Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0484c_(-)_573049_573804
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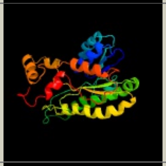
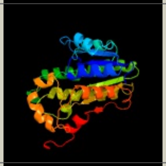
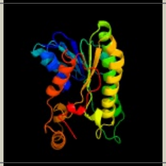
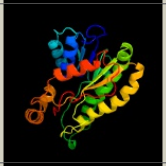
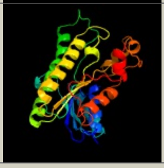
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6d9yB_	Alignment		100.0	25	**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
2	c3lf2B_	Alignment		100.0	26	**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
3	c5t2uC_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family **PDBTitle:** short chain dehydrogenase/reductase family protein
4	c5u9pB_	Alignment		100.0	22	**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
5	d1pr9a_	Alignment		100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
6	c4urfB_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cyclohexanol dehydrogenase; **PDBTitle:** molecular genetic and crystal structural analysis of 1-(4-2 hydroxyphenyl)-ethanol dehydrogenase from aromatoleum aromaticum ebn1
7	c3rihB_	Alignment		100.0	20	**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
8	c3svtA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
9	c3tzqD_	Alignment		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 from2 mycobacterium marinum
10	d1hdca_	Alignment		100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
11	c5idxB_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of an oxidoreductase from burkholderia vietnamiensis

12	c3cxtA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase with different specificities; **PDBTitle:** quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
13	c5epoD_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**7-alpha-hydroxysteroid deydrogenase; **PDBTitle:** the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
14	c5itvC_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dihydroanticapsin 7-dehydrogenase; **PDBTitle:** crystal structure of bacillus subtilis bacc dihydroanticapsin 7-2 dehydrogenase in complex with nadh
15	c5jy1C_	Alignment		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
16	c4nbvA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase putative short- **PDBTitle:** crystal structure of fabg from cupriavidus taiwanensis
17	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
18	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
19	d1w6ua_	Alignment		100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
20	c3awdD_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative polyol dehydrogenase; **PDBTitle:** crystal structure of gox2181
21	c4cr8D_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**n-acylmannosamine 1-dehydrogenase; **PDBTitle:** crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
22	c3rkuC_	Alignment	not modelled	100.0	38	**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+
23	c4afnB_	Alignment	not modelled	100.0	23	**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
24	d2ae2a_	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
25	d1fmca_	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
26	d1q7ba_	Alignment	not modelled	100.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
27	c4wecA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
28	c4npcA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sorbitol dehydrogenase; **PDBTitle:** crystal structure of an oxidoreductase, short-chain2

						dehydrogenase/reductase family protein from brucella suis
29	c5ojgB_	Alignment	not modelled	100.0	23	**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
30	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
31	d2bgka1	Alignment	not modelled	100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
32	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
33	d1ae1a_	Alignment	not modelled	100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
34	c2p68A_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of aq_1716 from aquifex aeolicus vf5
35	c4imrA_	Alignment	not modelled	100.0	22	**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
36	c5x8hA_	Alignment	not modelled	100.0	25	**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
37	c2pd6D_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**estradiol 17-beta-dehydrogenase 8; **PDBTitle:** structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
38	d1iy8a_	Alignment	not modelled	100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
39	c3gvcB_	Alignment	not modelled	100.0	25	**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
40	c4rziB_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-ketoacyl-acyl carrier protein reductase; **PDBTitle:** crystal structure of phab from synechocystis sp. pcc 6803
41	c4egfA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-xylulose reductase; **PDBTitle:** crystal structure of a l-xylulose reductase from mycobacterium2 smegmatis
42	c4iboA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gluconate dehydrogenase; **PDBTitle:** crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
43	c3wtcB_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of gox2036
44	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
45	c5h5xH_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor
46	c3pk0B_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
47	c5k9zB_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400
48	c4i5eC_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**alclohol dehydrogenase/short-chain dehydrogenase; **PDBTitle:** crystal structure of ralstonia sp. alcohol dehydrogenase in complex2 with nadp+
49	d1k2wa_	Alignment	not modelled	100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
50	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+ and2 tyramine
51	c4fc6B_	Alignment	not modelled	100.0	22	**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
52	c2zatC_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase/reductase sdr family member 4; **PDBTitle:** crystal structure of a mammalian reductase
53	c5jo9A_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribitol 2-dehydrogenase; **PDBTitle:** structural characterization of the thermostable

						bradyrhizobium2 japonicum d-sorbitol dehydrogenase
54	d1zema1	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
55	c4jroC_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**fabg protein; **PDBTitle:** crystal structure of 3-oxoacyl-[acyl-carrier protein]reductase (fabg)2 from listeria monocytogenes in complex with nadp+
56	c3ai3A_	Alignment	not modelled	100.0	27	**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
57	c4wuvB_	Alignment	not modelled	100.0	15	**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
58	c4m8sB_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative 3-oxoacyl-[acyl-carrier protein] reductase; **PDBTitle:** crystal structure of 3-ketoacyl -(acyl carrier protein) reductase2 (fabg) from neisseria meningitidis
59	c4g81A_	Alignment	not modelled	100.0	22	**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
60	c3ak4C_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-dependent quinuclidinone reductase; **PDBTitle:** crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
61	c3emkA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase from brucella2 melitensis
62	c3v2gA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
63	c2z1nA_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of ape0912 from aeropyrum pernix k1
64	c4mowB_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glucose 1-dehydrogenase; **PDBTitle:** crystal structure of a putative glucose 1-dehydrogenase from2 burkholderia cenocepacia j2315
65	c4j2hA_	Alignment	not modelled	100.0	25	**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)
66	c4dqxB_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable oxidoreductase protein; **PDBTitle:** crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42
67	c4nbrA_	Alignment	not modelled	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
68	d2c07a1	Alignment	not modelled	100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
69	c2c07A_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** oxoacyl-acp reductase of plasmodium falciparum
70	c4trrH_	Alignment	not modelled	100.0	25	**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
71	c4fn4A_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** short-chain nad(h)-dependent dehydrogenase/reductase from sulfolobus2 acidocaldarius
72	c5unlA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-ketoacyl-acp reductase; **PDBTitle:** crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
73	c3uf0A_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
74	c1w4zA_	Alignment	not modelled	100.0	19	**PDB header:**antibiotic biosynthesis **Chain:** A: **PDB Molecule:**ketoacyl reductase; **PDBTitle:** structure of actinorhodin polyketide (actiii) reductase
75	c4gh5B_	Alignment	not modelled	100.0	25	**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)
76	d1xkqa_	Alignment	not modelled	100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
						Fold:NAD(P)-binding Rossmann-fold domains

77	d1nffa_	Alignment	not modelled	100.0	22	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
78	c3vc7B_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
79	c6ixjK_	Alignment	not modelled	100.0	40	**PDB header:**cytosolic protein **Chain:** K: **PDB Molecule:**sulfoacetaldehyde reductase; **PDBTitle:** the crystal structure of sulfoacetaldehyde reductase from klebsiella2 oxytoca
80	c3toxG_	Alignment	not modelled	100.0	19	**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
81	c3nugA_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti
82	d1o5ia_	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
83	c2jahB_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**clavulanic acid dehydrogenase; **PDBTitle:** biochemical and structural analysis of the clavulanic acid2 dehydeogenase (cad) from streptomyces clavuligerus
84	c5tt0A_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** crystal structure of an oxidoreductase (short chain2 dehydrogenase/reductase family) from burkholderia thailandensis
85	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 chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'
86	c2cfcB_	Alignment	not modelled	100.0	27	**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
87	d2d1ya1	Alignment	not modelled	100.0	22	**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	22	**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	d2rhca1	Alignment	not modelled	100.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
90	d1bdba_	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
91	c3k31B_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of eonyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
92	c5jlaB_	Alignment	not modelled	100.0	28	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase from brucella2 melitensis 16m
93	c3gk3D_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**acetoacetyl-coa reductase; **PDBTitle:** crystal structure of acetoacetyl-coa reductase from burkholderia2 pseudomallei 1710b
94	c4hp8A_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-deoxy-d-gluconate 3-dehydrogenase; **PDBTitle:** crystal structure of a putative 2-deoxy-d-gluconate 3-dehydrogenase2 from agrobacterium tumefaciens (target efi-506435) with bound nadp
95	c4o5oA_	Alignment	not modelled	100.0	26	**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
96	c3gr6A_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of the staphylococcus aureus enoyl-acyl carrier2 protein reductase (fabi) in complex with nadp and triclosan
97	c4nbuD_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of fabg from bacillus sp
98	c5t5qC_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short-chain dehydrogenase/reductase sdr:glucose/ribitol **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase2 sdr:glucose/ribitol dehydrogenase from brucella melitensis
99	c5jc8C_	Alignment	not modelled	100.0	23	**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
100	c6ds1C_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of cj0485 dehydrogenase in complex with nadp+
101	d1ydea1	Alignment	not modelled	100.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

						Family: Tyrosine-dependent oxidoreductases
102	c6a41A_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehalogenase; **PDBTitle:** dehalogenation enzyme
103	c4xgnD_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase in complex with2 nad from burkholderia thailandensis
104	c2uvdE_	Alignment	not modelled	100.0	26	**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)
105	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
106	c3tscB_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of short chain dehydrogenase map_2410 from2 mycobacterium paratuberculosis bound to nad
107	d1cyda_	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
108	c3ftpD_	Alignment	not modelled	100.0	24	**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
109	c3rkrC_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain oxidoreductase; **PDBTitle:** crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp
110	c4qecB_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**elxo; **PDBTitle:** elxo with nadp bound
111	d1g0oa_	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
112	c2yz7B_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**d-3-hydroxybutyrate dehydrogenase; **PDBTitle:** x-ray analyses of 3-hydroxybutyrate dehydrogenase from2 alcaligenes faecalis
113	c3t7cC_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carveol dehydrogenase; **PDBTitle:** crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
114	d1ulsa_	Alignment	not modelled	100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
115	c5o30A_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of the novel halohydrin dehalogenase hheg
116	c4kwhA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**reductase homolog; **PDBTitle:** the crystal structure of angucycline c-6 ketoreductase lanv with bound2 nadp
117	d1h5qa_	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
118	c6f9qC_	Alignment	not modelled	100.0	21	**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+
119	c4nqzF_	Alignment	not modelled	100.0	12	**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
120	c2q2qG_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**beta-d-hydroxybutyrate dehydrogenase; **PDBTitle:** structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida