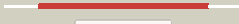



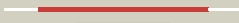



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2002_(fabG3)_2247668_2248450
Date	Mon Aug 5 13:25:11 BST 2019
Unique Job ID	ccdda57c45d9c01b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nffa_	 Alignment		100.0	99	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
2	d1hdca_	 Alignment		100.0	49	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
3	d1w6ua_	 Alignment		100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
4	c5idxB_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of an oxidoreductase from burkholderia vietnamiensis
5	c3gvcB_	 Alignment		100.0	36	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
6	c5epoD_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
7	c3tzqD_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: D: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
8	c3k31B_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of enoyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
9	c3cxtA_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
10	c4fc6B_	 Alignment		100.0	28	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
11	c4dqxB_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42

12	c3lf2B_	Alignment		100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: short chain oxidoreductase q9hya2; PDBTitle: nadph bound structure of the short chain oxidoreductase q9hya2 from2 pseudomonas aeruginosa pao1 containing an atypical catalytic center
13	c3emkA_	Alignment		100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose/ribitol dehydrogenase; PDBTitle: 2.5a crystal structure of glucose/ribitol dehydrogenase from brucella2 melitensis
14	c4wecA_	Alignment		100.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
15	c5itvC_	Alignment		100.0	40	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
16	d2c07a1	Alignment		100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
17	c2c07A_	Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acyl reductase of plasmodium falciparum
18	c4nqzF_	Alignment		100.0	26	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
19	c6ci9D_	Alignment		100.0	30	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
20	d1xhla_	Alignment		100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
21	d1yxma1	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
22	c5h5xH_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: H: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor
23	c4npcA_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: sorbitol dehydrogenase; PDBTitle: crystal structure of an oxidoreductase, short-chain2 dehydrogenase/reductase family protein from brucella suis
24	c5k9zB_	Alignment	not modelled	100.0	35	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
25	d2ae2a_	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
26	c4iboA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
27	d1q7ba_	Alignment	not modelled	100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
28	c3nugA_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti
						PDB header: oxidoreductase Chain: C: PDB Molecule: putative short-chain

29	c5jc8C_	Alignment	not modelled	100.0	34	dehydrogenase/reductase; PDBTitle: crystal structure of a putative short-chain dehydrogenase/reductase2 from burkholderia xenovorans
30	d1ae1a_	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
31	c3ai3A_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-p-sorbose reductase; PDBTitle: the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
32	c4afnB_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase fabg; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 (fabg) from pseudomonas aeruginosa at 2.3a resolution
33	d1iy8a_	Alignment	not modelled	100.0	36	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
34	c5u9pB_	Alignment	not modelled	100.0	33	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
35	c5ojgB_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of the dehydrogenase/reductase sdr family member 42 (dhrs4) from caenorhabditis elegans
36	d1geea_	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
37	c5jy1C_	Alignment	not modelled	100.0	33	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
38	c4nbvA_	Alignment	not modelled	100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from cupriavidus taiwanensis
39	c4urfB_	Alignment	not modelled	100.0	42	PDB header: oxidoreductase Chain: B: PDB Molecule: cyclohexanol dehydrogenase; PDBTitle: molecular genetic and crystal structural analysis of 1-(4-2 hydroxyphenyl)-ethanol dehydrogenase from aromatoleum aromaticum ebn1
40	c3svtA_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
41	d1k2wa_	Alignment	not modelled	100.0	36	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
42	c4j2hA_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain alcohol dehydrogenase-related dehydrogenase; PDBTitle: crystal structure of a putative short-chain alcohol dehydrogenase from2 sinorhizobium meliloti 1021 (target nysgrc-011708)
43	d1fmca_	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
44	c4cr8D_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: D: PDB Molecule: n-acylmannosamine 1-dehydrogenase; PDBTitle: crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
45	c6d9yB_	Alignment	not modelled	100.0	36	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 with partially occupied nad
46	c4gh5B_	Alignment	not modelled	100.0	36	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)
47	c5x8hA_	Alignment	not modelled	100.0	35	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
48	c3vc7B_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
49	c3wtcB_	Alignment	not modelled	100.0	38	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036
50	c3grkE_	Alignment	not modelled	100.0	25	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
51	c5un1A_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketoacyl-acp reductase; PDBTitle: crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
52	c6ds1C_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of cj0485 dehydrogenase in complex

						with nadp+
53	c4g81A_	Alignment	not modelled	100.0	35	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)
54	d1ydea1	Alignment	not modelled	100.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
55	c2pd6D_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
56	c4trrH_	Alignment	not modelled	100.0	30	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
57	c4egfA_	Alignment	not modelled	100.0	39	PDB header: oxidoreductase Chain: A: PDB Molecule: l-xylulose reductase; PDBTitle: crystal structure of a l-xylulose reductase from mycobacterium2 smegmatis
58	d1pr9a_	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
59	c3awdD_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: D: PDB Molecule: putative polyol dehydrogenase; PDBTitle: crystal structure of gox2181
60	c2q2qG_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: G: PDB Molecule: beta-d-hydroxybutyrate dehydrogenase; PDBTitle: structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
61	c3t7cC_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
62	c3itdA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: 17beta-hydroxysteroid dehydrogenase; PDBTitle: crystal structure of an inactive 17beta-hydroxysteroid dehydrogenase2 (y167f mutated form) from fungus cochliobolus lunatus
63	c5er6C_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: crystal structure of an oxidoreductase from brucella ovis
64	d2bgka1	Alignment	not modelled	100.0	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
65	d2ew8a1	Alignment	not modelled	100.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
66	c4imrA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of 3-oxoacyl (acyl-carrier-protein) reductase2 (target efi-506442) from agrobacterium tumefaciens c58 with nadp3 bound
67	d1zema1	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	c4lvuB_	Alignment	not modelled	100.0	36	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
69	c4m87B_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of enoyl-acyl carrier protein reductase (fabI) from2 neisseria meningitidis in complex with nad+
70	c3tscB_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of short chain dehydrogenase map_2410 from2 mycobacterium paratuberculosis bound to nad
71	d1hxha_	Alignment	not modelled	100.0	43	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
72	c4cqmj_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: J: PDB Molecule: carbonyl reductase family member 4; PDBTitle: crystal structure of heterotetrameric human ketoacyl2 reductase complexed with nad and nadp
73	c3ak4C_	Alignment	not modelled	100.0	38	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
74	c3rihB_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: short chain dehydrogenase or reductase; PDBTitle: crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
75	c5ff9C_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: noroxomaritidine/norcraugsodine reductase; PDBTitle: noroxomaritidine/norcraugsodine reductase in complex with nadp+ and2 tyramine
76	c4jroC_	Alignment	not modelled	100.0	38	PDB header: oxidoreductase Chain: C: PDB Molecule: fabg protein; PDBTitle: crystal structure of 3-oxoacyl-[acyl-carrier protein]reductase (fabg)2 from listeria monocytogenes in complex with nadp+

