-kda protein (nugm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
44	c3sokB	Alignment	not modelled	6.2	11	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
45	c5xpdA	Alignment	not modelled	6.1	17	PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
46	c4ikyA	Alignment	not modelled	6.1	12	PDB header: transport protein Chain: A: PDB Molecule: di-tripeptide abc transporter (permease); PDBTitle: crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
47	c4hlmD	Alignment	not modelled	6.0	17	PDB header: transferase Chain: D: PDB Molecule: tankyrase-2; PDBTitle: crystal structure of tankyrase 2 in complex with 3',4'-2 dihydroxyflavone
48	c5iwsA	Alignment	not modelled	5.9	13	PDB header: transferase Chain: A: PDB Molecule: protein-n(pi)-phosphohistidine-sugar phosphotransferase PDBTitle: crystal structure of the transporter malt, the eic domain from the2 maltose-specific phosphotransferase system
49	c4yzfA	Alignment	not modelled	5.9	12	PDB header: immune system Chain: A: PDB Molecule: band 3 anion transport protein; PDBTitle: crystal structure of the anion exchanger domain of human erythrocyte2 band 3
50	c2f1zB	Alignment	not modelled	5.8	18	PDB header: hydrolase Chain: B: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 7; PDBTitle: crystal structure of hausp
51	d1ttja	Alignment	not modelled	5.7	33	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
52	d1bwva1	Alignment	not modelled	5.6	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
53	c2dp3A	Alignment	not modelled	5.6	20	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
54	c5c2gD	Alignment	not modelled	5.5	13	PDB header: lyase Chain: D: PDB Molecule: form ii rubisco; PDBTitle: gws1b rubisco: form ii rubisco derived from uncultivated2

						gallionellacea species (cabp-bound).
55	c1izlj_	Alignment	not modelled	5.5	11	PDB header: photosynthesis Chain: J: PDB Molecule: photosystem ii: subunit psba; PDBTitle: crystal structure of photosystem ii
56	d1kv5a_	Alignment	not modelled	5.5	33	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
57	c2nq5A_	Alignment	not modelled	5.5	33	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of methyltransferase from streptococcus mutans
58	c2dexX_	Alignment	not modelled	5.4	25	PDB header: hydrolase Chain: X: PDB Molecule: protein-arginine deiminase type iv; PDBTitle: crystal structure of human peptidylarginine deiminase 4 in complex2 with histone h3 n-terminal peptide including arg17
59	d1wdda1	Alignment	not modelled	5.4	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
60	c4ztxA_	Alignment	not modelled	5.1	27	PDB header: transferase Chain: A: PDB Molecule: cobalamin-independent methionine synthase; PDBTitle: neurospora crassa cobalamin-independent methionine synthase complexed2 with zn2+
61	c3l7sA_	Alignment	not modelled	5.1	33	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of mete coordinated with zinc from streptococcus2 mutans
62	c3ppgA_	Alignment	not modelled	5.1	40	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of the candida albicans methionine synthase by2 surface entropy reduction, alanine variant with zinc
63	c5macD_	Alignment	not modelled	5.1	27	PDB header: lyase Chain: D: PDB Molecule: ribulose-1,5-bisphosphate carboxylase-oxygenase type iii; PDBTitle: crystal structure of decameric methanococcoides burtonii rubisco2 complexed with 2-carboxyarabinitol bisphosphate