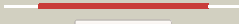



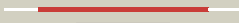



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0439c (-) _527382_528317
Date	Tue Jul 23 14:50:51 BST 2019
Unique Job ID	ec59be13b8982b0d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rd5A_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: mypaa.01249.c; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
2	d1n5da_	 Alignment		100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
3	c5ldgA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-isopiperitenone reductase; PDBTitle: isopiperitenone reductase from mentha piperita in complex with2 isopiperitenone and nadt
4	c3o26A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: salutaridine reductase; PDBTitle: the structure of salutaridine reductase from papaver somniferum.
5	d1wmaa1	 Alignment		100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
6	d1w6ua_	 Alignment		100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
7	c3cxtA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
8	c5ig2B_	 Alignment		100.0	17	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	c4lvuB_	 Alignment		100.0	24	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
10	d1yxma1	 Alignment		100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
11	c4egfA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: l-xylulose reductase; PDBTitle: crystal structure of a l-xylulose reductase from mycobacterium2 smegmatis

12	c4fn4A_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from sulfolobus2 acidocaldarius
13	c6ci9D_	Alignment		100.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
14	c4nbrA_	Alignment		100.0	19	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
15	c5h5xH_	Alignment		100.0	18	PDB header: oxidoreductase Chain: H: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor
16	c4afnB_	Alignment		100.0	19	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
17	c4nbvA_	Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from cupriavidus taiwanensis
18	d1oaaa_	Alignment		100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
19	c5u9pB_	Alignment		100.0	21	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
20	c3rihB_	Alignment		100.0	22	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
21	c5epoD_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
22	c5ojgB_	Alignment	not modelled	100.0	17	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
23	c4weoD_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: putative acetoin(diacetyl) reductase; PDBTitle: crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia
24	c3svtA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
25	c2zatC_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
26	d1xg5a_	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
27	c2c07A_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acyl carrier protein reductase of plasmodium falciparum
28	d2c07a1	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

29	c2p68A_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
30	c3ppiA_	Alignment	not modelled	100.0	19	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
31	c3lf2B_	Alignment	not modelled	100.0	19	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
32	d1iy8a_	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
33	c3pk0B_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
34	c3wtcB_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036
35	d1fmca_	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	c3rkuC_	Alignment	not modelled	100.0	21	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+
37	c4iboA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
38	c4trrH_	Alignment	not modelled	100.0	20	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
39	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+
40	c4urfB_	Alignment	not modelled	100.0	21	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
41	c3v2gA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
42	c5ff9C_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: noroxomaritidine/norcraftsodine reductase; PDBTitle: noroxomaritidine/norcraftsodine reductase in complex with nadp+ and2 tyramine
43	d1xsea_	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
44	d1xkqa_	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
45	c4j2hA_	Alignment	not modelled	100.0	22	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)
46	d1geea_	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
47	c3afnC_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of aldose reductase a1-r complexed with nadp
48	c4z0tA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family; PDBTitle: crystal structure of a putative oxoacyl-(acyl carrier protein)2 reductase from brucella ovis
49	c4g81A_	Alignment	not modelled	100.0	16	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
50	d1ae1a_	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
51	c4o0IA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph-dependent 3-quinuclidinone reductase; PDBTitle: crystal structure of nadph-dependent 3-quinuclidinone reductase from2 rhodotorula rubra
52	d2ae2a_	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

53	c5x8hA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain dehydrogenase reductase; PDBTitle: crystal structure of the ketone reductase chkred20 from the genome of <i>Chryseobacterium</i> sp. ca49
54	c3i1jB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: structure of a putative short chain dehydrogenase from <i>Pseudomonas</i> <i>syringae</i>
55	c3toxG_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: G: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase in complex with 2 nad(p) from <i>Sinorhizobium meliloti</i> 1021
56	c4xgnD_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase in complex with 2 nad from <i>Burkholderia thailandensis</i>
57	c4dqxB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a short chain dehydrogenase from <i>Rhizobium etli</i> 2 cfn 42
58	c2jahB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid 2 dehydrogenase (cad) from <i>Streptomyces clavuligerus</i>
59	c4imrA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of 3-oxoacyl (acyl-carrier-protein) reductase 2 (target efi-506442) from <i>Agrobacterium tumefaciens</i> c58 with nadp3 bound
60	c4m8sB_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: putative 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: crystal structure of 3-ketoacyl -(acyl carrier protein) reductase 2 (fabg) from <i>Neisseria meningitidis</i>
61	c3awdD_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: putative polyol dehydrogenase; PDBTitle: crystal structure of gox2181
62	c4jroC_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: fabg protein; PDBTitle: crystal structure of 3-oxoacyl-[acyl-carrier protein] reductase (fabg) 2 from <i>Listeria monocytogenes</i> in complex with nadp+
63	c5jc8C_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of a putative short-chain dehydrogenase/reductase 2 from <i>Burkholderia xenovorans</i>
64	c4gh5B_	Alignment	not modelled	100.0	18	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)
65	d1edoa_	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	c5itvC_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydroantipain 7-dehydrogenase; PDBTitle: crystal structure of <i>Bacillus subtilis</i> bacc dihydroantipain 7-2 dehydrogenase in complex with nadh
67	d1xhla_	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	c3imfA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: 1.99 angstrom resolution crystal structure of a short chain 2 dehydrogenase from <i>Bacillus anthracis</i> str. 'ames ancestor'
69	c4npcA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: sorbitol dehydrogenase; PDBTitle: crystal structure of an oxidoreductase, short-chain 2 dehydrogenase/reductase family protein from <i>Brucella suis</i>
70	c3tjrA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a rv0851c ortholog short chain dehydrogenase from <i>Mycobacterium paratuberculosis</i>
71	d1y5ma1	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
72	c3emkA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose/ribitol dehydrogenase; PDBTitle: 2.5a crystal structure of glucose/ribitol dehydrogenase from <i>Brucella</i> 2 melitensis
73	c5unlA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketoacyl-acyl carrier protein reductase; PDBTitle: crystal structure of a d-beta-hydroxybutyrate dehydrogenase from <i>Burkholderia multivorans</i>
74	d1q7ba_	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
75	c3lylB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: structure of 3-oxoacyl-acyl carrier protein reductase, fabg2 from <i>Francisella tularensis</i>
76	c4mowB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase; PDBTitle: crystal structure of a putative glucose 1-dehydrogenase from <i>Burkholderia cenocepacia</i> j2315
77	c4o5oA_	Alignment	not modelled	100.0	17	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 PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
78	c3o38D_	Alignment	not modelled	100.0	21	
79	c2z1nA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of ape0912 from aeropyrum pernix k1
80	c4fc6B_	Alignment	not modelled	100.0	18	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
81	c2uvdE_	Alignment	not modelled	100.0	22	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)
82	c3ijrF_	Alignment	not modelled	100.0	16	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+
83	c5er6C_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: crystal structure of an oxidoreductase from brucella ovis
84	c6d9yB_	Alignment	not modelled	100.0	20	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
85	c5jy1C_	Alignment	not modelled	100.0	16	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
86	c3ak4C_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
87	d1yb1a_	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
88	c4iuyB_	Alignment	not modelled	100.0	17	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
89	d1gz6a_	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
90	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
91	c1w4zA_	Alignment	not modelled	100.0	18	PDB header: antibiotic biosynthesis Chain: A: PDB Molecule: ketoacyl reductase; PDBTitle: structure of actinorhodin polyketide (actiii) reductase
92	c4wuvB_	Alignment	not modelled	100.0	16	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
93	d1x1ta1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
94	c1zbqB_	Alignment	not modelled	100.0	18	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
95	d1zbqa1	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
96	d1zema1	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
97	c3ftpD_	Alignment	not modelled	100.0	20	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
98	c3rkrC_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain oxidoreductase; PDBTitle: crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp
99	c5b1yB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of nadph bound carbonyl reductase from aeropyrum2 pernix
100	c3t7cC_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
101	c3wxbB_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase activator Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of nadph bound carbonyl reductase from chicken fatty2 liver
						Fold: NAD(P)-binding Rossmann-fold domains

102	d2o23a1	Alignment	not modelled	100.0	19	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
103	c3ioyB_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: structure of putative short-chain dehydrogenase (saro_0793) from2 novosphingobium aromaticivorans
104	c5g4kB_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: phloroglucinol reductase from clostridium sp. apo-form
105	c3gvcB_	Alignment	not modelled	100.0	21	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
106	c4iiuB_	Alignment	not modelled	100.0	15	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
107	d2bela_	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
108	d1xu9a_	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
109	c5idxB_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of an oxidoreductase from burkholderia vietnamiensis
110	c4yaiB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligl in complex with nadh and gge from2 sphingobium sp. strain syk-6
111	c3tzqD_	Alignment	not modelled	100.0	24	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
112	d1k2wa_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
113	c2pd6D_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
114	c5jydA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
115	c4kzpC_	Alignment	not modelled	100.0	19	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
116	d1e6wa_	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
117	c4dmmA_	Alignment	not modelled	100.0	22	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
118	d1hdca_	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
119	c3ai3A_	Alignment	not modelled	100.0	19	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
120	c5fydB_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: structural and biochemical insights into 7beta-2 hydroxysteroid dehydrogenase stereoselectivity