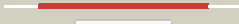


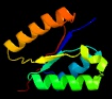
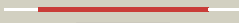
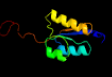













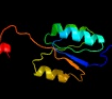




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1990A (-) _2233889_2234224
Date	Mon Aug 5 13:25:09 BST 2019
Unique Job ID	fa2407945636494e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2et6A_	 Alignment		99.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: (3r)-hydroxyacyl-coa dehydrogenase; PDBTitle: (3r)-hydroxyacyl-coa dehydrogenase domain of candida tropicalis2 peroxisomal multifunctional enzyme type 2
2	c5I53A_	 Alignment		99.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-menthone:(+)-neomenthol reductase; PDBTitle: menthone neomenthol reductase from mentha piperita in complex with2 nadp
3	c3ppiA_	 Alignment		99.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase type-2; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase type-2 from2 mycobacterium avium
4	c3omIA_	 Alignment		99.5	16	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: peroxisomal multifunctional enzyme type 2, cg3415; PDBTitle: structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster
5	c3ek2D_	 Alignment		99.5	16	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of enoyl-(acyl carrier protein) reductase from2 burkholderia pseudomallei 1719b
6	c4wuvB_	 Alignment		99.5	21	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-hydroxycyclohexanecarboxyl-coa dehydrogenase; PDBTitle: crystal structure of a putative d-mannonate oxidoreductase from2 haemophilus influenza (avi_5165, target efi-513796) with bound nad
7	c1zbqB_	 Alignment		99.5	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase 4; PDBTitle: crystal structure of human 17-beta-hydroxysteroid dehydrogenase type 42 in complex with nad
8	d1zbqa1	 Alignment		99.5	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
9	c5epoD_	 Alignment		99.5	29	PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
10	d2ag5a1	 Alignment		99.5	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
11	d1qsga_	 Alignment		99.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

12	c5jy1C_	Alignment		99.4	22	PDB header: oxidoreductase Chain: C: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400 bound to nad
13	c2qioA_	Alignment		99.4	19	PDB header: unknown function Chain: A: PDB Molecule: enoyl-(acyl-carrier-protein) reductase; PDBTitle: x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
14	c5jydA_	Alignment		99.4	28	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
15	c5f1pB_	Alignment		99.4	33	PDB header: oxidoreductase Chain: B: PDB Molecule: ptm08; PDBTitle: crystal structure of dehydrogenase from streptomyces platensis
16	d1yxma1	Alignment		99.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
17	c4zjuA_	Alignment		99.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: structure of a nadh-dependent enoyl-acp reductase from acinetobacter2 baumannii in complex with nad
18	c6ci9D_	Alignment		99.4	20	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
19	c3r3sD_	Alignment		99.4	23	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
20	c4q9nD_	Alignment		99.4	20	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: D: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of chlamydia trachomatis enoyl-acp reductase (fabI)2 in complex with nadh and afn-1252
21	d1xg5a_	Alignment	not modelled	99.4	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
22	c5g4kB_	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: phloroglucinol reductase from clostridium sp. apo-form
23	c5er6C_	Alignment	not modelled	99.4	27	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: crystal structure of an oxidoreductase from brucella ovis
24	c4nimA_	Alignment	not modelled	99.4	32	PDB header: oxidoreductase Chain: A: PDB Molecule: versicolorin reductase; PDBTitle: crystal structure of a short chain dehydrogenase from brucella2 melitensis
25	c4nk4E_	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of fabI from candidatus liberibacter asiaticus
26	c2wdzD_	Alignment	not modelled	99.4	22	PDB header: oxidoreductase Chain: D: PDB Molecule: short-chain dehydrogenase/reductase; PDBTitle: crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
27	c3pxxE_	Alignment	not modelled	99.4	35	PDB header: oxidoreductase Chain: E: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nicotinamide adenine dinucleotide
28	c4wecA_	Alignment	not modelled	99.4	32	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from

						mycobacterium2 smegmatis
29	c5jlaB_	Alignment	not modelled	99.4	23	PDB header: isomerase Chain: B: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of ribose-5-phosphate isomerase from brucella2 melitensis 16m
30	c5ig2B_	Alignment	not modelled	99.4	23	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of a short chain dehydrogenase/reductase sdr from2 burkholderia phymatum in complex with nad
31	d1nffa_	Alignment	not modelled	99.4	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
32	c3ctmH_	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: H: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
33	c4nqzF_	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: F: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh] fabi; PDBTitle: crystal structure of the pseudomonas aeruginosa enoyl-acyl carrier2 protein reductase (fabi) in apo form
34	c3toxG_	Alignment	not modelled	99.4	24	PDB header: oxidoreductase Chain: G: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
35	c3grkE_	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
36	d1zema1	Alignment	not modelled	99.3	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
37	c5un1A_	Alignment	not modelled	99.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketoacyl-acp reductase; PDBTitle: crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
38	c3t4xA_	Alignment	not modelled	99.3	25	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: short chain dehydrogenase/reductase family oxidoreductase from2 bacillus anthracis str. ames ancestor
39	c4euhA_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ca_c0462; PDBTitle: crystal structure of clostridium acetobutlicum trans-2-enoyl-coa2 reductase apo form
40	d2ae2a_	Alignment	not modelled	99.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
41	c5koiH_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: H: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of a possible enoyl-(acyl-carrier-protein) reductase2 from brucella melitensis
42	c5x8hA_	Alignment	not modelled	99.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain dehydrogenase reductase; PDBTitle: crystal structure of the ketone reductase chkred20 from the genome of2 chryseobacterium sp. ca49
43	c4lvuB_	Alignment	not modelled	99.3	28	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia thailandensis
44	c4fc6B_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxisomal 2,4-dienoyl-coa reductase; PDBTitle: studies on dcr shed new light on peroxisomal beta-oxidation: crystal2 structure of the ternary complex of pdcr
45	d1ulua_	Alignment	not modelled	99.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
46	d2a4ka1	Alignment	not modelled	99.3	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
47	d2pd4a1	Alignment	not modelled	99.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
48	c3tjrA_	Alignment	not modelled	99.3	28	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis
49	c3vc7B_	Alignment	not modelled	99.3	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
50	d1luaa1	Alignment	not modelled	99.3	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
51	c2pd6D_	Alignment	not modelled	99.3	25	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
52	c4iboA_	Alignment	not modelled	99.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)

53	c4j2hA_	Alignment	not modelled	99.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain alcohol dehydrogenase-related dehydrogenase; PDBTitle: crystal structure of a putative short-chain alcohol dehydrogenase from <i>Sinorhizobium meliloti</i> 1021 (target nysgrc-011708)
54	d2bgka1	Alignment	not modelled	99.3	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
55	d1xkqa_	Alignment	not modelled	99.3	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
56	c4nbvA_	Alignment	not modelled	99.3	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from <i>Cupriavidus taiwanensis</i>
57	d1hxha_	Alignment	not modelled	99.3	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
58	d1bdba_	Alignment	not modelled	99.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
59	c4pcvB_	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: bdca (yjgi); PDBTitle: the structure of bdca (yjgi) from <i>E. coli</i>
60	c3f9iB_	Alignment	not modelled	99.3	19	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 <i>Rickettsia prowazekii</i>
61	c3awdD_	Alignment	not modelled	99.3	24	PDB header: oxidoreductase Chain: D: PDB Molecule: putative polyol dehydrogenase; PDBTitle: crystal structure of gox2181
62	d1xhla_	Alignment	not modelled	99.3	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
63	c4urfB_	Alignment	not modelled	99.3	24	PDB header: oxidoreductase Chain: B: PDB Molecule: cyclohexanol dehydrogenase; PDBTitle: molecular genetic and crystal structural analysis of 1-(4-2-hydroxyphenyl)-ethanol dehydrogenase from <i>Aromatoleum aromaticum</i> ebn1
64	c3nugA_	Alignment	not modelled	99.3	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from <i>Mesorhizobium loti</i>
65	d1oaaa_	Alignment	not modelled	99.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
66	c4yacA_	Alignment	not modelled	99.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligo in complex with nadh from <i>Sphingobium</i> sp.2 strain syk-6
67	c5h5xH_	Alignment	not modelled	99.3	23	PDB header: oxidoreductase Chain: H: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of nadh bound carbonyl reductase from <i>Streptomyces</i> 2 <i>coelicolor</i>
68	c4fn4A_	Alignment	not modelled	99.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from <i>Sulfolobus</i> 2 <i>acidocaldarius</i>
69	d1xsea_	Alignment	not modelled	99.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
70	c4fgsB_	Alignment	not modelled	99.3	22	PDB header: oxidoreductase Chain: B: PDB Molecule: probable dehydrogenase protein; PDBTitle: crystal structure of a probable dehydrogenase protein
71	c4gh5B_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of s-2-hydroxypropyl coenzyme m dehydrogenase (s-2 hpcdh)
72	c3itdA_	Alignment	not modelled	99.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 17beta-hydroxysteroid dehydrogenase; PDBTitle: crystal structure of an inactive 17beta-hydroxysteroid dehydrogenase2 (y167f mutated form) from fungus <i>Cochliobolus lunatus</i>
73	c4npcA_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: sorbitol dehydrogenase; PDBTitle: crystal structure of an oxidoreductase, short-chain2 dehydrogenase/reductase family protein from <i>Brucella suis</i>
74	d1ae1a_	Alignment	not modelled	99.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
75	c4rgbB_	Alignment	not modelled	99.3	37	PDB header: oxidoreductase Chain: B: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of a putative carveol dehydrogenase from <i>Mycobacterium avium</i> bound to nad
76	c3ioyB_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: structure of putative short-chain dehydrogenase (saro_0793) from <i>Novosphingobium aromaticivorans</i>
77	c3rd5A_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: mypaa.01249.c; PDBTitle: crystal structure of a putative uncharacterized protein from <i>Mycobacterium paratuberculosis</i>
78	d1xqla_	Alignment	not modelled	99.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

				Family:Tyrosine-dependent oxidoreductases		
79	c5itvC_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydroantcapsin 7-dehydrogenase; PDBTitle: crystal structure of bacillus subtilis bacc dihydroantcapsin 7-2 dehydrogenase in complex with nadh
80	c5idxB_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of an oxidoreductase from burkholderia vietnamiensis
81	c4g81A_	Alignment	not modelled	99.3	25	PDB header: oxidoreductase Chain: A: PDB Molecule: putative hexonate dehydrogenase; PDBTitle: crystal structure of a hexonate dehydrogenase ortholog (target efi-2 506402 from salmonella enterica, unliganded structure
82	c3pk0B_	Alignment	not modelled	99.3	21	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
83	c5k9zB_	Alignment	not modelled	99.3	25	PDB header: oxidoreductase Chain: B: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400
84	c4trrH_	Alignment	not modelled	99.3	25	PDB header: oxidoreductase Chain: H: PDB Molecule: putative d-beta-hydroxybutyrate dehydrogenase; PDBTitle: crystal structure of a putative putative d-beta-hydroxybutyrate2 dehydrogenase from burkholderia cenocepacia j2315
85	c4egfA_	Alignment	not modelled	99.3	37	PDB header: oxidoreductase Chain: A: PDB Molecule: l-xylulose reductase; PDBTitle: crystal structure of a l-xylulose reductase from mycobacterium2 smegmatis
86	d1ulsa_	Alignment	not modelled	99.3	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
87	c3imfA_	Alignment	not modelled	99.3	23	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'
88	c4mowB_	Alignment	not modelled	99.3	31	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase; PDBTitle: crystal structure of a putative glucose 1-dehydrogenase from2 burkholderia cenocepacia j2315
89	d1zk4a1	Alignment	not modelled	99.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
90	c3gaff_	Alignment	not modelled	99.3	21	PDB header: oxidoreductase Chain: F: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: 2.2a crystal structure of 7-alpha-hydroxysteroid dehydrogenase from2 brucella melitensis
91	c5u9pB_	Alignment	not modelled	99.3	30	PDB header: oxidoreductase Chain: B: PDB Molecule: gluconate 5-dehydrogenase; PDBTitle: crystal structure of a gluconate 5-dehydrogenase from burkholderia2 cenocepacia j2315 in complex with nadp and tartrate
92	c3o38D_	Alignment	not modelled	99.3	19	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
93	c2p68A_	Alignment	not modelled	99.3	31	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
94	c4xgnD_	Alignment	not modelled	99.3	22	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase in complex with2 nad from burkholderia thailandensis
95	d1ja9a_	Alignment	not modelled	99.3	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
96	c2zatC_	Alignment	not modelled	99.3	24	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
97	c3qljB_	Alignment	not modelled	99.3	24	PDB header: oxidoreductase Chain: B: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 avium
98	d1spxa_	Alignment	not modelled	99.3	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
99	d1w6ua_	Alignment	not modelled	99.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
100	c3emkA_	Alignment	not modelled	99.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose/ribitol dehydrogenase; PDBTitle: 2.5a crystal structure of glucose/ribitol dehydrogenase from brucella2 melitensis
101	c5t5qC_	Alignment	not modelled	99.3	23	PDB header: oxidoreductase Chain: C: PDB Molecule: short-chain dehydrogenase/reductase sdr:glucose/ribitol PDBTitle: crystal structure of short-chain dehydrogenase/reductase2 sdr:glucose/ribitol dehydrogenase from brucella melitensis
102	d1vl8a_	Alignment	not modelled	99.3	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
103	d1iy8a_	Alignment	not modelled	99.3	37	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

				Family:Tyrosine-dependent oxidoreductases		
104	d1pr9a_	Alignment	not modelled	99.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
105	c3wtcB_	Alignment	not modelled	99.3	30	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036
106	c4iuyB_	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: short chain dehydrogenase/reductase; PDBTitle: crystal structure of short-chain dehydrogenase/reductase (apo-form)2 from a. baumannii clinical strain wm99c
107	d1y5ma1	Alignment	not modelled	99.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
108	c3gvcB_	Alignment	not modelled	99.3	26	PDB header: oxidoreductase Chain: B: PDB Molecule: probable short-chain type dehydrogenase/reductase; PDBTitle: crystal structure of probable short-chain dehydrogenase-reductase from2 mycobacterium tuberculosis
109	c4nbrA_	Alignment	not modelled	99.3	22	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: crystal structure of 3-oxoacyl-[acyl-carrier protein] reductase from2 brucella melitensis atcc 23457
110	c3zu3A_	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ypo4104/y4119/yp_4011; PDBTitle: structure of the enoyl-acp reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
111	c3ak4C_	Alignment	not modelled	99.3	30	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
112	c3ijrF_	Alignment	not modelled	99.3	22	PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
113	c3iccA_	Alignment	not modelled	99.3	25	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 3-oxoacyl-(acyl carrier protein) reductase; PDBTitle: crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
114	c3ftpD_	Alignment	not modelled	99.3	23	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 burkholderia pseudomallei at 2.05 a resolution
115	d2h7ma1	Alignment	not modelled	99.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
116	c3i1jB_	Alignment	not modelled	99.3	26	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: structure of a putative short chain dehydrogenase from pseudomonas2 syringae
117	d1geea_	Alignment	not modelled	99.3	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
118	c3ai3A_	Alignment	not modelled	99.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-sorbose reductase; PDBTitle: the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
119	c3cxtA_	Alignment	not modelled	99.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
120	c4kwhA_	Alignment	not modelled	99.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: reductase homolog; PDBTitle: the crystal structure of angucycline c-6 ketoreductase lanv with bound2 nadp