







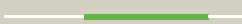


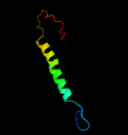

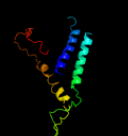

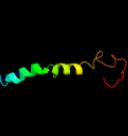


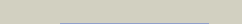


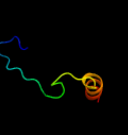
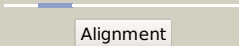


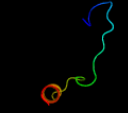


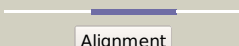

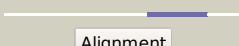

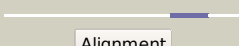
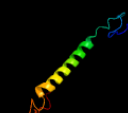
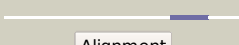
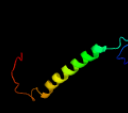






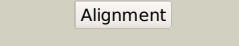
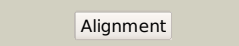
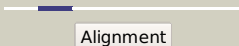
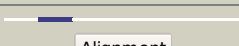
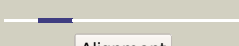
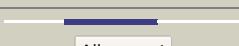


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1622c_cydB_1823367_1824407
 Date Fri Aug 2 13:30:21 BST 2019
 Unique Job ID fcc2e5c2c5484c96

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ir6B_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
2	c6cfwG_	 Alignment		87.9	10	PDB header: membrane protein Chain: G: PDB Molecule: monovalent cation/h+ antiporter subunit c; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
3	c6f0kC_	 Alignment		71.6	10	PDB header: membrane protein Chain: C: PDB Molecule: polysulphide reductase nrfd; PDBTitle: alternative complex iii
4	c3m7eA_	 Alignment		57.5	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein teha homolog; PDBTitle: crystal structure of plant slac1 homolog teha
5	c3m7bA_	 Alignment		57.5	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein teha homolog; PDBTitle: crystal structure of plant slac1 homolog teha
6	c2yevB_	 Alignment		45.1	14	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase
7	c4djiA_	 Alignment		35.3	15	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
8	d1fftb2	 Alignment		34.1	19	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
9	c5ir6A_	 Alignment		29.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: bd-type quinol oxidase subunit i; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
10	c6f0kF_	 Alignment		26.6	12	PDB header: membrane protein Chain: F: PDB Molecule: actf; PDBTitle: alternative complex iii
11	d1ejxc2	 Alignment		24.2	25	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain

12	c5wudA_		Alignment		24.1	28	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structural basis for conductance through tric cation channels
13	d1e9yb2		Alignment		22.3	22	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
14	c4lhdB_		Alignment		18.9	38	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine dehydrogenase [decarboxylating]; PDBTitle: crystal structure of synechocystis sp. pcc 6803 glycine decarboxylase2 (p-protein), holo form with pyridoxal-5'-phosphate and glycine,3 closed flexible loop
15	c4rymA_		Alignment		18.1	11	PDB header: membrane protein Chain: A: PDB Molecule: integral membrane protein; PDBTitle: crystal structure of bctspo iodo type1 monomer
16	d2r6gf1		Alignment		17.7	13	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
17	c1ar1B_		Alignment		16.6	9	PDB header: complex (oxidoreductase/antibody) Chain: B: PDB Molecule: cytochrome c oxidase; PDBTitle: structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
18	c1qleB_		Alignment		16.6	9	PDB header: oxidoreductase/immune system Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: cryo-structure of the paracoccus denitrificans four-subunit cytochrome2 c oxidase in the completely oxidized state complexed with an antibody3 fv fragment
19	c5fayA_		Alignment		14.9	19	PDB header: lyase Chain: A: PDB Molecule: choline trimethylamine-lyase; PDBTitle: y208f mutant of choline tma-lyase
20	c2bo9B_		Alignment		11.4	19	PDB header: hydrolase Chain: B: PDB Molecule: human latexin; PDBTitle: human carboxypeptidase a4 in complex with human latexin.
21	c2f3oB_		Alignment	not modelled	10.7	19	PDB header: unknown function Chain: B: PDB Molecule: pyruvate formate-lyase 2; PDBTitle: crystal structure of a glycy radical enzyme from archaeoglobus2 fulgidus
22	c5a0uA_		Alignment	not modelled	10.6	29	PDB header: lyase Chain: A: PDB Molecule: choline trimethylamine lyase; PDBTitle: structure of cutc choline lyase choline bound form from klebsiella2 pneumoniae.
23	c5ymrB_		Alignment	not modelled	10.3	19	PDB header: lyase Chain: B: PDB Molecule: formate acetyltransferase; PDBTitle: the crystal structure of iseg
24	c6hwhL_		Alignment	not modelled	10.3	12	PDB header: electron transport Chain: L: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
25	c5lnkn_		Alignment	not modelled	8.9	24	PDB header: oxidoreductase Chain: N: PDB Molecule: mitochondrial complex i, nd2 subunit; PDBTitle: entire ovine respiratory complex i
26	c5wufA_		Alignment	not modelled	8.1	23	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein; PDBTitle: structural basis for conductance through tric cation channels
27	c2ktaA_		Alignment	not modelled	7.9	42	PDB header: hydrolase Chain: A: PDB Molecule: putative helicase; PDBTitle: solution nmr structure of a domain of protein a6ky75 from bacteroides2 vulgatus, northeast structural genomics target bvr106a
28	c5xmjG_		Alignment	not modelled	7.8	14	PDB header: electron transport Chain: G: PDB Molecule: fumarate reductase respiratory complex; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas

29	c5h36E_	Alignment	not modelled	7.7	17	PDB header: membrane protein Chain: E; PDB Molecule: uncharacterized protein tric; PDBTitle: crystal structures of the tric trimeric intracellular cation channel2 orthologue from rhodobacter sphaeroides
30	c1fftG_	Alignment	not modelled	7.6	8	PDB header: oxidoreductase Chain: G; PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli
31	c5h35C_	Alignment	not modelled	7.6	16	PDB header: immune system/membrane protein Chain: C; PDB Molecule: membrane protein tric; PDBTitle: crystal structures of the tric trimeric intracellular cation channel2 orthologue from sulfolobus solfataricus
32	c5i1mV_	Alignment	not modelled	7.2	13	PDB header: membrane protein Chain: V; PDB Molecule: v-type proton atpase subunit a, vacuolar isoform; PDBTitle: yeast v-atpase average of densities, a subunit segment
33	c5jffC_	Alignment	not modelled	7.2	27	PDB header: transferase Chain: C; PDB Molecule: probable adenosine monophosphate-protein transferase fic; PDBTitle: e. coli ecfct mutant g55r in complex with ecfica
34	c4x2eA_	Alignment	not modelled	7.2	36	PDB header: transferase Chain: A; PDB Molecule: fic family protein putative filamentation induced by camp PDBTitle: clostridium difficile wild type fic protein
35	c4yifA_	Alignment	not modelled	7.2	60	PDB header: oxidoreductase Chain: A; PDB Molecule: dihydroorotate dehydrogenase b (nad(+)), electron transfer PDBTitle: insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
36	c5ly0B_	Alignment	not modelled	6.9	18	PDB header: transcription Chain: B; PDB Molecule: lob family transfactor ramosa2.1; PDBTitle: crystal structure of lob domain of ramosa2 from wheat
37	c4heaJ_	Alignment	not modelled	6.7	9	PDB header: oxidoreductase Chain: J; PDB Molecule: nadh-quinone oxidoreductase subunit 10; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
38	c4hkrB_	Alignment	not modelled	6.4	14	PDB header: transport protein Chain: B; PDB Molecule: calcium release-activated calcium channel protein 1; PDBTitle: calcium release-activated calcium (crac) channel orai
39	c2mgvA_	Alignment	not modelled	5.9	20	PDB header: membrane protein Chain: A; PDB Molecule: translocator protein; PDBTitle: solution structure of the mitochondrial translocator protein (tspo) in2 complex with its high-affinity ligand pk11195
40	c2hfaA_	Alignment	not modelled	5.5	23	PDB header: transferase Chain: A; PDB Molecule: rna-directed rna polymerase(ns5); PDBTitle: crystal structure of rna dependent rna polymerase domain2 from west Nile virus
41	c5voxb_	Alignment	not modelled	5.5	14	PDB header: hydrolase Chain: B; PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
42	c2v5iA_	Alignment	not modelled	5.3	63	PDB header: viral protein Chain: A; PDB Molecule: salmonella typhimurium db7155 bacteriophage det7 tailspike; PDBTitle: structure of the receptor-binding protein of bacteriophage det7: a2 podoviral tailspike in a myovirus
43	c4hkrA_	Alignment	not modelled	5.2	14	PDB header: transport protein Chain: A; PDB Molecule: calcium release-activated calcium channel protein 1; PDBTitle: calcium release-activated calcium (crac) channel orai
44	c6nbxG_	Alignment	not modelled	5.2	14	PDB header: oxidoreductase Chain: G; PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)