

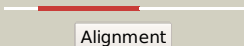

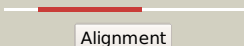






















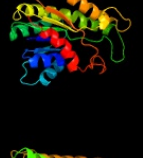
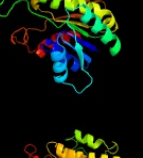
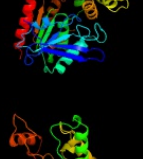
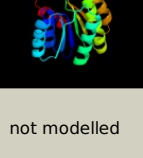


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2214c_ (ephD)_2479931_2481709
Date	Mon Aug 5 13:25:34 BST 2019
Unique Job ID	e51b4dd61ab03025

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2et6A_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: (3r)-hydroxyacyl-coa dehydrogenase; PDBTitle: (3r)-hydroxyacyl-coa dehydrogenase domain of candida tropicalis2 peroxisomal multifunctional enzyme type 2
2	c1cr6A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
3	c3i28A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
4	c4wuvB_	 Alignment		100.0	24	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
5	c5ig2B_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of a short chain dehydrogenase/reductase sdr from2 burkholderia phymatum in complex with nad
6	d1xu9a_	 Alignment		100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
7	d1xsea_	 Alignment		100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
8	c3ioyB_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: structure of putative short-chain dehydrogenase (saro_0793) from2 novosphingobium aromaticivorans
9	d1y5ma1	 Alignment		100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
10	c4yacA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligo in complex with nadh from sphingobium sp.2 strain syk-6
11	c3omIA_	 Alignment		100.0	29	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: peroxisomal multifunctional enzyme type 2, cg3415; PDBTitle: structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster

12	c3tjrA	Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis
13	c4qloA	Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
14	c4yaiB	Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligl in complex with nadh and gge from2 sphingobium sp. strain syk-6
15	c5f4zB	Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
16	c3llsB	Alignment		100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-ketoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 mycobacterium tuberculosis
17	c3o26A	Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: salutaridine reductase; PDBTitle: the structure of salutaridine reductase from papaver somniferum.
18	c5ldgA	Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-isopiperitenone reductase; PDBTitle: isopiperitenone reductase from mentha piperita in complex with2 isopiperitenone and nadp
19	c5yhpB	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
20	c3t7cC	Alignment		100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
21	c4qlaA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
22	d2b61a1	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
23	d1qo7a	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
24	d1zbqa1	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
25	c1zbqB	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase 4; PDBTitle: crystal structure of human 17-beta-hydroxysteroid dehydrogenase type 42 in complex with nad
26	c4qlaB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
27	c3om8A	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
28	c5w8pA	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
						PDB header: dehydrogenase

29	c1fdvA_	Alignment	not modelled	100.0	25	Chain: A: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase; PDBTitle: human 17-beta-hydroxysteroid-dehydrogenase type 1 mutant h221l2 complexed with nad+
30	c5d6oB_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
31	c4nqzF_	Alignment	not modelled	100.0	20	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
32	c4fc6B_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxisomal 2,4-dienoyl-coa reductase; PDBTitle: studies on dcr shed new light on peroxisomal beta-oxidation: crystal2 structure of the ternary complex of pdcr
33	c4i19A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
34	c3i1iA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
35	c4d9jl_	Alignment	not modelled	100.0	18	PDB header: de novo protein Chain: I: PDB Molecule: designed 16nm tetrahedral protein cage containing non-haem PDBTitle: structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains
36	d1jtva_	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
37	c3cxtA_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
38	c5jkjA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
39	d2ae2a_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
40	d1zema1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
41	c4j2hA_	Alignment	not modelled	100.0	27	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)
42	c3imfA_	Alignment	not modelled	100.0	24	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'
43	c4bmvH_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: H: PDB Molecule: short-chain dehydrogenase; PDBTitle: short-chain dehydrogenase from sphingobium yanoikuyae in2 complex with nadph
44	c6ci9D_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
45	c2qmqA_	Alignment	not modelled	100.0	13	PDB header: signaling protein Chain: A: PDB Molecule: protein ndr2; PDBTitle: crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
46	d1yb1a_	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
47	c3vvlA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
48	c2vavL_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
49	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
50	c5jy1C_	Alignment	not modelled	100.0	26	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
51	c3o38D_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
52	c3lylB_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: structure of 3-oxoacyl-acylcarrier protein reductase, fabq2 from francisella tularensis

53	c1yb1B	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase type xi; PDBTitle: crystal structure of human 17-beta-hydroxysteroid dehydrogenase type2 xi
54	c5epoD	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
55	d1xhla	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
56	d2c07a1	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
57	c2c07A	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acc reductase of plasmodium falciparum
58	c2e3jA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase ephb; PDBTitle: the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom
59	c5k9zB	Alignment	not modelled	100.0	31	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
60	d1geea	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
61	c5uroA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
62	c3svtA	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
63	c5o98A	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase 1; PDBTitle: binary complex of catharanthus roseus vitrosamine synthase with nadp+
64	c5nfqA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase belonging to alpha/beta hydrolase PDBTitle: novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
65	d2vata1	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
66	c4kzpC	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family PDBTitle: crystal structure of a putative short chain dehydrogenase from2 mycobacterium smegmatis
67	c4urfB	Alignment	not modelled	100.0	31	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
68	d1w6ua	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
69	c2y6vB	Alignment	not modelled	100.0	10	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
70	c3toxG	Alignment	not modelled	100.0	29	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
71	c3tscB	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of short chain dehydrogenase map_2410 from2 mycobacterium paratuberculosis bound to nad
72	c4z9yA	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-deoxy-d-gluconate 3-dehydrogenase; PDBTitle: crystal structure of 2-keto-3-deoxy-d-gluconate dehydrogenase from2 pectobacterium carotovorum
73	c3grkE	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nahh); PDBTitle: crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
74	d1ae1a	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
75	c4iiuB	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: crystal structure of a putative 3-oxoacyl-[acyl-carrier2 protein]reductase from escherichia coli strain cft073 complexed with3 nadp+ at 2.1 a resolution
76	c3wtcB	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036

77	c4afnB	Alignment	not modelled	100.0	26	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
78	c5fydB	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: structural and biochemical insights into 7beta-2 hydroxysteroid dehydrogenase stereoselectivity
79	d2bela	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
80	c6ixjK	Alignment	not modelled	100.0	24	PDB header: cytosolic protein Chain: K: PDB Molecule: sulfoacetaldehyde reductase; PDBTitle: the crystal structure of sulfoacetaldehyde reductase from klebsiella2 oxytoca
81	c4weoD	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: D: PDB Molecule: putative acetoin(diacetyl) reductase; PDBTitle: crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia
82	c4cr8D	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: D: PDB Molecule: n-acylmannosamine 1-dehydrogenase; PDBTitle: crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
83	c5efzC	Alignment	not modelled	100.0	10	PDB header: hydrolase Chain: C: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
84	c4iboA	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
85	c4dqxB	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42
86	c4dryA	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: the crystal structure of 3-oxoacyl-[acyl-carrier-protein] reductase2 from rhizobium meliloti
87	c2jahB	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
88	c2cfcB	Alignment	not modelled	100.0	31	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
89	c4m87B	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of enoyl-acyl carrier protein reductase (fabI) from2 neisseria meningitidis in complex with nad+
90	c3lf2B	Alignment	not modelled	100.0	25	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
91	d1yxma1	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
92	c3rkuC	Alignment	not modelled	100.0	27	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+
93	c4fn4A	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from sulfolobus2 acidocaldarius
94	d1oaaa	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
95	c4y98A	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligd-apo form from sphingobium sp. strain syk-6
96	c4lvuB	Alignment	not modelled	100.0	25	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
97	c5esrA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
98	c4zjuA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: structure of a nadh-dependent enoyl-acp reductase from acinetobacter2 baumannii in complex with nad
99	c3pgxB	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of a putative carveol dehydrogenase from2 mycobacterium paratuberculosis bound to nicotinamide adenine3 dinucleotide
100	c4nbvA	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from cupriavidus taiwanensis

101	c3awdD	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: D: PDB Molecule: putative polyol dehydrogenase; PDBTitle: crystal structure of gox2181
102	c3uveC	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase ((+)-trans-carveol dehydrogenase); PDBTitle: crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
103	c4nimA	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: versicolorin reductase; PDBTitle: crystal structure of a short chain dehydrogenase from brucella2 melitensis
104	c3itdA	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 17beta-hydroxysteroid dehydrogenase; PDBTitle: crystal structure of an inactive 17beta-hydroxysteroid dehydrogenase2 (y167f mutated form) from fungus cochliobolus lunatus
105	c4pw0A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
106	d1cr6a2	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
107	d1azwa	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
108	d1zd3a2	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
109	c3oecA	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: carveol dehydrogenase (mytha.01326.c, a0r518 homolog); PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
110	c3osuA	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of the 3-oxoacyl-acyl carrier protein reductase,2 fabg, from staphylococcus aureus
111	c3sc4A	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase (a0qtm2 homolog); PDBTitle: crystal structure of a short chain dehydrogenase (a0qtm2 homolog)2 mycobacterium thermoresistibile
112	c2r11D	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
113	d2bd0a1	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
114	c3k31B	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of enoyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
115	d1iy8a	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
116	c4g81A	Alignment	not modelled	100.0	25	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)
117	d2pl5a1	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
118	c3ppiA	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase type-2; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase type-2 from2 mycobacterium avium
119	c3kvoB	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: hydroxysteroid dehydrogenase-like protein 2; PDBTitle: crystal structure of the catalytic domain of human hydroxysteroid2 dehydrogenase like 2 (hsd12)
120	c3tzqD	Alignment	not modelled	100.0	28	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