Phyre2

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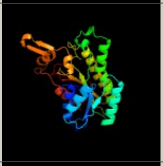
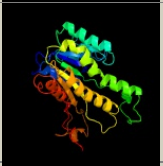
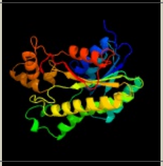
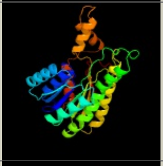
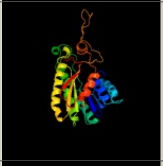
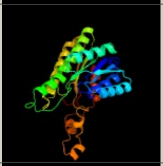
Description	RVBD1484_(inhA)_1674208_1675017
Date	Fri Aug 2 13:30:06 BST 2019
Unique Job ID	a60c2794ae174f0d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2h7ma1	Alignment		100.0	100	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
2	c3itdA_	Alignment		100.0	16	**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
3	c5unlA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-ketoacyl-acp reductase; **PDBTitle:** crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
4	c3gr6A_	Alignment		100.0	26	**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
5	c4nqzF_	Alignment		100.0	30	**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
6	c4nk4E_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of fabi from candidatus liberibacter asiaticus
7	c5ojgB_	Alignment		100.0	18	**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
8	c3ai3A_	Alignment		100.0	19	**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
9	d2pd4a1	Alignment		100.0	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
10	c5koiH_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of a possible enoyl-(acyl-carrier-protein) reductase2 from brucella melitensis
11	c2qioA_	Alignment		100.0	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan

12	c4zjuA_	Alignment		100.0	31	**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
13	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
14	d1xhla_	Alignment		100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
15	c3ek2D_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of eonyl-(acyl carrier protein) reductase from2 burkholderia pseudomallei 1719b
16	d1geea_	Alignment		100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
17	c3lf2B_	Alignment		100.0	15	**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
18	d1iy8a_	Alignment		100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
19	d1qsga_	Alignment		100.0	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
20	c6ci9D_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
21	c3toxG_	Alignment	not modelled	100.0	18	**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
22	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
23	c3t7cC_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carveol dehydrogenase; **PDBTitle:** crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
24	c2cfcB_	Alignment	not modelled	100.0	18	**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
25	c4m87B_	Alignment	not modelled	100.0	34	**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+
26	c5epoD_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**7-alpha-hydroxysteroid deydrogenase; **PDBTitle:** the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
27	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
28	c3grkE_	Alignment	not modelled	100.0	26	**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
29	c5h5xH_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor
30	c5idxB_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of an oxidoreductase from burkholderia vietnamiensis
31	c3rihB_	Alignment	not modelled	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
32	d1w6ua_	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
33	d1ja9a_	Alignment	not modelled	100.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
34	c4nbrA_	Alignment	not modelled	100.0	14	**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
35	c1w4zA_	Alignment	not modelled	100.0	14	**PDB header:**antibiotic biosynthesis **Chain:** A: **PDB Molecule:**ketoacyl reductase; **PDBTitle:** structure of actinorhodin polyketide (actiii) reductase
36	c2p91A_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of enoyl-[acyl-carrier-protein] reductase (nadh)2 from aquifex aeolicus vf5
37	d2rhca1	Alignment	not modelled	100.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
38	c4urfB_	Alignment	not modelled	100.0	19	**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
39	c3k31B_	Alignment	not modelled	100.0	23	**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
40	c3bmrA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pteridine reductase; **PDBTitle:** structure of pteridine reductase 1 (ptr1) from trypanosoma2 brucei in ternary complex with cofactor (nadp+) and3 inhibitor (compound ax6)
41	c3awdD_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative polyol dehydrogenase; **PDBTitle:** crystal structure of gox2181
42	c2yz7B_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**d-3-hydroxybutyrate dehydrogenase; **PDBTitle:** x-ray analyses of 3-hydroxybutyrate dehydrogenase from2 alcaligenes faecalis
43	c3wtcB_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of gox2036
44	c6f9qC_	Alignment	not modelled	100.0	16	**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+
45	d2bgka1	Alignment	not modelled	100.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
46	d1pr9a_	Alignment	not modelled	100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
47	c5u9pB_	Alignment	not modelled	100.0	17	**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
48	c3tzqD_	Alignment	not modelled	100.0	21	**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
49	c2zatC_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase/reductase sdr family member 4; **PDBTitle:** crystal structure of a mammalian reductase
50	c5x8hA_	Alignment	not modelled	100.0	17	**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
51	c6d9yB_	Alignment	not modelled	100.0	17	**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
52	c5k9zB_	Alignment	not modelled	100.0	22	**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

53	d1k2wa_	Alignment	not modelled	100.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
54	c3svtA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
55	c4wecA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
56	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
57	d1yxma1	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
58	c3pk0B_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
59	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
60	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
61	c5jydA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
62	c4wuvB_	Alignment	not modelled	100.0	14	**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
63	c2jjyD_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of francisella tularensis enoyl reductase2 (ftfabi) with bound nad
64	c3ijrF_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
65	c3ak4C_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-dependent quinuclidinone reductase; **PDBTitle:** crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
66	c4cr8D_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**n-acylmannosamine 1-dehydrogenase; **PDBTitle:** crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
67	c3gdfA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nadp-dependent mannitol dehydrogenase; **PDBTitle:** crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
68	d1ulua_	Alignment	not modelled	100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
69	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
70	c5jc8C_	Alignment	not modelled	100.0	20	**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
71	c3sjuA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**keto reductase; **PDBTitle:** hedamycin polyketide ketoreductase bound to nadph
72	c6ds1C_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of cj0485 dehydrogenase in complex with nadp+
73	c4npcA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sorbitol dehydrogenase; **PDBTitle:** crystal structure of an oxidoreductase, short-chain2 dehydrogenase/reductase family protein from brucella suis
74	d1fmca_	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
75	c4g81A_	Alignment	not modelled	100.0	18	**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
76	d1h5qa_	Alignment	not modelled	100.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
77	c5iv1C_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative short-chain dehydrogenase/reductase;

77	c5jy1C_	Alignment	not modelled	100.0	16	**PDBTitle:** crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400 bound to nad
78	c3uveC_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carveol dehydrogenase ((+)-trans-carveol dehydrogenase); **PDBTitle:** crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
79	c4nbvA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase putative short- **PDBTitle:** crystal structure of fabg from cupriavidus taiwanensis
80	c4trrH_	Alignment	not modelled	100.0	19	**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
81	d1zk4a1	Alignment	not modelled	100.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
82	c5jlaB_	Alignment	not modelled	100.0	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase from brucella2 melitensis 16m
83	c4afnB_	Alignment	not modelled	100.0	22	**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	c3r3sD_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase; **PDBTitle:** structure of the ygha oxidoreductase from salmonella enterica
85	d1zema1	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
86	c5o3zK_	Alignment	not modelled	100.0	11	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**sorbitol-6-phosphate dehydrogenase; **PDBTitle:** crystal structure of sorbitol-6-phosphate 2-dehydrogenase srld from2 erwinia amylovora
87	c3iccA_	Alignment	not modelled	100.0	15	**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
88	c3nugA_	Alignment	not modelled	100.0	17	**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
89	c2pd6D_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**estradiol 17-beta-dehydrogenase 8; **PDBTitle:** structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
90	c3oidA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadph]; **PDBTitle:** crystal structure of enoyl-acp reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)
91	d1bdba_	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
92	c4iboA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gluconate dehydrogenase; **PDBTitle:** crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
93	c4m8sB_	Alignment	not modelled	100.0	20	**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
94	c4jroC_	Alignment	not modelled	100.0	19	**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+
95	c4gh5B_	Alignment	not modelled	100.0	20	**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)
96	c4fn4A_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** short-chain nad(h)-dependent dehydrogenase/reductase from sulfolobus2 acidocaldarius
97	c3gvcB_	Alignment	not modelled	100.0	19	**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
98	c3ppiA_	Alignment	not modelled	100.0	18	**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
99	c4z9yA_	Alignment	not modelled	100.0	18	**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
100	c3u49B_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bacilysin biosynthesis oxidoreductase ywfh;

						PDBTitle: crystal structure of ywfh, nadph dependent reductase involved in2 bacilysin biosynthesis
101	c3tscB_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of short chain dehydrogenase map_2410 from2 mycobacterium paratuberculosis bound to nad
102	c4iuyB_	Alignment	not modelled	100.0	16	**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
103	c5t2uC_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family **PDBTitle:** short chain dehydrogenase/reductase family protein
104	d1ae1a_	Alignment	not modelled	100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
105	c4kwhA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**reductase homolog; **PDBTitle:** the crystal structure of angucycline c-6 ketoreductase lanv with bound2 nadp
106	c4i5eC_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**alclohol dehydrogenase/short-chain dehydrogenase; **PDBTitle:** crystal structure of ralstonia sp. alcohol dehydrogenase in complex2 with nadp+
107	c3o38D_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
108	d1q7ba_	Alignment	not modelled	100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
109	c3cxtA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase with different specificities; **PDBTitle:** quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
110	c6a41A_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehalogenase; **PDBTitle:** dehalogenation enzyme
111	c4j2hA_	Alignment	not modelled	100.0	21	**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)
112	c2p68A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of aq_1716 from aquifex aeolicus vf5
113	c4o0lA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-dependent 3-quinuclidinone reductase; **PDBTitle:** crystal structure of nadph-dependent 3-quinuclidinone reductase from2 rhodotorula rubra
114	c3imfA_	Alignment	not modelled	100.0	20	**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'
115	c4imrA_	Alignment	not modelled	100.0	16	**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
116	d1nffa_	Alignment	not modelled	100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
117	d1vl8a_	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
118	c3afnC_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of aldose reductase a1-r complexed with nadp
119	d1gega_	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	c4lvuB_	Alignment	not modelled	100.0	16	**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