







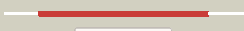















Phyre2

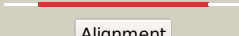

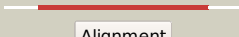
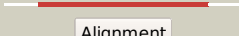






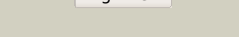

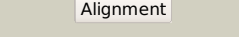
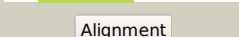
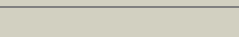
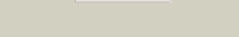

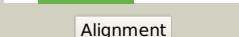

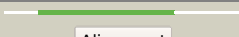
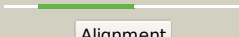


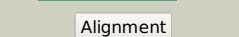
Email	mdejesus@rockefeller.edu
Description	RVBD2971 (-) _3326111_3326959
Date	Thu Aug 8 16:20:13 BST 2019
Unique Job ID	2f24eb50da7c6709

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4otkA_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterial enzyme rv2971; PDBTitle: a structural characterization of the isoniazid mycobacterium2 tuberculosis drug target, rv2971, in its unliganded form
2	d1mzra_	 Alignment		100.0	48	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
3	c3f7jB_	 Alignment		100.0	43	PDB header: oxidoreductase Chain: B: PDB Molecule: yvgn protein; PDBTitle: b.subtilis yvgn
4	d1frba_	 Alignment		100.0	37	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
5	c4fziA_	 Alignment		100.0	43	PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f synthase; PDBTitle: crystal structure of prostaglandin f synthase from trypanosoma cruzi
6	c3wbwA_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2,5-diketo-d-gluconic acid reductase; PDBTitle: crystal structure of gox0644 in complex with nadph
7	d1mi3a_	 Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
8	c3h7uA_	 Alignment		100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of the plant stress-response enzyme akr4c9
9	c2wztA_	 Alignment		100.0	67	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of a mycobacterium aldo-keto reductase in its apo2 and liganded form
10	d1hqta_	 Alignment		100.0	38	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
11	c4mhbF_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: F: PDB Molecule: putative aldo/keto reductase; PDBTitle: structure of a putative reductase from yersinia pestis

12	d1qwka_	Alignment		100.0	38	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
13	c3up8B_	Alignment		100.0	34	PDB header: oxidoreductase Chain: B: PDB Molecule: putative 2,5-diketo-d-gluconic acid reductase b; PDBTitle: crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b
14	c5az0A_	Alignment		100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of aldo-keto reductase (akr2e5) of the silkworm,2 bombyx mori
15	d1q5ma_	Alignment		100.0	35	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
16	d2alra_	Alignment		100.0	39	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
17	d1c9wa_	Alignment		100.0	38	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
18	c3wczA_	Alignment		100.0	41	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase 2e; PDBTitle: crystal structure of bombyx mori aldo-keto reductase (akr2e4) in2 complex with nadp
19	d1vp5a_	Alignment		100.0	42	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
20	c5ketA_	Alignment		100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase 1; PDBTitle: structure of the aldo-keto reductase from coptotermes gestroi
21	c1vbjB_	Alignment	not modelled	100.0	44	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f synthase; PDBTitle: the crystal structure of prostaglandin f synthase from trypanosoma2 brucei
22	c3b3dA_	Alignment	not modelled	100.0	41	PDB header: oxidoreductase Chain: A: PDB Molecule: putative morphine dehydrogenase; PDBTitle: b.subtilis ytbe
23	c4q3mF_	Alignment	not modelled	100.0	39	PDB header: hydrolase Chain: F: PDB Molecule: mgs-m4; PDBTitle: crystal structure of mgs-m4, an aldo-keto reductase enzyme from a2 medee basin deep-sea metagenome library
24	c3o0kB_	Alignment	not modelled	100.0	48	PDB header: oxidoreductase Chain: B: PDB Molecule: aldo/keto reductase; PDBTitle: crystal structure of aldo/keto reductase from brucella melitensis
25	d1j96a_	Alignment	not modelled	100.0	38	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
26	d1hw6a_	Alignment	not modelled	100.0	49	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
27	d1ah4a_	Alignment	not modelled	100.0	40	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
28	c2bgsA_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: aldose reductase; PDBTitle: holo aldose reductase from barley
						PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f2-alpha synthase/d-

29	c4f40B_	Alignment	not modelled	100.0	44	arabinose dehydrogenase; PDBTitle: x-ray crystal structure of apo prostaglandin f synthase from2 leishmania major friedlin
30	d1afsa_	Alignment	not modelled	100.0	37	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
31	d1s1pa_	Alignment	not modelled	100.0	37	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
32	c1zgdB_	Alignment	not modelled	100.0	35	PDB header: plant protein Chain: B: PDB Molecule: chalcone reductase; PDBTitle: chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution
33	d1us0a_	Alignment	not modelled	100.0	41	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
34	c3wg6C_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: C: PDB Molecule: conjugated polyketone reductase c1; PDBTitle: crystal structure of conjugated polyketone reductase c1 from candida2 parapsilosis complexed with nadph
35	c3h7rA_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of the plant stress-response enzyme akr4c8
36	c3buvB_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxo-5-beta-steroid 4-dehydrogenase; PDBTitle: crystal structure of human delta(4)-3-ketosteroid 5-beta-reductase in2 complex with nadp and hepes. resolution: 1.35 a.
37	c4hbka_	Alignment	not modelled	100.0	40	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase family 1, member b4 (aldose reductase); PDBTitle: structure of the aldose reductase from schistosoma japonicum
38	d1lqaa_	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
39	c4pmjA_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021 in complex with nadp
40	c3krbB_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: B: PDB Molecule: aldose reductase; PDBTitle: structure of aldose reductase from giardia lamblia at 1.75a resolution
41	d1ur3m_	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
42	c4xk2A_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo/keto reductase; PDBTitle: crystal structure of aldo-keto reductase from polaromonas sp. js666
43	c3erpA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
44	c3vxgA_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: conjugated polyketone reductase c2; PDBTitle: crystal structure of conjugated polyketone reductase c2 from candida2 parapsilosis
45	c6hg6A_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: l-glyceraldehyde 3-phosphate reductase; PDBTitle: clostridium beijerinckii aldo-keto reductase cbei_3974 with nadph
46	d3eaua1	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
47	d1pyfa_	Alignment	not modelled	100.0	27	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
48	c3lutA_	Alignment	not modelled	100.0	24	PDB header: membrane protein Chain: A: PDB Molecule: voltage-gated potassium channel subunit beta-2; PDBTitle: a structural model for the full-length shaker potassium channel kv1.2
49	c3n2tA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
50	c3n6qF_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: F: PDB Molecule: yghz aldo-keto reductase; PDBTitle: crystal structure of yghz from e. coli
51	d1pz1a_	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
52	c3v0tA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: perakine reductase; PDBTitle: crystal structure of perakine reductase, founder member of a novel akr2 subfamily with unique conformational changes during nadph binding
53	c5danA_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,5-diketo-d-gluconic acid reductase; PDBTitle: crystal structure of a novel aldo keto reductase tm1743 from2 thermotoga maritima in complex with nadp+
54	c4wghA_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde reductase; PDBTitle: crystal structure of aldo/keto reductase from klebsiella pneumoniae in2 complex with nadp and acetate at 1.8 a resolution

55	c4ijrA	 Alignment	not modelled	100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arabinose dehydrogenase [nad(p)+] heavy chain; PDBTitle: crystal structure of saccharomyces cerevisiae arabinose dehydrogenase2 ara1 complexed with nadph
56	d1gvea	 Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
57	c6gtmA	 Alignment	not modelled	100.0	19	PDB header: signaling protein Chain: A: PDB Molecule: aldo-keto reductase family protein; PDBTitle: crystal structure of smba in complex with ppgpp.
58	c1ynpA	 Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: aldo-keto reductase akr11c1 from bacillus halodurans (apo form)
59	c2bp1C	 Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: aflatoxin b1 aldehyde reductase member 2; PDBTitle: structure of the aflatoxin aldehyde reductase in complex with nadph
60	c4exaD	 Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the pa4992, the putative aldo-keto reductase from2 pseudomona aeruginosa
61	c3ln3A	 Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodiol dehydrogenase; PDBTitle: crystal structure of putative reductase (np_038806.2) from mus2 musculus at 1.18 a resolution
62	c3l2iB	 Alignment	not modelled	85.7	14	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinatase; PDBTitle: 1.85 angstrom crystal structure of the 3-dehydroquinatase2 (arod) from salmonella typhimurium lt2.
63	c4ph6A	 Alignment	not modelled	85.1	17	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinatase; PDBTitle: structure of 3-dehydroquinatase dehydratase from enterococcus faecalis
64	c3g8rA	 Alignment	not modelled	84.6	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
65	d1gqna	 Alignment	not modelled	80.0	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
66	c3js3C	 Alignment	not modelled	78.6	15	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinatase; PDBTitle: crystal structure of type i 3-dehydroquinatase dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
67	c1xuzA	 Alignment	not modelled	68.6	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein siaC; PDBTitle: crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
68	c1vliA	 Alignment	not modelled	63.8	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
69	c5c6mD	 Alignment	not modelled	58.0	19	PDB header: lyase Chain: D: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose-phosphate aldolase from shewanella2 halifaxensis
70	c6ncsB	 Alignment	not modelled	57.9	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-acetylneuraminic acid (sialic acid) synthetase; PDBTitle: crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
71	d1vliA2	 Alignment	not modelled	57.9	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
72	d1jpmA1	 Alignment	not modelled	57.5	10	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
73	d2zdra2	 Alignment	not modelled	50.0	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
74	c3oa3A	 Alignment	not modelled	44.3	21	PDB header: lyase Chain: A: PDB Molecule: aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
75	c4xbsA	 Alignment	not modelled	43.5	21	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
76	c2nqlB	 Alignment	not modelled	42.2	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: isomerase/lactonizing enzyme; PDBTitle: crystal structure of a member of the enolase superfamily from2 agrobacterium tumefaciens
77	d1sflA	 Alignment	not modelled	40.8	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
78	c5dbul	 Alignment	not modelled	39.1	23	PDB header: lyase Chain: I: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of 2-deoxyribose-5-phosphate aldolase

