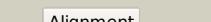
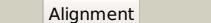
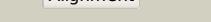
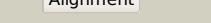
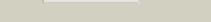
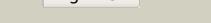
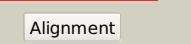
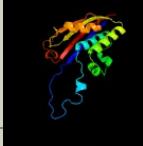
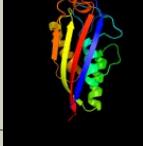
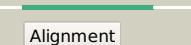
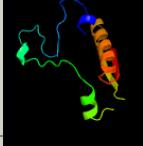
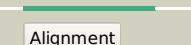
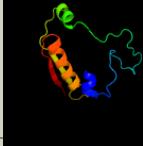
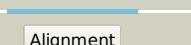
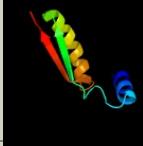
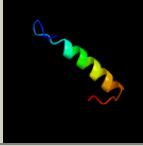
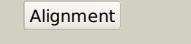
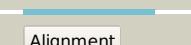
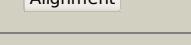
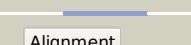
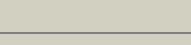


Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD3581c_(ispF)_4024047_4024526
Date	Fri Aug 9 18:20:26 BST 2019
Unique Job ID	adb785fdb5e233c4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f0gA			100.0	41	PDB header: lyase Chain: A; PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
2	c2pmpA			100.0	37	PDB header: lyase Chain: A; PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
3	d1gx1a			100.0	42	Fold: Bacillus chorismate mutase-like Superfamily: IpsF-like Family: IpsF-like
4	d1t0aa			100.0	41	Fold: Bacillus chorismate mutase-like Superfamily: IpsF-like Family: IpsF-like
5	c1w57A			100.0	32	PDB header: transferase Chain: A; PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
6	d1w55a2			100.0	32	Fold: Bacillus chorismate mutase-like Superfamily: IpsF-like Family: IpsF-like
7	c2uzhB			100.0	75	PDB header: lyase Chain: B; PDB Molecule: 2c-methyl-d-erythritol 2,4-cyclodiphosphate PDBTitle: mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
8	d1iv3a			100.0	43	Fold: Bacillus chorismate mutase-like Superfamily: IpsF-like Family: IpsF-like
9	d1vh8a			100.0	42	Fold: Bacillus chorismate mutase-like Superfamily: IpsF-like Family: IpsF-like
10	c5iwyD			100.0	41	PDB header: lyase Chain: D; PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from bacillus subtilis complexed with cmp and mg2+
11	c4c82A			100.0	33	PDB header: lyase Chain: A; PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: ispf (plasmodium falciparum) unliganded structure

12	c3re3B_			100.0	36	PDB header: lyase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
13	c3b6nA_			100.0	31	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase pv003920 from plasmodium vivax
14	c5eszG_			100.0	32	PDB header: immune system Chain: G: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase, PDBTitle: crystal structure of broadly neutralizing antibody ch04, isolated from2 donor ch0219, in complex with scaffolded trimeric hiv-1 env v1v23 domain from the clade ae strain a244
15	c3nbmA_			45.7	19	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
16	c6epzA_			40.6	10	PDB header: transport protein Chain: A: PDB Molecule: periplasmic alpha-galactoside-binding protein; PDBTitle: structure of the periplasmic binding protein melb (atu4661) in complex2 with melibiose from agrobacterium fabrum c58
17	c6i3gA_			40.2	9	PDB header: peptide binding protein Chain: A: PDB Molecule: abc transporter, substrate-binding protein, family 5; PDBTitle: crystal structure of a putative peptide binding protein appa from2 clostridium difficile
18	c1w25B_			38.1	11	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
19	c4onyB_			35.5	21	PDB header: transport protein Chain: B: PDB Molecule: extracellular solute-binding protein family 5; PDBTitle: crystal structure of a abc transporter, periplasmic substrate-binding2 protein from brucella melitensis
20	d1r57a_			35.4	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
21	c4mgeB_		not modelled	34.9	17	PDB header: transferase Chain: B: PDB Molecule: pts system, cellobiose-specific iib component; PDBTitle: 1.85 angstrom resolution crystal structure of pts system cellobiose2 specific transporter subunit iib from bacillus anthracis.
22	c6hlxA_		not modelled	32.6	10	PDB header: transport protein Chain: A: PDB Molecule: agaa; PDBTitle: structure of the ppb agaa in complex with agropinic acid from2 a.tumefaciens r10
23	c3bbIA_		not modelled	31.8	19	PDB header: regulatory protein Chain: A: PDB Molecule: regulatory protein of laci family; PDBTitle: crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
24	d2cc0a1		not modelled	28.5	9	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Nod-B-like polysaccharide deacetylase
25	c4f54A_		not modelled	27.6	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4136 family protein (bt2437) from2 bacteroides thetaiaomicron vpi-5482 at 1.60 a resolution
26	c2l2qA_		not modelled	27.5	11	PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
27	c5k9nB_		not modelled	26.8	18	PDB header: transferase Chain: B: PDB Molecule: polyamine n acetyltransferase; PDBTitle: structural and mechanistic analysis of drosophila melanogaster2 polyamine n acetyltransferase, an enzyme that catalyzes the formation3 of n acetylagmatine
28	d1s5ja2		not modelled	26.4	10	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases

						Family: DNA polymerase I
29	c5u4oA	Alignment	not modelled	25.4	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: a 2.05a x-ray structureof a bacterial extracellular solute-binding2 protein, family 5 for bacillus anthracis str. ames
30	c5noca	Alignment	not modelled	24.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: stage 0 sporulation protein j; PDBTitle: solution nmr structure of the c-terminal domain of parb (spo0j)
31	c2mdpA	Alignment	not modelled	24.5	33	PDB header: viral protein Chain: A: PDB Molecule: gene 1.2 protein; PDBTitle: the bacteriophage t7 encoded inhibitor (gp1.2) of e. coli dgtp2 triphosphohydrolase
32	c6dyrA	Alignment	not modelled	24.0	6	PDB header: biosynthetic protein Chain: A: PDB Molecule: ebony; PDBTitle: c-terminal condensation domain of ebony in complex with carcinine
33	c4fd5A	Alignment	not modelled	23.4	18	PDB header: transferase Chain: A: PDB Molecule: arylalkylamine n-acetyltransferase 2; PDBTitle: crystal structure of arylalkylamine n-acetyltransferase 2 from aedes2 aegypti
34	c5a29A	Alignment	not modelled	21.2	17	PDB header: lyase Chain: A: PDB Molecule: exopolygalacturonate lyase; PDBTitle: family 2 pectate lyase from vibrio vulnificus
35	d1iiba	Alignment	not modelled	21.0	35	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
36	c4l1gB	Alignment	not modelled	19.9	14	PDB header: hydrolase Chain: B: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the bc1960 peptidoglycan n-acetylglucosamine2 deacetylase from bacillus cereus
37	c4jj9A	Alignment	not modelled	19.8	20	PDB header: isomerase Chain: A: PDB Molecule: 5-carboxymethyl-2-hydroxymuconate delta-isomerase; PDBTitle: crystal structure of 5-carboxymethyl-2-hydroxymuconate delta-isomerase
38	c3te4A	Alignment	not modelled	19.4	12	PDB header: transferase Chain: A: PDB Molecule: dopamine n acetyltransferase, isoform a; PDBTitle: crystal structure of dopamine n acetyltransferase in complex with 2 acetyl-coa from drosophila melanogaster
39	c4m1bA	Alignment	not modelled	19.3	17	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: structural determination of ba0150, a polysaccharide deacetylase from2 bacillus anthracis
40	d1h4ra2	Alignment	not modelled	19.3	32	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Third domain of FERM
41	c5icqA	Alignment	not modelled	19.1	19	PDB header: periplasmic binding protein Chain: A: PDB Molecule: methylocystis parvus obbp mbne; PDBTitle: methanobactin periplasmic binding protein
42	d1q8ia2	Alignment	not modelled	18.6	19	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
43	c3qb8A	Alignment	not modelled	18.2	12	PDB header: transferase Chain: A: PDB Molecule: a654l protein; PDBTitle: paramecium chlorella bursaria virus1 putative orf a654l is a polyamine2 acetyltransferase
44	c5ipwA	Alignment	not modelled	18.1	7	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic oligopeptide- PDBTitle: oligopeptide-binding protein oppa
45	c5i0cA	Alignment	not modelled	18.0	18	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein yjdj; PDBTitle: crystal structure of predicted acyltransferase yjdj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12
46	d1d5aa2	Alignment	not modelled	15.5	11	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
47	c4fd7A	Alignment	not modelled	15.4	21	PDB header: transferase Chain: A: PDB Molecule: putative arylalkylamine n-acetyltransferase 7; PDBTitle: crystal structure of insect putative arylalkylamine n-2 acetyltransferase 7 from the yellow fever mosquito aedes aegypt
48	d1tgoa2	Alignment	not modelled	15.0	12	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
49	d2j13a1	Alignment	not modelled	14.9	17	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
50	c1xaxA	Alignment	not modelled	14.5	5	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0054 protein hi0004; PDBTitle: nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
51	d1f0la1	Alignment	not modelled	14.3	29	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Diphtheria toxin, C-terminal domain Family: Diphtheria toxin, C-terminal domain
52	c4fd4B	Alignment	not modelled	14.3	21	PDB header: transferase Chain: B: PDB Molecule: arylalkylamine n-acetyltransferase like 5b; PDBTitle: crystal structure of mosquito arylalkylamine n-acetyltransferase like2 5b
53	c6gr8B	Alignment	not modelled	14.0	14	PDB header: transferase Chain: B: PDB Molecule: inner centromere protein; PDBTitle: human aurkc incenp complex bound to brd-7880
						PDB header: transferase

54	c5mdnB	Alignment	not modelled	13.4	14	Chain: B: PDB Molecule: dna polymerase; PDBTitle: structure of the family b dna polymerase from the hyperthermophilic2 archaeon pyrobaculum calidifontis
55	d1qhta2	Alignment	not modelled	13.2	14	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
56	c2vfjA	Alignment	not modelled	12.7	25	PDB header: hydrolase Chain: A: PDB Molecule: tumor necrosis factor; PDBTitle: structure of the a20 ovarian tumour (otu) domain
57	d1wn7a2	Alignment	not modelled	12.5	12	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
58	c5gpoB	Alignment	not modelled	12.3	33	PDB header: transferase Chain: B: PDB Molecule: sensor protein czcs; PDBTitle: the sensor domain structure of the zinc-responsive histidine kinase2 czcs from pseudomonas aeruginosa
59	d2fi0a1	Alignment	not modelled	12.1	21	Fold: SP0561-like Superfamily: SP0561-like Family: SP0561-like
60	c5ncdA	Alignment	not modelled	12.1	9	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the polysaccharide deacetylase bc1974 from2 bacillus cereus in complex with (2s)-2-amino-5-3 (diaminomethylideneamino)-n-hydroxypentanamide
61	c4zebA	Alignment	not modelled	12.1	10	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein (agrocinopines a PDBTitle: pbp acca from a. tumefaciens c58 in complex with agrocinopine a
62	d1ny1a	Alignment	not modelled	11.6	17	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
63	d2c1ia1	Alignment	not modelled	11.6	17	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
64	c1s5jA	Alignment	not modelled	11.4	10	PDB header: transferase Chain: A: PDB Molecule: dna polymerase i; PDBTitle: insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfobolus solfataricus
65	c5ve9C	Alignment	not modelled	11.3	33	PDB header: protein binding Chain: C: PDB Molecule: microtubule-actin cross-linking factor 1, isoforms 1/2/3/5; PDBTitle: structure of hacf7 ef1-ef2-gar domains
66	c5lgcA	Alignment	not modelled	10.9	17	PDB header: hydrolase Chain: A: PDB Molecule: arce4a; PDBTitle: t48 deacetylase with substrate
67	c6e20B	Alignment	not modelled	10.8	28	PDB header: sugar binding protein Chain: B: PDB Molecule: galectin; PDBTitle: crystal structure of the dario rerio galectin-1-l2
68	c3dkbA	Alignment	not modelled	10.6	25	PDB header: hydrolase Chain: A: PDB Molecule: tumor necrosis factor, alpha-induced protein 3; PDBTitle: crystal structure of a20, 2.5 angstrom
69	c5us5B	Alignment	not modelled	10.6	18	PDB header: structural genomics Chain: B: PDB Molecule: upf0297 protein ef_1202; PDBTitle: solution structure of the ireb homodimer
70	c4bopA	Alignment	not modelled	10.3	25	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 1; PDBTitle: structure of otud1 otu domain
71	d1vr5a1	Alignment	not modelled	10.2	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
72	c6dx1A	Alignment	not modelled	9.9	19	PDB header: hydrolase, protein binding Chain: A: PDB Molecule: rna-dependent rna polymerase; PDBTitle: crystal structure of the viral otu domain protease from qalyub virus
73	c2bg5C	Alignment	not modelled	9.6	14	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
74	c2c7yB	Alignment	not modelled	9.6	18	PDB header: transferase Chain: B: PDB Molecule: 3-ketoacyl-coa thiolase 2; PDBTitle: plant enzyme
75	c1w17A	Alignment	not modelled	9.2	19	PDB header: hydrolase Chain: A: PDB Molecule: probable polysaccharide deacetylase pdaa; PDBTitle: structure of bacillus subtilis pdaa, a family 4 carbohydrate esterase.
76	c6dx3B	Alignment	not modelled	9.1	20	PDB header: hydrolase, protein binding Chain: B: PDB Molecule: rna-dependent rna polymerase; PDBTitle: crystal structure of the viral otu domain protease from taggart virus
77	c3pfyA	Alignment	not modelled	9.0	31	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 5; PDBTitle: the catalytic domain of human otud5
78	c4bouA	Alignment	not modelled	8.9	31	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 3; PDBTitle: structure of otud3 otu domain
79	c2ohiB	Alignment	not modelled	8.6	9	PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpfa; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpfa), a

						diiron2 flavoprotein, reduced state
80	c1ztyA	Alignment	not modelled	8.6	16	PDB header: sugar binding protein, signaling protein Chain: A: PDB Molecule: chitin oligosaccharide binding protein; PDBTitle: crystal structure of the chitin oligosaccharide binding2 protein
81	d1h1ca	Alignment	not modelled	8.5	22	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
82	c2grvC	Alignment	not modelled	8.5	21	PDB header: biosynthetic protein Chain: C: PDB Molecule: lpqw; PDBTitle: crystal structure of lpqw
83	c3iwgB	Alignment	not modelled	8.3	12	PDB header: transferase Chain: B: PDB Molecule: acetyltransferase, gnat family; PDBTitle: acetyltransferase from gnat family from colwellia psychrerythraea.
84	d1otga	Alignment	not modelled	8.3	16	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 5-carboxymethyl-2-hydroxymuconate isomerase (CHMI)
85	c3lkzB	Alignment	not modelled	8.3	19	PDB header: viral protein Chain: B: PDB Molecule: non-structural protein 5; PDBTitle: structural and functional analyses of a conserved hydrophobic pocket2 of flavivirus methyltransferase
86	c3b0vD	Alignment	not modelled	8.1	22	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: tRNA-dihydrouridine synthase; PDBTitle: tRNA-dihydrouridine synthase from thermus thermophilus in complex with 2 tRNA
87	d1v5ra1	Alignment	not modelled	7.9	33	Fold: N domain of copper amine oxidase-like Superfamily: GAS2 domain-like Family: GAS2 domain
88	d2pw9a1	Alignment	not modelled	7.8	26	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: FdhD/NarQ
89	c4fm4C	Alignment	not modelled	7.8	24	PDB header: lyase Chain: C: PDB Molecule: nitrile hydratase alpha subunit; PDBTitle: wild type fe-type nitrile hydratase from comamonas testosteroni ni1
90	c2mm0A	Alignment	not modelled	7.8	40	PDB header: toxin Chain: A: PDB Molecule: host-selective toxin protein; PDBTitle: solution structures of active ptr toxB and its inactive homolog2 highlight protein dynamics as a modulator of toxin activity
91	c5jp6A	Alignment	not modelled	7.7	17	PDB header: hydrolase Chain: A: PDB Molecule: putative polysaccharide deacetylase; PDBTitle: bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
92	c2wuaA	Alignment	not modelled	7.7	18	PDB header: transferase Chain: A: PDB Molecule: acetoacetyl coa thiolase; PDBTitle: structure of the peroxisomal 3-ketoacyl-coa thiolase from sunflower
93	d1wf3a2	Alignment	not modelled	7.6	27	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
94	d1is3a	Alignment	not modelled	7.6	25	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
95	d1ef1a2	Alignment	not modelled	7.6	28	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Third domain of FERM
96	d1cmca	Alignment	not modelled	7.5	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Met repressor, MetR (MetR)
97	c3huuC	Alignment	not modelled	7.5	22	PDB header: transcription regulator Chain: C: PDB Molecule: transcription regulator like protein; PDBTitle: crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
98	c2oq2B	Alignment	not modelled	7.4	13	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
99	d1xmta	Alignment	not modelled	7.3	7	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT