













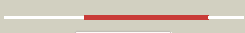









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1844c_gnd1_2093738_2095195
Date	Fri Aug 2 13:30:45 BST 2019
Unique Job ID	49203ba72341c8db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1pgqA_	 Alignment		100.0	52	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
2	c2iz1C_	 Alignment		100.0	51	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
3	c6fqzB_	 Alignment		100.0	41	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
4	c3fwnB_	 Alignment		100.0	54	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
5	c2p4qA_	 Alignment		100.0	49	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
6	c1pgjA_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
7	d2pgda1	 Alignment		100.0	56	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
8	d1pgja1	 Alignment		100.0	30	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
9	c4e21B_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase (decarboxylating); PDBTitle: the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
10	c4dllB_	 Alignment		100.0	21	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
11	c2cvzD_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8

12	c1yb4A_	Alignment		100.0	23	PDB header: oxidoreductase Chain: A; PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
13	c1vpdA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A; PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
14	c4ezbA_	Alignment		100.0	16	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
15	c3cumA_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A; PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
16	c5u5gC_	Alignment		100.0	26	PDB header: oxidoreductase Chain: C; PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: psf3 in complex with nadp+ and 2-opp
17	c3g0oA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
18	c3w6uA_	Alignment		100.0	23	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
19	d2pgda2	Alignment		100.0	44	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
20	c4gjbB_	Alignment		100.0	18	PDB header: oxidoreductase Chain: B; PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
21	c3ckyA_	Alignment	not modelled	100.0	24	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
22	c3qsgA_	Alignment	not modelled	100.0	13	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
23	c3l6dB_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B; PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
24	c3pefA_	Alignment	not modelled	100.0	24	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+
25	c5je8A_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: the crystal structure of bacillus cereus 3-hydroxyisobutyrate2 dehydrogenase in complex with nad
26	c3pduF_	Alignment	not modelled	100.0	27	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	c3dciA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A; PDB Molecule: dehydrogenase-like protein;

27	c3u9jA	Alignment	not modelled	100.0	41	PDBTitle: structure of glyoxylate reductase 1 from arabidopsis (atglyr1) 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
28	c1i36A	Alignment	not modelled	100.0	17	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
29	c2uyyD	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
30	d1pgja2	Alignment	not modelled	100.0	45	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthbadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
31	c5y8mA	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
32	d1vpda2	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
33	c5g6sD	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
34	c5a9tA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
35	c2gf2B	Alignment	not modelled	100.0	21	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
36	c6grlA	Alignment	not modelled	100.0	19	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
37	c5ocmA	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
38	d2cvza2	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: imine reductase; PDBTitle: bcsired from bacillus cereus in complex with nadph
39	c4d3fB	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
40	c3qhaB	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: r-imine reductase; PDBTitle: r-imine reductase from streptomyces kanamyceticus in2 complex with nadp.
41	c3zhbC	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase
42	c4oqzA	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from nocardiosis halophila
43	c4d3sA	Alignment	not modelled	100.0	18	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	c5ojlA	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
45	d3cuma2	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: (s)-imine reductase; PDBTitle: streptomyces sp. gf3546 imine reductase
46	c4oqyA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cap50; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap502 from staphylococcus aureus
47	c3ojlA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 418aa long hypothetical udp-n-acetyl-d-mannosaminuronic PDBTitle: structure of udp-d-mannac dehdrogeanse from pyrococcus horikoshii
48	c4r16A	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized udgd, udp-glucose dehydrogenase from sphingomonas2 elodea
49	c4a7pA	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: cals8; PDBTitle: crystal structure of cals8 from micromonospora echinospora (p294s2 mutant)
50	c4wb1B	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum
51	c3vtfA	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-

52	c3gg2B_	Alignment	not modelled	99.9	16	mannose dehydrogenase PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from porphyromonas2 gingivalis bound to product udp-glucuronate
53	c2y0dB_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
54	c4edfC_	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: dimeric hugdh, k94e
55	c3plnA_	Alignment	not modelled	99.9	16	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
56	c1m67A_	Alignment	not modelled	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
57	c1mv8A_	Alignment	not modelled	99.9	15	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
58	c2o3jC_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
59	c2q3eH_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
60	c3prjB_	Alignment	not modelled	99.9	16	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.
61	c3g79A_	Alignment	not modelled	99.9	17	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
62	c3k96B_	Alignment	not modelled	99.9	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
63	c5t57A_	Alignment	not modelled	99.9	16	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
64	c1dliA_	Alignment	not modelled	99.9	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
65	d1i36a2	Alignment	not modelled	99.9	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
66	c2pv7B_	Alignment	not modelled	99.9	13	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
67	c3d1lB_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
68	c6c4jA_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: ligand bound full length hugdh with a104l substitution
69	c2vzC_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: C: PDB Molecule: metalloreductase steap4; PDBTitle: rat steap4 oxidoreductase domain complexed with nadp
70	c4wjia_	Alignment	not modelled	99.9	21	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
71	c2f1kD_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis aroenate dehydrogenase
72	c3b1fA_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
73	c1np3B_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
74	c2graA_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
75	c4kqxB_	Alignment	not modelled	99.8	10	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
						PDB header: oxidoreductase

76	c2lzzE	Alignment	not modelled	99.8	11	Chain: E; PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase
77	c3hn2A	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
78	c2rafC	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: C; PDB Molecule: putative dinucleotide-binding oxidoreductase; PDBTitle: crystal structure of putative dinucleotide-binding oxidoreductase2 (np_786167.1) from lactobacillus plantarum at 1.60 a resolution
79	c3dzbA	Alignment	not modelled	99.8	17	PDB header: biosynthetic protein Chain: A; PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
80	c2g5cD	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: D; PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
81	c4xdzB	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: B; PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
82	c3triB	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B; PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
83	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
84	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)
85	c4o19A	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A; PDB Molecule: putative 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of putative 2-dehydropantoate 2-reductase pane from2 mycobacterium tuberculosis complexed with nadp and oxamate
86	d2pv7a2	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
87	c5n2iC	Alignment	not modelled	99.8	23	PDB header: oxidoreductase Chain: C; PDB Molecule: reduced coenzyme f420:nadp oxidoreductase; PDBTitle: f420:nadph oxidoreductase from thermobifida fusca with nadp+ bound
88	c1txgA	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A; PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
89	c3gt0A	Alignment	not modelled	99.8	8	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
90	c1z82A	Alignment	not modelled	99.8	14	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
91	c3hwrA	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution
92	c5bseF	Alignment	not modelled	99.8	16	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)
93	c3wfiD	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: D; PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: the complex structure of d-mandelate dehydrogenase with nadh
94	c1ks9A	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
95	c4xdyB	Alignment	not modelled	99.8	10	PDB header: oxidoreductase Chain: B; PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaean
96	c5zikC	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: C; PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of ketopantoate reductase from pseudomonas2 aeruginosa
97	c2i76B	Alignment	not modelled	99.8	14	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein tm1727 from thermotoga maritima
98	c4hujB	Alignment	not modelled	99.8	12	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein sma0349 from sinorhizobium2 meliloti
99	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 caenorhadbitis elegans in p1 space group PDB header: oxidoreductase

100	c2ofpB	Alignment	not modelled	99.8	16	Chain: B: PDB Molecule: ketopantoate reductase; PDBTitle: crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
101	c4e12A	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: diketoreductase; PDBTitle: substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
102	c5t8xA	Alignment	not modelled	99.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean
103	c1bg6A	Alignment	not modelled	99.7	13	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
104	c4ypoB	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
105	c4tskA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase, isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
106	c3ktdC	Alignment	not modelled	99.7	15	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
107	c2ew2B	Alignment	not modelled	99.7	15	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
108	c3ggpA	Alignment	not modelled	99.7	15	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+
109	c5ayvB	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of archaeal ketopantoate reductase complexed with2 coenzyme a and 2-oxopantoate
110	d2g5ca2	Alignment	not modelled	99.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
111	c2ag8A	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
112	c2vq3B	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: metalloreductase steap3; PDBTitle: crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
113	d1jaya	Alignment	not modelled	99.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
114	c1yj8C	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
115	c3g17H	Alignment	not modelled	99.7	15	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: similar to 2-dehydropantoate 2-reductase; PDBTitle: structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
116	d2i76a2	Alignment	not modelled	99.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
117	c3dttA	Alignment	not modelled	99.7	19	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
118	c5uscB	Alignment	not modelled	99.6	16	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
119	d1mv8a2	Alignment	not modelled	99.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
120	d2f1ka2	Alignment	not modelled	99.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain