

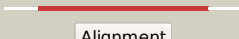

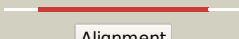



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0687_(fabG)_787102_787929
Date	Fri Jul 26 01:50:25 BST 2019
Unique Job ID	9aacffa26de6d99

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pgxB_	 Alignment		100.0	82	PDB header: oxidoreductase Chain: B: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of a putative carveol dehydrogenase from2 mycobacterium paratuberculosis bound to nicotinamide adenine3 dinucleotide
2	c3tscB_	 Alignment		100.0	48	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of short chain dehydrogenase map_2410 from2 mycobacterium paratuberculosis bound to nad
3	c3t7cC_	 Alignment		100.0	43	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
4	c3uveC_	 Alignment		100.0	45	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase ((+)-trans-carveol dehydrogenase); PDBTitle: crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
5	c3oecA_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: A: PDB Molecule: carveol dehydrogenase (mytha.01326.c, a0r518 homolog); PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
6	c4rgbB_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of a putative carveol dehydrogenase from2 mycobacterium avium bound to nad
7	c4trrH_	 Alignment		100.0	24	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
8	c3lf2B_	 Alignment		100.0	21	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
9	d1geea_	 Alignment		100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
10	d1iy8a_	 Alignment		100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
11	c3wtcB_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036

12	d1xhla_	Alignment		100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
13	d2ae2a_	Alignment		100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	c4wuvB_	Alignment		100.0	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
15	c3cxtA_	Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
16	c2q2qG_	Alignment		100.0	29	PDB header: oxidoreductase Chain: G: PDB Molecule: beta-d-hydroxybutyrate dehydrogenase; PDBTitle: structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
17	c3svtA_	Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
18	c5ojgB_	Alignment		100.0	24	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
19	d1w6ua_	Alignment		100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
20	d1g0oa_	Alignment		100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
21	c5o30A_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of the novel halohydrin dehalogenase hheg
22	d1yxma1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
23	c4cr8D_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: D: PDB Molecule: n-acylmannosamine 1-dehydrogenase; PDBTitle: crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
24	c4z9yA_	Alignment	not modelled	100.0	28	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
25	c5x8hA_	Alignment	not modelled	100.0	28	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
26	d2bgka1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
27	c3sx2F_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: F: PDB Molecule: putative 3-ketoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of a putative 3-ketoacyl-(acyl-carrier-protein)2 reductase from mycobacterium paratuberculosis in complex with nad
28	c6ci9D_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol

					dehydrogenase nadp +2 aminoacetone holo-structure 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)
29	c4g81A_	Alignment	not modelled	100.0	28
30	c4nqzF_	Alignment	not modelled	100.0	24
31	c4fc6B_	Alignment	not modelled	100.0	25
32	c3rihB_	Alignment	not modelled	100.0	31
33	c5jc8C_	Alignment	not modelled	100.0	31
34	c4urfB_	Alignment	not modelled	100.0	31
35	c5jy1C_	Alignment	not modelled	100.0	27
36	c5jydA_	Alignment	not modelled	100.0	29
37	c4egfA_	Alignment	not modelled	100.0	33
38	c5h5xH_	Alignment	not modelled	100.0	33
39	c3itdA_	Alignment	not modelled	100.0	26
40	c3toxG_	Alignment	not modelled	100.0	33
41	c3gvCB_	Alignment	not modelled	100.0	33
42	c3nugA_	Alignment	not modelled	100.0	31
43	d1xkqa_	Alignment	not modelled	100.0	23
44	c5itvC_	Alignment	not modelled	100.0	27
45	c4j2hA_	Alignment	not modelled	100.0	31
46	c3awdD_	Alignment	not modelled	100.0	27
47	d1ja9a_	Alignment	not modelled	100.0	28
48	c6d9yB_	Alignment	not modelled	100.0	26
49	c1w4zA_	Alignment	not modelled	100.0	31
50	d1k2wa_	Alignment	not modelled	100.0	29
51	d2ew8a1	Alignment	not modelled	100.0	31
52	c4fn4A_	Alignment	not modelled	100.0	24

52	c4m4A_	Alignment	not modelled	100.0	24	PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from sulfobolbus2 acidocaldarius
53	d2rhca1	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
54	d1zema1	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
55	d1ae1a_	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
56	c2zatC_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
57	c5un1A_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketoacyl-acp reductase; PDBTitle: crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
58	c3ak4C_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
59	c3tzqD_	Alignment	not modelled	100.0	26	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
60	c3ijrF_	Alignment	not modelled	100.0	24	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+
61	c6ds1C_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of cj0485 dehydrogenase in complex with nadp+
62	c3iccA_	Alignment	not modelled	100.0	22	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
63	c4afnB_	Alignment	not modelled	100.0	31	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
64	c4nimA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: versicolorin reductase; PDBTitle: crystal structure of a short chain dehydrogenase from brucella2 melitensis
65	c5k9zB_	Alignment	not modelled	100.0	27	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
66	c5epoD_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
67	c4npcA_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: sorbitol dehydrogenase; PDBTitle: crystal structure of an oxidoreductase, short-chain2 dehydrogenase/reductase family protein from brucella suis
68	c5u9pB_	Alignment	not modelled	100.0	27	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
69	c3o38D_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
70	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)
71	c3ai3A_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph-sorbitose reductase; PDBTitle: the crystal structure of l-sorbitose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbitose
72	c4imrA_	Alignment	not modelled	100.0	23	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
73	c5o3zK_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: K: PDB Molecule: sorbitol-6-phosphate dehydrogenase; PDBTitle: crystal structure of sorbitol-6-phosphate 2-dehydrogenase srlid from2 erwinia amylovora
74	c2yz7B_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: d-3-hydroxybutyrate dehydrogenase; PDBTitle: x-ray analyses of 3-hydroxybutyrate dehydrogenase from2 alcaligenes faecalis
75	c3grkE_	Alignment	not modelled	100.0	23	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
						PDB header: oxidoreductase

76	c4gh5B_	Alignment	not modelled	100.0	26	Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of s-2-hydroxypropyl coenzyme m dehydrogenase (s-2 hpcdh)
77	c4nbvA_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from cupriavidus taiwanensis
78	d2c07a1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
79	c2c07A_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acp reductase of plasmodium falciparum
80	d1nffa_	Alignment	not modelled	100.0	37	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
81	c3imfA_	Alignment	not modelled	100.0	30	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'
82	d1h5qa_	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
83	c3r3sD_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
84	d1hdca_	Alignment	not modelled	100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
85	c6f9qC_	Alignment	not modelled	100.0	23	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+
86	c3sjuA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: keto reductase; PDBTitle: hedamycin polyketide ketoreductase bound to nadph
87	d1fmca_	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
88	d1zk4a1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
89	d2pd4a1	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
90	c5thkH_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: H: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of a putative dehydrogenase from burkholderia2 cenocepacia with bound nadp
91	c4iiuB_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: crystal structure of a putative 3-oxoacyl-[acyl-carrier2 protein]reductase from escherichia coli strain cft073 complexed with3 nadp+ at 2.1 a resolution
92	c4lvuB_	Alignment	not modelled	100.0	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
93	c6oz7A_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized oxidoreductase yohf; PDBTitle: putative oxidoreductase from escherichia coli str. k-12
94	c3pk0B_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
95	c2cfcB_	Alignment	not modelled	100.0	27	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
96	c4wecA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
97	d1gega_	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
98	c5ff9C_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: noroxomaritidine/norcraugsodine reductase; PDBTitle: noroxomaritidine/norcraugsodine reductase in complex with nadp+ and2 tyramine
99	c4jroC_	Alignment	not modelled	100.0	32	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+
100	c3k31B_	Alignment	not modelled	100.0	22	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
						PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain dehydrogenase/reductase sdr;

101	c3uf0A_	Alignment	not modelled	100.0	26	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)
102	c2pd6D_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
103	c4iuyB_	Alignment	not modelled	100.0	26	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
104	c4zjuA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nahd]; PDBTitle: structure of a nahd-dependent enoyl-acp reductase from acinetobacter2 baumannii in complex with nad
105	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
106	c3v2gA_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
107	c4kwhA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: reductase homolog; PDBTitle: the crystal structure of angucycline c-6 ketoreductase lanv with bound2 nadp
108	c4m87B_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nahd]; PDBTitle: crystal structure of enoyl-acyl carrier protein reductase (fabI) from2 neisseria meningitidis in complex with nad+
109	d1ydea1	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
110	c5g4kB_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: phloroglucinol reductase from clostridium sp. apo-form
111	c5idxB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of an oxidoreductase from burkholderia vietnamiensis
112	c2uvdE_	Alignment	not modelled	100.0	32	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)
113	c5er6C_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: crystal structure of an oxidoreductase from brucella ovis
114	c3pxxE_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: E: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nicotinamide adenine dinucleotide
115	c4dqxB_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42
116	c4qecB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: elxo; PDBTitle: elxo with nadp bound
117	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 (ftfabI) with bound nad
118	c4ni5A_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family PDBTitle: crystal structure of a short chain dehydrogenase from brucella suis
119	c4k6fD_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: D: PDB Molecule: putative acetoacetyl-coa reductase; PDBTitle: x-ray crystal structure of a putative acetoacetyl-coa reductase from2 burkholderia cenocepacia bound to the co-factor nadp
120	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