







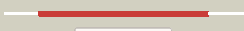















# Phyre2

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Description	RVBD1941 (-) _2193671_2194441
Date	Mon Aug 5 13:25:03 BST 2019
Unique Job ID	54edded4d9022a1e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gvcB_</a>	 Alignment		100.0	98	<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 from2 mycobacterium tuberculosis
2	<a href="#">c3lf2B_</a>	 Alignment		100.0	28	<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
3	<a href="#">c5itvC_</a>	 Alignment		100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroantcapsin 7-dehydrogenase; <b>PDBTitle:</b> crystal structure of bacillus subtilis bacc dihydroantcapsin 7-2 dehydrogenase in complex with nadh
4	<a href="#">c5idxB_</a>	 Alignment		100.0	27	<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 burkholderia vietnamiensis
5	<a href="#">c3tzqD_</a>	 Alignment		100.0	38	<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
6	<a href="#">c5u9pB_</a>	 Alignment		100.0	30	<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
7	<a href="#">c3cxtA_</a>	 Alignment		100.0	32	<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
8	<a href="#">d1hdca</a>	 Alignment		100.0	37	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
9	<a href="#">c5ojgB_</a>	 Alignment		100.0	29	<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
10	<a href="#">d2ae2a_</a>	 Alignment		100.0	29	<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="#">c4dqxB_</a>	 Alignment		100.0	35	<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

12	<a href="#">c3wtcB_</a>	Alignment		100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of gox2036
13	<a href="#">d1iy8a_</a>	Alignment		100.0	34	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
14	<a href="#">c2q2qG_</a>	Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> beta-d-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
15	<a href="#">c6d9yB_</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 an oxidoreductase, short-chain dehydrogenase/reductase sdr from2 burkholderia phymatum with partially occupied nad
16	<a href="#">d1k2wa_</a>	Alignment		100.0	34	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
17	<a href="#">c4npcA_</a>	Alignment		100.0	41	<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
18	<a href="#">c4j2hA_</a>	Alignment		100.0	34	<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)
19	<a href="#">d1q7ba_</a>	Alignment		100.0	33	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
20	<a href="#">c4trrH_</a>	Alignment		100.0	31	<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
21	<a href="#">c3ak4C_</a>	Alignment	not modelled	100.0	35	<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
22	<a href="#">c4iboA_</a>	Alignment	not modelled	100.0	33	<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)
23	<a href="#">d1yxma1</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
24	<a href="#">c3ai3A_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-sorbose reductase; <b>PDBTitle:</b> the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
25	<a href="#">c4fc6B_</a>	Alignment	not modelled	100.0	27	<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
26	<a href="#">c2zatC_</a>	Alignment	not modelled	100.0	34	<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
27	<a href="#">c4wuvB_</a>	Alignment	not modelled	100.0	26	<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
28	<a href="#">d1fmca_</a>	Alianment	not modelled	100.0	33	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains

				Family:Tyrosine-dependent oxidoreductases		
29	<a href="#">c3awdD</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative polyol dehydrogenase; <b>PDBTitle:</b> crystal structure of gox2181
30	<a href="#">c5unlA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-acyl carrier protein reductase; <b>PDBTitle:</b> crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
31	<a href="#">c4lvuB</a>	Alignment	not modelled	100.0	32	<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
32	<a href="#">c5epoD</a>	Alignment	not modelled	100.0	31	<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
33	<a href="#">c4wecA</a>	Alignment	not modelled	100.0	34	<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 mycobacterium2 smegmatis
34	<a href="#">c4z9yA</a>	Alignment	not modelled	100.0	29	<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
35	<a href="#">c4g81A</a>	Alignment	not modelled	100.0	32	<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)
36	<a href="#">c4urfB</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclohexanol dehydrogenase; <b>PDBTitle:</b> molecular genetic and crystal structural analysis of 1-(4-2 hydroxyphenyl)-ethanol dehydrogenase from aromatoleum aromaticum ebn1
37	<a href="#">d1geea</a>	Alignment	not modelled	100.0	31	<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="#">c5jy1C</a>	Alignment	not modelled	100.0	31	<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
39	<a href="#">d1xhla</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
40	<a href="#">c6ds1C</a>	Alignment	not modelled	100.0	28	<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+
41	<a href="#">c4i5eC</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> alcohol dehydrogenase/short-chain dehydrogenase; <b>PDBTitle:</b> crystal structure of ralstonia sp. alcohol dehydrogenase in complex2 with nadp+
42	<a href="#">c3svtA</a>	Alignment	not modelled	100.0	29	<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
43	<a href="#">d1ae1a</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
44	<a href="#">c5k9zB</a>	Alignment	not modelled	100.0	30	<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 from2 burkholderia xenovorans lb400
45	<a href="#">c4cr8D</a>	Alignment	not modelled	100.0	28	<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
46	<a href="#">c4afnB</a>	Alignment	not modelled	100.0	31	<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
47	<a href="#">d1nffa</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
48	<a href="#">d1xkqa</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
49	<a href="#">c6ci9D</a>	Alignment	not modelled	100.0	28	<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
50	<a href="#">c3nugA</a>	Alignment	not modelled	100.0	33	<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
51	<a href="#">c4nbvA</a>	Alignment	not modelled	100.0	40	<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 cupriavidus taiwanensis
52	<a href="#">c5t2uC</a>	Alignment	not modelled	100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family

