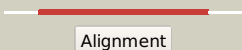







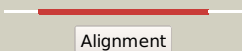

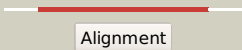



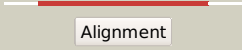









Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0468_fadB2_558898_559758
 Date Tue Jul 23 14:50:54 BST 2019
 Unique Job ID ebd9b18a120fdfe1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mogA_	 Alignment		100.0	41	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
2	c6hrdD_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of m. tuberculosis fadB2 (rv0468)
3	c2d3tB_	 Alignment		100.0	37	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
4	c6iunB_	 Alignment		100.0	35	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
5	c4b3hA_	 Alignment		100.0	33	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
6	c2x58B_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: the crystal structure of mfe1 liganded with coa
7	c1zciA_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase
8	c4kueA_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 clostridium butyricum
9	c5zqzC_	 Alignment		100.0	32	PDB header: lyase,hydrolase/transferase Chain: C: PDB Molecule: trifunctional enzyme subunit alpha, mitochondrial; PDBTitle: structure of human mitochondrial trifunctional protein, tetramer
10	c3rqsB_	 Alignment		100.0	39	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
11	c3k6jA_	 Alignment		100.0	26	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

12	c1m75B_	Alignment		100.0	41	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
13	c4pzdB_	Alignment		100.0	40	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+
14	c4om8B_	Alignment		100.0	30	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.
15	c2wtbA_	Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: fatty acid multifunctional protein (atmfp2); PDBTitle: arabidopsis thaliana multifunctional protein, mfp2
16	c1zejA_	Alignment		100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of the 3-hydroxyacyl-coa dehydrogenase (hbd-9,2 af2017) from archaeoglobus fulgidus dsm 4304 at 2.00 a resolution
17	c4e12A_	Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: diketoreductase; PDBTitle: substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
18	c4j0eB_	Alignment		100.0	38	PDB header: oxidoreductase Chain: B: PDB Molecule: probable 3-hydroxyacyl-coa dehydrogenase f54c8.1; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase from2 caenorhadbitis elegans in p1 space group
19	c2ep9A_	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: l-gulonate 3-dehydrogenase; PDBTitle: crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
20	d1wdka3	Alignment		100.0	36	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
21	d1f0ya2	Alignment	not modelled	100.0	36	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
22	c1vpdA_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
23	d3hdha1	Alignment	not modelled	99.9	48	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
24	d1f0ya1	Alignment	not modelled	99.9	52	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
25	d1wdka1	Alignment	not modelled	99.9	38	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
26	c3pduF_	Alignment	not modelled	99.9	14	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+
27	c4gbjB_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
						PDB header: oxidoreductase

28	c4xdzB_	Alignment	not modelled	99.9	11	Chain: B; PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
29	c5je8A_	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: A; PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: the crystal structure of bacillus cereus 3-hydroxyisobutyrate2 dehydrogenase in complex with nad
30	c6grlA_	Alignment	not modelled	99.9	16	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
31	d1dlja2	Alignment	not modelled	99.9	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
32	c3pefA_	Alignment	not modelled	99.9	14	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+
33	c4xdyB_	Alignment	not modelled	99.9	11	PDB header: oxidoreductase Chain: B; PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaean
34	c4oqyA_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A; PDB Molecule: (s)-imine reductase; PDBTitle: streptomyces sp. gf3546 imine reductase
35	c3ckyA_	Alignment	not modelled	99.8	15	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
36	c4wjia_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A; PDB Molecule: putative cyclohexadienyl dehydrogenase and adh prephenate PDBTitle: crystal structure of cyclohexadienyl dehydrogenase from sinorhizobium2 melliloti in complex with nadp and tyrosine
37	c5ocmA_	Alignment	not modelled	99.8	15	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
38	c4d3fB_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B; PDB Molecule: imine reductase; PDBTitle: bcsired from bacillus cereus in complex with nadph
39	c4wb1B_	Alignment	not modelled	99.8	24	PDB header: oxidoreductase Chain: B; PDB Molecule: cals8; PDBTitle: crystal structure of cal8 from micromonospora echinospora (p294s2 mutant)
40	c3d1lB_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B; PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
41	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
42	c4r16A_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A; PDB Molecule: 418aa long hypothetical udp-n-acetyl-d-mannosaminuronic PDBTitle: structure of udp-d-mannac dehydrogeanse from pyrococcus horikoshii
43	c5ojjA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A; PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus terreus in complex with nadph4 and2 dibenz[c,e]azepine
44	c4d3sA_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A; PDB Molecule: imine reductase; PDBTitle: imine reductase from nocardiosis halophila
45	c3vtfA_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A; PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaean pyrobaculum islandicum
46	c2y0dB_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B; PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
47	c3gg2B_	Alignment	not modelled	99.8	18	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
48	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 archaean pyrobaculum calidifontis
49	c3cumA_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A; PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
50	c3prjB_	Alignment	not modelled	99.8	17	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.
51	c3zhhC_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: C; PDB Molecule: r-imine reductase; PDBTitle: r-imine reductase from streptomyces kanamyceticus in2 complex with nadp.

52	c3l6dB_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
53	c3ojlA_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cap5o; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
54	c3dojA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis (atglyr1)
55	c1mv8A_	Alignment	not modelled	99.8	16	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
56	c3g79A_	Alignment	not modelled	99.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; PDBTitle: crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1
57	c5y8mA_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
58	c3g0oA_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
59	c1yb4A_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
60	c2q3eH_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
61	c5u5gC_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: psf3 in complex with nadp+ and 2-opp
62	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
63	c4a7pA_	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized ugdg, udp-glucose dehydrogenase from sphingomonas2 elodea
64	c2o3jC_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
65	c2pv7B_	Alignment	not modelled	99.8	17	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
66	d1ez4a1	Alignment	not modelled	99.8	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
67	d1wdka2	Alignment	not modelled	99.8	32	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
68	c5g6sD_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
69	d1uxja1	Alignment	not modelled	99.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
70	c2gf2B_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
71	c3dzbA_	Alignment	not modelled	99.7	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
72	c2g5cD_	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
73	c3b1fA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
74	c3qhaB_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
75	c5uscB_	Alignment	not modelled	99.7	14	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
76	c3ggpA_	Alignment	not modelled	99.7	19	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+
77	c4oqzA	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase
78	c4dllB	Alignment	not modelled	99.7	14	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
79	c5a9tA	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
80	c5t57A	Alignment	not modelled	99.7	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
81	c3triB	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
82	c4ypoB	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
83	c1np3B	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroeductase from2 pseudomonas aeruginosa
84	c3ctvA	Alignment	not modelled	99.7	25	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of central domain of 3-hydroxyacyl-coa dehydrogenase2 from archaeoglobus fulgidus
85	c1dliA	Alignment	not modelled	99.7	16	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
86	c1m67A	Alignment	not modelled	99.7	17	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
87	d1ojuA1	Alignment	not modelled	99.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
88	c2cvzD	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
89	c2ahrB	Alignment	not modelled	99.7	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
90	c3k96B	Alignment	not modelled	99.7	15	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
91	d1mv8a2	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
92	c4edfC	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: dimeric hugdh, k94e
93	c2f1kD	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogonate dehydrogenase
94	c6fqzB	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: plasmodium falciparum 6-phosphogluconate dehydrogenase in its apo2 form, in complex with its cofactor nadp+ and in complex with its3 substrate 6-phosphogluconate
95	c6aqjB	Alignment	not modelled	99.7	13	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 that3 have biocidal activity.
96	c2ag8A	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
97	c5bseF	Alignment	not modelled	99.7	14	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)
98	c3gt0A	Alignment	not modelled	99.7	13	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
99	c4hujB	Alignment	not modelled	99.6	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein sma0349 from sinorhizobium2 meliloti
100	c2i76B	Alignment	not modelled	99.6	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein tm1727 from thermotoga

						maritima
101	c2iz1C_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
102	c1pgjA_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
103	d1guza1	Alignment	not modelled	99.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
104	d2ahra2	Alignment	not modelled	99.6	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
105	c3dttA_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp oxidoreductase; PDBTitle: crystal structure of a putative f420 dependent nadp-reductase2 (arth_0613) from arthrobacter sp. fb24 at 1.70 a resolution
106	d1ldma1	Alignment	not modelled	99.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
107	c3hn2A_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
108	d3cuma2	Alignment	not modelled	99.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
109	d2g5ca2	Alignment	not modelled	99.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
110	d1gv0a1	Alignment	not modelled	99.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
111	c3ktdC_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cg10226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
112	d1ldna1	Alignment	not modelled	99.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
113	d1yqga2	Alignment	not modelled	99.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
114	c3fwnB_	Alignment	not modelled	99.6	13	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
115	c1i36A_	Alignment	not modelled	99.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth1747; PDBTitle: structure of conserved protein mth1747 of unknown function reveals2 structural similarity with 3-hydroxyacid dehydrogenases
116	c2p4qA_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
117	d9dta1	Alignment	not modelled	99.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
118	d2f1ka2	Alignment	not modelled	99.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
119	d1t2da1	Alignment	not modelled	99.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
120	d1n1ea2	Alignment	not modelled	99.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain