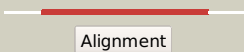

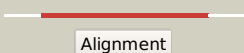

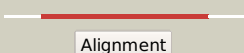

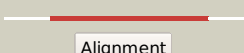



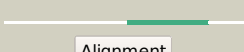

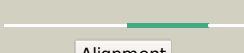

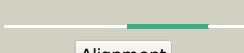




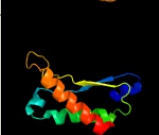


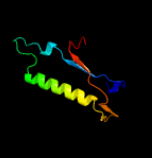
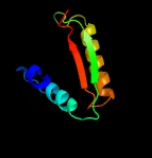


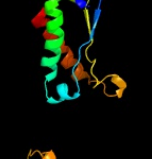


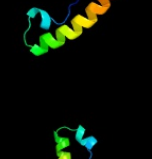
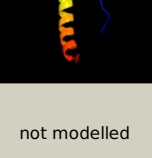


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1920_(-)_2171630_2172493
Date	Fri Aug 2 13:30:54 BST 2019
Unique Job ID	24abcae64e7c6caf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kymA_	 Alignment		100.0	26	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		99.2	16	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		98.9	13	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		98.0	18	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
5	c2dp3A_	 Alignment		52.0	13	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
6	d1ttja_	 Alignment		44.8	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
7	c3qstA_	 Alignment		44.5	12	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase, putative; PDBTitle: crystal structure of trichomonas vaginalis triosephosphate isomerase2 tvag_096350 gene (val-45 variant)
8	c4ohqB_	 Alignment		42.3	13	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase, chloroplastic; PDBTitle: crystal structure of chloroplast triose phosphate isomerase from2 arabidopsis thaliana
9	c4x22A_	 Alignment		41.5	13	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of leptospira interrogans triosephosphate isomerase2 (litim)
10	c4mknA_	 Alignment		40.6	13	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
11	c5eywB_	 Alignment		40.0	11	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of litopenaeus vannamei triosephosphate isomerase2 complexed with 2-phosphoglycolic acid

12	d1np7a2	Alignment		37.6	11	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
13	c4wbdA	Alignment		37.0	17	PDB header: ligase Chain: A: PDB Molecule: bshc; PDBTitle: the crystal structure of bshc from bacillus subtilis complexed with2 citrate and adp
14	d1suxa	Alignment		36.2	17	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
15	c1yyaA	Alignment		35.5	19	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8
16	c5uprA	Alignment		35.2	8	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: x-ray structure of a putative triosephosphate isomerase from2 toxoplasma gondii me49
17	d1m6ja	Alignment		33.7	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
18	c4y8fA	Alignment		33.6	16	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from clostridium2 perfringens
19	c1zggA	Alignment		32.5	10	PDB header: hydrolase Chain: A: PDB Molecule: putative low molecular weight protein-tyrosine- PDBTitle: solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
20	c4etiA	Alignment		32.5	10	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine-phosphatase ywle; PDBTitle: crystal structure of ywle from bacillus subtilis
21	c3m9yB	Alignment	not modelled	31.2	15	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
22	d1o5xa	Alignment	not modelled	30.7	10	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
23	d1sw3a	Alignment	not modelled	30.5	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
24	d1r2ra	Alignment	not modelled	30.3	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
25	d1n55a	Alignment	not modelled	29.9	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
26	c5zg5B	Alignment	not modelled	28.8	12	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase sadsubaaa mutant from2 opisthorchis viverrini
27	c5ibxB	Alignment	not modelled	28.0	16	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: 1.65 angstrom crystal structure of triosephosphate isomerase (tim)2 from streptococcus pneumoniae
28	d1mo0a	Alignment	not modelled	25.5	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM) PDB header: isomerase

29	c3krsB	Alignment	not modelled	25.3	10	Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
30	d1b9ba	Alignment	not modelled	24.4	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
31	c4y9aB	Alignment	not modelled	24.1	17	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from streptomyces2 coelicolor
32	d1kv5a	Alignment	not modelled	22.8	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
33	c4y96B	Alignment	not modelled	22.2	13	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from gemmata2 obscuriglobus
34	c3gvgA	Alignment	not modelled	20.1	13	PDB header: isomerase Chain: A; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from mycobacterium2 tuberculosis
35	c4obtA	Alignment	not modelled	19.9	14	PDB header: isomerase Chain: A; PDB Molecule: triosephosphate isomerase, cytosolic; PDBTitle: crystal structure of arabidopsis thaliana cytosolic triose phosphate2 isomerase
36	c1np7A	Alignment	not modelled	18.9	11	PDB header: lyase Chain: A; PDB Molecule: dna photolyase; PDBTitle: crystal structure analysis of synechocystis sp. pcc6803 cryptochrome
37	c2kelB	Alignment	not modelled	18.3	33	PDB header: transcription repressor Chain: B; PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
38	d2btma	Alignment	not modelled	15.9	16	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
39	c3bq9A	Alignment	not modelled	15.7	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: predicted rossmann fold nucleotide-binding domain- PDBTitle: crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
40	c6gfmA	Alignment	not modelled	13.1	16	PDB header: hydrolase Chain: A; PDB Molecule: pyrimidine/purine nucleotide 5'-monophosphate nucleosidase; PDBTitle: crystal structure of the escherichia coli nucleosidase ppnn (ppppp-2 form)
41	d1trea	Alignment	not modelled	12.9	13	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
42	c5ujwD	Alignment	not modelled	11.8	15	PDB header: isomerase Chain: D; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from francisella2 tularensis subsp. tularensis schu s4
43	d1aw1a	Alignment	not modelled	10.8	18	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
44	c4g1kB	Alignment	not modelled	9.9	16	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from burkholderia2 thailandensis
45	c2fekA	Alignment	not modelled	9.1	8	PDB header: hydrolase Chain: A; PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
46	c4y90B	Alignment	not modelled	9.0	18	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from deinococcus2 radiodurans
47	c2g18K	Alignment	not modelled	8.7	10	PDB header: oxidoreductase Chain: K; PDB Molecule: phycocyanobilin:ferredoxin oxidoreductase; PDBTitle: crystal structure of nostoc sp. 7120 phycocyanobilin:ferredoxin2 oxidoreductase (pcya) apoprotein
48	c3th6B	Alignment	not modelled	8.0	11	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.
49	c1r0ID	Alignment	not modelled	7.7	23	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
50	c3gh1A	Alignment	not modelled	7.5	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: predicted nucleotide-binding protein; PDBTitle: crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
51	c1f0xA	Alignment	not modelled	7.4	37	PDB header: oxidoreductase Chain: A; PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme.
52	c6bveA	Alignment	not modelled	7.3	21	PDB header: isomerase Chain: A; PDB Molecule: triosephosphate isomerase; PDBTitle: triosephosphate isomerase of synechocystis in complex with 2-2 phosphoglycolic acid
53	d1t33a2	Alignment	not modelled	6.9	11	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
						PDB header: transferase Chain: B; PDB Molecule: 5' polynucleotide kinase-3' phosphatase

54	c1vj5B_	Alignment	not modelled	6.9	18	catalytic domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
55	d2ioja1	Alignment	not modelled	6.7	21	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: DRTGG domain
56	d1neya_	Alignment	not modelled	6.5	9	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
57	c2d1eA_	Alignment	not modelled	6.4	9	PDB header: oxidoreductase Chain: A: PDB Molecule: phycocyanobilin:ferredoxin oxidoreductase; PDBTitle: crystal structure of pcya-biliverdin complex
58	d1bg5a1	Alignment	not modelled	6.3	22	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
59	d1v7za_	Alignment	not modelled	6.3	21	Fold: Creatininase Superfamily: Creatininase Family: Creatininase
60	c4picA_	Alignment	not modelled	5.8	18	PDB header: hydrolase Chain: A: PDB Molecule: arginine phosphatase ywle; PDBTitle: ywle arginine phosphatase from geobacillus stearothermophilus
61	c1emsB_	Alignment	not modelled	5.5	8	PDB header: antitumor protein Chain: B: PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
62	d2q8za1	Alignment	not modelled	5.4	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
63	c4ug3C_	Alignment	not modelled	5.4	3	PDB header: cell cycle Chain: C: PDB Molecule: cell cycle protein gpsb; PDBTitle: b. subtilis gpsb n-terminal domain
64	c4bc9C_	Alignment	not modelled	5.3	33	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase, peroxisomal; PDBTitle: mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl