

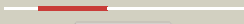























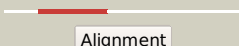

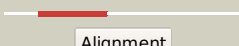
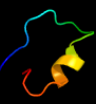
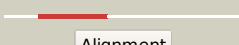






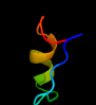

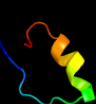
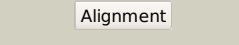
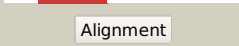
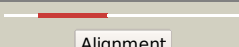


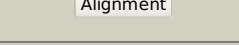
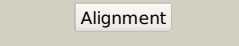
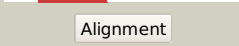


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2614A (-) _2943386_2943613
Date	Wed Aug 7 12:50:25 BST 2019
Unique Job ID	98f3dc7879ebd1e4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4mknA_</a>	 Alignment		94.6	48	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of chloroplastic triosephosphate isomerase from2 chlamydomonas reinhardtii at 1.1 a of resolution
2	<a href="#">c3m9yB_</a>	 Alignment		94.6	39	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
3	<a href="#">c5zg5B_</a>	 Alignment		94.6	48	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase sadsubaa mutant from2 opisthorchis viverrini
4	<a href="#">d1ttja_</a>	 Alignment		94.6	48	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
5	<a href="#">c5eywB_</a>	 Alignment		94.5	43	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of litopenaeus vannamei triosephosphate isomerase2 complexed with 2-phosphoglycolic acid
6	<a href="#">d1o5xa_</a>	 Alignment		94.4	43	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
7	<a href="#">d1neva_</a>	 Alignment		94.3	39	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
8	<a href="#">c4y9aB_</a>	 Alignment		94.3	35	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from streptomyces2 coelicolor
9	<a href="#">c4x22A_</a>	 Alignment		94.3	43	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of leptospira interrogans triosephosphate isomerase2 (litim)
10	<a href="#">d1mo0a_</a>	 Alignment		94.3	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
11	<a href="#">c2dp3A_</a>	 Alignment		94.3	30	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia

12	<a href="#">c3qstA</a>	 Alignment		94.2	52	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase, putative; <b>PDBTitle:</b> crystal structure of trichomonas vaginalis triosephosphate isomerase2 tvag_096350 gene (val-45 variant)
13	<a href="#">c3th6B</a>	 Alignment		94.2	35	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.
14	<a href="#">c3gvgA</a>	 Alignment		94.2	61	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from mycobacterium2 tuberculosis
15	<a href="#">d1m6ja</a>	 Alignment		94.2	43	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
16	<a href="#">d1kv5a</a>	 Alignment		94.1	48	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
17	<a href="#">d1sw3a</a>	 Alignment		94.1	48	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
18	<a href="#">d2btma</a>	 Alignment		94.0	43	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
19	<a href="#">c5ujwD</a>	 Alignment		94.0	35	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from francisella2 tularensis subsp. tularensis schu s4
20	<a href="#">d1r2ra</a>	 Alignment		94.0	48	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
21	<a href="#">c4obtA</a>	 Alignment	not modelled	94.0	43	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase, cytosolic; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana cytosolic triose phosphate2 isomerase
22	<a href="#">c1yyaA</a>	 Alignment	not modelled	94.0	52	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8
23	<a href="#">c4nvtD</a>	 Alignment	not modelled	93.9	48	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from brucella2 melitensis
24	<a href="#">c5uprA</a>	 Alignment	not modelled	93.9	43	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> x-ray structure of a putative triosephosphate isomerase from2 toxoplasma gondii me49
25	<a href="#">c4ohqB</a>	 Alignment	not modelled	93.8	39	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase, chloroplastic; <b>PDBTitle:</b> crystal structure of chloroplast triose phosphate isomerase from2 arabidopsis thaliana
26	<a href="#">c4y8fA</a>	 Alignment	not modelled	93.8	35	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from clostridium2 perfringens
27	<a href="#">d1n55a</a>	 Alignment	not modelled	93.8	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
28	<a href="#">d1b9ba</a>	 Alignment	not modelled	93.7	48	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
						<b>PDB header:</b> isomerase

29	<a href="#">c4y90B_</a>	Alignment	not modelled	93.7	39	<b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from deinococcus2 radiodurans
30	<a href="#">d1trea_</a>	Alignment	not modelled	93.7	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
31	<a href="#">c2jqgB_</a>	Alignment	not modelled	93.7	30	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
32	<a href="#">d1suxa_</a>	Alignment	not modelled	93.6	39	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
33	<a href="#">c3krsB_</a>	Alignment	not modelled	93.6	39	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
34	<a href="#">c6bveA_</a>	Alignment	not modelled	93.5	35	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> triosephosphate isomerase of synechocystis in complex with 2-2 phosphoglycolic acid
35	<a href="#">d1aw1a_</a>	Alignment	not modelled	93.4	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
36	<a href="#">c3kxqB_</a>	Alignment	not modelled	93.3	39	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from bartonella2 henselae at 1.6a resolution
37	<a href="#">c4g1kB_</a>	Alignment	not modelled	93.2	39	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from burkholderia2 thailandensis
38	<a href="#">c4y96B_</a>	Alignment	not modelled	92.6	43	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from gemmata2 obscuriglobus
39	<a href="#">c5ibxB_</a>	Alignment	not modelled	92.4	50	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> 1.65 angstrom crystal structure of triosephosphate isomerase (tim)2 from streptococcus pneumoniae
40	<a href="#">c3s6dA_</a>	Alignment	not modelled	91.8	39	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis
41	<a href="#">d1ed7a_</a>	Alignment	not modelled	31.2	44	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
42	<a href="#">c2d49A_</a>	Alignment	not modelled	18.1	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase c; <b>PDBTitle:</b> solution structure of the chitin-binding domain of2 streptomyces griseus chitinase c
43	<a href="#">c4nz3A_</a>	Alignment	not modelled	16.8	56	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deacetylase da1; <b>PDBTitle:</b> structure of vibrio cholerae chitin de-n-acetylase in complex with2 di(n-acetyl-d-glucosamine) (cbs) in p 21 21 21
44	<a href="#">c4n71A_</a>	Alignment	not modelled	16.7	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted hd phosphohydrolase phnz; <b>PDBTitle:</b> x-ray crystal structure of 2-amino-1-hydroxyethylphosphonate-bound2 phnz
45	<a href="#">d1goia1</a>	Alignment	not modelled	14.7	38	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
46	<a href="#">c4m6tA_</a>	Alignment	not modelled	14.1	39	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase ii-associated factor 1 homolog, linker, rna <b>PDBTitle:</b> structure of human paf1 and leo1 complex
47	<a href="#">d1aiwa_</a>	Alignment	not modelled	13.5	31	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
48	<a href="#">d2phcb1</a>	Alignment	not modelled	13.3	32	<b>Fold:</b> Cyclophilin-like <b>Superfamily:</b> Cyclophilin-like <b>Family:</b> PH0987 C-terminal domain-like
49	<a href="#">d2j01i1</a>	Alignment	not modelled	10.3	38	<b>Fold:</b> Ribosomal protein L9 C-domain <b>Superfamily:</b> Ribosomal protein L9 C-domain <b>Family:</b> Ribosomal protein L9 C-domain
50	<a href="#">c1txkA_</a>	Alignment	not modelled	9.8	29	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> glucans biosynthesis protein g; <b>PDBTitle:</b> crystal structure of escherichia coli oppg
51	<a href="#">d1txka2</a>	Alignment	not modelled	9.2	29	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> MdoG-like
52	<a href="#">c6npaD_</a>	Alignment	not modelled	9.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> tmbp, (r)-1-hydroxy-2-trimethylaminoethylphosphonate <b>PDBTitle:</b> x-ray crystal structure of tmbp, (r)-1-hydroxy-2-2 trimethylaminoethylphosphonate oxygenase, with (r)-1-hydroxy-2-3 trimethylaminoethylphosphonate
53	<a href="#">c2rtsA_</a>	Alignment	not modelled	9.0	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase; <b>PDBTitle:</b> chitin binding domain1
54	<a href="#">d1hg3a_</a>	Alignment	not modelled	8.5	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
						<b>Fold:</b> H-NS histone-like proteins

55	<a href="#">d1hnra_</a>	Alignment	not modelled	8.3	35	<b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins
56	<a href="#">d2asba1</a>	Alignment	not modelled	7.9	40	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
57	<a href="#">d1jhsa_</a>	Alignment	not modelled	6.8	38	<b>Fold:</b> Mog1p/PsbP-like <b>Superfamily:</b> Mog1p/PsbP-like <b>Family:</b> Ran-binding protein mog1p
58	<a href="#">d1jxa2</a>	Alignment	not modelled	6.5	38	<b>Fold:</b> beta-Trefoil <b>Superfamily:</b> Agglutinin <b>Family:</b> Agglutinin
59	<a href="#">d1od6a_</a>	Alignment	not modelled	6.3	50	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenylyltransferase
60	<a href="#">c5yfgA_</a>	Alignment	not modelled	6.2	34	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ran guanine nucleotide release factor; <b>PDBTitle:</b> solution structure of human mog1
61	<a href="#">d1v6ga2</a>	Alignment	not modelled	5.9	45	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
62	<a href="#">d2diga1</a>	Alignment	not modelled	5.7	46	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Tudor/PWWP/MBT <b>Family:</b> Tudor domain
63	<a href="#">d1gdva_</a>	Alignment	not modelled	5.7	33	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
64	<a href="#">c4wwxY_</a>	Alignment	not modelled	5.6	57	<b>PDB header:</b> hydrolase, ligase <b>Chain:</b> Y: <b>PDB Molecule:</b> v(d)j recombination-activating protein 2; <b>PDBTitle:</b> crystal structure of the core rag1/2 recombinase