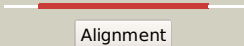

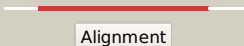

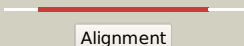







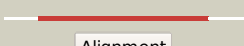









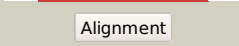







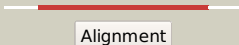

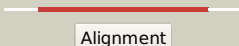

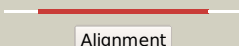



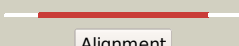


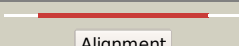
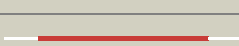
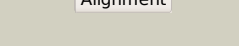

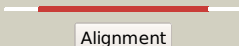

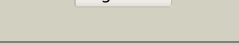


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0769 (-) _862415_863161
Date	Fri Jul 26 01:50:35 BST 2019
Unique Job ID	fd0314a49a0c4899

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5epoD	 Alignment		100.0	34	PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
2	c3toxG	 Alignment		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
3	c4urfB	 Alignment		100.0	35	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	d1fmca	 Alignment		100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
5	c4nbvA	 Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from cupriavidus taiwanensis
6	c6ci9D	 Alignment		100.0	27	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
7	c3svtA	 Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
8	c3wtcB	 Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036
9	c5jy1C	 Alignment		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
10	c2uvdE	 Alignment		100.0	33	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)
11	c2zatC	 Alignment		100.0	33	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase

12	c3awdD_			100.0	32	PDB header: oxidoreductase Chain: D: PDB Molecule: putative polyol dehydrogenase; PDBTitle: crystal structure of gox2181
13	d1iy8a_			100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	d2ae2a_			100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
15	c4afnB_			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
16	c5x8hA_			100.0	32	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
17	d1xhla_			100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
18	d1yxma1			100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
19	c4trrH_			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
20	c4nbrA_			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
21	c3cxtA_		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 suis type 2
22	c5u9pB_		not modelled	100.0	28	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
23	c5ojgB_		not modelled	100.0	33	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
24	c4fc6B_		not modelled	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
25	c5h5xH_		not modelled	100.0	35	PDB header: oxidoreductase Chain: H: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor
26	c3lf2B_		not modelled	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
27	c3rihB_		not modelled	100.0	29	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
28	c2cfcB_		not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-(r)-hydroxypropyl-com dehydrogenase;