77	c5t2uC	Alignment	not modelled	100.0	38	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family PDBTitle: short chain dehydrogenase/reductase family protein
78	c2p68A	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vF5
79	c2cfcB	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-(r)-hydroxypropyl-com dehydrogenase; PDBTitle: structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
80	c2zatC	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
81	c3gk3D	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: D: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetoacetyl-coa reductase from burkholderia2 pseudomallei 1710b
82	d2pd4a1	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
83	c4wuvB	Alignment	not modelled	100.0	23	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
84	c2jyD	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of francisella tularensis enoyl reductase2 (ftfab) with bound nad
85	c4z9yA	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-deoxy-d-gluconate 3-dehydrogenase; PDBTitle: crystal structure of 2-keto-3-deoxy-d-gluconate dehydrogenase from2 pectobacterium carotovorum
86	d1xkqa	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
87	c3ijrF	Alignment	not modelled	100.0	27	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+
88	c3imfA	Alignment	not modelled	100.0	29	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'
89	c4i5eC	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol dehydrogenase/short-chain dehydrogenase; PDBTitle: crystal structure of ralstonia sp. alcohol dehydrogenase in complex2 with nadp+
90	c3r3sD	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
91	c5jlaB	Alignment	not modelled	100.0	27	PDB header: isomerase Chain: B: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of ribose-5-phosphate isomerase from brucella2 melitensis 16m
92	c3toxG	Alignment	not modelled	100.0	33	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
93	c4ni5A	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family PDBTitle: crystal structure of a short chain dehydrogenase from brucella suis
94	c4m8sB	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: putative 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: crystal structure of 3-ketoacyl -(acyl carrier protein) reductase2 (fabg) from neisseria meningitidis
95	d2d1ya1	Alignment	not modelled	100.0	36	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
96	c3ek2D	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nahh); PDBTitle: crystal structure of enoyl-(acyl carrier protein) reductase from2 burkholderia pseudomallei 1719b
97	c4nk4E	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nahh]; PDBTitle: crystal structure of fabi from candidatus liberibacter asiaticus
98	c1w4zA	Alignment	not modelled	100.0	36	PDB header: antibiotic biosynthesis Chain: A: PDB Molecule: ketoacyl reductase; PDBTitle: structure of actinorhodin polyketide (actiii) reductase
99	c3lylB	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
100	d2rhca1	Alignment	not modelled	100.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

						Family: Tyrosine-dependent oxidoreductases
101	c3o38D_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
102	c4zjuA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nahh]; PDBTitle: structure of a nahh-dependent enoyl-acp reductase from acinetobacter2 baumannii in complex with nad
103	c6f9qC_	Alignment	not modelled	100.0	31	PDB header: biosynthetic protein Chain: C: PDB Molecule: 7s-cis-cis-nepetalactol cyclase; PDBTitle: binary complex of a 7s-cis-cis-nepetalactol cyclase from nepeta2 mussinii with nad+
104	c4gloC_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: crystal structure of a short chain dehydrogenase homolog (target efi-2 505321) from burkholderia multivorans, with bound nad
105	c2z1nA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of ape0912 from aeropyrum pernix k1
106	c4fgsB_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: probable dehydrogenase protein; PDBTitle: crystal structure of a probable dehydrogenase protein
107	c2yz7B_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: d-3-hydroxybutyrate dehydrogenase; PDBTitle: x-ray analyses of 3-hydroxybutyrate dehydrogenase from2 alcaligenes faecalis
108	c3uf0A_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
109	c3ftpD_	Alignment	not modelled	100.0	34	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
110	c2uvdE_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: E: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: the crystal structure of a 3-oxoacyl-(acyl carrier protein) reductase2 from bacillus anthracis (ba3989)
111	d1ulua_	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
112	c4rziB_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-ketoacyl-acyl carrier protein reductase; PDBTitle: crystal structure of phab from synechocystis sp. pcc 6803
113	d1zk4a1	Alignment	not modelled	100.0	43	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
114	c3iccA_	Alignment	not modelled	100.0	24	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
115	c5o30A_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of the novel halohydrin dehalogenase hheg
116	c5bt9B_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of folm alternative dihydrofolate reductase 1 from2 brucella canis complexed with nadp
117	c4fn4A_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from sulfobolus2 acidocaldarius
118	c5jo9A_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: ribitol 2-dehydrogenase; PDBTitle: structural characterization of the thermostable bradyrhizobium2 japonicum d-sorbitol dehydrogenase
119	d1qsga_	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
120	c5jydA_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia