





















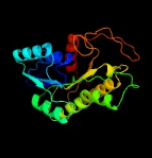




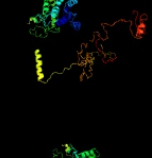
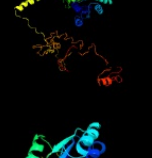
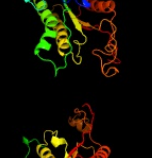



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1663_(pks17)_1886519_1888027
Date	Fri Aug 2 13:30:26 BST 2019
Unique Job ID	b9a17241690b5988

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vz8B_	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
2	c2vz8A_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
3	c6fn6A_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase 1, isoform a; PDBTitle: modifying region (dh-er-kr) of an insect fatty acid synthase (fas)
4	c3slkB_	 Alignment		100.0	54	PDB header: oxidoreductase Chain: B: PDB Molecule: polyketide synthase extender module 2; PDBTitle: structure of ketoreductase and enoylreductase didomain from modular2 polyketide synthase
5	c3mjsA_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: A: PDB Molecule: amphb; PDBTitle: structure of a-type ketoreductases from modular polyketide synthase
6	c4impB_	 Alignment		100.0	39	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
7	c2fr1A_	 Alignment		100.0	45	PDB header: oxidoreductase Chain: A: PDB Molecule: erythromycin synthase, eryai; PDBTitle: the first ketoreductase of the erythromycin synthase2 (crystal form 2)
8	c2uv9B_	 Alignment		100.0	15	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase alpha subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
9	c3qp9C_	 Alignment		100.0	36	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
10	c2uv8C_	 Alignment		100.0	14	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha (fas2); PDBTitle: crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
11	c2vkzC_	 Alignment		100.0	14	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex

12	c4pivB_	Alignment		100.0	32	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
13	c2z5IA_	Alignment		100.0	45	PDB header: transferase Chain: A: PDB Molecule: tylactone synthase starter module and modules 1 & 2; PDBTitle: the first ketoreductase of the tylosin pks
14	c4l4xA_	Alignment		100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: amphi; PDBTitle: an a2-type ketoreductase from a modular polyketide synthase
15	c3hmjB_	Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: saccharomyces cerevisiae fas type i
16	c2pffA_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase
17	c2pffD_	Alignment		100.0	15	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase
18	c2pffG_	Alignment		100.0	15	PDB header: transferase Chain: G: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase
19	c4di7A_	Alignment		100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: amphi; PDBTitle: structure of a2-type ketoreductase of modular polyketide synthases
20	c5d2eA_	Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: mlne; PDBTitle: crystal structure of an n-terminal ketoreductase from macrolactin2 assembly line
21	c4hxyA_	Alignment	not modelled	100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: plm1; PDBTitle: plmkr1-ketoreductase from the first module of phoslactomycin2 biosynthesis in streptomyces sp. hk803
22	c4jlSA_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide synthase pksj; PDBTitle: crystal structure of a ketoreductase domain from the bacillaene2 assembly line
23	c5ktkA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide synthase pksj; PDBTitle: ketoreductase from module 3 of the bacillaene synthase from bacillus2 subtilis 168
24	c4b3yB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
25	c3s8mA_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acp reductase; PDBTitle: the crystal structure of fabv
26	c4ggoA_	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: trans-2-enoyl-coa reductase; PDBTitle: crystal structure of trans-2-enoyl-coa reductase from treponema2 denticola
27	c3llsB_	Alignment	not modelled	100.0	22	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
28	d2fr1a1	Alignment	not modelled	100.0	44	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

29	c5xi0B_	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of fabv, a new class of enyl-acyl carrier protein2 reductase from vibrio fischeri
30	c2et6A_	Alignment	not modelled	99.9	26	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
31	c3m11A_	Alignment	not modelled	99.9	22	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
32	d1zbqa1	Alignment	not modelled	99.9	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
33	c1zbqB_	Alignment	not modelled	99.9	25	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
34	c3om1A_	Alignment	not modelled	99.9	25	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
35	d1gz6a_	Alignment	not modelled	99.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
36	c3ioyB_	Alignment	not modelled	99.9	23	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: structure of putative short-chain dehydrogenase (saro_0793) from2 novosphingobium aromaticivorans
37	c4wuvB_	Alignment	not modelled	99.9	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
38	c4yacA_	Alignment	not modelled	99.8	20	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
39	c3pvzD_	Alignment	not modelled	99.8	14	PDB header: lyase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
40	d1xsea_	Alignment	not modelled	99.8	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
41	d1jtva_	Alignment	not modelled	99.8	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
42	c5o98A_	Alignment	not modelled	99.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase 1; PDBTitle: binary complex of catharanthus roseus vitrosamine synthase with nadp+
43	c4y98A_	Alignment	not modelled	99.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligd-apo form from sphingobium sp. strain syk-6
44	d1xu9a_	Alignment	not modelled	99.8	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
45	c1fdvA_	Alignment	not modelled	99.8	21	PDB header: dehydrogenase Chain: A: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase; PDBTitle: human 17-beta-hydroxysteroid-dehydrogenase type 1 mutant h221f2 complexed with nad+
46	c3lylB_	Alignment	not modelled	99.8	21	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
47	c4kzpC_	Alignment	not modelled	99.8	27	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
48	c5ig2B_	Alignment	not modelled	99.8	24	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
49	c3e03C_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative dehydrogenase from xanthomonas2 campestris
50	c4iiuB_	Alignment	not modelled	99.8	21	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
51	c3osuA_	Alignment	not modelled	99.8	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
52	c4trrh_	Alignment	not modelled	99.8	22	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

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53	d1y5ma1	Alignment	not modelled	99.8	20 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
54	c3qljB_	Alignment	not modelled	99.8	27 PDB header: oxidoreductase Chain: B: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 avium
55	d1geea_	Alignment	not modelled	99.8	17 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
56	c6ci9D_	Alignment	not modelled	99.8	21 PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
57	c2c07A_	Alignment	not modelled	99.8	23 PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acp reductase of plasmodium falciparum
58	d2c07a1	Alignment	not modelled	99.8	23 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
59	c4j2hA_	Alignment	not modelled	99.8	20 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)
60	c3nzoB_	Alignment	not modelled	99.8	12 PDB header: lyase Chain: B: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
61	c3iccA_	Alignment	not modelled	99.8	16 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
62	c3tjrA_	Alignment	not modelled	99.8	21 PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis
63	c4nimA_	Alignment	not modelled	99.8	25 PDB header: oxidoreductase Chain: A: PDB Molecule: versicolorin reductase; PDBTitle: crystal structure of a short chain dehydrogenase from brucella2 melitensis
64	c4nbwA_	Alignment	not modelled	99.8	20 PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of fabg from pleisocystis pacifica
65	c4fc6B_	Alignment	not modelled	99.8	24 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
66	c4m87B_	Alignment	not modelled	99.8	18 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+
67	c6ixjK_	Alignment	not modelled	99.7	24 PDB header: cytosolic protein Chain: K: PDB Molecule: sulfoacetaldehyde reductase; PDBTitle: the crystal structure of sulfoacetaldehyde reductase from klebsiella2 oxytoca
68	c5epoD_	Alignment	not modelled	99.7	15 PDB header: oxidoreductase Chain: D: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
69	c3oecA_	Alignment	not modelled	99.7	22 PDB header: oxidoreductase Chain: A: PDB Molecule: carveol dehydrogenase (mytha.01326.c, a0r518 homolog); PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
70	c2jahB_	Alignment	not modelled	99.7	26 PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
71	c3grkE_	Alignment	not modelled	99.7	14 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
72	c4z9yA_	Alignment	not modelled	99.7	16 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	c4urfB_	Alignment	not modelled	99.7	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
74	c3cxtA_	Alignment	not modelled	99.7	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
75	c4nqzF_	Alignment	not modelled	99.7	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
76	c3c26A_	Alignment	not modelled	99.7	24 PDB header: oxidoreductase Chain: A: PDB Molecule: salutaridine reductase;

76	c30z0A	Alignment	not modelled	99.7	24	PDBTitle: the structure of salutaridine reductase from papaver somniferum.
77	c6h0jA	Alignment	not modelled	99.7	49	PDB header: protein binding Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: a1-type acp domain from module 5 of mlsA1
78	c3imfA	Alignment	not modelled	99.7	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'
79	c3oidA	Alignment	not modelled	99.7	16	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)
80	c4dryA	Alignment	not modelled	99.7	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
81	c3wtcB	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036
82	d1oaaa	Alignment	not modelled	99.7	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
83	c4lvuB	Alignment	not modelled	99.7	20	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
84	c4nk4E	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of fabi from candidatus liberibacter asiaticus
85	c4bmvH	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: H: PDB Molecule: short-chain dehydrogenase; PDBTitle: short-chain dehydrogenase from sphingobium yanoikuyae in2 complex with nadph
86	d2ae2a	Alignment	not modelled	99.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
87	d1ae1a	Alignment	not modelled	99.7	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
88	c4kwhA	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: reductase homolog; PDBTitle: the crystal structure of angucycline c-6 ketoreductase lanv with bound2 nadp
89	c3uf0A	Alignment	not modelled	99.7	25	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)
90	c3t7cC	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
91	c3zu3A	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ypo4104/y4119/yp_4011; PDBTitle: structure of the enoyl-acp reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
92	d1edoa	Alignment	not modelled	99.7	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
93	c5x8hA	Alignment	not modelled	99.7	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
94	c2ju2A	Alignment	not modelled	99.7	48	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase; PDBTitle: minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
95	c3tfoD	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: D: PDB Molecule: putative 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of a putative 3-oxoacyl-(acyl-carrier-protein)2 reductase from sinorhizobium meliloti
96	c3v8bC	Alignment	not modelled	99.7	29	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
97	c4e4yA	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase family protein; PDBTitle: the crystal structure of a short chain dehydrogenase family protein2 from francisella tularensis subsp. tularensis schu s4
98	c3kzvA	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized oxidoreductase yir035c; PDBTitle: the crystal structure of a cytoplasmic protein with unknown function2 from saccharomyces cerevisiae
99	d1zema1	Alignment	not modelled	99.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
100	c4iboA	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase

					from2 agrobacterium tumefaciens (target efi-506446)
101	c4ni5A_	Alignment	not modelled	99.7	30 PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family PDBTitle: crystal structure of a short chain dehydrogenase from brucella suis
102	c3itdA_	Alignment	not modelled	99.7	18 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
103	c2cfcB_	Alignment	not modelled	99.7	24 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
104	c3ezlA_	Alignment	not modelled	99.7	17 PDB header: oxidoreductase Chain: A: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetyacetyl-coa reductase from2 burkholderia pseudomallei 1710b
105	c3afnC_	Alignment	not modelled	99.7	21 PDB header: oxidoreductase Chain: C: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of aldose reductase a1-r complexed with nadp
106	c2uvdE_	Alignment	not modelled	99.7	22 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)
107	c4dqxB_	Alignment	not modelled	99.7	18 PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42
108	c4weoD_	Alignment	not modelled	99.7	19 PDB header: oxidoreductase Chain: D: PDB Molecule: putative acetoin(diacetyl) reductase; PDBTitle: crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia
109	c4zjuA_	Alignment	not modelled	99.7	17 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
110	c3h7aC_	Alignment	not modelled	99.7	20 PDB header: oxidoreductase Chain: C: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of short-chain dehydrogenase from rhodopseudomonas2 palustris
111	c5jy1C_	Alignment	not modelled	99.7	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
112	c5bt9B_	Alignment	not modelled	99.7	18 PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of folm alternative dihydrofolate reductase 1 from2 brucella canis complexed with nadp
113	c4e3zA_	Alignment	not modelled	99.7	28 PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase protein; PDBTitle: crystal structure of a oxidoreductase from rhizobium etli cfn 42
114	c4gh5B_	Alignment	not modelled	99.7	22 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)
115	d2pd4a1	Alignment	not modelled	99.7	11 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
116	c3r3sD_	Alignment	not modelled	99.7	21 PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
117	c2nwgA_	Alignment	not modelled	99.7	26 PDB header: oxidoreductase Chain: A: PDB Molecule: probable short-chain dehydrogenase; PDBTitle: short chain dehydrogenase from pseudomonas aeruginosa
118	c4nbvA_	Alignment	not modelled	99.7	23 PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from cupriavidus taiwanensis
119	c4mowB_	Alignment	not modelled	99.7	19 PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase; PDBTitle: crystal structure of a putative glucose 1-dehydrogenase from2 burkholderia cenocepacia j2315
120	c5ldgA_	Alignment	not modelled	99.7	23 PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-isopiperitenone reductase; PDBTitle: isopiperitenone reductase from mentha piperita in complex with2 isopiperitenone and nadp