

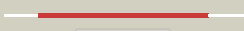
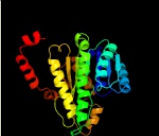




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3057c_(-)_3417796_3418659
Date	Thu Aug 8 16:20:23 BST 2019
Unique Job ID	2cf18af39942924e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ig2B_</a>	 Alignment		100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase/reductase sdr from2 burkholderia phymatum in complex with nad
2	<a href="#">d1xsea_</a>	 Alignment		100.0	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
3	<a href="#">d1xu9a_</a>	 Alignment		100.0	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
4	<a href="#">d1y5ma1</a>	 Alignment		100.0	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
5	<a href="#">c3tjrA_</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis
6	<a href="#">c4yaiB_</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> c alpha-dehydrogenase; <b>PDBTitle:</b> crystal structure of lig1 in complex with nadh and gge from2 sphingobium sp. strain syk-6
7	<a href="#">c4yacA_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> c alpha-dehydrogenase; <b>PDBTitle:</b> crystal structure of ligo in complex with nadh from sphingobium sp.2 strain syk-6
8	<a href="#">c3lf2B_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain oxidoreductase q9hya2; <b>PDBTitle:</b> nadph bound structure of the short chain oxidoreductase q9hya2 from2 pseudomonas aeruginosa pao1 containing an atypical catalytic center
9	<a href="#">c3ioyB_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> structure of putative short-chain dehydrogenase (saro_0793) from2 novosphingobium aromaticivorans
10	<a href="#">d2bela_</a>	 Alignment		100.0	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
11	<a href="#">c3rihB_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain dehydrogenase or reductase; <b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus

12	<a href="#">c4egfA_</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-xylulose reductase; <b>PDBTitle:</b> crystal structure of a l-xylulose reductase from mycobacterium2 smegmatis
13	<a href="#">c5fydB_</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase <b>PDBTitle:</b> structural and biochemical insights into 7beta-2 hydroxysteroid dehydrogenase stereoselectivity
14	<a href="#">d1w6ua_</a>	Alignment		100.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
15	<a href="#">c4fc6B_</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> studies on dcr shed new light on peroxisomal beta-oxidation: crystal2 structure of the ternary complex of pdcr
16	<a href="#">c3wtcB_</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of gox2036
17	<a href="#">c1fdvA_</a>	Alignment		100.0	26	<b>PDB header:</b> dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> 17-beta-hydroxysteroid dehydrogenase; <b>PDBTitle:</b> human 17-beta-hydroxysteroid-dehydrogenase type 1 mutant h221I2 complexed with nad+
18	<a href="#">d1yb1a_</a>	Alignment		100.0	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
19	<a href="#">c4bmvH_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> short-chain dehydrogenase; <b>PDBTitle:</b> short-chain dehydrogenase from sphingobium yanoikuyae in2 complex with nadph
20	<a href="#">c5itvC_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroantocapsin 7-dehydrogenase; <b>PDBTitle:</b> crystal structure of bacillus subtilis bacc dihydroantocapsin 7-2 dehydrogenase in complex with nadh
21	<a href="#">c4g81A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hexonate dehydrogenase; <b>PDBTitle:</b> crystal structure of a hexonate dehydrogenase ortholog (target efi-2 506402 from salmonella enterica, unliganded structure
22	<a href="#">c1yb1B_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 17-beta-hydroxysteroid dehydrogenase type xi; <b>PDBTitle:</b> crystal structure of human 17-beta-hydroxysteroid dehydrogenase type2 xi
23	<a href="#">c3pk0B_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
24	<a href="#">c4trrH_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> putative d-beta-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative putative d-beta-hydroxybutyrate2 dehydrogenase from burkholderia cenocepacia j2315
25	<a href="#">d1iy8a_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
26	<a href="#">d1jtva_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
27	<a href="#">c6ci9D_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
28	<a href="#">c465aA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase;

28	<a href="#">c803vA</a>	Alignment	not modelled	100.0	24	<b>PDBTitle:</b> x-ray crystal structure of a 3-hydroxyacyl-coa dehydrogenase from2 brucella suis
29	<a href="#">d2ae2a</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
30	<a href="#">c5epoD</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 7-alpha-hydroxysteroid dehydrogenase; <b>PDBTitle:</b> the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
31	<a href="#">c5ojgB</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase/reductase sdr family member 4; <b>PDBTitle:</b> crystal structure of the dehydrogenase/reductase sdr family member 42 (dhrs4) from caenorhabditis elegans
32	<a href="#">c4y98A</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> c alpha-dehydrogenase; <b>PDBTitle:</b> crystal structure of ligd-apo form from sphingobium sp. strain syk-6
33	<a href="#">c6ixjK</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> cytosolic protein <b>Chain:</b> K: <b>PDB Molecule:</b> sulfoacetaldehyde reductase; <b>PDBTitle:</b> the crystal structure of sulfoacetaldehyde reductase from klebsiella2 oxytoca
34	<a href="#">c4j2hA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain alcohol dehydrogenase-related dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative short-chain alcohol dehydrogenase from2 sinorhizobium meliloti 1021 (target nysgrc-011708)
35	<a href="#">d1zema1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
36	<a href="#">c3ak4C</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-dependent quinuclidinone reductase; <b>PDBTitle:</b> crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
37	<a href="#">d2bgka1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
38	<a href="#">d1k2wa</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
39	<a href="#">c3toxG</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
40	<a href="#">c3ai3A</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-p-sorbose reductase; <b>PDBTitle:</b> the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
41	<a href="#">c5jy1C</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400 bound to nad
42	<a href="#">c4fn4A</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> short-chain nad(h)-dependent dehydrogenase/reductase from sulfolobus2 acidocaldarius
43	<a href="#">c3t7cC</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carveol dehydrogenase; <b>PDBTitle:</b> crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
44	<a href="#">d1xhla</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
45	<a href="#">c4wuvB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-hydroxycyclohexanecarboxyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative d-mannonate oxidoreductase from2 haemophilus influenza (avi_5165, target efi-513796) with bound nad
46	<a href="#">c4npcA</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sorbitol dehydrogenase; <b>PDBTitle:</b> crystal structure of an oxidoreductase, short-chain2 dehydrogenase/reductase family protein from brucella suis
47	<a href="#">c3o38D</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
48	<a href="#">c3svtA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase; <b>PDBTitle:</b> structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
49	<a href="#">d1ae1a</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
50	<a href="#">c4jroC</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> fabg protein; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier protein]reductase (fabg)2 from listeria monocytogenes in complex with nadp+
51	<a href="#">c4iuyB</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of short-chain dehydrogenase/reductase (apo-form)2 from a. baumannii clinical strain wm99c
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclohexanol dehydrogenase;

52	<a href="#">c4urfB</a>	Alignment	not modelled	100.0	25	<b>PDBTitle:</b> molecular genetic and crystal structural analysis of 1-(4-2 hydroxyphenyl)-ethanol dehydrogenase from aromatoleum aromaticum ebn1
53	<a href="#">c4afnB</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase fabg; <b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 (fabg) from pseudomonas aeruginosa at 2.3a resolution
54	<a href="#">c5h5xH</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor
55	<a href="#">c2zatC</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase/reductase sdr family member 4; <b>PDBTitle:</b> crystal structure of a mammalian reductase
56	<a href="#">d1yxma1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
57	<a href="#">c2p68A</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of aq_1716 from aquifex aeolicus vf5
58	<a href="#">c3rkuC</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase ymr226c; <b>PDBTitle:</b> substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+
59	<a href="#">c4dqxB</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42
60	<a href="#">d1ydea1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
61	<a href="#">d1geea</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
62	<a href="#">c3cxtA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase with different specificities; <b>PDBTitle:</b> quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
63	<a href="#">c4iboA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gluconate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
64	<a href="#">c2c07A</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) reductase; <b>PDBTitle:</b> oxoacyl-acyl reductase of plasmodium falciparum
65	<a href="#">d2c07a1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
66	<a href="#">c3awdD</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative polyol dehydrogenase; <b>PDBTitle:</b> crystal structure of gox2181
67	<a href="#">c3rkrC</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short chain oxidoreductase; <b>PDBTitle:</b> crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp
68	<a href="#">c3emkA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose/ribitol dehydrogenase; <b>PDBTitle:</b> 2.5a crystal structure of glucose/ribitol dehydrogenase from brucella2 melitensis
69	<a href="#">c5ff9C</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> noroxomaritidine/norcraugsodine reductase; <b>PDBTitle:</b> noroxomaritidine/norcraugsodine reductase in complex with nadp+ and2 tyramine
70	<a href="#">c5u9pB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gluconate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of a gluconate 5-dehydrogenase from burkholderia2 cenocepacia j2315 in complex with nadp and tartrate
71	<a href="#">c1w4zA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> antibiotic biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> ketoacyl reductase; <b>PDBTitle:</b> structure of actinorhodin polyketide (actiii) reductase
72	<a href="#">c2jahB</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> clavulanic acid dehydrogenase; <b>PDBTitle:</b> biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
73	<a href="#">c4xgnD</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase in complex with2 nad from burkholderia thailandensis
74	<a href="#">c3nugA</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) reductase; <b>PDBTitle:</b> crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti
75	<a href="#">c3tzqD</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
76	<a href="#">c4lvuB</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase from2 burkholderia thailandensis
						<b>PDB header:</b> oxidoreductase

77	<a href="#">c5un1A_</a>	Alignment	not modelled	100.0	25	<b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-acp reductase; <b>PDBTitle:</b> crystal structure of a d-beta-hydroxybutyrate dehydrogenase from <i>Burkholderia multivorans</i>
78	<a href="#">c4nbvA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase putative short- <b>PDBTitle:</b> crystal structure of fabg from <i>Cupriavidus taiwanensis</i>
79	<a href="#">c4imrA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of 3-oxoacyl (acyl-carrier-protein) reductase2 (target efi-506442) from <i>Agrobacterium tumefaciens</i> c58 with nadp3 bound
80	<a href="#">c3gvcB_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable short-chain type dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of probable short-chain dehydrogenase-reductase from <i>Mycobacterium tuberculosis</i>
81	<a href="#">c2z1nA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure of ape0912 from <i>Aeropyrum pernix</i> k1
82	<a href="#">d1hdca_</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
83	<a href="#">c4z0tA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, short-chain dehydrogenase/reductase family; <b>PDBTitle:</b> crystal structure of a putative oxoacyl-(acyl carrier protein)2 reductase from <i>Brucella ovis</i>
84	<a href="#">c4dmmA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> 3-oxoacyl-[acyl-carrier-protein] reductase from <i>Synechococcus</i> 2 elongatus pcc 7942 in complex with nadp
85	<a href="#">c3itdA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 17beta-hydroxysteroid dehydrogenase; <b>PDBTitle:</b> crystal structure of an inactive 17beta-hydroxysteroid dehydrogenase2 (y167f mutated form) from fungus <i>Cochliobolus lunatus</i>
86	<a href="#">c4nqzF_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh] fabi; <b>PDBTitle:</b> crystal structure of the <i>Pseudomonas aeruginosa</i> enoyl-acyl carrier2 protein reductase (fabi) in apo form
87	<a href="#">c2et6A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> (3r)-hydroxyacyl-coa dehydrogenase domain of <i>Candida tropicalis</i> 2 peroxisomal multifunctional enzyme type 2
88	<a href="#">c4cr8D_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> n-acylmannosamine 1-dehydrogenase; <b>PDBTitle:</b> crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
89	<a href="#">c5er6C_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from <i>Brucella ovis</i>
90	<a href="#">d2rhca1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
91	<a href="#">c6ds1C_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of cj0485 dehydrogenase in complex with nadp+
92	<a href="#">c5idxB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of an oxidoreductase from <i>Burkholderia vietnamiensis</i>
93	<a href="#">c5x8hA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase reductase; <b>PDBTitle:</b> crystal structure of the ketone reductase chkred20 from the genome of <i>Chryseobacterium</i> sp. ca49
94	<a href="#">c4dryA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> the crystal structure of 3-oxoacyl-[acyl-carrier-protein] reductase2 from <i>Rhizobium meliloti</i>
95	<a href="#">c3imfA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from <i>Bacillus anthracis</i> str. 'ames ancestor'
96	<a href="#">d1pr9a_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
97	<a href="#">c4wecA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from <i>Mycobacterium</i> 2 smegmatis
98	<a href="#">d1fmca_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
99	<a href="#">d1oaaa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
100	<a href="#">d1xkqa_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
101	<a href="#">c5k9zB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of putative short-chain dehydrogenase/reductase from <i>Burkholderia xenovorans</i> lb400

102	<a href="#">d2o23a1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
103	<a href="#">d1h5qa</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
104	<a href="#">c4weoD</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative acetoin(diacetyl) reductase; <b>PDBTitle:</b> crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia
105	<a href="#">d1q7ba</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
106	<a href="#">c6f9qC</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> 7s-cis-cis-nepetalactol cyclase; <b>PDBTitle:</b> binary complex of a 7s-cis-cis-nepetalactol cyclase from nepeta2 mussinii with nad+
107	<a href="#">c4mowB</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose 1-dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative glucose 1-dehydrogenase from2 burkholderia cenocepacia j2315
108	<a href="#">c6d9yB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase/reductase sdr from2 burkholderia phymatum with partially occupied nad
109	<a href="#">d1sbya1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
110	<a href="#">c3vc7B</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
111	<a href="#">c3lylB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
112	<a href="#">c5u4sB</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from burkholderia2 cenocepacia j2315 in complex with nadp.
113	<a href="#">c3iljB</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> structure of a putative short chain dehydrogenase from pseudomonas2 syringae
114	<a href="#">c3sjuA</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> keto reductase; <b>PDBTitle:</b> hedamycin polyketide ketoreductase bound to nadph
115	<a href="#">d1zbqa1</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
116	<a href="#">c1zbqB</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 17-beta-hydroxysteroid dehydrogenase 4; <b>PDBTitle:</b> crystal structure of human 17-beta-hydroxysteroid dehydrogenase type 42 in complex with nad
117	<a href="#">c2cfcB</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-(r)-hydroxypropyl-com dehydrogenase; <b>PDBTitle:</b> structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
118	<a href="#">c4z9yA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-deoxy-d-gluconate 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxy-d-gluconate dehydrogenase from2 pectobacterium carotovorum
119	<a href="#">c2yz7B</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-3-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> x-ray analyses of 3-hydroxybutyrate dehydrogenase from2 alcaligenes faecalis
120	<a href="#">d1x1ta1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases