

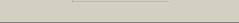
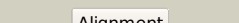
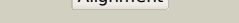
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mogA_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from <i>Escherichia coli</i> K12 substr. mg1655
2	c2x58B_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: the crystal structure of mfe1 liganded with coa
3	c1zcjA_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase
4	c2d3tB_	 Alignment		100.0	35	PDB header: lyase, oxidoreductase/transferase Chain: B: PDB Molecule: fatty acid oxidation complex alpha subunit; PDBTitle: fatty acid beta-oxidation multienzyme complex from <i>Pseudomonas fragi</i> , form v
5	c4b3hA_	 Alignment		100.0	29	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	c2wtbA_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: fatty acid multifunctional protein (atmfp2); PDBTitle: arabidopsis thaliana multifunctional protein, mfp2
7	c3k6jA_	 Alignment		100.0	24	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 <i>C. elegans</i>
8	c3rqsB_	 Alignment		100.0	40	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
9	c4kueA_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from <i>Clostridium butyricum</i>
10	c1m75B_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa
11	c1zejA_	 Alignment		100.0	33	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 <i>Archaeoglobus fulgidus</i> DSM 4304 at 2.00 a resolution

12	c4e12A_	Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: diketoreductase; PDBTitle: substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
13	c4j0eB_	Alignment		100.0	39	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
14	c2ep9A_	Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: l-gulonate 3-dehydrogenase; PDBTitle: crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
15	d1wdka3	Alignment		100.0	42	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
16	d1f0ya2	Alignment		100.0	40	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
17	d3hdha1	Alignment		100.0	45	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
18	d1f0ya1	Alignment		100.0	45	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
19	d1wdka1	Alignment		99.9	33	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
20	c1vpdA_	Alignment		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]
21	d1dlja2	Alignment	not modelled	99.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
22	c4wjiA_	Alignment	not modelled	99.9	22	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
23	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
24	c3pduF_	Alignment	not modelled	99.9	16	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+
25	d1wdka2	Alignment	not modelled	99.9	24	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HCDH C-domain-like
26	c4gbjB_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
27	d1ez4a1	Alignment	not modelled	99.8	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
						PDB header: oxidoreductase

28	c4oqyA_	Alignment	not modelled	99.8	12	Chain: A: PDB Molecule: (s)-imine reductase; PDBTitle: streptomyces sp. gf3546 imine reductase
29	c3ckyA_	Alignment	not modelled	99.8	14	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
30	c2g5cD_	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
31	c3pefA_	Alignment	not modelled	99.8	13	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+
32	c3dzbA_	Alignment	not modelled	99.8	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
33	c3ggpA_	Alignment	not modelled	99.8	20	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+
34	c3zhbC_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: C: PDB Molecule: r-imine reductase; PDBTitle: r-imine reductase from streptomyces kanamyceticus in2 complex with nadp.
35	c2pv7B_	Alignment	not modelled	99.8	18	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
36	c1np3B_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroeductase from2 pseudomonas aeruginosa
37	c3ctvA_	Alignment	not modelled	99.8	35	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of central domain of 3-hydroxyacyl-coa2 dehydrogenase from archaeoglobus fulgidus
38	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
39	c2uyyD_	Alignment	not modelled	99.7	13	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
40	c3l6dB_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
41	d2g5ca2	Alignment	not modelled	99.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
42	d1uxja1	Alignment	not modelled	99.7	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
43	c3dojA_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
44	c3cumA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
45	c2f1kD_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis aroenate dehydrogenase
46	c3w6uA_	Alignment	not modelled	99.7	20	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
47	c3g0oA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
48	c2gf2B_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
49	d2b0ja2	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
50	d1ldma1	Alignment	not modelled	99.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
51	d2ahra2	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
52	c2ahrB_	Alignment	not modelled	99.7	16	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
53	c2i76B_	Alignment	not modelled	99.7	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein tm1727 from thermotoga maritima
54	d1mv8a2	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
55	d2f1ka2	Alignment	not modelled	99.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
56	c1yb4A_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from <i>Salmonella typhimurium</i> lt2
57	d1l1ca1	Alignment	not modelled	99.6	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
58	d1ojua1	Alignment	not modelled	99.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
59	c2y0dB_	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
60	d1ldna1	Alignment	not modelled	99.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
61	c4oqzA_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase
62	c3k96B_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from <i>Coxiella burnetii</i>
63	d1pzga1	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
64	d9ldta1	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
65	d1yqga2	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
66	c3triB_	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from <i>Coxiella burnetii</i>
67	c1mv8A_	Alignment	not modelled	99.6	17	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 <i>Pseudomonas aeruginosa</i>
68	c4hujB_	Alignment	not modelled	99.6	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein sma0349 from <i>Sinorhizobium meliloti</i>
69	c4wb1B_	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: cals8; PDBTitle: crystal structure of cals8 from <i>Micromonospora echinospora</i> (p294s2 mutant)
70	d1guza1	Alignment	not modelled	99.6	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
71	d1t2da1	Alignment	not modelled	99.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
72	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 (arh_0613) from <i>Arthrobacter</i> sp. fb24 at 1.70 a resolution
73	c3qt0A_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of pyrroline 5-carboxylate reductase from <i>Bacillus cereus</i> . northeast structural genomics consortium target bcr38b
74	c3ojlA_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: cap5o; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from <i>Staphylococcus aureus</i>
75	c3qhaB_	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from <i>Mycobacterium avium</i> 104
76	c3ktdC_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from <i>Corynebacterium glutamicum</i> atcc 13032 at 2.60 a resolution
77	c2ag8A_	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from <i>Neisseria meningitidis</i>
						PDB header: oxidoreductase Chain: B: PDB Molecule: suqar dehydrogenase, udp-glucose/adp-

