

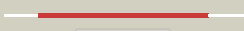








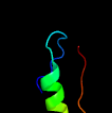











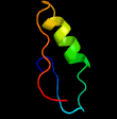




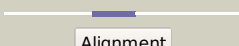

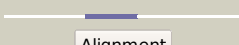

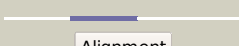






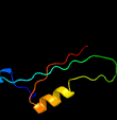

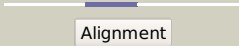

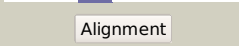

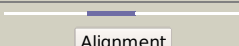
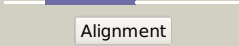



Phyre2

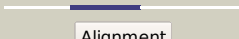
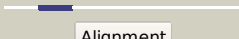
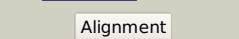
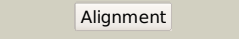
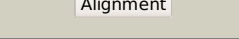
Email	mdejesus@rockefeller.edu
Description	RVBD3814c_(-)_4279408_4280193
Date	Fri Aug 9 18:20:52 BST 2019
Unique Job ID	37de9685018e1e12

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kymA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: 1-acyl-sn-glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of the 1-acyl-sn-glycerophosphate (lpa)2 acyltransferase, plsc, from thermotoga maritima
2	c5f34A_	 Alignment		99.8	14	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannoside acyltransferase; PDBTitle: crystal structure of membrane associated pata from mycobacterium2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
3	c5knkB_	 Alignment		99.7	17	PDB header: transferase Chain: B: PDB Molecule: lipid a biosynthesis lauroyl acyltransferase; PDBTitle: lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
4	d1iuga_	 Alignment		99.1	14	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
5	c6g2dC_	 Alignment		35.5	12	PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
6	c4mxnB_	 Alignment		31.7	8	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative glycosyl hydrolase (parmer_00599) from2 parabacteroides merdae atcc 43184 at 1.95 a resolution
7	c3hkxA_	 Alignment		22.7	14	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure analysis of an amidase from nesterenkonia sp.
8	c2ov3A_	 Alignment		21.9	13	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein component of an abc type zinc PDBTitle: crystal structure of 138-173 znua deletion mutant plus zinc bound
9	c3zppA_	 Alignment		20.3	19	PDB header: cell adhesion Chain: A: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structure of the streptococcus pneumoniae surface protein2 and adhesin pfba
10	c4cyyA_	 Alignment		19.4	12	PDB header: hydrolase Chain: A: PDB Molecule: pantetheinase; PDBTitle: the structure of vanin-1: defining the link between metabolic disease,2 oxidative stress and inflammation
11	c3jurA_	 Alignment		18.5	16	PDB header: hydrolase Chain: A: PDB Molecule: exo-poly-alpha-d-galacturonidase; PDBTitle: the crystal structure of a hyperthermoactive exopolysaccharonase from2 thermotoga maritima

12	c5olpB_		Alignment		17.3	19	PDB header: hydrolase Chain: B: PDB Molecule: pectate lyase; PDBTitle: galacturonidase
13	d1pq4a_		Alignment		17.1	12	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
14	c2e11B_		Alignment		16.0	16	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
15	c5khaA_		Alignment		15.1	12	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad+ synthetase; PDBTitle: structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
16	c1r0lD_		Alignment		15.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph
17	c2ogwB_		Alignment		14.5	18	PDB header: transport protein Chain: B: PDB Molecule: high-affinity zinc uptake system protein znua PDBTitle: structure of abc type zinc transporter from e. coli
18	c5uyvA_		Alignment		14.0	18	PDB header: metal transport Chain: A: PDB Molecule: periplasmic chelated iron-binding protein yfea; PDBTitle: yfea ancillary sites that do not co-load with site 2
19	c4hnbB_		Alignment		12.9	13	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
20	d1v7za_		Alignment		12.5	17	Fold: Creatininase Superfamily: Creatininase Family: Creatininase
21	c6r6kB_		Alignment	not modelled	12.0	17	PDB header: protein transport Chain: B: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: structure of a fpvc mutant from pseudomonas aeruginosa
22	c3a14B_		Alignment	not modelled	11.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of dxr from thermotoga maritima, in complex with2 nadph
23	d2ffca1		Alignment	not modelled	11.6	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
24	c2pyhB_		Alignment	not modelled	11.0	16	PDB header: isomerase Chain: B: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: azotobacter vinelandii mannuronan c-5 epimerase alge4 a-module2 complexed with mannuronan trisaccharide
25	c5n6mA_		Alignment	not modelled	10.8	12	PDB header: membrane protein Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: structure of the membrane integral lipoprotein n-acyltransferase lnt2 from p. aeruginosa
26	c5vrhA_		Alignment	not modelled	10.7	9	PDB header: transferase Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: apolipoprotein n-acyltransferase c387s active site mutant
27	c3va7A_		Alignment	not modelled	10.4	21	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
28	c3w7bB_		Alignment	not modelled	10.4	17	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase

						from thermus2 thermophilus hb8
29	c3bg5B_	Alignment	not modelled	10.0	13	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
30	c2o1eB_	Alignment	not modelled	9.8	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ycdh; PDBTitle: crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
31	c2ps3A_	Alignment	not modelled	9.8	18	PDB header: metal transport Chain: A: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: structure and metal binding properties of znua, a periplasmic zinc2 transporter from escherichia coli
32	c4cl2A_	Alignment	not modelled	9.7	15	PDB header: transport protein Chain: A: PDB Molecule: periplasmic solute binding protein; PDBTitle: structure of periplasmic metal binding protein from candidatus2 liberibacter asiaticus
33	c3ve9B_	Alignment	not modelled	9.4	10	PDB header: lyase Chain: B: PDB Molecule: orotidine-5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-monophosphate decarboxylase from2 metallosphaera sedula
34	c1emsB_	Alignment	not modelled	9.1	10	PDB header: antitumor protein Chain: B: PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
35	d1ki7a_	Alignment	not modelled	8.7	15	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
36	c2uveA_	Alignment	not modelled	8.7	15	PDB header: hydrolase Chain: A: PDB Molecule: exopolygalacturonase; PDBTitle: structure of yersinia enterocolitica family 282 exopolygalacturonase
37	d1hrua_	Alignment	not modelled	8.5	29	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
38	d2q8za1	Alignment	not modelled	8.4	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
39	d1o59a2	Alignment	not modelled	8.2	18	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Allantoicase repeat
40	c4imyl_	Alignment	not modelled	8.2	9	PDB header: transferase Chain: I: PDB Molecule: af4/fmr2 family member 4; PDBTitle: the aff4 scaffold binds human p-tefb adjacent to hiv tat
41	c4imyG_	Alignment	not modelled	8.2	9	PDB header: transferase Chain: G: PDB Molecule: af4/fmr2 family member 4; PDBTitle: the aff4 scaffold binds human p-tefb adjacent to hiv tat
42	c4imyH_	Alignment	not modelled	8.1	9	PDB header: transferase Chain: H: PDB Molecule: af4/fmr2 family member 4; PDBTitle: the aff4 scaffold binds human p-tefb adjacent to hiv tat
43	d1lg7a_	Alignment	not modelled	8.1	22	Fold: VSV matrix protein Superfamily: VSV matrix protein Family: VSV matrix protein
44	d1o59a1	Alignment	not modelled	7.9	27	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Allantoicase repeat
45	d1aopa2	Alignment	not modelled	7.5	21	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
46	c3eqnB_	Alignment	not modelled	7.4	14	PDB header: hydrolase Chain: B: PDB Molecule: glucan 1,3-beta-glucosidase; PDBTitle: crystal structure of beta-1,3-glucanase from phanerochaete2 chryso sporium (lam55a)
47	c4xrvB_	Alignment	not modelled	7.4	19	PDB header: metal binding protein Chain: B: PDB Molecule: periplasmic solute binding protein; PDBTitle: structure of a zn abc transporter substrate binding protein from2 paracoccus denitrificans
48	c2eghA_	Alignment	not modelled	6.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
49	d2fdsa1	Alignment	not modelled	6.7	8	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
50	c2fdsA_	Alignment	not modelled	6.7	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: orotidine-monophosphate-decarboxylase; PDBTitle: crystal structure of plasmodium berghei orotidine 5'-monophosphate2 decarboxylase (ortholog of plasmodium falciparum pf10_0225)
51	d1q0qa2	Alignment	not modelled	6.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
52	d1w98b1	Alignment	not modelled	6.2	15	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
53	d1rmga_	Alignment	not modelled	6.1	8	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Galacturonase

54	c3mfqB_	 Alignment	not modelled	6.0	14	<p>PDB header:metal binding protein Chain: B: PDB Molecule:high-affinity zinc uptake system protein znua; PDBTitle: a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center</p>
55	c2zo7A_	 Alignment	not modelled	5.4	31	<p>PDB header:luminescent protein Chain: A: PDB Molecule:cyan/green-emitting gfp-like protein, kusabira-cyan mutant PDBTitle: crystal structure of a kusabira-cyan mutant (kcy-r1), a cyan/green-2 emitting gfp-like protein</p>
56	c4qskB_	 Alignment	not modelled	5.3	19	<p>PDB header:ligase Chain: B: PDB Molecule:pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp</p>
57	c3obiC_	 Alignment	not modelled	5.3	11	<p>PDB header:hydrolase Chain: C: PDB Molecule:formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution</p>
58	d1xvla1	 Alignment	not modelled	5.2	13	<p>Fold:Chelatase-like Superfamily:"Helical backbone" metal receptor Family:TroA-like</p>