

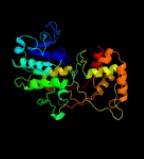










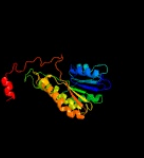













Phyre2

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 Description RVBD3391_(acrA1_3805801_3807753)
 Date Fri Aug 9 18:20:06 BST 2019
 Unique Job ID 356af1bf2067da63

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2et6A_	 Alignment		100.0	22	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	c5msuC_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: C; PDB Molecule: carboxylic acid reductase; PDBTitle: structure of the r domain of carboxylic acid reductase (car) from2 mycobacterium marinum in complex with nadp, p21 form
3	c4dqvA_	 Alignment		100.0	22	PDB header: ligase Chain: A; PDB Molecule: probable peptide synthetase nrp (peptide synthase); PDBTitle: crystal structure of reductase (r) domain of non-ribosomal peptide2 synthetase from mycobacterium tuberculosis
4	c1z7eC_	 Alignment		100.0	15	PDB header: hydrolase Chain: C; PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
5	c1z45A_	 Alignment		100.0	20	PDB header: isomerase Chain: A; PDB Molecule: gal10 bifunctional protein; PDBTitle: crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose
6	c4f6cA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: ausa reductase domain protein; PDBTitle: crystal structure of aureusimine biosynthetic cluster reductase domain
7	c4w4tA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A; PDB Molecule: mxaa; PDBTitle: the crystal structure of the terminal r domain from the myxalamid pks-2 nrps biosynthetic pathway
8	c2vz8B_	 Alignment		100.0	15	PDB header: transferase Chain: B; PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
9	c4j1sA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: polyketide synthase pksj; PDBTitle: crystal structure of a ketoreductase domain from the bacillaene2 assembly line
10	c3llsB_	 Alignment		100.0	26	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
11	c4l4xA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A; PDB Molecule: amphi; PDBTitle: an a2-type ketoreductase from a modular polyketide synthase

12	c5d2eA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: mlne; PDBTitle: crystal structure of an n-terminal ketoreductase from macrolactin2 assembly line
13	c5df1A_	Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: iridoid synthase; PDBTitle: iridoid synthase from catharanthus roseus - ternary complex with nadp+2 and geranic acid
14	c4pivB_	Alignment		100.0	15	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: human fatty acid synthase psi/kr tri-domain with nadph and gsk2194069
15	c4di7A_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: amphi; PDBTitle: structure of a2-type ketoreductase of modular polyketide synthases
16	c4wuvB_	Alignment		100.0	20	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
17	c3omlA_	Alignment		100.0	32	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
18	c3qp9C_	Alignment		100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: type i polyketide synthase pikaii; PDBTitle: the structure of a c2-type ketoreductase from a modular polyketide2 synthase
19	c1zbqB_	Alignment		100.0	30	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
20	d1zbqa1	Alignment		100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
21	c5msvB_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the phosphopantetheine modified pcp-r didomain of2 carboxylic acid reductase (car) in complex with nadp
22	d1xsea_	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
23	c3slkB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: polyketide synthase extender module 2; PDBTitle: structure of ketoreductase and enoylreductase didomain from modular2 polyketide synthase
24	c5ldgA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-isopiperitenone reductase; PDBTitle: isopiperitenone reductase from mentha piperita in complex with2 isopiperitenone and nadp
25	c3o26A_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: salutaridine reductase; PDBTitle: the structure of salutaridine reductase from papaver somniferum.
26	c3ioyB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: structure of putative short-chain dehydrogenase (saro_0793) from2 novosphingobium aromaticivorans
27	c3mjsA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: amphb; PDBTitle: structure of a-type ketoreductases from modular polyketide synthase
28	d1xu9a_	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

29	c2z5IA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: tylactone synthase starter module and modules 1 & 2; PDBTitle: the first ketoreductase of the tylosin pks
30	c2vz8A	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
31	c3oh8A	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
32	d1i24a	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
33	c2v6gA	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: progesterone 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
34	c4yacA	Alignment	not modelled	100.0	21	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
35	c4impB	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: polyketide synthase extender modules 3-4; PDBTitle: the missing linker: a dimerization motif located within polyketide2 synthase modules
36	c5ig2B	Alignment	not modelled	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 in complex with nad
37	d1y5ma1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
38	c2fr1A	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: erythromycin synthase, eryai; PDBTitle: the first ketoreductase of the erythromycin synthase2 (crystal form 2)
39	c4hxyA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: plm1; PDBTitle: plmkr1-ketoreductase from the first module of phoslactomycin2 biosynthesis in streptomyces sp. hk803
40	c3tjrA	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis
41	c3pvzD	Alignment	not modelled	100.0	17	PDB header: lyase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
42	c5o98A	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase 1; PDBTitle: binary complex of catharanthus roseus vitrosamine synthase with nadp+
43	c4nqzF	Alignment	not modelled	100.0	17	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
44	c3cxtA	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
45	c3t7cC	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
46	c4kzpC	Alignment	not modelled	100.0	24	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
47	c3lylB	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
48	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
49	c5ktaA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide synthase pksj; PDBTitle: ketoreductase from module 3 of the bacillaene synthase from bacillus2 subtilis 168
50	d2bela	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
51	c3e03C	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative dehydrogenase from xanthomonas2 campestris
52	c4m87B	Alignment	not modelled	100.0	19	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+
						Fold: NAD(P)-binding Rossmann-fold domains

53	d1xhla_	Alignment	not modelled	100.0	27	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
54	c5zedA_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein adh; PDBTitle: crystal structure of kluyveromyces polyspora adh (kpadh) mutant2 (e214v/t215s)
55	c2c07A_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acp reductase of plasmodium falciparum
56	d2c07a1	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
57	c4pvcB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent methylglyoxal reductase gre2; PDBTitle: crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2
58	c5epoD_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
59	c4fc6B_	Alignment	not modelled	100.0	20	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
60	c4j2hA_	Alignment	not modelled	100.0	26	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)
61	d1ae1a_	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
62	c5jy1C_	Alignment	not modelled	100.0	25	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
63	c4yaiB_	Alignment	not modelled	100.0	23	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
64	c4dryA_	Alignment	not modelled	100.0	25	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
65	c4y98A_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligd-apo form from sphingobium sp. strain syk-6
66	c3w1vA_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap8e; PDBTitle: crystal structure of capsular polysaccharide synthesizing enzyme cape2 from staphylococcus aureus in complex with inhibitor
67	c3v8bC_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase, possibly 3-oxoacyl-[acyl-carrier PDBTitle: crystal structure of a 3-ketoacyl-acp reductase from sinorhizobium2 meliloti 1021
68	d2ew8a1	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
69	c3imfA_	Alignment	not modelled	100.0	23	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'
70	c3grkE_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
71	c4urfB_	Alignment	not modelled	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
72	c4weoD_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: D: PDB Molecule: putative acetoin(diacetyl) reductase; PDBTitle: crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia
73	c3rkrC_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain oxidoreductase; PDBTitle: crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp
74	c3rkuC_	Alignment	not modelled	100.0	26	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+
75	d1yb1a_	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
76	c6el3A_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxo-delta(4,5)-steroid 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from

						arabidopsis thaliana in2 complex with nadp
77	d2bd0a1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
78	c3svtA	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
79	c4bmvH	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: H: PDB Molecule: short-chain dehydrogenase; PDBTitle: short-chain dehydrogenase from sphingobium yanoikuyae in2 complex with nadph
80	c4cr8D	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: n-acylmannosamine 1-dehydrogenase; PDBTitle: crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
81	c4fn4A	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from sulfobolbus2 acidocaldarius
82	c5k9zB	Alignment	not modelled	100.0	24	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
83	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
84	c4e3zA	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase protein; PDBTitle: crystal structure of a oxidoreductase from rhizobium etli cfn 42
85	c6aqyD	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: D: PDB Molecule: gdp-l-fucose synthetase; PDBTitle: crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
86	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
87	c5ff9C	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: noroxomaritidine/norcraugsodine reductase; PDBTitle: noroxomaritidine/norcraugsodine reductase in complex with nadp+ and2 tyramine
88	c1fdvA	Alignment	not modelled	100.0	28	PDB header: dehydrogenase Chain: A: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase; PDBTitle: human 17-beta-hydroxysteroid-dehydrogenase type 1 mutant h221l2 complexed with nad+
89	c3kvoB	Alignment	not modelled	100.0	23	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 (hsdl2)
90	c2jahB	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
91	c5I53A	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-menthone:(+)-neomenthol reductase; PDBTitle: menthone neomenthol reductase from mentha piperita in complex with2 nadp
92	c2cfcB	Alignment	not modelled	100.0	29	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
93	c6bwIA	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: pal; PDBTitle: x-ray structure of pal from bacillus thuringiensis
94	c3o38D	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
95	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
96	c4lvuB	Alignment	not modelled	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
97	d1e6wa	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
98	c5fydB	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: structural and biochemical insights into 7beta-2 hydroxysteroid dehydrogenase stereoselectivity
99	c3I1jB	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: structure of a putative short chain dehydrogenase from pseudomonas2 syringae
100	c5f1pB	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: ptmo8; PDBTitle: crystal structure of dehydrogenase from streptomyces

						platensis
101	c4dqxB_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42
102	c4nimA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: versicolorin reductase; PDBTitle: crystal structure of a short chain dehydrogenase from brucella2 melitensis
103	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
104	c3qljB_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: B: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 avium
105	c4ni5A_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family PDBTitle: crystal structure of a short chain dehydrogenase from brucella suis
106	d1yxma1	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
107	c3toxG_	Alignment	not modelled	100.0	30	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
108	c5jydA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
109	c4o5oA_	Alignment	not modelled	100.0	23	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
110	c2zatC_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
111	d1gz6a_	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
112	c4iboA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
113	c3awdD_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: putative polyol dehydrogenase; PDBTitle: crystal structure of gox2181
114	c1yb1B_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase type xi; PDBTitle: crystal structure of human 17-beta-hydroxysteroid dehydrogenase type2 xi
115	c3tzqD_	Alignment	not modelled	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
116	d1gy8a_	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
117	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
118	c4nbvA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from cupriavidus taiwanensis
119	d2c5aa1	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
120	c3m1IA_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of a c-terminal truncated mutant of a putative2 ketoacyl reductase (fabg4) from mycobacterium tuberculosis h37rv at3 2.5 angstrom resolution