
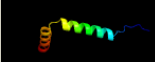
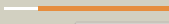
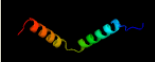



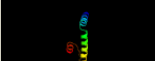



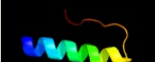





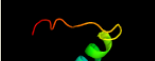

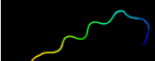

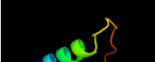


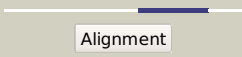
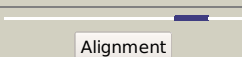
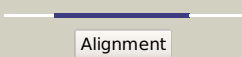
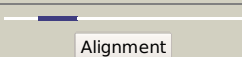
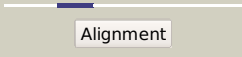
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1489A (-) _1678948_1679178
Date	Fri Aug 2 13:30:07 BST 2019
Unique Job ID	9e9eef460bc79eaf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d7reqa1	 Alignment		90.2	53	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Methylmalonyl-CoA mutase, N-terminal (CoA-binding) domain
2	c1e1cA	 Alignment		87.9	50	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
3	c3bicA	 Alignment		61.6	39	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase
4	c4r3uB	 Alignment		57.7	29	PDB header: isomerase Chain: B: PDB Molecule: 2-hydroxyisobutyryl-coa mutase large subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
5	c4xc8B	 Alignment		39.9	24	PDB header: isomerase Chain: B: PDB Molecule: isobutyryl-coa mutase fused; PDBTitle: isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
6	c5ngyA	 Alignment		19.4	41	PDB header: transferase Chain: A: PDB Molecule: dsr-m glucansucrase inactive mutant e715q; PDBTitle: crystal structure of leuconostoc citreum nrri1 b-1299 dextransucrase2 dsr-m
7	d1nsoa	 Alignment		15.7	41	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
8	d1ls9a	 Alignment		13.4	30	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
9	c3hz3A	 Alignment		12.9	44	PDB header: transferase Chain: A: PDB Molecule: glucansucrase; PDBTitle: lactobacillus reuteri n-terminally truncated glucansucrase2 gtf180(d1025n)-sucrose complex
10	c1yd7A	 Alignment		12.2	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-keto acid:ferredoxin oxidoreductase subunit alpha; PDBTitle: conserved hypothetical protein pfu-1647980-001 from pyrococcus2 furiosus
11	c6hvgA	 Alignment		12.0	48	PDB header: transferase Chain: A: PDB Molecule: alternansucrase; PDBTitle: crystal structure of truncated alternansucrase from leuconostoc2 mesenteroides nrri1 b-1355

12	c3ov5A_	Alignment		11.7	36	PDB header: protein transport Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: atomic structure of the xanthomonas citri virb7 globular domain.
13	c5lfcA_	Alignment		11.0	41	PDB header: transferase Chain: A: PDB Molecule: dsrv; PDBTitle: crystal structure of leuconostoc citreum nrml b-1299 n-terminally2 truncated dextranucrase dsr-m
14	d2in5a1	Alignment		10.5	45	Fold: YmcC-like Superfamily: YmcC-like Family: YmcC-like
15	d1r3ea1	Alignment		10.0	13	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
16	c4aygB_	Alignment		8.7	48	PDB header: transferase Chain: B: PDB Molecule: glucansucrase; PDBTitle: lactobacillus reuteri n-terminally truncated glucansucrase gtf180 in2 orthorhombic apo-form
17	c5z81A_	Alignment		8.6	23	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 15; PDBTitle: trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
18	d2cx1a1	Alignment		8.4	50	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
19	d2ey4a1	Alignment		8.2	50	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
20	c3r90E_	Alignment		8.0	63	PDB header: rna binding protein Chain: E: PDB Molecule: malignant t cell-amplified sequence 1; PDBTitle: crystal structure of malignant t cell-amplified sequence 1 protein
21	c3ttoD_	Alignment	not modelled	7.8	41	PDB header: transferase Chain: D: PDB Molecule: dextranucrase; PDBTitle: crystal structure of leuconostoc mesenteroides nrml b-1299 n-2 terminally truncated dextranucrase dsr-e in triclinic form
22	c5vaeH_	Alignment	not modelled	7.4	44	PDB header: cell adhesion Chain: H: PDB Molecule: accessory sec system protein asp3; PDBTitle: crystal structure of accessory secretion protein 1 and 3
23	c1q7hA_	Alignment	not modelled	6.6	63	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: structure of a conserved pua domain protein from thermoplasma2 acidophilum
24	c1zs7A_	Alignment	not modelled	6.5	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ape0525; PDBTitle: the structure of gene product ape0525 from aeropyrum pernix
25	c2mc5A_	Alignment	not modelled	6.5	50	PDB header: protein binding Chain: A: PDB Molecule: 45l; PDBTitle: a bacteriophage transcription regulator inhibits bacterial2 transcription initiation by -factor displacement
26	c3aicC_	Alignment	not modelled	6.5	48	PDB header: transferase Chain: C: PDB Molecule: glucosyltransferase-si; PDBTitle: crystal structure of glucansucrase from streptococcus mutans
27	c5jfbB_	Alignment	not modelled	6.4	52	PDB header: transferase Chain: B: PDB Molecule: inactive glucansucrase; PDBTitle: 4,6-alpha-glucanotransferase gtfb (d1015n mutant) from lactobacillus2 reuteri 121 complexed with maltopentaose
28	c2ve7A_	Alignment	not modelled	5.9	33	PDB header: cell cycle Chain: A: PDB Molecule: kinetochore protein hec1, kinetochore protein spc25; PDBTitle: crystal structure of a bonsai version of the human ndc80 complex

29	d2rspa_	 Alignment	not modelled	5.5	32	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
30	d1iq8a3	 Alignment	not modelled	5.4	25	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
31	c2rkhA_	 Alignment	not modelled	5.4	45	PDB header: transcription Chain: A: PDB Molecule: putative apha-like transcription factor; PDBTitle: crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution
32	c1debA_	 Alignment	not modelled	5.2	64	PDB header: structural protein Chain: A: PDB Molecule: adenomatous polyposis coli protein; PDBTitle: crystal structure of the n-terminal coiled coil domain from apc
33	c5jzB_	 Alignment	not modelled	5.1	69	PDB header: transferase Chain: B: PDB Molecule: uncharacterized protein yhfg; PDBTitle: e. coli ecfict in complex with ecfica mutant e28g