						<b>PDBTitle:</b> short chain dehydrogenase/reductase family protein <b>PDB header:</b> oxidoreductase
53	<a href="#">c4fn4A_</a>	Alignment	not modelled	100.0	31	<b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> short-chain nad(h)-dependent dehydrogenase/reductase from <i>sulfolobus2 acidocaldarius</i>
54	<a href="#">c2yz7B_</a>	Alignment	not modelled	100.0	33	<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 from <i>2 alcaligenes faecalis</i>
55	<a href="#">c2cfcB_</a>	Alignment	not modelled	100.0	34	<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)- and 2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
56	<a href="#">c4imrA_</a>	Alignment	not modelled	100.0	31	<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 c58</i> with nadp3 bound
57	<a href="#">c3emkA_</a>	Alignment	not modelled	100.0	31	<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 <i>brucella2 melitensis</i>
58	<a href="#">d1pr9a_</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
59	<a href="#">d2rhca1</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
60	<a href="#">c1w4zA_</a>	Alignment	not modelled	100.0	32	<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
61	<a href="#">c4egfA_</a>	Alignment	not modelled	100.0	36	<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 <i>mycobacterium2 smegmatis</i>
62	<a href="#">c5h5xH_</a>	Alignment	not modelled	100.0	33	<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 <i>streptomyces2 coelicolor</i>
63	<a href="#">c4gh5B_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of s-2-hydroxypropyl coenzyme m dehydrogenase (s-2 hpcdh)
64	<a href="#">c3uf0A_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from <i>beutenbergia cavernae</i> (efi target efi-502044) with3 bound nadp (low occupancy)
65	<a href="#">d2c07a1</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
66	<a href="#">c2c07A_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) reductase; <b>PDBTitle:</b> oxoacyl-acc reductase of <i>plasmodium falciparum</i>
67	<a href="#">d1ydea1</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
68	<a href="#">d1zema1</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
69	<a href="#">c3tscB_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of short chain dehydrogenase map_2410 from <i>2 mycobacterium paratuberculosis</i> bound to nad
70	<a href="#">c3itdA_</a>	Alignment	not modelled	100.0	29	<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>
71	<a href="#">d1w6ua_</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
72	<a href="#">c5o30A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of the novel halohydrin dehalogenase hheg
73	<a href="#">c4iuyB_</a>	Alignment	not modelled	100.0	26	<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 <i>a. baumannii</i> clinical strain wm99c
74	<a href="#">c4jroC_</a>	Alignment	not modelled	100.0	34	<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 <i>listeria monocytogenes</i> in complex with nadp+
75	<a href="#">d2bgka1</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
76	<a href="#">c3rihB_</a>	Alignment	not modelled	100.0	27	<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 <i>mycobacterium abscessus</i>
77	<a href="#">d1hxha_</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
						<b>PDB header:</b> oxidoreductase