78	c3gg2B_	Alignment	not modelled	99.6	18	mannose PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
79	d1i10a1	Alignment	not modelled	99.6	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
80	c3vtfA_	Alignment	not modelled	99.5	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
81	d1llda1	Alignment	not modelled	99.5	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
82	d1gv0a1	Alignment	not modelled	99.5	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
83	d1y6ja1	Alignment	not modelled	99.5	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
84	c1m67A_	Alignment	not modelled	99.5	14	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
85	d1i0za1	Alignment	not modelled	99.5	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
86	c3prjB_	Alignment	not modelled	99.5	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.
87	c2vq3B_	Alignment	not modelled	99.5	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
88	d3cuma2	Alignment	not modelled	99.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
89	c3hn2A_	Alignment	not modelled	99.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
90	c3plnA_	Alignment	not modelled	99.5	18	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
91	c4dllB_	Alignment	not modelled	99.5	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
92	c3c24A_	Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution
93	c2vhyB_	Alignment	not modelled	99.5	24	PDB header: oxidoreductase Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
94	c2izzE_	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate2 reductase
95	d1n1ea2	Alignment	not modelled	99.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
96	c4a7pA_	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized ugdg, udp-glucose dehydrogenase from2 sphingomonas elodea
97	d2ldxa1	Alignment	not modelled	99.4	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
98	c3g79A_	Alignment	not modelled	99.4	18	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
99	c2o3jC_	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
100	c2q3eH_	Alignment	not modelled	99.4	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
101	c4tskA_	Alignment	not modelled	99.4	19	PDB header: oxidoreductase,isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
102	d2pgda2	Alignment	not modelled	99.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
103	c2cvzD_	Alignment	not modelled	99.4	12	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8

104	c1wpqB_	 Alignment	not modelled	99.4	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
105	d1vpda2	 Alignment	not modelled	99.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
106	d1np3a2	 Alignment	not modelled	99.3	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
107	d5ldha1	 Alignment	not modelled	99.3	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
108	d1pgja2	 Alignment	not modelled	99.3	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
109	d1hyha1	 Alignment	not modelled	99.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
110	c1pgjA_	 Alignment	not modelled	99.3	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
111	d1bg6a2	 Alignment	not modelled	99.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
112	c2graA_	 Alignment	not modelled	99.3	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
113	c1i36A_	 Alignment	not modelled	99.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth1747; PDBTitle: structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
114	c1dliA_	 Alignment	not modelled	99.3	15	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
115	c2iz1C_	 Alignment	not modelled	99.3	14	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
116	d1jaya_	 Alignment	not modelled	99.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
117	d2pv7a2	 Alignment	not modelled	99.3	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
118	c4ol9A_	 Alignment	not modelled	99.2	16	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
119	c1ks9A_	 Alignment	not modelled	99.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
120	c2p4qA_	 Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae