

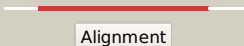

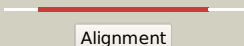







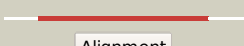









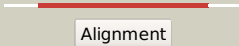

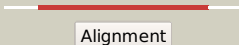

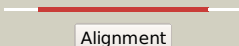



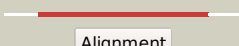

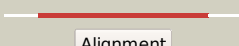

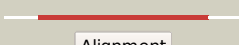







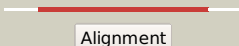






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1122_(gnd2)_1245134_1246156
Date	Wed Jul 31 22:05:20 BST 2019
Unique Job ID	1d94e4b36999090f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fwnB_	 Alignment		100.0	29	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
2	c1pgjA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A; PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan parasite t. brucei
3	c2p4qA_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: A; PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
4	c1pggA_	 Alignment		100.0	32	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
5	c2iz1C_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: C; PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
6	c6fqzB_	 Alignment		100.0	30	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
7	c4e21B_	 Alignment		100.0	56	PDB header: oxidoreductase Chain: B; PDB Molecule: 6-phosphogluconate dehydrogenase (decarboxylating); PDBTitle: the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
8	c2cvzD_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: D; PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
9	c1yb4A_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
10	c4dllB_	 Alignment		100.0	20	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	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

12	c1vpdA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
13	c5u5gC_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: psf3 in complex with nadp+ and 2-opp
14	c4ezbA_	 Alignment		100.0	20	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	c3g0aA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
16	c3ckyA_	 Alignment		100.0	23	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
17	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
18	c4gjbB_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
19	c5je8A_	 Alignment		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
20	c5y8mA_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
21	c3qhaB_	 Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
22	c3qsgA_	 Alignment	not modelled	100.0	19	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	c2gf2B_	 Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
24	c3l6dB_	 Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
25	c3dojA_	 Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis (atglyr1)
26	c3pefA_	 Alignment	not modelled	100.0	21	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+
27	c3pduF_	 Alignment	not modelled	100.0	21	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+
28	c4wb1B_	Alignment	not modelled	100.0	22 PDB header: oxidoreductase Chain: B: PDB Molecule: cals8; PDBTitle: crystal structure of cal8 from micromonospora echinospora (p294s2 mutant)
29	c2uyvD_	Alignment	not modelled	100.0	18 PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
30	c1m67A_	Alignment	not modelled	100.0	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
31	c5a9tA_	Alignment	not modelled	100.0	15 PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
32	c5g6sD_	Alignment	not modelled	100.0	11 PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
33	c1mv8A_	Alignment	not modelled	100.0	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
34	c2y0dB_	Alignment	not modelled	100.0	15 PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
35	c3k96B_	Alignment	not modelled	100.0	12 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
36	c1i36A_	Alignment	not modelled	100.0	18 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
37	c3vtfA_	Alignment	not modelled	100.0	15 PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum
38	d2pgda2	Alignment	not modelled	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
39	c3gg2B_	Alignment	not modelled	100.0	13 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
40	c4a7pA_	Alignment	not modelled	100.0	14 PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized ugdg, udp-glucose dehydrogenase from sphingomonas2 elodea
41	c3zhbC_	Alignment	not modelled	100.0	17 PDB header: oxidoreductase Chain: C: PDB Molecule: r-imine reductase; PDBTitle: r-imine reductase from streptomyces kanamyceticus in2 complex with nadp.
42	c5ojlA_	Alignment	not modelled	100.0	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
43	c4r16A_	Alignment	not modelled	100.0	20 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
44	c4d3sA_	Alignment	not modelled	100.0	15 PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from nocardiosis halophila
45	c6grlA_	Alignment	not modelled	100.0	17 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
46	c5ocmA_	Alignment	not modelled	100.0	18 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
47	d1pgja2	Alignment	not modelled	100.0	29 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
48	c4oqzA_	Alignment	not modelled	100.0	14 PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase
49	c4oqyA_	Alignment	not modelled	100.0	17 PDB header: oxidoreductase Chain: A: PDB Molecule: (s)-imine reductase; PDBTitle: streptomyces sp. gf3546 imine reductase
50	c4d3fB_	Alignment	not modelled	100.0	13 PDB header: oxidoreductase Chain: B: PDB Molecule: imine reductase; PDBTitle: bcsired from bacillus cereus in complex with nadph
51	c3ojlA_	Alignment	not modelled	100.0	16 PDB header: oxidoreductase Chain: A: PDB Molecule: cap5o; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
52	c2g3eH_	Alignment	not modelled	100.0	13 PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase;

52	c2qpe1_	Alignment	not modelled	100.0	13	PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose PDB header: oxidoreductase
53	c3prjB_	Alignment	not modelled	100.0	13	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.
54	c1yj8C_	Alignment	not modelled	100.0	10	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
55	d1vpda2	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
56	c1dliA_	Alignment	not modelled	100.0	11	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	c2o3jC_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
58	c4edfC_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: dimeric hugdh, k94e
59	c1txgA_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p+); PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
60	d2cvza2	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
61	c3plnA_	Alignment	not modelled	100.0	14	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
62	c1wpqB_	Alignment	not modelled	100.0	12	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
63	c3g79A_	Alignment	not modelled	100.0	11	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
64	c1z82A_	Alignment	not modelled	100.0	10	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
65	c4kqxB_	Alignment	not modelled	100.0	14	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
66	d3cuma2	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
67	c1bg6A_	Alignment	not modelled	99.9	14	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
68	c4xdzB_	Alignment	not modelled	99.9	10	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
69	c6c4jA_	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: ligand bound full length hugdh with a104l substitution
70	c5t57A_	Alignment	not modelled	99.9	14	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
71	c6aqjB_	Alignment	not modelled	99.9	14	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.
72	c1np3B_	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetoxy acid isomeroreductase from2 pseudomonas aeruginosa
73	c3wfdD_	Alignment	not modelled	99.9	11	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: the complex structure of d-mandelate dehydrogenase with nadh
74	c3d1lB_	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
75	d1i36a2	Alignment	not modelled	99.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
76	c5zikC_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: C: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of ketopantoate reductase from

						pseudomonas2 aeruginosa PDB header: oxidoreductase
77	c4xdyB_	Alignment	not modelled	99.9	13	Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaean
78	c5n2iC_	Alignment	not modelled	99.9	22	PDB header: oxidoreductase Chain: C: PDB Molecule: reduced coenzyme f420:nadp oxidoreductase; PDBTitle: f420:nadph oxidoreductase from thermobifida fusca with nadp+ bound
79	c2izzE_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase
80	c5bseF_	Alignment	not modelled	99.9	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)
81	d2pgda1	Alignment	not modelled	99.9	29	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
82	c2ep9A_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: l-gulonate 3-dehydrogenase; PDBTitle: crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
83	c4oI9A_	Alignment	not modelled	99.9	14	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
84	c2graA_	Alignment	not modelled	99.9	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
85	c3hn2A_	Alignment	not modelled	99.9	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
86	c2ew2B_	Alignment	not modelled	99.9	12	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
87	c4fgwA_	Alignment	not modelled	99.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(+)] 1; PDBTitle: structure of glycerol-3-phosphate dehydrogenase, gpd1, from2 sacharomyces cerevisiae
88	c3g17H_	Alignment	not modelled	99.9	13	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
89	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
90	c5ayvB_	Alignment	not modelled	99.9	14	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
91	c3hwrA_	Alignment	not modelled	99.9	14	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	c2ahrB_	Alignment	not modelled	99.9	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
93	c4wjiA_	Alignment	not modelled	99.9	20	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
94	c1ks9A_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
95	c2f1kD_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
96	c4ypoB_	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
97	c2ofpB_	Alignment	not modelled	99.9	16	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
98	c3triB_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
99	c5yeqB_	Alignment	not modelled	99.9	11	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: the structure of sac-kari protein
						PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase;

100	c3gt0A_	Alignment	not modelled	99.9	13	PDBTitle: crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
101	d1mv8a2	Alignment	not modelled	99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
102	d1pgja1	Alignment	not modelled	99.8	32	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
103	c3ghyA_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
104	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
105	d1jaya_	Alignment	not modelled	99.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
106	c3dzbA_	Alignment	not modelled	99.8	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
107	c2g5cD_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
108	c2ag8A_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
109	d2f1ka2	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
110	c3b1fA_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
111	c2yzC_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: C: PDB Molecule: metalloreductase steap4; PDBTitle: rat steap4 oxidoreductase domain complexed with nadp
112	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
113	d1n1ea2	Alignment	not modelled	99.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
114	d1txga2	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
115	d2pv7a2	Alignment	not modelled	99.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
116	c3dttA_	Alignment	not modelled	99.8	17	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
117	c4e12A_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: diketoreductase; PDBTitle: substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
118	c2rcyB_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline carboxylate reductase; PDBTitle: crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
119	c5t8xA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean
120	c2i76B_	Alignment	not modelled	99.8	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein tm1727 from thermotoga maritima