						(1-220) from2 streptococcus suis
79	d1r0ma1	Alignment	not modelled	38.8	16	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
80	d1ub3a	Alignment	not modelled	38.4	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
81	c2ph5A	Alignment	not modelled	37.1	15	PDB header: transferase Chain: A: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
82	c5c2xB	Alignment	not modelled	36.9	20	PDB header: lyase Chain: B: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose-phosphate aldolase from colwellia2 psychrerythraea (tetragonal form)
83	d2ijqa1	Alignment	not modelled	36.6	16	Fold: Hyaluronidase domain-like Superfamily: TTHA0068-like Family: TTHA0068-like
84	c4pIpB	Alignment	not modelled	34.3	19	PDB header: transferase Chain: B: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad
85	d1o0ya	Alignment	not modelled	33.8	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
86	c3ngjC	Alignment	not modelled	32.4	17	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
87	c5m31A	Alignment	not modelled	31.9	32	PDB header: antitoxin Chain: A: PDB Molecule: appr-1-p processing domain protein; PDBTitle: macrodomain of thermus aquaticus darg
88	d1i27a	Alignment	not modelled	29.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of the rap74 subunit of TFIIF
89	c6ei9A	Alignment	not modelled	27.2	11	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
90	c2o7qA	Alignment	not modelled	26.2	16	PDB header: oxidoreductase,transferase Chain: A: PDB Molecule: bifunctional 3-dehydroquininate dehydratase/shikimate PDBTitle: crystal structure of the a. thaliana dhq-dehydroshikimate-sdh-2 shikimate-nadp(h)
91	c6ewvA	Alignment	not modelled	26.0	38	PDB header: peptide binding protein Chain: A: PDB Molecule: nrps kj12c-ndd, nrps kj12b-cdd; PDBTitle: solution structure of docking domain complex of rxp nrps: kj12c ndd -2 kj12b cdd
92	c2eeeA	Alignment	not modelled	25.9	15	PDB header: gene regulation Chain: A: PDB Molecule: uncharacterized protein c6orf130; PDBTitle: solution structure of the a1pp domain from human protein2 c6orf130
93	c3c5yD	Alignment	not modelled	25.5	13	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
94	d1mzha	Alignment	not modelled	24.9	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
95	c3ejfA	Alignment	not modelled	24.3	30	PDB header: hydrolase Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of ibv x-domain at ph 8.5
96	c3smaD	Alignment	not modelled	23.8	17	PDB header: transferase Chain: D: PDB Molecule: frbf; PDBTitle: a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
97	d1vcva1	Alignment	not modelled	23.3	30	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
98	d2fg1a1	Alignment	not modelled	22.8	19	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
99	c5d88A	Alignment	not modelled	22.1	34	PDB header: hydrolase Chain: A: PDB Molecule: predicted protease of the collagenase family; PDBTitle: the structure of the u32 peptidase mk0906
100	d1p1xa	Alignment	not modelled	21.7	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
101	c1tx2A	Alignment	not modelled	21.1	15	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
102	d1tx2a	Alignment	not modelled	21.1	15	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
103	d1wlza1	Alignment	not modelled	20.5	19	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins