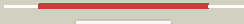



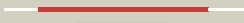















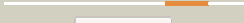
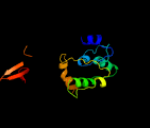
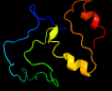


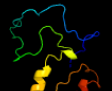
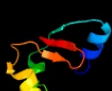
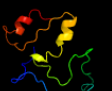
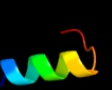

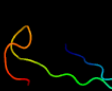


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3779 (-) _4225163_4227163
Date	Fri Aug 9 18:20:48 BST 2019
Unique Job ID	a64eb13e4f649994

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6eznF_	 Alignment		99.9	14	PDB header: membrane protein Chain: F: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
2	c3wajA_	 Alignment		99.8	13	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
3	c3rceA_	 Alignment		99.6	12	PDB header: transferase/peptide Chain: A: PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb
4	c5f15A_	 Alignment		99.4	11	PDB header: transferase Chain: A: PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
5	c3vu0B_	 Alignment		98.5	15	PDB header: transferase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-s2, af_0040, o30195_arcfu) from3 archaeoglobus fulgidus
6	c3vgpA_	 Alignment		98.3	17	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase, putative; PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (af_0329) from archaeoglobus fulgidus
7	c6p2rB_	 Alignment		96.3	13	PDB header: transferase Chain: B: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
8	c6p25A_	 Alignment		95.5	14	PDB header: transferase Chain: A: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 1; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
9	c2lgzA_	 Alignment		94.2	11	PDB header: transferase, membrane protein Chain: A: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: solution structure of stt3p
10	c3waiA_	 Alignment		92.6	16	PDB header: transferase, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, transmembrane PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion
11	c3vu1A_	 Alignment		83.0	19	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein ph0242; PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (phaglb-l, o74088_pyrho) from pyrococcus3 horikoshii

12	c2nacA	Alignment		67.5	13	PDB header: oxidoreductase(aldehyde(d),nad+(a)) Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: high resolution structures of holo and apo formate dehydrogenase
13	c5svbD	Alignment		57.2	16	PDB header: ligase Chain: D: PDB Molecule: acetone carboxylase alpha subunit; PDBTitle: mechanism of atp-dependent acetone carboxylation, acetone carboxylase2 amp bound structure
14	c5j9wA	Alignment		55.8	10	PDB header: ligase Chain: A: PDB Molecule: acetophenone carboxylase delta subunit; PDBTitle: crystal structure of the apc core complex
15	c3fn4A	Alignment		52.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: apo-form of nad-dependent formate dehydrogenase from bacterium2 moraxella sp.c-1 in closed conformation
16	c2b5dX	Alignment		50.6	4	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
17	d2naca2	Alignment		46.5	13	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
18	d2odgc1	Alignment		40.6	19	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
19	c2hyxA	Alignment		35.8	15	PDB header: unknown function Chain: A: PDB Molecule: protein dipz; PDBTitle: structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
20	d1c01a	Alignment		34.8	21	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Plant antimicrobial protein MIAMP1
21	c3fo5A	Alignment	not modelled	33.5	22	PDB header: lipid transport Chain: A: PDB Molecule: thioesterase, adipose associated, isoform bfit2; PDBTitle: human start domain of acyl-coenzyme a thioesterase 11 (acot11)
22	d1t9ba2	Alignment	not modelled	29.5	10	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
23	c3qocD	Alignment	not modelled	27.9	21	PDB header: hydrolase Chain: D: PDB Molecule: putative metallopeptidase; PDBTitle: crystal structure of n-terminal domain (creatinase/prolidase like2 domain) of putative metallopeptidase from corynebacterium diphtheriae
24	d1ufaa2	Alignment	not modelled	27.4	18	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
25	c2xznU	Alignment	not modelled	25.4	20	PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein l7ae containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
26	c2opkC	Alignment	not modelled	24.5	5	PDB header: isomerase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
27	c4hzbE	Alignment	not modelled	22.6	11	PDB header: hydrolase Chain: E: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
						PDB header: structural protein

28	c5t0zB_	Alignment	not modelled	22.4	22	Chain: B: PDB Molecule: lipoprotein, putative; PDBTitle: pelc from geobacter metallireducens
29	c2zagB_	Alignment	not modelled	21.4	14	PDB header: transferase Chain: B: PDB Molecule: oligosaccharyl transferase stt3 subunit related protein; PDBTitle: crystal structure of the semet-substituted soluble domain of stt3 from <i>S. aureus</i>
30	d1xzwa2	Alignment	not modelled	21.2	6	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
31	c2miiA_	Alignment	not modelled	20.8	8	PDB header: protein binding Chain: A: PDB Molecule: penicillin-binding protein activator lpob; PDBTitle: nmr structure of e. coli lpob
32	c3zk4A_	Alignment	not modelled	20.5	9	PDB header: oxidoreductase Chain: A: PDB Molecule: diphosphonucleotide phosphatase 1; PDBTitle: structure of purple acid phosphatase ppd1 isolated from yellow lupin (<i>lupinus luteus</i>) seeds
33	d1pvda2	Alignment	not modelled	19.8	7	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
34	c2ou2A_	Alignment	not modelled	19.6	29	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase htatip; PDBTitle: acetyltransferase domain of human hiv-1 tat interacting2 protein, 60kda, isoform 3
35	d2ozua1	Alignment	not modelled	19.2	24	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
36	c5ujwD_	Alignment	not modelled	18.9	14	PDB header: isomerase Chain: D: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from francisella2 tularensis subsp. tularensis schu s4
37	c3zey1_	Alignment	not modelled	18.7	9	PDB header: ribosome Chain: 1: PDB Molecule: 40s ribosomal protein s4, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
38	d1fy7a_	Alignment	not modelled	18.6	24	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
39	c5oxwD_	Alignment	not modelled	18.5	24	PDB header: splicing Chain: D: PDB Molecule: neq068; PDBTitle: structure of neqn from nanoarchaeum equitans
40	c5azaA_	Alignment	not modelled	18.5	19	PDB header: sugar binding protein, transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein, oligosaccharyl PDBTitle: crystal structure of mbp-sagIb fusion protein with a 20-residue spacer2 in the connector helix
41	d2b5dx2	Alignment	not modelled	18.4	4	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
42	d1zpa2	Alignment	not modelled	18.4	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
43	c2givA_	Alignment	not modelled	18.3	19	PDB header: transferase Chain: A: PDB Molecule: probable histone acetyltransferase myst1; PDBTitle: human myst histone acetyltransferase 1
44	d2giva1	Alignment	not modelled	18.3	19	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
45	c1ufaA_	Alignment	not modelled	18.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tt1467 protein; PDBTitle: crystal structure of tt1467 from thermus thermophilus hb8
46	c3izbD_	Alignment	not modelled	17.8	12	PDB header: ribosome Chain: D: PDB Molecule: 40s ribosomal protein rps4 (s4e); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
47	d3bfxa1	Alignment	not modelled	17.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
48	c5gk9A_	Alignment	not modelled	17.5	29	PDB header: transferase/metal binding protein Chain: A: PDB Molecule: histone acetyltransferase kat7; PDBTitle: crystal structure of human hbo1 in complex with brpf2
49	d1ovma2	Alignment	not modelled	17.4	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
50	d2pjua1	Alignment	not modelled	16.9	9	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
51	c4hrvB_	Alignment	not modelled	16.7	11	PDB header: lipid binding protein Chain: B: PDB Molecule: putative lipoprotein gna1162; PDBTitle: crystal structure of lipoprotein gna1162 from neisseria meningitidis
52	c2xwgA_	Alignment	not modelled	16.3	18	PDB header: hydrolase Chain: A: PDB Molecule: sortase; PDBTitle: crystal structure of sortase c-1 from actinomyces oris (formerly2 actinomyces naeslundii)
53	d2z06a1	Alignment	not modelled	16.2	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
54	c4n1kB_	Alignment	not modelled	15.8	9	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase;

54	c4g1kB	Alignment	not modelled	13.8	9	PDBTitle: crystal structure of triosephosphate isomerase from burkholderia2 thailandensis PDB header: unknown function
55	c4x9tA	Alignment	not modelled	15.6	10	Chain: A; PDB Molecule: uncharacterized protein upf0065; PDBTitle: crystal structure of a tctc solute binding protein from polaromonas2 (bpro_3516, target efi-510338), no ligand
56	d1w2za3	Alignment	not modelled	15.4	11	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
57	d2obba1	Alignment	not modelled	15.1	9	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
58	c2q5cA	Alignment	not modelled	15.0	7	PDB header: transcription Chain: A; PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
59	c3j20E	Alignment	not modelled	14.8	11	PDB header: ribosome Chain: E; PDB Molecule: 30s ribosomal protein s4e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
60	c3n92A	Alignment	not modelled	14.6	4	PDB header: transferase Chain: A; PDB Molecule: alpha-amylase, gh57 family; PDBTitle: crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose
61	d1r5aa2	Alignment	not modelled	14.4	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
62	c5ohxB	Alignment	not modelled	14.4	8	PDB header: lyase Chain: B; PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
63	c5essB	Alignment	not modelled	14.2	15	PDB header: transferase Chain: B; PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- PDBTitle: crystal structure of m. tuberculosis mend bound to mg2+ and covalent2 intermediate i (a thdp and decarboxylated 2-oxoglutarate adduct)
64	c4y90B	Alignment	not modelled	14.0	0	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from deinococcus2 radiodurans
65	d1suxa	Alignment	not modelled	13.9	11	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
66	c2x58B	Alignment	not modelled	13.9	14	PDB header: oxidoreductase Chain: B; PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: the crystal structure of mfe1 liganded with coa
67	d1sw3a	Alignment	not modelled	13.7	5	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
68	c4y8fA	Alignment	not modelled	13.6	11	PDB header: isomerase Chain: A; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from clostridium2 perfringens
69	c4mknA	Alignment	not modelled	13.6	5	PDB header: isomerase Chain: A; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of chloroplastic triosephosphate isomerase from2 chlamydomonas reinhardtii at 1.1 a of resolution
70	c6bveA	Alignment	not modelled	13.5	11	PDB header: isomerase Chain: A; PDB Molecule: triosephosphate isomerase; PDBTitle: triosephosphate isomerase of synechocystis in complex with 2-2 phosphoglycolic acid
71	c3th6B	Alignment	not modelled	13.5	5	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.
72	c2jgqB	Alignment	not modelled	13.5	17	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
73	c5z95B	Alignment	not modelled	13.4	0	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase sadsubaaa mutant from2 opisthorchis viverrini
74	d1kv5a	Alignment	not modelled	13.3	11	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
75	c5xyiE	Alignment	not modelled	13.2	12	PDB header: ribosome Chain: E; PDB Molecule: 40s ribosomal protein s4; PDBTitle: small subunit of trichomonas vaginalis ribosome
76	c1kbpB	Alignment	not modelled	13.0	7	PDB header: hydrolase (phosphoric monoester) Chain: B; PDB Molecule: purple acid phosphatase; PDBTitle: kidney bean purple acid phosphatase
77	c2pjuD	Alignment	not modelled	13.0	9	PDB header: transcription Chain: D; PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon regulatory protein2 prpr
78	d1o5xa	Alignment	not modelled	12.9	22	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
79	d1n55a	Alignment	not modelled	12.9	0	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)

80	c4nvtD_	Alignment	not modelled	12.9	5	PDB header: isomerase Chain: D: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from bruceella2 melitensis
81	c5eywB_	Alignment	not modelled	12.9	0	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of litopenaeus vannamei triosephosphate isomerase2 complexed with 2-phosphoglycolic acid
82	d1r2ra_	Alignment	not modelled	12.6	5	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
83	c5ibxB_	Alignment	not modelled	12.4	5	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: 1.65 angstrom crystal structure of triosephosphate isomerase (tim)2 from streptococcus pneumoniae
84	d1neva_	Alignment	not modelled	12.4	11	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
85	d1kfia4	Alignment	not modelled	12.3	18	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
86	d2btma_	Alignment	not modelled	12.2	11	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
87	c1yyaA_	Alignment	not modelled	12.2	16	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8
88	c6faqA_	Alignment	not modelled	12.2	13	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding protein; PDBTitle: structure of h. salinarum rosr (vng0258) grown from kbr
89	c5dynA_	Alignment	not modelled	12.2	13	PDB header: hydrolase Chain: A: PDB Molecule: putative peptidase; PDBTitle: b. fragilis cysteine protease
90	c3m9yB_	Alignment	not modelled	12.2	16	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
91	d3pmga4	Alignment	not modelled	12.2	25	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
92	c3u5cE_	Alignment	not modelled	12.2	12	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal protein s4-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
93	c4y9aB_	Alignment	not modelled	12.2	11	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from streptomyces2 coelicolor
94	d1mo0a_	Alignment	not modelled	12.1	11	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
95	d1vpqa_	Alignment	not modelled	12.1	13	Fold: TIM beta/alpha-barrel Superfamily: TM1631-like Family: TM1631-like
96	c5uprA_	Alignment	not modelled	12.1	11	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: x-ray structure of a putative triosephosphate isomerase from2 toxoplasma gondii me49
97	d1b9ba_	Alignment	not modelled	12.1	11	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
98	d1m6ja_	Alignment	not modelled	12.0	5	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
99	c3s6dA_	Alignment	not modelled	12.0	0	PDB header: isomerase Chain: A: PDB Molecule: putative triosephosphate isomerase; PDBTitle: crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis