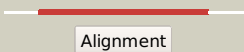

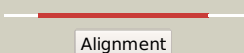

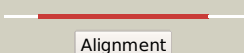
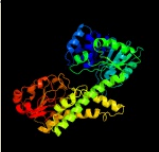
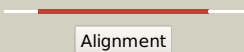


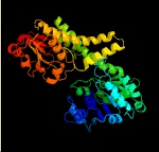
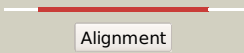

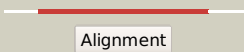

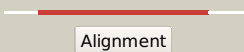

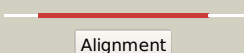



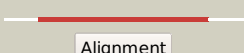



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0322_(udgA)_389260_390591
Date	Tue Jul 23 14:50:39 BST 2019
Unique Job ID	5191083d38c16dd6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2q3eH_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
2	c3prjB_	 Alignment		100.0	32	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.
3	c2y0dB_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
4	c4a7pA_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized udgd, udp-glucose dehydrogenase from sphingomonas2 elodea
5	c2o3jC_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
6	c3g79A_	 Alignment		100.0	28	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
7	c4wb1B_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: cals8; PDBTitle: crystal structure of cal8 from micromonospora echinospora (p294s2 mutant)
8	c3gg2B_	 Alignment		100.0	37	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
9	c3vtfA_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum
10	c4r16A_	 Alignment		100.0	29	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
11	c6c4jA_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: ligand bound full length hugdh with a104l substitution

12	c4edfC_	Alignment		100.0	33	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: dimeric hugdh, k94e
13	c3ojlA_	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: cap5o; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
14	c1mv8A_	Alignment		100.0	30	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
15	c1dliA_	Alignment		100.0	27	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
16	c3plnA_	Alignment		100.0	29	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
17	c1vpdA_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
18	c3w6uA_	Alignment		100.0	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
19	c4dllB_	Alignment		100.0	19	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
20	c3cumA_	Alignment		100.0	17	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	c2cvzD_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
22	c3ckyA_	Alignment	not modelled	100.0	16	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
23	c1yb4A_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
24	c3g0oA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
25	c4e21B_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase (decarboxylating); PDBTitle: the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
26	d1mv8a2	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
27	c5u5gC_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: psf3 in complex with nadp+ and 2-opp
28	c4ezbA_	Alignment	not modelled	100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of the conserved hypothetical protein

					from2 sinorhizobium melliloti 1021
29	c4gjbB	Alignment	not modelled	100.0	20 PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
30	d1dlja2	Alignment	not modelled	100.0	31 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
31	d1mv8a1	Alignment	not modelled	100.0	32 Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
32	c1pgjA	Alignment	not modelled	100.0	19 PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
33	d1dlja1	Alignment	not modelled	100.0	30 Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
34	c3fwnB	Alignment	not modelled	99.9	17 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
35	c2p4qA	Alignment	not modelled	99.9	16 PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
36	c3qhaB	Alignment	not modelled	99.9	21 PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
37	c5y8mA	Alignment	not modelled	99.9	20 PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
38	c1pgqA	Alignment	not modelled	99.9	18 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
39	c3qsgA	Alignment	not modelled	99.9	16 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
40	c5je8A	Alignment	not modelled	99.9	15 PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: the crystal structure of bacillus cereus 3-hydroxyisobutyrate2 dehydrogenase in complex with nad
41	c2iz1C	Alignment	not modelled	99.9	15 PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
42	c6fqzB	Alignment	not modelled	99.9	9 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
43	c4tskA	Alignment	not modelled	99.9	13 PDB header: oxidoreductase,isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
44	c2uyyD	Alignment	not modelled	99.9	15 PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
45	c3dojA	Alignment	not modelled	99.9	13 PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis (atglyr1)
46	c3pduF	Alignment	not modelled	99.9	18 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+
47	c2gf2B	Alignment	not modelled	99.9	18 PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
48	c3l6dB	Alignment	not modelled	99.9	18 PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
49	c3pefA	Alignment	not modelled	99.9	19 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+
50	c1m67A	Alignment	not modelled	99.9	18 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 PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
51	c5a9tA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
52	c5g6sD_	Alignment	not modelled	99.9	14	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
53	c5ocmA_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: (s)-imine reductase; PDBTitle: streptomyces sp. gf3546 imine reductase
54	c4oqyA_	Alignment	not modelled	99.9	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: UDP-glucose/GDP-mannose dehydrogenase C-terminal domain Family: UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
55	d1mv8a3	Alignment	not modelled	99.9	19	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
56	c1bg6A_	Alignment	not modelled	99.9	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
57	c1i36A_	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: imine reductase; PDBTitle: bcsired from bacillus cereus in complex with nadph
58	c4d3fB_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: C: PDB Molecule: r-imine reductase; PDBTitle: r-imine reductase from streptomyces kanamyceticus in2 complex with nadp.
59	c3zhhC_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from nocardioptis halophila
60	c4d3sA_	Alignment	not modelled	99.9	14	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
61	c6grlA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase
62	c4oqzA_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus terreus in complex with nadph4 and2 dibenz[c,e]azepine
63	c5ojlA_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
64	c1vj8C_	Alignment	not modelled	99.8	10	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
65	c1txgA_	Alignment	not modelled	99.8	19	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
66	c2ew2B_	Alignment	not modelled	99.8	14	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
67	c3k96B_	Alignment	not modelled	99.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
68	d2pgda2	Alignment	not modelled	99.8	16	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
69	c1wpgB_	Alignment	not modelled	99.8	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
70	d1pgja2	Alignment	not modelled	99.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
71	d1vpda2	Alignment	not modelled	99.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
72	c4e12A_	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: diketoreductase; PDBTitle: substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
73	c5zikC_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: C: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of ketopantoate reductase from pseudomonas2 aeruginosa
74	d3cuma2	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

75	c5ayvB	Alignment	not modelled	99.7	12	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
76	c3ghyA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
77	c2ofpB	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ketopantoate reductase; PDBTitle: crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
78	d1dlja3	Alignment	not modelled	99.7	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: UDP-glucose/GDP-mannose dehydrogenase C-terminal domain Family: UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
79	c2ep9A	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l-gulonate 3-dehydrogenase; PDBTitle: crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
80	c3hn2A	Alignment	not modelled	99.7	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
81	c3d1lB	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
82	c4wjia	Alignment	not modelled	99.7	11	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
83	c2f1kD	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
84	c3wfid	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: the complex structure of d-mandelate dehydrogenase with nadh
85	c1ks9A	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
86	c1z82A	Alignment	not modelled	99.7	18	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
87	d2cvza2	Alignment	not modelled	99.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
88	c3hwrA	Alignment	not modelled	99.7	16	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
89	c6hrdD	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of m. tuberculosis fadB2 (rv0468)
90	c4ol9A	Alignment	not modelled	99.6	18	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
91	c5t57A	Alignment	not modelled	99.6	18	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
92	c2g5cD	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
93	c5uscB	Alignment	not modelled	99.6	15	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
94	d1n1ea2	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
95	c5n2iC	Alignment	not modelled	99.6	26	PDB header: oxidoreductase Chain: C: PDB Molecule: reduced coenzyme f420:nadp oxidoreductase; PDBTitle: f420:nadph oxidoreductase from thermobifida fusca with nadp+ bound
96	d2f1ka2	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
97	d1f0ya2	Alignment	not modelled	99.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
98	c3egoB	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of probable 2-dehydropantoate 2-reductase pane from2 bacillus subtilis
99	c3triB	Alignment	not modelled	99.6	10	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase;

99	c3ubB_	Alignment	not modelled	99.6	19	PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
100	d1i36a2	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
101	c1m75B_	Alignment	not modelled	99.5	20	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
102	c2izzE_	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase
103	c3g17H_	Alignment	not modelled	99.5	14	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
104	c3dzba_	Alignment	not modelled	99.5	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
105	c4j0eB_	Alignment	not modelled	99.5	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
106	c4fgwA_	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(+)] 1; PDBTitle: structure of glycerol-3-phosphate dehydrogenase, gpd1, from2 saccharomyces cerevisiae
107	c2pv7B_	Alignment	not modelled	99.5	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
108	c4xdyB_	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaeon
109	c5bseF_	Alignment	not modelled	99.5	15	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)
110	c2graA_	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
111	c5t8xA_	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean
112	c4om8B_	Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 5-formyl-3-hydroxy-2-methylpyridine 4-carboxylic2 acid (fhmpc) 5-dehydrogenase, an nad+ dependent dismutase.
113	c3b1fA_	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
114	c3rqsB_	Alignment	not modelled	99.5	19	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
115	d1bg6a2	Alignment	not modelled	99.5	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
116	d1jaya_	Alignment	not modelled	99.5	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
117	c4xdzB_	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
118	c3ggpA_	Alignment	not modelled	99.4	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+
119	c3k6jA_	Alignment	not modelled	99.4	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
120	c3dttA_	Alignment	not modelled	99.4	21	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