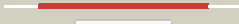
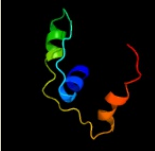


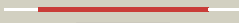






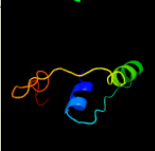









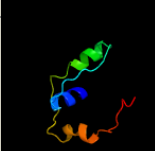


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2970A (-) _3325944_3326114
Date	Thu Aug 8 16:20:13 BST 2019
Unique Job ID	c74fc1be82070b77

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5az0A_	 Alignment		99.2	24	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of aldo-keto reductase (akr2e5) of the silkworm,2 bombyx mori
2	c3ln3A_	 Alignment		99.2	21	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
3	d1q5ma_	 Alignment		99.1	24	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
4	d2alra_	 Alignment		99.1	38	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
5	c3h7uA_	 Alignment		99.1	32	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of the plant stress-response enzyme akr4c9
6	d1ah4a_	 Alignment		99.1	45	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
7	d1hqta_	 Alignment		99.1	38	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
8	d1s1pa_	 Alignment		99.1	26	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
9	d1c9wa_	 Alignment		99.1	49	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
10	d1frba_	 Alignment		99.1	47	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
11	c4hbka_	 Alignment		99.1	37	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

12	d1afsa_	Alignment		99.1	20	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
13	d1j96a_	Alignment		99.1	28	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
14	c4mhbF_	Alignment		99.0	27	PDB header: oxidoreductase Chain: F: PDB Molecule: putative aldo/keto reductase; PDBTitle: structure of a putative reductase from yersinia pestis
15	c2bgsA_	Alignment		99.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: aldose reductase; PDBTitle: holo aldose reductase from barley
16	c4otkA_	Alignment		99.0	42	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
17	d1us0a_	Alignment		99.0	42	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
18	c3buvB_	Alignment		99.0	38	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.
19	c5ketA_	Alignment		99.0	40	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase 1; PDBTitle: structure of the aldo-keto reductase from coptotermes gestroi
20	c4ijrA_	Alignment		99.0	31	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
21	c1zgdB_	Alignment	not modelled	99.0	23	PDB header: plant protein Chain: B: PDB Molecule: chalcone reductase; PDBTitle: chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution
22	c3vxgA_	Alignment	not modelled	99.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: conjugated polyketone reductase c2; PDBTitle: crystal structure of conjugated polyketone reductase c2 from candida2 parapsilosis
23	c3wcZA_	Alignment	not modelled	99.0	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
24	c4q3mF_	Alignment	not modelled	98.9	41	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
25	d1mi3a_	Alignment	not modelled	98.9	37	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
26	d1vp5a_	Alignment	not modelled	98.9	32	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
27	c3wg6C_	Alignment	not modelled	98.9	25	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
28	c3h7rA_	Alignment	not modelled	98.9	27	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of the plant stress-response enzyme akr4c8
						Fold: TIM beta/alpha-barrel

29	d1qwka_	Alignment	not modelled	98.9	31	Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
30	c1vbjB_	Alignment	not modelled	98.9	39	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f synthase; PDBTitle: the crystal structure of prostaglandin f synthase from trypanosoma2 brucei
31	d1mzra_	Alignment	not modelled	98.9	48	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
32	d1hw6a_	Alignment	not modelled	98.9	41	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
33	c4f40B_	Alignment	not modelled	98.9	39	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f2-alpha synthase/d-arabinose dehydrogenase; PDBTitle: x-ray crystal structure of apo prostaglandin f synthase from2 leishmania major friedlin
34	c3up8B_	Alignment	not modelled	98.8	28	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
35	c3wbwA_	Alignment	not modelled	98.8	43	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2,5-diketo-d-gluconic acid reductase; PDBTitle: crystal structure of gox0644 in complex with nadph
36	c4fziA_	Alignment	not modelled	98.7	40	PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f synthase; PDBTitle: crystal structure of prostaglandin f synthase from trypanosoma cruzi
37	c3o0kB_	Alignment	not modelled	98.7	52	PDB header: oxidoreductase Chain: B: PDB Molecule: aldo/keto reductase; PDBTitle: crystal structure of aldo/keto reductase from brucella melitensis
38	c4pmjA_	Alignment	not modelled	98.7	28	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021 in complex with nadp
39	c2wztA_	Alignment	not modelled	98.7	49	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
40	c3b3dA_	Alignment	not modelled	98.7	34	PDB header: oxidoreductase Chain: A: PDB Molecule: putative morphine dehydrogenase; PDBTitle: b.subtilis ytbe
41	c4wghA_	Alignment	not modelled	98.7	24	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
42	c3f7jB_	Alignment	not modelled	98.7	36	PDB header: oxidoreductase Chain: B: PDB Molecule: syvgn protein; PDBTitle: b.subtilis yvgn
43	c5danA_	Alignment	not modelled	98.6	17	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+
44	c3v0tA_	Alignment	not modelled	98.6	13	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
45	c3krbB_	Alignment	not modelled	98.6	33	PDB header: oxidoreductase Chain: B: PDB Molecule: aldose reductase; PDBTitle: structure of aldose reductase from giardia lamblia at 1.75a resolution
46	c3n2tA_	Alignment	not modelled	98.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
47	c4xk2A_	Alignment	not modelled	98.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo/keto reductase; PDBTitle: crystal structure of aldo-keto reductase from polaromonas sp. js666
48	d1ur3m_	Alignment	not modelled	98.4	22	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
49	c3erpA_	Alignment	not modelled	98.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
50	d1pyfa_	Alignment	not modelled	98.4	16	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
51	d3eaua1	Alignment	not modelled	98.3	15	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
52	c6hg6A_	Alignment	not modelled	98.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-glyceraldehyde 3-phosphate reductase; PDBTitle: clostridium beijerinckii aldo-keto reductase cbei_3974 with nadph
53	d1lqaa_	Alignment	not modelled	98.3	5	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
54	c3lutA_	Alignment	not modelled	98.3	15	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
55	c1ynpA_	Alignment	not modelled	98.3	12 PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: aldo-keto reductase akr11c1 from bacillus halodurans (apo form)
56	c3n6qF_	Alignment	not modelled	98.2	14 PDB header: oxidoreductase Chain: F: PDB Molecule: yghz aldo-keto reductase; PDBTitle: crystal structure of yghz from e. coli
57	d1pz1a_	Alignment	not modelled	98.1	12 Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
58	c2bp1C_	Alignment	not modelled	98.1	21 PDB header: oxidoreductase Chain: C: PDB Molecule: afatoxin b1 aldehyde reductase member 2; PDBTitle: structure of the aflatoxin aldehyde reductase in complex with nadph
59	d1gvea_	Alignment	not modelled	97.9	19 Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
60	c6gtmA_	Alignment	not modelled	97.5	7 PDB header: signaling protein Chain: A: PDB Molecule: aldo-keto reductase family protein; PDBTitle: crystal structure of smba in complex with pggpp.
61	c4exaD_	Alignment	not modelled	96.0	18 PDB header: oxidoreductase Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the pa4992, the putative aldo-keto reductase from2 pseudomona aeruginosa
62	c6oswA_	Alignment	not modelled	11.0	37 PDB header: cell cycle Chain: A: PDB Molecule: forkhead box m1; PDBTitle: an order-to-disorder structural switch activates the foxm12 transcription factor
63	c1wizD_	Alignment	not modelled	7.1	3 PDB header: unknown function Chain: D: PDB Molecule: cap-binding protein complex interacting protein PDBTitle: crystal structure of djbp fragment which was obtained by2 limited proteolysis
64	d1wlza1	Alignment	not modelled	6.9	3 Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins