




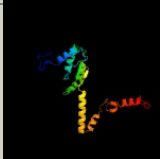



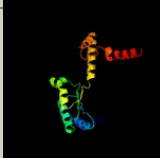

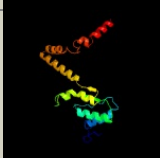





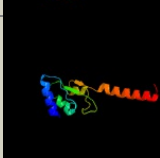

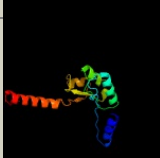

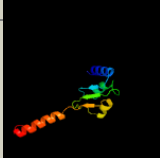
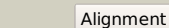
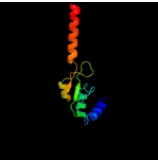





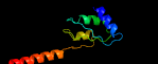




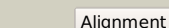

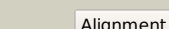

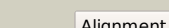
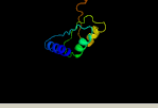
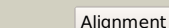

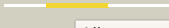
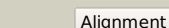
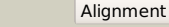
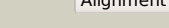




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1916_(aceAb)_2161573_2162769
Date	Fri Aug 2 13:30:53 BST 2019
Unique Job ID	6a18d71bb784db52

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dqua_	 Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
2	c5e9fD_	 Alignment		100.0	37	PDB header: lyase Chain: D: PDB Molecule: isocitrate lyase; PDBTitle: structural insights of isocitrate lyases from magnaporthe oryzae
3	d1f61a_	 Alignment		100.0	40	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
4	c3eolB_	 Alignment		100.0	40	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.0a crystal structure of isocitrate lyase from brucella melitensis2 (p43212)
5	c3i4eA_	 Alignment		100.0	36	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: crystal structure of isocitrate lyase from burkholderia2 pseudomallei
6	c3e5bB_	 Alignment		100.0	39	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.4 a crystal structure of isocitrate lyase from brucella melitensis
7	d1igwa_	 Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
8	c6g1oA_	 Alignment		100.0	26	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: structure of pseudomonas aeruginosa isocitrate lyase, icl
9	c3fa4D_	 Alignment		97.9	24	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
10	c4lsbA_	 Alignment		97.8	24	PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
11	c3b8iF_	 Alignment		97.7	20	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.

12	c3eooL_	 Alignment		97.6	27	PDB header: lyase Chain: L; PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from burkholderia pseudomallei
13	c3lyeA_	 Alignment		97.2	25	PDB header: hydrolase Chain: A; PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
14	d1ujqa_	 Alignment		97.2	27	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
15	d1s2wa_	 Alignment		97.1	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
16	c1zlpA_	 Alignment		97.0	18	PDB header: lyase Chain: A; PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
17	c3ih1A_	 Alignment		96.9	21	PDB header: lyase Chain: A; PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
18	d1muma_	 Alignment		95.9	30	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
19	c4mg4G_	 Alignment		91.9	24	PDB header: unknown function Chain: G; PDB Molecule: phosphonomutase; PDBTitle: crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
20	c5uncB_	 Alignment		85.1	18	PDB header: isomerase Chain: B; PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
21	c2ze3A_	 Alignment	not modelled	81.3	19	PDB header: isomerase Chain: A; PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
22	c2qiwa_	 Alignment	not modelled	81.0	14	PDB header: transferase Chain: A; PDB Molecule: pep phosphonomutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
23	c2hjpA_	 Alignment	not modelled	73.6	13	PDB header: hydrolase Chain: A; PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
24	d3bxda1	 Alignment	not modelled	61.9	26	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: MioX-like
25	c2huoA_	 Alignment	not modelled	61.9	26	PDB header: oxidoreductase Chain: A; PDB Molecule: inositol oxygenase; PDBTitle: crystal structure of mouse myo-inositol oxygenase in complex with2 substrate
26	d2ibna1	 Alignment	not modelled	53.3	23	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: MioX-like
27	c2p2gD_	 Alignment	not modelled	52.5	14	PDB header: transferase Chain: D; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
28	c5mp4C_	 Alignment	not modelled	43.5	17	PDB header: oxidoreductase Chain: C; PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae

29	c2x48B_	Alignment	not modelled	41.4	26	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1
30	c2yfkA_	Alignment	not modelled	39.9	16	PDB header: transferase Chain: A: PDB Molecule: aspartate/ornithine carbamoyltransferase; PDBTitle: crystal structure of a putative transcarbamoylase from2 enterococcus faecalis
31	c6c4IC_	Alignment	not modelled	38.7	19	PDB header: oxidoreductase Chain: C: PDB Molecule: yersinopine dehydrogenase; PDBTitle: yersinopine dehydrogenase (ypodh) - apo
32	d2j8ga2	Alignment	not modelled	37.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: 1,4-beta-N-acetylmuraminidase
33	d3bfxa1	Alignment	not modelled	35.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
34	d1vyra_	Alignment	not modelled	33.6	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
35	c5n6yC_	Alignment	not modelled	32.4	33	PDB header: oxidoreductase Chain: C: PDB Molecule: nitrogenase vanadium-iron protein delta chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
36	c4bhhZ_	Alignment	not modelled	31.5	28	PDB header: viral protein/rna Chain: Z: PDB Molecule: nucleoprotein; PDBTitle: crystal structure of tetramer of la crosse virus nucleoprotein in2 complex with ssrna
37	d2fiqa1	Alignment	not modelled	29.5	30	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
38	d1knwa2	Alignment	not modelled	28.2	12	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
39	c2f61A_	Alignment	not modelled	26.9	29	PDB header: hydrolase Chain: A: PDB Molecule: acid beta-glucosidase; PDBTitle: crystal structure of partially deglycosylated acid beta-glucosidase
40	c1stzB_	Alignment	not modelled	25.8	18	PDB header: transcription Chain: B: PDB Molecule: heat-inducible transcription repressor hrca homolog; PDBTitle: crystal structure of a hypothetical protein at 2.2 a resolution
41	c1zd1B_	Alignment	not modelled	24.9	26	PDB header: transferase Chain: B: PDB Molecule: sulfotransferase 4a1; PDBTitle: human sulfotransferase sult4a1
42	c3c6cA_	Alignment	not modelled	24.3	12	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
43	c3euhF_	Alignment	not modelled	23.6	26	PDB header: cell cycle Chain: F: PDB Molecule: muke; PDBTitle: crystal structure of the muke-mukf complex
44	c6b4cH_	Alignment	not modelled	23.0	22	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
45	c6nmiD_	Alignment	not modelled	22.1	25	PDB header: transcription Chain: D: PDB Molecule: general transcription factor iih subunit 4, p52; PDBTitle: cryo-em structure of the human tfiih core complex
46	c6fvjB_	Alignment	not modelled	22.1	13	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: tesa a major thioesterase from mycobacterium tuberculosis
47	d2a3ra1	Alignment	not modelled	21.7	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
48	c2j8fA_	Alignment	not modelled	21.7	14	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of the modular cpl-1 endolysin complexed with a2 peptidoglycan analogue (e94q mutant in complex with a disaccharide-3 pentapeptide)
49	c6cckA_	Alignment	not modelled	20.4	42	PDB header: transferase Chain: A: PDB Molecule: d-glycerate 3-kinase; PDBTitle: d-glycerate 3-kinase from cryptococcus neoformans var. grubii serotype2 a (h99 / atcc 208821 / cbs 10515 / fgsc 9487)
50	c3bkhA_	Alignment	not modelled	20.2	17	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
51	c2h8kA_	Alignment	not modelled	19.9	15	PDB header: transferase Chain: A: PDB Molecule: sult1c3 splice variant d; PDBTitle: human sulfotranferase sult1c3 in complex with pap
52	c4qblF_	Alignment	not modelled	19.7	15	PDB header: hydrolase Chain: F: PDB Molecule: vrr-nuc; PDBTitle: vrr_nuc domain protein
53	c2aapA_	Alignment	not modelled	19.6	56	PDB header: toxin Chain: A: PDB Molecule: jingzhaotoxin-vii; PDBTitle: solution structure of jingzhaotoxin-vii
54	d1xmba2	Alianment	not modelled	19.3	39	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain

						Family: Bacterial exopeptidase dimerisation domain
55	d2cyya2	Alignment	not modelled	19.3	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
56	c3pnnA	Alignment	not modelled	19.3	18	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
57	d2rbia_	Alignment	not modelled	19.3	15	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Bacterial ribonucleases
58	c6e10c_	Alignment	not modelled	18.0	50	PDB header: protein transport Chain: C: PDB Molecule: exported protein 2; PDBTitle: ptex core complex in the engaged (extended) state
59	d1goua_	Alignment	not modelled	17.9	17	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Bacterial ribonucleases
60	c4rapD_	Alignment	not modelled	17.7	14	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase tbc; PDBTitle: crystal structure of bacterial iron-containing dodecameric2 glycosyltransferase tbc from enterotoxigenic e.coli h10407
61	d2c7fa2	Alignment	not modelled	17.7	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
62	c4c0xA_	Alignment	not modelled	17.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: frm-dependent nadh-azoreductase 1; PDBTitle: the crystal structure of ppazor in complex with anthraquinone-2-2 sulfonate
63	c2yxgD_	Alignment	not modelled	17.4	13	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
64	c1oahA_	Alignment	not modelled	17.3	13	PDB header: reductase Chain: A: PDB Molecule: cytochrome c nitrite reductase; PDBTitle: cytochrome c nitrite reductase from desulfovibrio2 desulfuricans atcc 27774: the relevance of the two3 calcium sites in the structure of the catalytic subunit4 (nrfa).
65	d1oaha_	Alignment	not modelled	17.3	13	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
66	c6n2fB_	Alignment	not modelled	16.9	15	PDB header: lyase Chain: B: PDB Molecule: diaminopimelate decarboxylase 2, chloroplastic; PDBTitle: meso-diaminopimelate decarboxylase from arabidopsis thaliana (isoform2 2)
67	d2csta_	Alignment	not modelled	16.8	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
68	c3b6iB_	Alignment	not modelled	16.6	21	PDB header: flavoprotein Chain: B: PDB Molecule: flavoprotein wrba; PDBTitle: wrba from escherichia coli, native structure
69	c6o4nB_	Alignment	not modelled	16.5	19	PDB header: hydrolase Chain: B: PDB Molecule: enolase; PDBTitle: crystal structure of enolase from chlamydia trachomatis
70	c2wagA_	Alignment	not modelled	16.1	12	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme, putative; PDBTitle: the structure of a family 25 glycosyl hydrolase from2 bacillus anthracis.
71	c3bdkB_	Alignment	not modelled	15.9	29	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
72	c3rfaA_	Alignment	not modelled	15.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
73	c5ywwA_	Alignment	not modelled	15.3	17	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
74	c3w26A_	Alignment	not modelled	15.3	16	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 10; PDBTitle: the high-resolution crystal structure of tsxyla, intracellular2 xylanase from /thermoanaerobacterium saccharolyticum jw/si-ys485/:3 the complex of the e146a mutant with xylotriose
75	c1y9jA_	Alignment	not modelled	15.2	46	PDB header: protein transport Chain: A: PDB Molecule: sec1 family domain containing protein 1; PDBTitle: solution structure of the rat sly1 n-terminal domain
76	d1ewqa4	Alignment	not modelled	15.2	33	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
77	c5tv7A_	Alignment	not modelled	15.2	24	PDB header: hydrolase Chain: A: PDB Molecule: putative peptidoglycan-binding/hydrolysing protein; PDBTitle: 2.05 angstrom resolution crystal structure of peptidoglycan-binding2 protein from clostridioides difficile in complex with glutamine3 hydroxamate.
78	c4wnyA_	Alignment	not modelled	15.1	16	PDB header: signaling protein Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei PDB header: lyase Chain: C: PDB Molecule: uncharacterized protein

79	c4eacC_	Alignment	not modelled	15.0	28	Chain: C; PDB Molecule: mannonate dehydratase; PDBTitle: crystal structure of mannonate dehydratase from escherichia coli2 strain k12
80	d1qw9a2	Alignment	not modelled	14.4	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
81	d1se7a_	Alignment	not modelled	13.8	18	Fold: DNA polymerase III theta subunit-like Superfamily: DNA polymerase III theta subunit-like Family: DNA polymerase III theta subunit-like
82	d1tz9a_	Alignment	not modelled	12.9	33	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like
83	d1tdha3	Alignment	not modelled	12.9	78	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
84	c1knwA_	Alignment	not modelled	12.8	6	PDB header: lyase Chain: A; PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase
85	c1cpbA_	Alignment	not modelled	12.8	8	PDB header: hydrolase (c-terminal peptidase) Chain: A; PDB Molecule: carboxypeptidase b; PDBTitle: structure of carboxypeptidase b at 2.8 angstroms resolution
86	d1h3na3	Alignment	not modelled	12.7	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
87	c2ehhE_	Alignment	not modelled	12.7	12	PDB header: lyase Chain: E; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
88	d1vqom1	Alignment	not modelled	12.5	50	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
89	d1us3a2	Alignment	not modelled	12.5	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
90	c3ps9A_	Alignment	not modelled	12.4	27	PDB header: transferase Chain: A; PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mnmC from e. coli
91	c6hq8B_	Alignment	not modelled	12.3	30	PDB header: hydrolase Chain: B; PDB Molecule: beta-1,3-oligosaccharide phosphorylase; PDBTitle: bacterial beta-1,3-oligosaccharide phosphorylase from gh149 with2 laminarihexaose bound at a surface site
92	d1q8ia2	Alignment	not modelled	12.3	15	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
93	c4j1jA_	Alignment	not modelled	12.2	26	PDB header: viral protein/dna Chain: A; PDB Molecule: nucleocapsid; PDBTitle: leanyer orthobunyavirus nucleoprotein-ssdna complex
94	d1mhyd_	Alignment	not modelled	12.2	23	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
95	c3u7iB_	Alignment	not modelled	12.1	11	PDB header: oxidoreductase Chain: B; PDB Molecule: fmn-dependent nadh-azoreductase 1; PDBTitle: the crystal structure of fmn-dependent nadh-azoreductase 1 (gbaa0966)2 from bacillus anthracis str. ames ancestor
96	c3d7nA_	Alignment	not modelled	12.1	15	PDB header: electron transport Chain: A; PDB Molecule: flavodoxin, wrba-like protein; PDBTitle: the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
97	d1tgoa2	Alignment	not modelled	11.8	31	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
98	c3eukL_	Alignment	not modelled	11.8	28	PDB header: cell cycle Chain: L; PDB Molecule: chromosome partition protein muke; PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head domain)-2 atpgammass complex, asymmetric dimer
99	c4r81C_	Alignment	not modelled	11.6	11	PDB header: oxidoreductase Chain: C; PDB Molecule: nadh dehydrogenase; PDBTitle: nad(p)h:quinone oxidoreductase from methanothermobacter marburgensis