

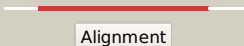

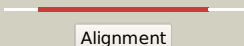







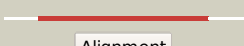











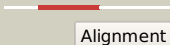

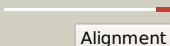

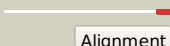





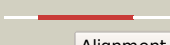







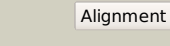
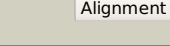

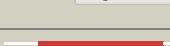




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2870c_dxr_3181780_3183021
Date	Wed Aug 7 12:50:54 BST 2019
Unique Job ID	e4b6aebb543b69d9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jcyA_	 Alignment		100.0	99	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium tuberculosis
2	c5kqoA_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from vibrio vulnificus
3	c3au9A_	 Alignment		100.0	36	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of the quaternary complex-1 of an isomerase
4	c2eghA_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
5	c4zn6B_	 Alignment		100.0	41	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: x-ray crystal structure of 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase (ispc) from acinetobacter baumannii
6	c1k5hB_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose-5-phosphate reductoisomerase
7	c1r0lD_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: D: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph
8	c3a14B_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of dxr from thermotoga maritima, in complex with2 nadph
9	d1q0qa3	 Alignment		100.0	48	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
10	d1r0ka3	 Alignment		100.0	48	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
11	d1r0ka2	 Alignment		100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

12	d1q0qa2	 Alignment		100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
13	d1t1ra2	 Alignment		100.0	40	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
14	d1q0qa1	 Alignment		100.0	41	Fold: Left-handed superhelix Superfamily: 1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain Family: 1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
15	d1r0ka1	 Alignment		100.0	36	Fold: Left-handed superhelix Superfamily: 1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain Family: 1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
16	c3upyB	 Alignment		99.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the brucella abortus enzyme catalyzing the first2 committed step of the methylerythritol 4-phosphate pathway.
17	c3mtjA	 Alignment		99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
18	c6dzsD	 Alignment		99.8	25	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
19	c3c8mA	 Alignment		99.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
20	c4pg8B	 Alignment		99.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of s. aureus homoserine dehydrogenase at pH8.5
21	c4xb1B	 Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 319aa long hypothetical homoserine dehydrogenase; PDBTitle: hyperthermophilic archaeal homoserine dehydrogenase in complex with2 nadph
22	c3do5A	 Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
23	c2ejwB	 Alignment	not modelled	99.6	25	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase from thermus thermophilus hb8
24	c1ebuA	 Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase complex with nad analogue and l-2 homoserine
25	c5avoA	 Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of the reduced form of homoserine dehydrogenase from2 sulfobolus tokodaii.
26	c3ingA	 Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
27	c3e9mC	 Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
28	c3nt5B	 Alignment	not modelled	99.1	21	PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase;

						PDBTitle: crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
29	c3db2C_	Alignment	not modelled	99.1	12	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
30	d1ebfa1	Alignment	not modelled	99.1	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
31	c1h6dL_	Alignment	not modelled	99.1	16	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
32	c3moiA_	Alignment	not modelled	99.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
33	c1ofgF_	Alignment	not modelled	99.1	16	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
34	c5uibA_	Alignment	not modelled	99.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase protein; PDBTitle: crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
35	c1zh8B_	Alignment	not modelled	99.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
36	c3ezyB_	Alignment	not modelled	99.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima
37	c3evnA_	Alignment	not modelled	99.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
38	c3m2tA_	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from chromobacterium2 violaceum
39	c2glxD_	Alignment	not modelled	99.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: 1,5-anhydro-d-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase
40	c2o48X_	Alignment	not modelled	99.0	21	PDB header: oxidoreductase Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase
41	c3e18A_	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
42	c2nvwB_	Alignment	not modelled	99.0	15	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal scture of transcriptional regulator gal80p from2 kluveromyces lactis
43	c2ixaA_	Alignment	not modelled	99.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyme, n-acetylgalactosaminidase
44	c5a06E_	Alignment	not modelled	99.0	19	PDB header: oxidoreductase Chain: E: PDB Molecule: aldose-aldose oxidoreductase; PDBTitle: crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol
45	c2q4eB_	Alignment	not modelled	99.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase at4g09670; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
46	c4mkzA_	Alignment	not modelled	98.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol dehydrogenase; PDBTitle: crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
47	c4gqaC_	Alignment	not modelled	98.9	29	PDB header: oxidoreductase Chain: C: PDB Molecule: nad binding oxidoreductase; PDBTitle: crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae
48	c5b3uB_	Alignment	not modelled	98.9	28	PDB header: transferase Chain: B: PDB Molecule: biliverdin reductase; PDBTitle: crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
49	c3ceaA_	Alignment	not modelled	98.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
50	c4h3vA_	Alignment	not modelled	98.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: oxidoreductase domain protein; PDBTitle: crystal structure of oxidoreductase domain protein from kribbella2 flavida
51	c3ec7C_	Alignment	not modelled	98.9	18	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
52	c4hktA_	Alignment	not modelled	98.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol 2-dehydrogenase; PDBTitle: crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
						PDB header: oxidoreductase

53	c6g1mA_	Alignment	not modelled	98.8	16	Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: amine dehydrogenase from petrotoga mobilis; open and closed form
54	c4miyB_	Alignment	not modelled	98.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from lactobacillus2 casei in complex with nad and myo-inositol
55	c3euwB_	Alignment	not modelled	98.8	23	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
56	c3kuxA_	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis
57	c4hadD_	Alignment	not modelled	98.8	22	PDB header: oxidoreductase Chain: D: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
58	c3gfgB_	Alignment	not modelled	98.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
59	c3rbvA_	Alignment	not modelled	98.8	27	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar 3-ketoreductase; PDBTitle: crystal structure of kjd10, a 3-ketoreductase from actinomadura2 kijaniata in complex with nadp
60	c6norB_	Alignment	not modelled	98.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad dependent dehydrogenase; PDBTitle: crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
61	c3fd8A_	Alignment	not modelled	98.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
62	c3q2kB_	Alignment	not modelled	98.8	26	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaa
63	d1zh8a1	Alignment	not modelled	98.8	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
64	c5yabD_	Alignment	not modelled	98.8	23	PDB header: oxidoreductase Chain: D: PDB Molecule: scyllo-inositol dehydrogenase with l-glucose dehydrogenase PDBTitle: crystal structure of scyllo-inositol dehydrogenase with l-glucose2 dehydrogenase activity
65	c6a3fB_	Alignment	not modelled	98.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putative dehydrogenase; PDBTitle: levoglucosan dehydrogenase, apo form
66	c1xeaD_	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
67	c6iauB_	Alignment	not modelled	98.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: amine dehydrogenase; PDBTitle: amine dehydrogenase from cystobacter fuscus in complex with nadp+ and2 cyclohexylamine
68	c4gmfD_	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: D: PDB Molecule: yersiniabactin biosynthetic protein ybtu; PDBTitle: apo structure of a thiazoliny imine reductase from yersinia2 enterocolitica (irp3)
69	c3c1aB_	Alignment	not modelled	98.8	27	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
70	d2nvwa1	Alignment	not modelled	98.8	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
71	c3fhiC_	Alignment	not modelled	98.8	16	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
72	c1evjC_	Alignment	not modelled	98.7	17	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
73	c3dtyA_	Alignment	not modelled	98.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae
74	c5ugjC_	Alignment	not modelled	98.7	16	PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis
75	c2ho3D_	Alignment	not modelled	98.7	21	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
76	c3e82A_	Alignment	not modelled	98.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
77	c2czcD_	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate

						dehydrogenase from2 pyrococcus horikoshii ot3
78	c3btuD_	Alignment	not modelled	98.7	15	PDB header: transcription Chain: D: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
79	c6iaqA_	Alignment	not modelled	98.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase n-terminus domain-containing PDBTitle: structure of amine dehydrogenase from mycobacterium smegmatis
80	d1h6da1	Alignment	not modelled	98.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
81	c3v5nA_	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from sinorhizobium meliloti
82	c3f4fF_	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: F: PDB Molecule: putative oxidoreductase yhhx; PDBTitle: crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
83	d1ydwal	Alignment	not modelled	98.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
84	c3oqbF_	Alignment	not modelled	98.6	14	PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
85	c3wycB_	Alignment	not modelled	98.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate d-dehydrogenase; PDBTitle: structure of a meso-diaminopimelate dehydrogenase in complex with nadp
86	c2axqA_	Alignment	not modelled	98.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
87	c4ew6A_	Alignment	not modelled	98.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: d-galactose-1-dehydrogenase protein; PDBTitle: crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
88	c1cf2Q_	Alignment	not modelled	98.5	16	PDB header: oxidoreductase Chain: Q: PDB Molecule: protein (glyceraldehyde-3-phosphate dehydrogenase); PDBTitle: three-dimensional structure of d-glyceraldehyde-3-phosphate2 dehydrogenase from the hyperthermophilic archaeon methanothermus3 fervidus
89	c5I78A_	Alignment	not modelled	98.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-aminoadipic semialdehyde synthase, mitochondrial; PDBTitle: crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
90	c4fb5A_	Alignment	not modelled	98.5	25	PDB header: oxidoreductase Chain: A: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a probable oxidoreductase protein
91	c1e5IA_	Alignment	not modelled	98.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
92	c6jnkA_	Alignment	not modelled	98.5	31	PDB header: oxidoreductase Chain: A: PDB Molecule: l-arabinose 1-dehydrogenase (nad(p)(+)); PDBTitle: crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form)
93	c2dc1A_	Alignment	not modelled	98.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
94	c1lc3A_	Alignment	not modelled	98.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
95	c1drwA_	Alignment	not modelled	98.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
96	c5kt0A_	Alignment	not modelled	98.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
97	c1b7gO_	Alignment	not modelled	98.4	17	PDB header: oxidoreductase Chain: O: PDB Molecule: protein (glyceraldehyde 3-phosphate dehydrogenase); PDBTitle: glyceraldehyde 3-phosphate dehydrogenase
98	c5z2fA_	Alignment	not modelled	98.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: nadph/pda bound dihydrodipicolinate reductase from paenisporsarcina2 sp. tg-14
99	c3u3xJ_	Alignment	not modelled	98.4	13	PDB header: oxidoreductase Chain: J: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
100	c4f3yA_	Alignment	not modelled	98.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis
101	d1ryda1	Alignment	not modelled	98.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

102	d1cf2o1	Alignment	not modelled	98.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
103	d1f06a1	Alignment	not modelled	98.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
104	c3ip3D_	Alignment	not modelled	98.3	16	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, putative; PDBTitle: structure of putative oxidoreductase (tm_0425) from thermotoga2 maritima
105	c3uuwB_	Alignment	not modelled	98.3	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase with nad(p)-binding rossmann-fold PDBTitle: 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
106	c2yyvB_	Alignment	not modelled	98.3	19	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
107	c3ic5A_	Alignment	not modelled	98.3	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
108	c2ep5B_	Alignment	not modelled	98.3	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 350aa long hypothetical aspartate-semialdehyde PDBTitle: structural study of project id st1242 from sulfolobus tokodaii strain7
109	c3dapB_	Alignment	not modelled	98.3	22	PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
110	c2g17A_	Alignment	not modelled	98.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: the structure of n-acetyl-gamma-glutamyl-phosphate reductase from2 salmonella typhimurium.
111	d1j5pa4	Alignment	not modelled	98.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
112	c2ozpA_	Alignment	not modelled	98.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (ttha1904) from thermus thermophilus
113	c3wzgB_	Alignment	not modelled	98.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate dehydrogenase; PDBTitle: crystal structure of meso-dapdh q154l/t173l/r199m/p248s/h249n/n276s2 mutant with d-leucine of from clostridium tetani e88
114	c2p2sA_	Alignment	not modelled	98.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
115	c5tenH_	Alignment	not modelled	98.2	18	PDB header: oxidoreductase Chain: H: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
116	c3wb9A_	Alignment	not modelled	98.2	26	PDB header: oxidoreductase Chain: A: PDB Molecule: diaminopimelate dehydrogenase; PDBTitle: crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum
117	c4oo3A_	Alignment	not modelled	98.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative oxidoreductase (parmer_00841) from2 parabacteroides merdae atcc 43184 at 2.23 a resolution
118	c3ketA_	Alignment	not modelled	98.1	13	PDB header: transcription/dna Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
119	c4dpkB_	Alignment	not modelled	98.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: malonyl-coa/succinyl-coa reductase; PDBTitle: structure of malonyl-coenzyme a reductase from crenarchaeota
120	c1ys4A_	Alignment	not modelled	98.1	27	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: structure of aspartate-semialdehyde dehydrogenase from methanococcus2 jannaschii