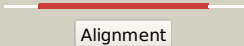

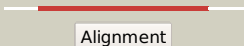

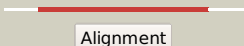







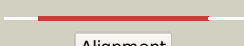











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2766c_(fabG)_3075598_3076380
Date	Wed Aug 7 12:50:42 BST 2019
Unique Job ID	0296a5cbee7c4c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6d9yB_	 Alignment		100.0	32	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
2	c5epoD_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
3	c4urfB_	 Alignment		100.0	33	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
4	c5idxB_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of an oxidoreductase from burkholderia vietnamiensis
5	c3svtA_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
6	d1w6ua_	 Alignment		100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
7	c6ci9D_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
8	c5k9zB_	 Alignment		100.0	30	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
9	c3awdD_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: D: PDB Molecule: putative polyol dehydrogenase; PDBTitle: crystal structure of gox2181
10	c4npcA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: sorbitol dehydrogenase; PDBTitle: crystal structure of an oxidoreductase, short-chain2 dehydrogenase/reductase family protein from brucella suis
11	c3tzqD_	 Alignment		100.0	36	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

12	c5jy1C_	Alignment		100.0	31	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	c3rihB_	Alignment		100.0	25	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
14	c4fc6B_	Alignment		100.0	29	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
15	d1q7ba_	Alignment		100.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
16	c3lf2B_	Alignment		100.0	24	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
17	c4nbvA_	Alignment		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
18	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
19	d1iy8a_	Alignment		100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
20	d1k2wa_	Alignment		100.0	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
21	c5u9pB_	Alignment	not modelled	100.0	29	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
22	c5t2uC_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family PDBTitle: short chain dehydrogenase/reductase family protein
23	d2ae2a_	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
24	c3cxtA_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus sulis type 2
25	d1hdca_	Alignment	not modelled	100.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
26	c4m8sB_	Alignment	not modelled	100.0	33	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
27	c4egfA_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: l-xylulose reductase; PDBTitle: crystal structure of a l-xylulose reductase from mycobacterium2 smegmatis
28	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

29	c4afnB	Alignment	not modelled	100.0	29	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
30	c5x8hA	Alignment	not modelled	100.0	31	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
31	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
32	c5itvC	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydroantipain 7-dehydrogenase; PDBTitle: crystal structure of bacillus subtilis bacc dihydroantipain 7-2 dehydrogenase in complex with nadh
33	c3wtcB	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036
34	d1xhla	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
35	d1ae1a	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
36	c5t5qC	Alignment	not modelled	100.0	28	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
37	d1geea	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
38	c3toxG	Alignment	not modelled	100.0	35	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
39	d1bdba	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
40	c4z9yA	Alignment	not modelled	100.0	29	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
41	c3pk0B	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
42	c4lvuB	Alignment	not modelled	100.0	29	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
43	c3uf0A	Alignment	not modelled	100.0	30	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)
44	c4cr8D	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: D: PDB Molecule: n-acylmannosamine 1-dehydrogenase; PDBTitle: crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
45	c4jroC	Alignment	not modelled	100.0	30	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+
46	d1pr9a	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
47	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
48	c4j2hA	Alignment	not modelled	100.0	35	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)
49	c5ojgB	Alignment	not modelled	100.0	40	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
50	c2zatC	Alignment	not modelled	100.0	38	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
51	c4g81A	Alignment	not modelled	100.0	31	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)
52	c3nugA	Alignment	not modelled	100.0	31	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
53	c5h5xH_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: H: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor
54	c4nbrA_	Alignment	not modelled	100.0	27	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
55	d1zema1	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
56	c3gvcB_	Alignment	not modelled	100.0	34	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
57	c3emkA_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose/ribitol dehydrogenase; PDBTitle: 2.5a crystal structure of glucose/ribitol dehydrogenase from brucella2 melitensis
58	c4wuvB_	Alignment	not modelled	100.0	28	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
59	c4o0IA_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph-dependent 3-quinuclidinone reductase; PDBTitle: crystal structure of nadph-dependent 3-quinuclidinone reductase from2 rhodotorula rubra
60	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
61	c4xgnD_	Alignment	not modelled	100.0	24	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
62	d1ydea1	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
63	c2pd6D_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
64	c5unlA_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketoacyl-acyl carrier protein reductase; PDBTitle: crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
65	c4iboA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
66	c4imrA_	Alignment	not modelled	100.0	28	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	c5ff9C_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: C: PDB Molecule: noroxomaritidine/norcraugsodine reductase; PDBTitle: noroxomaritidine/norcraugsodine reductase in complex with nadp+ and2 tyramine
68	c4fn4A_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from sulfobolbus2 acidocaldarius
69	c2p68A_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
70	d1yxma1	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
71	d2bgka1	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
72	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
73	c4i5eC_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol dehydrogenase/short-chain dehydrogenase; PDBTitle: crystal structure of ralstonia sp. alcohol dehydrogenase in complex2 with nadp+
74	c4iuyB_	Alignment	not modelled	100.0	28	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
75	c3gdfA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: probable nadp-dependent mannitol dehydrogenase; PDBTitle: crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.

76	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
77	d2c07a1	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
78	c2c07A_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acyl reductase of plasmodium falciparum
79	c4mowB_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase; PDBTitle: crystal structure of a putative glucose 1-dehydrogenase from2 burkholderia cenocepacia j2315
80	c4rziB_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-ketoacyl-acyl carrier protein reductase; PDBTitle: crystal structure of phab from synechocystis sp. pcc 6803
81	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
82	c3ai3A_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph-sorbose reductase; PDBTitle: the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
83	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+
84	c3gk3D_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetoacetyl-coa reductase from burkholderia2 pseudomallei 1710b
85	c4o5oA_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: x-ray crystal structure of a 3-hydroxyacyl-coa dehydrogenase from2 brucella suis
86	d1nffa_	Alignment	not modelled	100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
87	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+
88	d1xkqa_	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
89	c3gr6A_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of the staphylococcus aureus enoyl-acyl carrier2 protein reductase (fabI) in complex with nadp and triclosan
90	d1ulsA_	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
91	c4nbuD_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of fabg from bacillus sp
92	c2z1nA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of ape0912 from aeropyrum pernix k1
93	c3t7cC_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
94	c3v2gA_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of a dehydrogenase/reductase from sinorhizobium2 melliloti 1021
95	c5g4kB_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: phloroglucinol reductase from clostridium sp. apo-form
96	d2pd4a1	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
97	c6a41A_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: dehalogenase; PDBTitle: dehalogenation enzyme
98	c3iccA_	Alignment	not modelled	100.0	28	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
99	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'
100	c5tt0A_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: crystal structure of an oxidoreductase (short chain2 dehydrogenase/reductase family) from burkholderia thailandensis

101	c3afnC_	Alignment	not modelled	100.0	32	Chain: C; PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of aldose reductase a1-r complexed with nadp
102	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)
103	c4nqzF_	Alignment	not modelled	100.0	23	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
104	c4nbwA_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A; PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of fabg from pleisiocystis pacifica
105	c2p91A_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A; PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of enoyl-[acyl-carrier-protein] reductase (nadh)2 from aquifex aeolicus vf5
106	c2b4qB_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B; PDB Molecule: rhamnolipids biosynthesis 3-oxoacyl-[acyl-carrier-protein] PDBTitle: pseudomonas aeruginosa rhlg/nadp active-site complex
107	c4gh5B_	Alignment	not modelled	100.0	33	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)
108	c2q2qG_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: G; PDB Molecule: beta-d-hydroxybutyrate dehydrogenase; PDBTitle: structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
109	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
110	c4hp8A_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-deoxy-d-gluconate 3-dehydrogenase; PDBTitle: crystal structure of a putative 2-deoxy-d-gluconate 3-dehydrogenase2 from agrobacterium tumefaciens (target efi-506435) with bound nadp
111	c3ppiA_	Alignment	not modelled	100.0	28	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
112	c3ftpD_	Alignment	not modelled	100.0	33	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
113	c3rkuC_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: C; PDB Molecule: oxidoreductase ymr226c; PDBTitle: substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+
114	c3r3sD_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: D; PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
115	c5bt9B_	Alignment	not modelled	100.0	25	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
116	c4zjuA_	Alignment	not modelled	100.0	22	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
117	c5jlaB_	Alignment	not modelled	100.0	31	PDB header: isomerase Chain: B; PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of ribose-5-phosphate isomerase from brucella2 melitensis 16m
118	c5o3zK_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: K; PDB Molecule: sorbitol-6-phosphate dehydrogenase; PDBTitle: crystal structure of sorbitol-6-phosphate 2-dehydrogenase srid from2 erwinia amylovora
119	c3itdA_	Alignment	not modelled	100.0	20	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
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