28	c2c1cB	Alignment	not modelled	100.0	34	PDBTitle: structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
29	d2rhca1	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
30	c3tzqD	Alignment	not modelled	100.0	33	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
31	c4lvuB	Alignment	not modelled	100.0	26	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
32	c4iboA	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
33	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
34	c4gh5B	Alignment	not modelled	100.0	28	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)
35	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
36	d1geea	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
37	c5jc8C	Alignment	not modelled	100.0	28	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
38	c6d9yB	Alignment	not modelled	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
39	c1w4zA	Alignment	not modelled	100.0	28	PDB header: antibiotic biosynthesis Chain: A: PDB Molecule: ketoacyl reductase; PDBTitle: structure of actinorhodin polyketide (actiii) reductase
40	c4g81A	Alignment	not modelled	100.0	30	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
41	c3jirF	Alignment	not modelled	100.0	23	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+
42	d1w6ua	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
43	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 sulfobolus2 acidocaldarius
44	c3ftpD	Alignment	not modelled	100.0	32	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
45	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
46	c4egfA	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: l-xylulose reductase; PDBTitle: crystal structure of a l-xylulose reductase from mycobacterium2 smegmatis
47	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
48	d1xkqa	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
49	c5k9zB	Alignment	not modelled	100.0	32	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
50	c2c07A	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acyl reductase of plasmodium falciparum
51	d2c07a1	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
52	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
53	c5idxB	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of an oxidoreductase from burkholderia vietnamiensis
54	d1q7ba	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
55	c2yz7B	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: d-3-hydroxybutyrate dehydrogenase; PDBTitle: x-ray analyses of 3-hydroxybutyrate dehydrogenase from2 alcaligenes faecalis
56	c5itvC	Alignment	not modelled	100.0	30	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
57	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
58	c4nbwA	Alignment	not modelled	100.0	40	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of fabg from plasiocystis pacifica
59	d2pd4a1	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
60	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
61	c5jydA	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
62	c4jroC	Alignment	not modelled	100.0	31	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+
63	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
64	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
65	d1g0oa	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
66	c5unlA	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketoacyl-acp reductase; PDBTitle: crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
67	d1k2wa	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	c4j2hA	Alignment	not modelled	100.0	29	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)
69	c2p91A	Alignment	not modelled	100.0	23	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
70	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
71	d1gega	Alignment	not modelled	100.0	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
72	d1ja9a	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
73	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'
74	d1hdca	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
75	c4m8sB	Alignment	not modelled	100.0	30	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
76	c3grkE	Alignment	not modelled	100.0	21	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
77	c2q2qG_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: G: PDB Molecule: beta-d-hydroxybutyrate dehydrogenase; PDBTitle: structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
78	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 from 2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
79	c5ff9C_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: noroxomaritidine/norcraugsodine reductase; PDBTitle: noroxomaritidine/norcraugsodine reductase in complex with nadp+ and 2 tyramine
80	c4dqxB_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42
81	d1qsga_	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
82	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
83	c5o3zK_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: K: PDB Molecule: sorbitol-6-phosphate dehydrogenase; PDBTitle: crystal structure of sorbitol-6-phosphate 2-dehydrogenase srid from 2 erwinia amylovora
84	c4kwhA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: reductase homolog; PDBTitle: the crystal structure of angucycline c-6 ketoreductase lanv with bound 2 nadp
85	c5koiH_	Alignment	not modelled	100.0	24	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
86	c5er6C_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: crystal structure of an oxidoreductase from brucella ovis
87	c3ai3A_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-sorbose reductase; PDBTitle: the crystal structure of l-sorbose reductase from gluconobacter 2 frateurii complexed with nadph and l-sorbose
88	c3ak4C_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from 2 agrobacterium tumefaciens
89	c3uf0A_	Alignment	not modelled	100.0	31	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) with 3 bound nadp (low occupancy)
90	d1bdba_	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
91	c4zjuA_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: structure of a nadh-dependent enoyl-ACP reductase from acinetobacter 2 baumannii in complex with nad
92	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 from 2 pectobacterium carotovorum
93	c3afnC_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of aldose reductase a1-r complexed with nadp
94	c3nugA_	Alignment	not modelled	100.0	29	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
95	c4nbuD_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of fabg from bacillus sp
96	d1pr9a_	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
97	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 carrier 2 protein reductase (fabi) in apo form
98	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 v5
99	d1zk4a1	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
100	c6ov4A_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketoacyl-ACP reductase; PDBTitle: putative fabg from acinetobacter baumannii crystal form 1
						PDB header: oxidoreductase

101	c3sjuA_	Alignment	not modelled	100.0	30	Chain: A: PDB Molecule: keto reductase; PDBTitle: hedamycin polyketide ketoreductase bound to nadph
102	c4m87B_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nah]; PDBTitle: crystal structure of enoyl-acyl carrier protein reductase (fabI) from2 neisseria meningitidis in complex with nad+
103	c2pd6D_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
104	d1ulsA_	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
105	c3t7cC_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
106	c4weoD_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: D: PDB Molecule: putative acetoin(diacetyl) reductase; PDBTitle: crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia
107	d1h5qa_	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
108	d1nffa_	Alignment	not modelled	100.0	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
109	c3itdA_	Alignment	not modelled	100.0	23	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
110	c3tscB_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of short chain dehydrogenase map_2410 from2 mycobacterium paratuberculosis bound to nad
111	c4i5eC_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol dehydrogenase/short-chain dehydrogenase; PDBTitle: crystal structure of ralstonia sp. alcohol dehydrogenase in complex2 with nadp+
112	c3r3sD_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
113	c3bmrA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: pteridine reductase; PDBTitle: structure of pteridine reductase 1 (ptr1) from trypanosoma2 brucei in ternary complex with cofactor (nadp+) and3 inhibitor (compound ax6)
114	c3gvCB_	Alignment	not modelled	100.0	35	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
115	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
116	c3gr6A_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nah]; PDBTitle: crystal structure of the staphylococcus aureus enoyl-acyl carrier2 protein reductase (fabI) in complex with nadp and triclosan
117	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
118	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
119	d1x1ta1	Alignment	not modelled	100.0	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
120	c4mowB_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase; PDBTitle: crystal structure of a putative glucose 1-dehydrogenase from2 burkholderia cenocepacia j2315