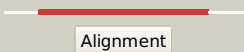

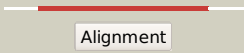

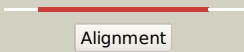

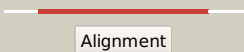

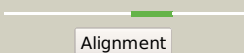

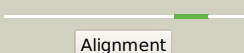
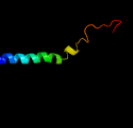


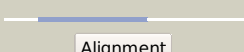

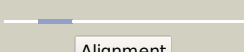

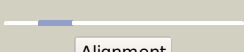
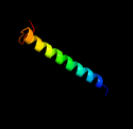
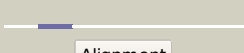
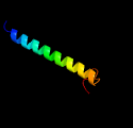











Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2156c_(mraY)_2416404_2417483
 Date Mon Aug 5 13:25:28 BST 2019
 Unique Job ID 4105969620b63232

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4j72A_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: crystal structure of polyprenyl-phosphate n-acetyl hexosamine 1-2 phosphate transferase
2	c5jnqA_	 Alignment		100.0	35	PDB header: transferase/antibiotic Chain: A: PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: mray tunicamycin complex
3	c4j72B_	 Alignment		100.0	33	PDB header: transferase Chain: B: PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: crystal structure of polyprenyl-phosphate n-acetyl hexosamine 1-2 phosphate transferase
4	c5levA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine--dolichyl-phosphate n- PDBTitle: crystal structure of human udp-n-acetylglucosamine-dolichyl-phosphate2 n-acetylglucosaminephosphotransferase (dpagt1) (v264g mutant)
5	c6m97A_	 Alignment		57.5	23	PDB header: transport protein Chain: A: PDB Molecule: chimera protein of high affinity copper uptake protein 1 PDBTitle: crystal structure of the high-affinity copper transporter ctr1
6	c2k74A_	 Alignment		55.0	24	PDB header: membrane protein, oxidoreductase Chain: A: PDB Molecule: disulfide bond formation protein b; PDBTitle: solution nmr structure of dsbb-ubiquinone complex
7	d1o5ha_	 Alignment		25.6	17	Fold: Methenyltetrahydrofolate cyclohydrolase-like Superfamily: Methenyltetrahydrofolate cyclohydrolase-like Family: Methenyltetrahydrofolate cyclohydrolase-like
8	c5gasN_	 Alignment		23.7	21	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
9	c4ntfA_	 Alignment		23.0	10	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: mus musculus itc4 synthase in s-hexyl-gsh complex form
10	c2uuiA_	 Alignment		21.0	13	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
11	c3b29A_	 Alignment		18.6	13	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: human leukotriene c4 synthase in complex with dodecyl-beta-d-2 selenomaltoside

12	c6btmD	Alignment		16.8	14	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
13	c2pnoH	Alignment		16.7	13	PDB header: lyase Chain: H: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
14	c2pnoC	Alignment		16.7	13	PDB header: lyase Chain: C: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
15	c2pnoK	Alignment		16.7	13	PDB header: lyase Chain: K: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
16	c2pnoB	Alignment		16.7	13	PDB header: lyase Chain: B: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
17	c2pnoL	Alignment		16.7	13	PDB header: lyase Chain: L: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
18	c2pnoE	Alignment		16.7	13	PDB header: lyase Chain: E: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
19	c2pnoF	Alignment		16.7	13	PDB header: lyase Chain: F: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
20	c2pnoD	Alignment		16.7	13	PDB header: lyase Chain: D: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
21	c2pnoA	Alignment	not modelled	16.7	13	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
22	c2pnoG	Alignment	not modelled	16.7	13	PDB header: lyase Chain: G: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
23	c2pnoJ	Alignment	not modelled	16.7	13	PDB header: lyase Chain: J: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
24	d2uuia1	Alignment	not modelled	16.7	13	Fold: MAPEG domain-like Superfamily: MAPEG domain-like Family: MAPEG domain
25	c2pnoI	Alignment	not modelled	16.7	13	PDB header: lyase Chain: I: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
26	c3hkkA	Alignment	not modelled	14.5	13	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: structure of human leukotriene c4 synthase in complex with glutathione2 sulfonate
27	c3pcvA	Alignment	not modelled	14.4	13	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure analysis of human leukotriene c4 synthase at 1.92 angstrom resolution
28	c2uuhA	Alignment	not modelled	12.9	13	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase in2 complex with substrate glutathione
29	c2pnoC	Alignment	not modelled	12.3	21	PDB header: protein fibril Chain: C: PDB Molecule: small s protein;

29	c2imlc_	Alignment	not modelled	12.5	31	PDBTitle: structure of the het-s(218-289) prion in its amyloid form obtained by2 solid-state nmr PDB header: lyase
30	c3leoA_	Alignment	not modelled	10.8	13	Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: structure of human leukotriene c4 synthase mutant r31q in complex with2 glutathione
31	c2jxpA_	Alignment	not modelled	10.4	28	PDB header: lipoprotein Chain: A: PDB Molecule: putative lipoprotein b; PDBTitle: solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
32	d2q7ra1	Alignment	not modelled	8.2	11	Fold: MAPEG domain-like Superfamily: MAPEG domain-like Family: MAPEG domain
33	c3tu8A_	Alignment	not modelled	8.2	38	PDB header: unknown function Chain: A: PDB Molecule: burkholderia lethal factor 1 (blf1); PDBTitle: crystal structure of the burkholderia lethal factor 1 (blf1)
34	d2c42a2	Alignment	not modelled	7.9	38	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
35	c5mlc7_	Alignment	not modelled	7.5	29	PDB header: ribosome Chain: 7: PDB Molecule: psrp5alpha, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
36	c3e61A_	Alignment	not modelled	7.4	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional repressor of ribose operon; PDBTitle: crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
37	c3nk4C_	Alignment	not modelled	7.1	31	PDB header: cell adhesion Chain: C: PDB Molecule: zona pellucida 3; PDBTitle: crystal structure of full-length sperm receptor zp3 at 2.0 a2 resolution
38	c3nk3C_	Alignment	not modelled	7.0	31	PDB header: cell adhesion Chain: C: PDB Molecule: zona pellucida 3; PDBTitle: crystal structure of full-length sperm receptor zp3 at 2.6 a2 resolution
39	c2k21A_	Alignment	not modelled	6.3	14	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c
40	c5un8B_	Alignment	not modelled	6.3	33	PDB header: hydrolase Chain: B: PDB Molecule: protein o-glcnacase; PDBTitle: crystal structure of human o-glcnacase in complex with glycopeptide2 p53
41	d2cbia2	Alignment	not modelled	6.0	33	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
42	c5mmi6_	Alignment	not modelled	5.7	29	PDB header: ribosome Chain: 6: PDB Molecule: plastid ribosomal protein cl37, psrp5; PDBTitle: structure of the large subunit of the chloroplast ribosome
43	d1kf6d_	Alignment	not modelled	5.7	17	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
44	c2mfrA_	Alignment	not modelled	5.6	24	PDB header: transferase Chain: A: PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
45	d2choa2	Alignment	not modelled	5.5	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
46	c2m0qA_	Alignment	not modelled	5.4	14	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 2; PDBTitle: solution nmr analysis of intact kcne2 in detergent micelles2 demonstrate a straight transmembrane helix