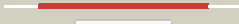



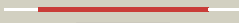





















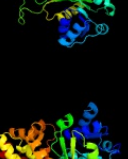



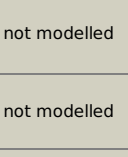


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3001c_(ilvC)_3359595_3360596
Date	Thu Aug 8 16:20:17 BST 2019
Unique Job ID	bc99a82d65dbe04b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5e4rA_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of domain-duplicated synthetic class ii ketol-acid2 reductoisomerase 2ia_kari-dd
2	c1yr1D_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: D: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: escherichia coli ketol-acid reductoisomerase
3	c4kqxB_	 Alignment		100.0	54	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: mutant slackia exigua kari ddv in complex with nad and an inhibitor
4	c6jczL_	 Alignment		100.0	31	PDB header: isomerase Chain: L: PDB Molecule: putative ketol-acid reductoisomerase 2; PDBTitle: cryo-em structure of sulfolobus solfataricus ketol-acid2 reductoisomerase (sso-kari) in complex with mg2+, nadph, and cpd at3 ph7.5
5	c6aaqjB_	 Alignment		100.0	56	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that have biocidal activity.
6	c5yegB_	 Alignment		100.0	45	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: the structure of sac-kari protein
7	c1yveK_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: K: PDB Molecule: acetoxy acid isomeroeductase; PDBTitle: acetoxy acid isomeroeductase complexed with nadph,2 magnesium and inhibitor ipoha (n-hydroxy-n-3 isopropylxamate)
8	c4ypoB_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
9	c4xdzB_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
10	c1np3B_	 Alignment		100.0	56	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetoxy acid isomeroeductase from2 pseudomonas aeruginosa
11	c4xdyB_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaean

12	c4tskA	Alignment		100.0	52	PDB header: oxidoreductase, isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
13	d1qmgA2	Alignment		100.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
14	d1np3a2	Alignment		100.0	53	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
15	d1np3a1	Alignment		100.0	59	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Acetohydroxy acid isomero-reductase (ketol-acid reductoisomerase, KARI)
16	c5t57A	Alignment		99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: semialdehyde dehydrogenase nad-binding protein; PDBTitle: crystal structure of a semialdehyde dehydrogenase nad-binding protein2 from cupriavidus necator in complex with calcium and nad
17	c3k96B	Alignment		99.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
18	c3d11B	Alignment		99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
19	c1m67A	Alignment		99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
20	c3cumA	Alignment		99.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
21	c1yj8C	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
22	c2y0dB	Alignment	not modelled	99.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
23	c3triB	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
24	c3c24A	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution
25	c1wpgB	Alignment	not modelled	99.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad+], PDBTitle: ternary complex of glycerol 3-phosphate dehydrogenase 12 with nad and dihydroxyactone
26	c4oqzA	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase
27	c3gg2B	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose dehydrogenase PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from porphyromonas2 gingivalis bound to product udp-glucuronate
28	c1vpdA	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde

						reductase2 [salmonella typhimurium lt2]
29	c3gt0A_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
30	c4a7pA_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized ugdg, udp-glucose dehydrogenase from sphingomonas2 elodea
31	c4gbjB_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
32	c4d3fB_	Alignment	not modelled	99.8	9	PDB header: oxidoreductase Chain: B: PDB Molecule: imine reductase; PDBTitle: bcsired from bacillus cereus in complex with nadph
33	c2iz1C_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
34	c1txgA_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p+); PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
35	c4wb1B_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: cals8; PDBTitle: crystal structure of cal8 from micromonospora echinospora (p294s2 mutant)
36	c3w6uA_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, nad-binding protein; PDBTitle: crystal structure of nadp bound l-serine 3-dehydrogenase from2 hyperthermophilic archaeon pyrobaculum calidifontis
37	c4dlIB_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-hydroxy-3-oxopropionate reductase; PDBTitle: crystal structure of a 2-hydroxy-3-oxopropionate reductase from2 polaromonas sp. js666
38	c2izzE_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase
39	c2ahrB_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative pyrroline carboxylate reductase; PDBTitle: crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes
40	c4e21B_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase (decarboxylating); PDBTitle: the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
41	c5bseF_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of medicago truncatula (delta)1-pyrroline-5-2 carboxylate reductase (mtp5cr)
42	c2ag8A_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
43	c4r16A_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 418aa long hypothetical udp-n-acetyl-d-mannosaminuronic PDBTitle: structure of udp-d-mannac dehydrogenase from pyrococcus horikoshii
44	c3vtfA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum
45	c2p4qA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
46	c3g0oA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
47	c1yb4A_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
48	c3fwnB_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
49	c2graA_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
50	c5y8mA_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
51	c6fzrB_	Alignment	not modelled	99.8	10	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating;

51	c0iqzB_	Alignment	not modelled	99.8	10	PDBTitle: plasmodium falciparum 6-phosphogluconate dehydrogenase in its apo2 form, in complex with its cofactor nadp+ and in complex with its3 substrate 6-phosphogluconate
52	c1pgjA_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
53	c1pgqA_	Alignment	not modelled	99.8	10	PDB header: oxidoreductase (choh(d)-nadp+(a)) Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
54	c3l6dB_	Alignment	not modelled	99.8	10	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
55	c3qhaB_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
56	c1dliA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
57	c5u5gC_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: psf3 in complex with nadp+ and 2-opp
58	c2q3eH_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
59	c2ep9A_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-gulonate 3-dehydrogenase; PDBTitle: crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
60	c4om8B_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 5-formly-3-hydroxy-2-methylpyridine 4-carboxylic2 acid (fhmpc) 5-dehydrogenase, an nad+ dependent dismutase.
61	c5je8A_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: the crystal structure of bacillus cereus 3-hydroxyisobutyrate2 dehydrogenase in complex with nad
62	c5ocmA_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nad_gly3p_dh, nad-dependent glycerol-3-phosphate PDBTitle: imine reductase from streptosporangium roseum in complex with nadp+2 and 2,2,2-trifluoroacetophenone hydrate
63	c3prjB_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
64	c1mv8A_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: gdp-mannose 6-dehydrogenase; PDBTitle: 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
65	c3ckyA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxymethyl glutarate dehydrogenase; PDBTitle: structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
66	d1n1ea2	Alignment	not modelled	99.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
67	c4wjiA_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative cyclohexadienyl dehydrogenase and adh prephenate PDBTitle: crystal structure of cyclohexadienyl dehydrogenase from sinorhizobium2 meliloti in complex with nadp and tyrosine
68	c2o3jC_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
69	c5g6sD_	Alignment	not modelled	99.8	10	PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
70	d1txga2	Alignment	not modelled	99.8	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
71	c2cvzD_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
72	c2f1kD_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
73	c4e12A_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: diketoreductase; PDBTitle: substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
74	c5a9tA_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
75	c3plnA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: crystal structure of klebsiella pneumoniae udp-glucose 6-

						dehydrogenase2 complexed with udp-glucose PDB header: oxidoreductase
76	c2rcyB_	Alignment	not modelled	99.8	15	Chain: B: PDB Molecule: pyrroline carboxylate reductase; PDBTitle: crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
77	c4j0eB_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: probable 3-hydroxyacyl-coa dehydrogenase f54c8.1; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase from2 caenorhabditis elegans in p1 space group
78	c4ezbA_	Alignment	not modelled	99.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of the conserved hypothetical protein from2 sinorhizobium meliloti 1021
79	c3pduF_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: F: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase family protein; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
80	c3k6jA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: protein f01g10.3, confirmed by transcript evidence; PDBTitle: crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
81	c1z82A_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of glycerol-3-phosphate dehydrogenase (tm0378) from2 thermotoga maritima at 2.00 a resolution
82	c3rqsB_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: hydroxyacyl-coenzyme a dehydrogenase, mitochondrial; PDBTitle: crystal structure of human l-3- hydroxyacyl-coa dehydrogenase2 (ec1.1.1.35) from mitochondria at the resolution 2.0 a, northeast3 structural genomics consortium target hr487, mitochondrial protein4 partnership
83	c3b1fA_	Alignment	not modelled	99.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
84	c6grlA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: beta-hydroxyacid dehydrogenase, 3-hydroxyisobutyrate PDBTitle: structure of imine reductase (apo form) at 1.6 a resolution from2 saccharomonospora xinjiangensis
85	c2pv7B_	Alignment	not modelled	99.8	16	PDB header: isomerase, oxidoreductase Chain: B: PDB Molecule: t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
86	c4d3sA_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from nocardioptis halophila
87	d1qmga1	Alignment	not modelled	99.8	19	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Acetohydroxy acid isomeroeductase (ketol-acid reductoisomerase, KARI)
88	c3mogA_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
89	c2uyyD_	Alignment	not modelled	99.8	13	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
90	c1m75B_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of the n208s mutant of l-3-hydroxyacyl-coa2 dehydrogenase in complex with nad and acetoacetyl-coa
91	c5uscB_	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: B: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
92	c4oqyA_	Alignment	not modelled	99.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: (s)-imine reductase; PDBTitle: streptomyces sp. gf3546 imine reductase
93	c3zhbC_	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: C: PDB Molecule: r-imine reductase; PDBTitle: r-imine reductase from streptomyces kanamyceticus in2 complex with nadp.
94	c3qsgA_	Alignment	not modelled	99.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-binding phosphogluconate dehydrogenase-like protein; PDBTitle: crystal structure of nad-binding phosphogluconate dehydrogenase-like2 protein from alicyclobacillus acidocaldarius
95	d1vpda2	Alignment	not modelled	99.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
96	c2gf2B_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
97	c3ojlA_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: cap50; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap502 from staphylococcus aureus
98	c3dciA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein;

98	c3u0jA	Alignment	not modelled	99.7	14	PDBTitle: structure of glyoxylate reductase 1 from arabidopsis (atglyr1)
99	d3cuma2	Alignment	not modelled	99.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
100	c4pzdB	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of (s)-3-hydroxybutyryl-coa dehydrogenase paah1 in2 complex with nad+
101	c5ojjA	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus terreus in complex with nadph4 and2 dibenz[c,e]zajepine
102	c1zcgA	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase
103	c6hrdD	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of m. tuberculosis fadB2 (rv0468)
104	c3dzbA	Alignment	not modelled	99.7	9	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
105	c5t8xA	Alignment	not modelled	99.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean
106	c2g5cD	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
107	c1bg6A	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; PDBTitle: crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
108	c4fgwA	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(+)] 1; PDBTitle: structure of glycerol-3-phosphate dehydrogenase, gpd1, from2 sacharomyces cerevisiae
109	c4kueA	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 clostridium butyricum
110	c3ggpA	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
111	c3pefA	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, nad-binding; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
112	c4b3hA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase/transferase Chain: A: PDB Molecule: fatty acid beta-oxidation complex alpha-chain fadB; PDBTitle: crystal structure of mycobacterium tuberculosis fatty acid2 beta-oxidation complex
113	c2wtbA	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fatty acid multifunctional protein (atmfp2); PDBTitle: arabidopsis thaliana multifunctional protein, mfp2
114	c3ktdC	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
115	c4edfC	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: dimeric hugdh, k94e
116	c6iunB	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-coa hydratase/delta(3)-cis-delta(2)-trans-enoyl-coa PDBTitle: crystal structure of enoyl-coa hydratase (ech) from ralstonia eutropha2 h16 in complex with nad
117	c2d3tB	Alignment	not modelled	99.7	14	PDB header: lyase, oxidoreductase/transferase Chain: B: PDB Molecule: fatty oxidation complex alpha subunit; PDBTitle: fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
118	c2x58B	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: the crystal structure of mfe1 liganded with coa
119	c2ew2B	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase, putative; PDBTitle: crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
120	c6huxA	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: h(2)-forming methylenetetrahydromethanopterin PDBTitle: hmdii from methanocaldococcus jannaschii reconstituted with fe-2 guanylylpyridinol (fegp) cofactor and co-crystallized with methenyl-3 tetrahydromethanopterin at 2.5 a resolution