











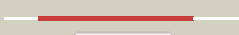

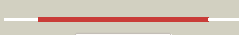









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1543_(-)_1745070_1746095
Date	Fri Aug 2 13:30:13 BST 2019
Unique Job ID	39868a4a46c04091

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2et6A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: (3r)-hydroxyacyl-coa dehydrogenase; PDBTitle: (3r)-hydroxyacyl-coa dehydrogenase domain of candida tropicalis2 peroxisomal multifunctional enzyme type 2
2	d1xsea_	 Alignment		100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
3	d1xu9a_	 Alignment		100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
4	d1y5ma1	 Alignment		100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
5	c4nqzF_	 Alignment		100.0	16	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
6	c4wuvB_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-hydroxycyclohexanecarboxyl-coa dehydrogenase; PDBTitle: crystal structure of a putative d-mannonate oxidoreductase from2 haemophilus influenza (avi_5165, target efi-513796) with bound nad
7	d1xhla_	 Alignment		100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
8	c5ig2B_	 Alignment		100.0	24	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 in complex with nad
9	d1zbqa1	 Alignment		100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
10	c1zbqB_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase 4; PDBTitle: crystal structure of human 17-beta-hydroxysteroid dehydrogenase type 42 in complex with nad
11	c5ldgA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-isopiperitenone reductase; PDBTitle: isopiperitenone reductase from mentha piperita in complex with2 isopiperitenone and nadt

12	c3ioyB_	Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: structure of putative short-chain dehydrogenase (saro_0793) from2 novosphingobium aromaticivorans
13	c1fdvA_	Alignment		100.0	25	PDB header: dehydrogenase Chain: A: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase; PDBTitle: human 17-beta-hydroxysteroid-dehydrogenase type 1 mutant h221I2 complexed with nad+
14	c3t7cC_	Alignment		100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
15	c3tjrA_	Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis
16	c3llsB_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-ketoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 mycobacterium tuberculosis
17	d1jtva_	Alignment		100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
18	c4yaiB_	Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligI in complex with nadh and gge from2 sphingobium sp. strain syk-6
19	c3i1jB_	Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: structure of a putative short chain dehydrogenase from pseudomonas2 syringae
20	c4yacA_	Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligo in complex with nadh from sphingobium sp.2 strain syk-6
21	c3rkuC_	Alignment	not modelled	100.0	28	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+
22	c3grkE_	Alignment	not modelled	100.0	19	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
23	c3o26A_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: salutaridine reductase; PDBTitle: the structure of salutaridine reductase from papaver somniferum.
24	c5fydB_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: structural and biochemical insights into 7beta-2 hydroxysteroid dehydrogenase stereoselectivity
25	c3svtA_	Alignment	not modelled	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
26	c3k31B_	Alignment	not modelled	100.0	18	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: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase

27	c4m87B_	Alignment	not modelled	100.0	17	[nadh]; PDBTitle: crystal structure of enoyl-acyl carrier protein reductase (fabI) from <i>Neisseria meningitidis</i> in complex with nad+
28	c3cxtA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from <i>Streptococcus suis</i> type 2
29	c4dryA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: the crystal structure of 3-oxoacyl-[acyl-carrier-protein] reductase2 from <i>Rhizobium meliloti</i>
30	c6ixjK_	Alignment	not modelled	100.0	24	PDB header: cytosolic protein Chain: K: PDB Molecule: sulfoacetaldehyde reductase; PDBTitle: the crystal structure of sulfoacetaldehyde reductase from <i>Klebsiella oxytoca</i>
31	d2bela_	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	c4fc6B_	Alignment	not modelled	100.0	21	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
33	d2ew8a1	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
34	c5epoD_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of <i>Clostridium absconum</i> 7alpha-2 hydroxysteroid dehydrogenase
35	d1yb1a_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
36	d2bd0a1	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
37	c3om1A_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: peroxisomal multifunctional enzyme type 2, cg3415; PDBTitle: structure of full-length peroxisomal multifunctional enzyme type 22 from <i>Drosophila melanogaster</i>
38	c5ff9C_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: noroxomaritidine/norcraugsodine reductase; PDBTitle: noroxomaritidine/norcraugsodine reductase in complex with nadp+ and 2 tyramine
39	c3o38D_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from <i>Mycobacterium smegmatis</i>
40	c5k9zB_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of putative short-chain dehydrogenase/reductase from <i>Mycobacterium xenovorans</i> lb400
41	d1iy8a_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
42	c2jyD_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of <i>Francisella tularensis</i> enoyl reductase2 (ftfabI) with bound nad
43	c3uveC_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase ((+)-trans-carveol dehydrogenase); PDBTitle: crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from <i>Mycobacterium avium</i>
44	c3tzqD_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: crystal structure of a short-chain type dehydrogenase/reductase from <i>Mycobacterium marinum</i>
45	d1zema1	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
46	c3rkrC_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain oxidoreductase; PDBTitle: crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp
47	c4bmvH_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: H: PDB Molecule: short-chain dehydrogenase; PDBTitle: short-chain dehydrogenase from <i>Sphingobium yanoikuyae</i> in2 complex with nadph
48	d1oaaa_	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
49	d1ae1a_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
50	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 <i>Pseudomonas aeruginosa</i> at 2.3a resolution
51	c1yb1B_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase type xi; PDBTitle: crystal structure of human 17-beta-hydroxysteroid

						dehydrogenase type2 xi
52	c4kzpC	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family PDBTitle: crystal structure of a putative short chain dehydrogenase from2 mycobacterium smegmatis
53	c3e03C	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative dehydrogenase from xanthomonas2 campestris
54	c3lylB	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
55	c4j2hA	Alignment	not modelled	100.0	28	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)
56	c2cfcB	Alignment	not modelled	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
57	d2c07a1	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
58	c2c07A	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acp reductase of plasmodium falciparum
59	d1xkqa	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
60	d1ulua	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
61	d1w6ua	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
62	c4fn4A	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from sulfolobus2 acidocaldarius
63	c3toxG	Alignment	not modelled	100.0	23	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
64	c5jy1C	Alignment	not modelled	100.0	22	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
65	d1yxma1	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
66	c3lf2B	Alignment	not modelled	100.0	27	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
67	c4ni5A	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family PDBTitle: crystal structure of a short chain dehydrogenase from brucella suis
68	c5jydA	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
69	c4y98A	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligd-apo form from sphingobium sp. strain syk-6
70	c6ci9D	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
71	c4weoD	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: putative acetoin(diacetyl) reductase; PDBTitle: crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia
72	c5o98A	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase 1; PDBTitle: binary complex of catharanthus roseus vitrosamine synthase with nadp+
73	c5x8hA	Alignment	not modelled	100.0	24	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
74	d2ae2a	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
75	c4urfB	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: cyclohexanol dehydrogenase; PDBTitle: molecular genetic and crystal structural analysis of 1-(4-2 hydroxyphenyl)-ethanol dehydrogenase from aromatelem aromaticum ebn1

76	c5h5xH	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: H: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor
77	c6d9yB	Alignment	not modelled	100.0	26	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
78	d2o23a1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
79	c3ijrF	Alignment	not modelled	100.0	22	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+
80	c4lvuB	Alignment	not modelled	100.0	23	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
81	d1qsga	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
82	c3iccA	Alignment	not modelled	100.0	19	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
83	c4cr8D	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: n-acylmannosamine 1-dehydrogenase; PDBTitle: crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
84	c3pgxB	Alignment	not modelled	100.0	24	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
85	c2zatC	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
86	c3kvoB	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: hydroxysteroid dehydrogenase-like protein 2; PDBTitle: crystal structure of the catalytic domain of human hydroxysteroid2 dehydrogenase like 2 (hsdI2)
87	c4trrH	Alignment	not modelled	100.0	26	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
88	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
89	d1e6wa	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
90	c4zjuA	Alignment	not modelled	100.0	16	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
91	d1geea	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
92	c2jahB	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
93	c3ppiA	Alignment	not modelled	100.0	17	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
94	c3sc4A	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase (a0qtm2 homolog); PDBTitle: crystal structure of a short chain dehydrogenase (a0qtm2 homolog)2 mycobacterium thermoresistibile
95	c5u4sB	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putative short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from burkholderia2 cenocepacia j2315 in complex with nadp.
96	d1nffa	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
97	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'
98	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
99	c4dgvB	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase protein;

99	c9uq4B_	Alignment	not modelled	100.0	47	PDBTitle: crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42
100	d2pd4a1	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
101	c4o5oA_	Alignment	not modelled	100.0	24	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
102	c5f1pB_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: ptm08; PDBTitle: crystal structure of dehydrogenase from streptomyces platensis
103	c3awdD_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: putative polyol dehydrogenase; PDBTitle: crystal structure of gox2181
104	c4iboA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
105	c5jc8C_	Alignment	not modelled	100.0	25	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
106	c4gh5B_	Alignment	not modelled	100.0	26	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)
107	c4nk4E_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of fabi from candidatus liberibacter asiaticus
108	c3tscB_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of short chain dehydrogenase map_2410 from2 mycobacterium paratuberculosis bound to nad
109	c4dmmA_	Alignment	not modelled	100.0	26	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
110	c5b1yB_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of nadph bound carbonyl reductase from aeropyrum2 pernix
111	c4hsyA_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: ketoreductase siam; PDBTitle: crystal structure of ketoreductase siam from streptomyces sp. a7248
112	c5ojgB_	Alignment	not modelled	100.0	21	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
113	c3qljB_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 avium
114	d1gz6a_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
115	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
116	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
117	c3oecA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: carveol dehydrogenase (mytha.01326.c, a0r518 homolog); PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
118	c2nwgA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: probable short-chain dehydrogenase; PDBTitle: short chain dehydrogenase from pseudomonas aeruginosa
119	c6f9qC_	Alignment	not modelled	100.0	22	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+
120	c5mlnB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase 3; PDBTitle: the crystal structure of alcohol dehydrogenase 10 from candida2 magnoliae