78	<a href="#">c3vc7B_</a>	Alignment	not modelled	100.0	33	<b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
79	<a href="#">c5x8hA_</a>	Alignment	not modelled	100.0	35	<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 of2 chryseobacterium sp. ca49
80	<a href="#">c2p68A_</a>	Alignment	not modelled	100.0	33	<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
81	<a href="#">d1g0oa_</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
82	<a href="#">c3sjuA_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> keto reductase; <b>PDBTitle:</b> hedamycin polyketide ketoreductase bound to nadph
83	<a href="#">c4m8sB_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative 3-oxoacyl-[acyl-carrier protein] reductase; <b>PDBTitle:</b> crystal structure of 3-ketoacyl -(acyl carrier protein) reductase2 (fabg) from neisseria meningitidis
84	<a href="#">c3toxG_</a>	Alignment	not modelled	100.0	38	<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
85	<a href="#">c2pd6D_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> estradiol 17-beta-dehydrogenase 8; <b>PDBTitle:</b> structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
86	<a href="#">c3gk3D_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> acetoacetyl-coa reductase; <b>PDBTitle:</b> crystal structure of acetoacetyl-coa reductase from burkholderia2 pseudomallei 1710b
87	<a href="#">c5jc8C_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a putative short-chain dehydrogenase/reductase2 from burkholderia xenovorans
88	<a href="#">c5er6C_</a>	Alignment	not modelled	100.0	35	<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 brucella ovis
89	<a href="#">c4hp8A_</a>	Alignment	not modelled	100.0	26	<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 a putative 2-deoxy-d-gluconate 3-dehydrogenase2 from agrobacterium tumefaciens (target efi-506435) with bound nadp
90	<a href="#">c3u49B_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bacilysin biosynthesis oxidoreductase ywfh; <b>PDBTitle:</b> crystal structure of ywfh, nadph dependent reductase involved in2 bacilysin biosynthesis
91	<a href="#">c3t7cC_</a>	Alignment	not modelled	100.0	29	<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
92	<a href="#">c5ff9C_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> noroxomaritidine/norcroagsodine reductase; <b>PDBTitle:</b> noroxomaritidine/norcroagsodine reductase in complex with nadp+ and2 tyramine
93	<a href="#">c3jirF_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
94	<a href="#">c5o3zK_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> sorbitol-6-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of sorbitol-6-phosphate 2-dehydrogenase srlid from2 erwinia amylovora
95	<a href="#">d1gega_</a>	Alignment	not modelled	100.0	37	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
96	<a href="#">d2ew8a1</a>	Alignment	not modelled	100.0	35	<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="#">c4ni5A_</a>	Alignment	not modelled	100.0	35	<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 short chain dehydrogenase from brucella suis
98	<a href="#">d1ja9a_</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
99	<a href="#">c5jo9A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribitol 2-dehydrogenase; <b>PDBTitle:</b> structural characterization of the thermostable bradyrhizobium2 japonicum d-sorbitol dehydrogenase
100	<a href="#">c4cqmJ_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> carbonyl reductase family member 4; <b>PDBTitle:</b> crystal structure of heterotetrameric human ketoacyl2 reductase complexed with nad and nadp
101	<a href="#">c6f9qC_</a>	Alignment	not modelled	100.0	26	<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+
						<b>Fold:</b> NAD(P)-binding Rossmann-fold domains

102	<a href="#">d1zk4a1</a>	Alignment	not modelled	100.0	33	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
103	<a href="#">c3k31B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of enoyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
104	<a href="#">c3pk0B</a>	Alignment	not modelled	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 short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
105	<a href="#">c4nqzF</a>	Alignment	not modelled	100.0	23	<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 pseudomonas aeruginosa enoyl-acyl carrier2 protein reductase (fabi) in apo form
106	<a href="#">c3uxyC</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> the crystal structure of short chain dehydrogenase from rhodobacter2 sphaeroides
107	<a href="#">c3gr6A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of the staphylococcus aureus enoyl-acyl carrier2 protein reductase (fabi) in complex with nadp and triclosan
108	<a href="#">d2d1ya1</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
109	<a href="#">c4mowB</a>	Alignment	not modelled	100.0	27	<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
110	<a href="#">c3iccA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 3-oxoacyl-(acyl carrier protein) reductase; <b>PDBTitle:</b> crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
111	<a href="#">c2uvdE</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> the crystal structure of a 3-oxoacyl-(acyl carrier protein) reductase2 from bacillus anthracis (ba3989)
112	<a href="#">c3imfA</a>	Alignment	not modelled	100.0	29	<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 bacillus anthracis str. 'ames ancestor'
113	<a href="#">d1h5qa</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
114	<a href="#">c2z1nA</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure of ape0912 from aeropyrum pernix k1
115	<a href="#">c4nbrA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 3-oxoacyl-(acyl-carrier protein) reductase; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier protein] reductase from2 brucella melitensis atcc 23457
116	<a href="#">c3v2gA</a>	Alignment	not modelled	100.0	35	<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 a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
117	<a href="#">c5jlaB</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase from brucella2 melitensis 16m
118	<a href="#">c3ftpD</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein] reductase; <b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 burkholderia pseudomallei at 2.05 a resolution
119	<a href="#">c5tt0A</a>	Alignment	not modelled	100.0	32	<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 an oxidoreductase (short chain2 dehydrogenase/reductase family) from burkholderia thailandensis
120	<a href="#">c5g4kB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase <b>PDBTitle:</b> phloroglucinol reductase from clostridium sp. apo-form