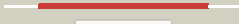



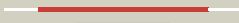





















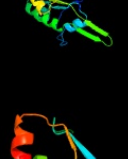
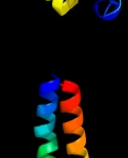


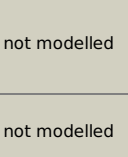


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1448c_(tal)_1626965_1628086
Date	Fri Aug 2 13:30:02 BST 2019
Unique Job ID	80d91164ac1d0c1f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r5eA_	 Alignment		100.0	62	PDB header: transferase Chain: A; PDB Molecule: transaldolase; PDBTitle: transaldolase from corynebacterium glutamicum
2	c3clmA_	 Alignment		100.0	40	PDB header: lyase Chain: A; PDB Molecule: transaldolase; PDBTitle: crystal structure of transaldolase (yp_208650.1) from neisseria2 gonorrhoeae fa 1090 at 1.14 a resolution
3	c3hja_	 Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: transaldolase b; PDBTitle: the structure of an aldolase from prochlorococcus marinus
4	d2e1da1	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
5	c3m16A_	 Alignment		100.0	24	PDB header: transferase Chain: A; PDB Molecule: transaldolase; PDBTitle: structure of a transaldolase from oleispira antarctica
6	d1f05a_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
7	c3igxA_	 Alignment		100.0	22	PDB header: transferase Chain: A; PDB Molecule: transaldolase; PDBTitle: 1.85 angstrom resolution crystal structure of transaldolase b (tala)2 from francisella tularensis.
8	c3cq0B_	 Alignment		100.0	24	PDB header: transferase Chain: B; PDB Molecule: putative transaldolase ygr043c; PDBTitle: crystal structure of tal2_ yeast
9	d1onra_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
10	c3s1vD_	 Alignment		100.0	29	PDB header: transferase Chain: D; PDB Molecule: probable transaldolase; PDBTitle: transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate
11	d1vpxA_	 Alignment		100.0	32	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase

12	d1wx0a1	Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
13	d1l6wa	Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
14	c3r8rj	Alignment		100.0	40	PDB header: transferase Chain: J; PDB Molecule: transaldolase; PDBTitle: transaldolase from bacillus subtilis
15	d1o66a	Alignment		78.7	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
16	c3ez4B	Alignment		69.1	15	PDB header: transferase Chain: B; PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
17	c3i10A	Alignment		38.5	16	PDB header: hydrolase Chain: A; PDB Molecule: putative glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (np_812074.1) from bacteroides thetaiotaomicron3 vpi-5482 at 1.35 a resolution
18	c3eziB	Alignment		31.3	14	PDB header: transferase Chain: B; PDB Molecule: nitrate/nitrite sensor protein narx; PDBTitle: crystal structure of the e. coli histidine kinase narx sensor domain2 without ligand
19	c4kbxA	Alignment		23.7	20	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein yhfx; PDBTitle: crystal structure of the pyridoxal-5'-phosphate dependent protein yhfx2 from escherichia coli
20	c1gqkB	Alignment		22.9	20	PDB header: hydrolase Chain: B; PDB Molecule: alpha-d-glucuronidase; PDBTitle: structure of pseudomonas cellulosa alpha-d-glucuronidase complexed2 with glucuronic acid
21	c2v4iA	Alignment	not modelled	22.6	31	PDB header: transferase Chain: A; PDB Molecule: glutamate n-acetyltransferase 2 alpha chain; PDBTitle: structure of a novel n-acyl-enzyme intermediate of an n-2 terminal nucleophile (ntn) hydrolase, oat2
22	c2penE	Alignment	not modelled	21.7	18	PDB header: chaperone Chain: E; PDB Molecule: orf134; PDBTitle: crystal structure of rbcx, crystal form i
23	d1x87a	Alignment	not modelled	20.5	22	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
24	d1uwka	Alignment	not modelled	20.4	20	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
25	d1h41a1	Alignment	not modelled	19.6	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
26	c2gr2A	Alignment	not modelled	19.5	13	PDB header: oxidoreductase Chain: A; PDB Molecule: ferredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase, bpha4 (oxidized form)
27	d1itza3	Alignment	not modelled	19.1	23	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
28	c3dx5A	Alignment	not modelled	19.0	10	PDB header: lyase Chain: A; PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis PDB header: chaperone/nuclear protein

29	c2jssA_	Alignment	not modelled	18.8	17	Chain: A: PDB Molecule: chimera of histone h2b.1 and histone h2a.z; PDBTitle: nmr structure of chaperone chz1 complexed with histone2 h2a.z-h2b
30	c2csuB_	Alignment	not modelled	18.6	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
31	c1vraA_	Alignment	not modelled	18.2	17	PDB header: transferase Chain: A: PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
32	d2peqa1	Alignment	not modelled	17.4	18	Fold: RbcX-like Superfamily: RbcX-like Family: RbcX-like
33	c4f48A_	Alignment	not modelled	16.4	22	PDB header: signaling protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the x-ray structural of fimxal-c-di-gmp-pilz complexes from2 xanthomonas campestris
34	c1mqrA_	Alignment	not modelled	16.2	25	PDB header: hydrolase Chain: A: PDB Molecule: alpha-d-glucuronidase; PDBTitle: the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 steartothermophilus t-6
35	d2f06a1	Alignment	not modelled	15.5	22	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
36	c4a1cO_	Alignment	not modelled	14.8	21	PDB header: ribosome Chain: O: PDB Molecule: rpl19; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
37	c3it4C_	Alignment	not modelled	14.3	18	PDB header: transferase Chain: C: PDB Molecule: arginine biosynthesis bifunctional protein argj PDBTitle: the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
38	c2h2wA_	Alignment	not modelled	14.2	48	PDB header: transferase Chain: A: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
39	c4eyeA_	Alignment	not modelled	13.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: probable oxidoreductase; PDBTitle: crystal structure of a probable oxidoreductase from mycobacterium2 abscessus solved by iodide ion sad
40	c4mz0B_	Alignment	not modelled	13.6	16	PDB header: transferase Chain: B: PDB Molecule: curl; PDBTitle: structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase
41	c3o6cA_	Alignment	not modelled	13.2	19	PDB header: transferase Chain: A: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
42	c2bt7A_	Alignment	not modelled	12.6	40	PDB header: viral protein Chain: A: PDB Molecule: sigma c; PDBTitle: structure of the c-terminal receptor-binding domain of avian reovirus2 fibre sigmac, cd crystal form
43	c1zlpA_	Alignment	not modelled	12.5	9	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
44	d1grja1	Alignment	not modelled	12.2	29	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
45	c4a1eO_	Alignment	not modelled	11.9	21	PDB header: ribosome Chain: O: PDB Molecule: rpl19; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
46	d1d7ya2	Alignment	not modelled	11.6	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
47	c2zkrp_	Alignment	not modelled	11.4	21	PDB header: ribosomal protein/rna Chain: P: PDB Molecule: rna expansion segment es31 part i; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
48	c4jesA_	Alignment	not modelled	11.2	29	PDB header: heme binding protein, transport protein Chain: A: PDB Molecule: hemophore hasa; PDBTitle: 1.6a resolution apo structure of the hemophore hasa from yersinia2 pestis (hexagonal form)
49	d2f23a1	Alignment	not modelled	11.2	29	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
50	d1gpua3	Alignment	not modelled	10.9	15	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
51	c3rlgA_	Alignment	not modelled	10.9	19	PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelin phosphodiesterase d liscitox-alphaia1a; PDBTitle: crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant
52	c2vrsC_	Alignment	not modelled	10.7	40	PDB header: viral protein Chain: C: PDB Molecule: sigma-c capsid protein; PDBTitle: structure of avian reovirus sigmac117-326, c2 crystal form PDB header: ribosome

53	c4a17O_	Alignment	not modelled	10.5	21	Chain: O: PDB Molecule: rpl19; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 2.
54	d1v93a_	Alignment	not modelled	10.5	20	Fold: TIM beta/alpha-barrel Superfamily: FAD-linked oxidoreductase Family: Methylene tetrahydrofolate reductase
55	d2ieaa3	Alignment	not modelled	10.3	15	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
56	d1xm3a_	Alignment	not modelled	10.3	20	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
57	c4oecD	Alignment	not modelled	10.2	12	PDB header: hydrolase Chain: D: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase from2 thermococcus kodakarensis kod1
58	c2k85A_	Alignment	not modelled	10.2	14	PDB header: protein binding Chain: A: PDB Molecule: glucocorticoid receptor dna-binding factor 1; PDBTitle: p190-a rhogap ff1 domain
59	c3mz2A_	Alignment	not modelled	10.1	20	PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of a glycerophosphoryl diester phosphodiesterase2 (bdi_3922) from parabacteroides distasonis atcc 8503 at 1.55 a3 resolution
60	d1m5wa_	Alignment	not modelled	10.1	23	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
61	c3iz5T_	Alignment	not modelled	10.1	21	PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein l19 (l19e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
62	c2htmB_	Alignment	not modelled	10.1	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
63	c2y0fD_	Alignment	not modelled	10.1	13	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
64	d1bd3a_	Alignment	not modelled	10.1	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
65	c4b6aR_	Alignment	not modelled	10.1	18	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein l19-b; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
66	c3ih1A_	Alignment	not modelled	9.9	11	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
67	d1reoal	Alignment	not modelled	9.9	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
68	d1l8na1	Alignment	not modelled	9.8	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
69	c3gk0H_	Alignment	not modelled	9.8	24	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
70	c3jz1Q_	Alignment	not modelled	9.7	21	PDB header: ribosome Chain: Q: PDB Molecule: 50s ribosomal protein l19e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
71	c2hjjA_	Alignment	not modelled	9.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ykff; PDBTitle: solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
72	d2hjjal	Alignment	not modelled	9.7	23	Fold: dsRBD-like Superfamily: Ycfa/nrd intein domain Family: Ykff-like
73	c4hhuA_	Alignment	not modelled	9.6	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: or280; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
74	d1vqop1	Alignment	not modelled	9.6	18	Fold: Ribosomal protein L19 (L19e) Superfamily: Ribosomal protein L19 (L19e) Family: Ribosomal protein L19 (L19e)
75	d2gtsa1	Alignment	not modelled	9.6	21	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
76	d2r8oa3	Alignment	not modelled	9.5	23	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
77	c2fmoA_	Alignment	not modelled	9.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methylene tetrahydrofolate reductase; PDBTitle: ala177val mutant of e. coli methylene tetrahydrofolate2 reductase PDB header: isomerase

78	c2vx2D_	Alignment	not modelled	9.4	13	Chain: D: PDB Molecule: enoyl-coa hydratase domain-containing protein 3; PDBTitle: crystal structure of human enoyl coenzyme a hydratase2 domain-containing protein 3 (echdc3)
79	c2hjpA_	Alignment	not modelled	9.4	6	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
80	c2qw5B_	Alignment	not modelled	9.3	22	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase-like tim barrel; PDBTitle: crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
81	c2py8B_	Alignment	not modelled	9.1	23	PDB header: chaperone Chain: B: PDB Molecule: hypothetical protein rbcx; PDBTitle: rbcx
82	d2ozlb2	Alignment	not modelled	8.9	23	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
83	c3j39R_	Alignment	not modelled	8.9	24	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein l19; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
84	c2f9rC_	Alignment	not modelled	8.7	22	PDB header: hydrolase Chain: C: PDB Molecule: sphingomyelinase d 1; PDBTitle: crystal structure of the inactive state of the smase i, a2 sphingomyelinase d from loxosceles laeta venom
85	c1ofpA_	Alignment	not modelled	8.7	27	PDB header: lyase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: crystal structure of the tyrosine-regulated 3-deoxy-d-arabino-2 heptulosonate-7-phosphate synthase from saccharomyces cerevisiae
86	c3noyA_	Alignment	not modelled	8.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
87	d1vz6a_	Alignment	not modelled	8.4	31	Fold: DmpA/ArgJ-like Superfamily: DmpA/ArgJ-like Family: ArgJ-like
88	c5xyiN_	Alignment	not modelled	8.3	17	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
89	c3ktcB_	Alignment	not modelled	8.2	16	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
90	c4hjfA_	Alignment	not modelled	8.2	12	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: eal domain of phosphodiesterase pdea in complex with c-di-gmp and ca++
91	c2qsfX_	Alignment	not modelled	8.1	27	PDB header: dna binding protein Chain: X: PDB Molecule: uv excision repair protein rad23; PDBTitle: crystal structure of the rad4-rad23 complex
92	c3zf7T_	Alignment	not modelled	7.9	24	PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein l19, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
93	c3k4iC_	Alignment	not modelled	7.9	14	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
94	c3cqkB_	Alignment	not modelled	7.6	23	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
95	d1xhca2	Alignment	not modelled	7.5	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
96	d1z0xa2	Alignment	not modelled	7.3	18	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
97	c3rlhA_	Alignment	not modelled	7.3	12	PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelin phosphodiesterase d liscix-alpha1a; PDBTitle: crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom
98	c3dufD_	Alignment	not modelled	7.2	29	PDB header: oxidoreductase/transferase Chain: D: PDB Molecule: pyruvate dehydrogenase e1 component subunit beta; PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
99	d1zcca1	Alignment	not modelled	7.1	16	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase