

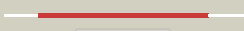














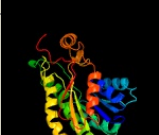






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3485c (-)_3904801_3905745
Date	Fri Aug 9 18:20:16 BST 2019
Unique Job ID	519318ce37538dc0

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3svtA_	 Alignment		100.0	86	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
2	c5jy1C_	 Alignment		100.0	25	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
3	c3rihB_	 Alignment		100.0	30	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
4	d2ae2a_	 Alignment		100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
5	c4egfA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: l-xylulose reductase; PDBTitle: crystal structure of a l-xylulose reductase from mycobacterium2 smegmatis
6	c4fc6B_	 Alignment		100.0	26	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
7	d1w6ua_	 Alignment		100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
8	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
9	c6ci9D_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
10	c3awdD_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: D: PDB Molecule: putative polyol dehydrogenase; PDBTitle: crystal structure of gox2181
11	d1xhla_	 Alignment		100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

12	c5jydA_	Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
13	c5epoD_	Alignment		100.0	28	PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
14	c2cfcB_	Alignment		100.0	24	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
15	c6d9yB_	Alignment		100.0	25	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
16	d1geea_	Alignment		100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
17	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
18	c5ojgB_	Alignment		100.0	26	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	c5k9zB_	Alignment		100.0	31	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
20	c3pk0B_	Alignment		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
21	d1ae1a_	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
22	c4j2hA_	Alignment	not modelled	100.0	30	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)
23	c4iboA_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
24	c2zatC_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
25	d1iy8a_	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
26	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+
27	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
						PDB header: oxidoreductase

28	c3toxG	Alignment	not modelled	100.0	28	Chain: G: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
29	c3wtcB	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036
30	c5x8hA	Alignment	not modelled	100.0	30	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	c4g81A	Alignment	not modelled	100.0	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)
32	c3lf2B	Alignment	not modelled	100.0	23	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
33	c4cr8D	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: n-acylmannosamine 1-dehydrogenase; PDBTitle: crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
34	c4z9yA	Alignment	not modelled	100.0	25	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
35	d2pd4a1	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
36	c3gr6A	Alignment	not modelled	100.0	23	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
37	d1zema1	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
38	c5koiH	Alignment	not modelled	100.0	23	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
39	c5u9pB	Alignment	not modelled	100.0	25	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
40	c3r3sD	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
41	c3cxtA	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
42	c4nbvA	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from cupriavidus taiwanensis
43	c3tzqD	Alignment	not modelled	100.0	30	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
44	c4nqzF	Alignment	not modelled	100.0	27	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
45	c3iccA	Alignment	not modelled	100.0	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
46	c5ff9C	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: C: PDB Molecule: noroxomaritidine/norcraugsodine reductase; PDBTitle: noroxomaritidine/norcraugsodine reductase in complex with nadp+ and2 tyramine
47	c4nbrA	Alignment	not modelled	100.0	29	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
48	c4fn4A	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from sulfolobus2 acidocaldarius
49	c4npcA	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: sorbitol dehydrogenase; PDBTitle: crystal structure of an oxidoreductase, short-chain2 dehydrogenase/reductase family protein from brucella suis
50	c4trrH	Alignment	not modelled	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
51	c4jroC	Alignment	not modelled	100.0	26	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+
52	c4nk4E_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of fabi from candidatus liberibacter asiaticus
53	c4lvuB_	Alignment	not modelled	100.0	25	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
54	c3k31B_	Alignment	not modelled	100.0	23	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
55	d1g0oa_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
56	c4afnB_	Alignment	not modelled	100.0	25	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
57	d1k2wa_	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
58	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
59	c3itdA_	Alignment	not modelled	100.0	25	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
60	c4iuyB_	Alignment	not modelled	100.0	23	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
61	c5h5xH_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: H: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor
62	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
63	d1qsga_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
64	d1fmca_	Alignment	not modelled	100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
65	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)
66	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
67	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
68	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
69	c2qioA_	Alignment	not modelled	100.0	24	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
70	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
71	c4rgbB_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of a putative carveol dehydrogenase from2 mycobacterium avium bound to nad
72	d1h5qa_	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
73	c5idxB_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of an oxidoreductase from burkholderia vietnamiensis
74	c3oidA_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadph]; PDBTitle: crystal structure of enoyl-acp reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)
75	c3ai3A_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph-sorbose reductase;

75	c3a12A	Alignment	not modelled	100.0	20	PDBTitle: the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose PDB header: oxidoreductase
76	c3o38D	Alignment	not modelled	100.0	24	Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
77	c5jc8C	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of a putative short-chain dehydrogenase/reductase2 from burkholderia xenovorans
78	c3ak4C	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
79	c3t7cC	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
80	c2p68A	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
81	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
82	d1ja9a	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
83	d1hdca	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
84	c5o30A	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of the novel halohydrin dehalogenase hheg
85	c3imfA	Alignment	not modelled	100.0	25	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'
86	c5itvC	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydroantocapsin 7-dehydrogenase; PDBTitle: crystal structure of bacillus subtilis bacc dihydroantocapsin 7-2 dehydrogenase in complex with nadh
87	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
88	d1vl8a	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
89	c5g4kB	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: phloroglucinol reductase from clostridium sp. apo-form
90	d1pr9a	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
91	c4m87B	Alignment	not modelled	100.0	26	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+
92	c5unlA	Alignment	not modelled	100.0	30	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
93	c2yz7B	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: d-3-hydroxybutyrate dehydrogenase; PDBTitle: x-ray analyses of 3-hydroxybutyrate dehydrogenase from2 alcaligenes faecalis
94	c3afnC	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: C: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of aldose reductase a1-r complexed with nadp
95	d1ulua	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
96	c1w4zA	Alignment	not modelled	100.0	22	PDB header: antibiotic biosynthesis Chain: A: PDB Molecule: ketoacyl reductase; PDBTitle: structure of actinorhodin polyketide (actiii) reductase
97	c5o3zK	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: K: PDB Molecule: sorbitol-6-phosphate dehydrogenase; PDBTitle: crystal structure of sorbitol-6-phosphate 2-dehydrogenase srlid from2 erwinia amylovora
98	c6a41A	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: dehalogenase; PDBTitle: dehalogenation enzyme
99	c3nugA	Alignment	not modelled	100.0	27	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
100	c4hp8A	Alignment	not modelled	100.0	27	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
101	c2uvdE_	Alignment	not modelled	100.0	27	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)
102	d2bgka1	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
103	c3rkuC_	Alignment	not modelled	100.0	20	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+
104	c3tscB_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of short chain dehydrogenase map_2410 from2 mycobacterium paratuberculosis bound to nad
105	d2rhca1	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
106	d1q7ba_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
107	c4ni5A_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family PDBTitle: crystal structure of a short chain dehydrogenase from brucella suis
108	c3ek2D_	Alignment	not modelled	100.0	23	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
109	c6ds1C_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of cj0485 dehydrogenase in complex with nadp+
110	c4gh5B_	Alignment	not modelled	100.0	27	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)
111	c2q2qG_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: G: PDB Molecule: beta-d-hydroxybutyrate dehydrogenase; PDBTitle: structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
112	c4mowB_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase; PDBTitle: crystal structure of a putative glucose 1-dehydrogenase from2 burkholderia cenocepacia j2315
113	c4dmmA_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: 3-oxoacyl-[acyl-carrier-protein] reductase from synechococcus2 elongatus pcc 7942 in complex with nadp
114	c5t2uC_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family PDBTitle: short chain dehydrogenase/reductase family protein
115	c3v2qA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
116	c4o0IA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph-dependent 3-quinuclidinone reductase; PDBTitle: crystal structure of nadph-dependent 3-quinuclidinone reductase from2 rhodotorula rubra
117	d1zk4a1	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
118	c4iiuB_	Alignment	not modelled	100.0	26	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
119	c3gk3D_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetoacetyl-coa reductase from burkholderia2 pseudomallei 1710b
120	c3uveC_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase ((+)-trans-carveol dehydrogenase); PDBTitle: crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium