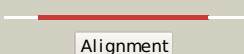
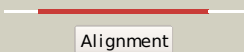
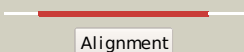
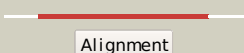
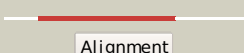
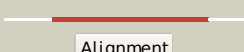
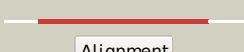
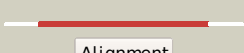
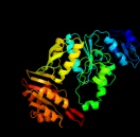
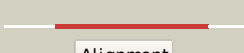


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3uagA_	 Alignment		100.0	98	PDB header: ligase Chain: A: PDB Molecule: protein (udp-n-acetyl muramoyl-l-alanine:d-glutamate ligase PDBTitle: udp-n-acetyl muramoyl-l-alanine:d-glutamate ligase
2	c3lk7A_	 Alignment		100.0	29	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetyl muramoyl alanine-d-glutamate ligase; PDBTitle: the crystal structure of udp-n-acetyl muramoyl alanine-d-2 glutamate (murd) ligase from streptococcus agalactiae to3 1.5a
3	c2f00A_	 Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetyl muramate--l-alanine ligase; PDBTitle: escherichia coli murc
4	c3hn7A_	 Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetyl muramate-l-alanine ligase; PDBTitle: crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
5	c1j6uA_	 Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetyl muramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetyl muramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
6	c1gqgA_	 Alignment		100.0	19	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetyl muramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus2 influenzae
7	c3eagA_	 Alignment		100.0	20	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetyl muramate:l-alanyl-gamma-d-glutamyl-meso- PDBTitle: the crystal structure of udp-n-acetyl muramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitidis
8	c2am1A_	 Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetyl muramoyl alanine-d-glutamyl-lysine-d-alanyl-d- PDBTitle: sp protein ligand 1
9	c1e8cB_	 Alignment		100.0	22	PDB header: ligase Chain: B: PDB Molecule: udp-n-acetyl muramoyl alanyl-d-glutamate--2,6- PDBTitle: structure of mure the udp-n-acetyl muramyl tripeptide2 synthetase from e. coli
10	c1gg4A_	 Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetyl muramoyl alanyl-d-glutamyl-2,6- PDBTitle: crystal structure of escherichia coli udpmurnac-tripeptide2 d-alanyl-d-alanine-adding enzyme (murf) at 2.3 angstrom3 resolution
11	c2wtzC_	 Alignment		100.0	24	PDB header: ligase Chain: C: PDB Molecule: udp-n-acetyl muramoyl-l-alanyl-d-glutamate- PDBTitle: mure ligase of mycobacterium tuberculosis

12	c2vosA	Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase protein folc; PDBTitle: mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
13	c1w78A	Alignment		100.0	22	PDB header: synthase Chain: A: PDB Molecule: folc bifunctional protein; PDBTitle: e.coli folc in complex with dhpp and adp
14	c2gc6A	Alignment		100.0	16	PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase; PDBTitle: s73a mutant of l. casei fpgs
15	c3n2aA	Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: bifunctional folylpolyglutamate synthase/dihydrofolate PDBTitle: crystal structure of bifunctional folylpolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
16	c1o5za	Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase/dihydrofolate synthase; PDBTitle: crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
17	d2jfga3	Alignment		100.0	97	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
18	d2jfga2	Alignment		100.0	100	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
19	d1p3da3	Alignment		100.0	19	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
20	d1e8ca3	Alignment		100.0	27	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
21	d1j6ua3	Alignment	not modelled	100.0	32	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
22	d2gc6a2	Alignment	not modelled	100.0	15	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
23	d1gg4a4	Alignment	not modelled	100.0	22	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
24	d1o5za2	Alignment	not modelled	100.0	20	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
25	d1gg4a1	Alignment	not modelled	99.7	18	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
26	d2jfga1	Alignment	not modelled	99.7	100	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
27	d1j6ua1	Alignment	not modelled	99.7	14	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
28	d1p3da1	Alignment	not modelled	99.7	19	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
29	d1e8ca2	Alignment	not modelled	99.6	18	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain

						Family: MurCDEF C-terminal domain
30	c3mvnA	Alignment	not modelled	99.5	16	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetyl muramate:l-alanyl-gamma-d-glutamyl-medo- PDBTitle: crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
31	d1p3da2	Alignment	not modelled	99.5	17	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
32	d1j6ua2	Alignment	not modelled	99.1	11	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
33	d1o5za1	Alignment	not modelled	98.9	25	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folypolyglutamate synthetase, C-terminal domain
34	d2gc6a1	Alignment	not modelled	98.7	20	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folypolyglutamate synthetase, C-terminal domain
35	d1pjqa1	Alignment	not modelled	98.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
36	c3d4oA	Alignment	not modelled	98.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
37	c3gg2B	Alignment	not modelled	97.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
38	c2y0dB	Alignment	not modelled	97.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
39	c3cumA	Alignment	not modelled	97.9	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
40	c1mv8A	Alignment	not modelled	97.8	23	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
41	c2rirA	Alignment	not modelled	97.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
42	c1pjtB	Alignment	not modelled	97.8	17	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelataase for4 siroheme synthesis
43	c1gdhA	Alignment	not modelled	97.8	14	PDB header: oxidoreductase(choh (d)-nad(p)+ (a)) Chain: A: PDB Molecule: d-glycerate dehydrogenase; PDBTitle: crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
44	d3cuma2	Alignment	not modelled	97.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
45	c3dhyc	Alignment	not modelled	97.8	21	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
46	c3dfzB	Alignment	not modelled	97.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: precorrin-2 dehydrogenase; PDBTitle: sir, precorrin-2 dehydrogenase
47	d1nya1	Alignment	not modelled	97.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
48	c3gvpB	Alignment	not modelled	97.8	19	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
49	c2g5cD	Alignment	not modelled	97.8	19	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
50	c1d4fD	Alignment	not modelled	97.7	20	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
51	d1mx3a1	Alignment	not modelled	97.7	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
52	d2naca1	Alignment	not modelled	97.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
53	c3g79A	Alignment	not modelled	97.7	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 PDB header: oxidoreductase

54	c2hk8B	Alignment	not modelled	97.7	17	Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
55	c1np3B	Alignment	not modelled	97.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroeductase from2 pseudomonas aeruginosa
56	c3oneA	Alignment	not modelled	97.7	19	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
57	d1li4a1	Alignment	not modelled	97.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
58	c1nytC	Alignment	not modelled	97.7	15	PDB header: oxidoreductase Chain: C: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: shikimate dehydrogenase aroe complexed with nadp+
59	d1gdha1	Alignment	not modelled	97.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
60	c3n7uD	Alignment	not modelled	97.7	22	PDB header: oxidoreductase Chain: D: PDB Molecule: formate dehydrogenase; PDBTitle: nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
61	d1np3a2	Alignment	not modelled	97.7	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
62	c2o3jC	Alignment	not modelled	97.7	18	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
63	c2j6iC	Alignment	not modelled	97.7	16	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
64	c2dbqA	Alignment	not modelled	97.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
65	d1vpda2	Alignment	not modelled	97.6	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
66	d1a4ia1	Alignment	not modelled	97.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
67	c3oj1A	Alignment	not modelled	97.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cap5o; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
68	c2g76A	Alignment	not modelled	97.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
69	c3n58D	Alignment	not modelled	97.6	20	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
70	d2dl1a1	Alignment	not modelled	97.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
71	d1v8ba1	Alignment	not modelled	97.6	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
72	d1leha1	Alignment	not modelled	97.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
73	c1wwkA	Alignment	not modelled	97.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
74	c2ek1A	Alignment	not modelled	97.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
75	d1j4aa1	Alignment	not modelled	97.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
76	c2omeA	Alignment	not modelled	97.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
77	c2nacA	Alignment	not modelled	97.5	14	PDB header: oxidoreductase(aldehyde(d),nad+(a)) Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: high resolution structures of holo and apo formate dehydrogenase
78	d1l7da1	Alignment	not modelled	97.5	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
79	c2gcbB	Alignment	not modelled	97.5	23	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
						Fold: NAD(P)-binding Rossmann-fold domains

80	d1c1da1	Alignment	not modelled	97.5	21	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
81	d2cvza2	Alignment	not modelled	97.5	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
82	d1bg6a2	Alignment	not modelled	97.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
83	c1yb4A_	Alignment	not modelled	97.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
84	d1mv8a2	Alignment	not modelled	97.5	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
85	d1p77a1	Alignment	not modelled	97.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
86	c1v8bA_	Alignment	not modelled	97.5	20	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
87	c3g0oA_	Alignment	not modelled	97.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
88	c1vpdA_	Alignment	not modelled	97.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
89	d1ygya1	Alignment	not modelled	97.5	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
90	c1ygyA_	Alignment	not modelled	97.5	26	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
91	c3prjB_	Alignment	not modelled	97.5	17	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.
92	d1b0aa1	Alignment	not modelled	97.5	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
93	c3pefA_	Alignment	not modelled	97.4	14	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+
94	c1bg6A_	Alignment	not modelled	97.4	15	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
95	c3d64A_	Alignment	not modelled	97.4	22	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
96	d1f0ya2	Alignment	not modelled	97.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
97	c2f1kD_	Alignment	not modelled	97.4	20	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
98	d1luxa1	Alignment	not modelled	97.4	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
99	d1e5qa1	Alignment	not modelled	97.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
100	c1j4aA_	Alignment	not modelled	97.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
101	c2uyyD_	Alignment	not modelled	97.4	21	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
102	d1qp8a1	Alignment	not modelled	97.4	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
103	c2pi1C_	Alignment	not modelled	97.4	19	PDB header: oxidoreductase Chain: C: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
104	c3hn2A_	Alignment	not modelled	97.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
105	c3gg9C_	Alignment	not modelled	97.4	13	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase oxidoreductase protein;

						PDBTitle: crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
106	c3evtA_	Alignment	not modelled	97.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
107	c1e5lA_	Alignment	not modelled	97.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
108	c3hg7A_	Alignment	not modelled	97.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase family PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from aeromonas salmonicida subsp. salmonicida a449
109	c2eggA_	Alignment	not modelled	97.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
110	d1pjca1	Alignment	not modelled	97.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
111	c3o8qB_	Alignment	not modelled	97.3	14	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase i alpha; PDBTitle: 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
112	c3bazA_	Alignment	not modelled	97.3	22	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of human udp-glucose dehydrogenase from colex blumei in2 complex with nadp+
113	c2q3eH_	Alignment	not modelled	97.3	15	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
114	c2axqA_	Alignment	not modelled	97.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
115	c2d0iC_	Alignment	not modelled	97.3	19	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase; PDBTitle: crystal structure ph0520 protein from pyrococcus horikoshii ot3
116	d2f1ka2	Alignment	not modelled	97.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
117	c2w2kB_	Alignment	not modelled	97.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: d-mandelate dehydrogenase; PDBTitle: crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
118	c3l6dB_	Alignment	not modelled	97.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
119	c3gvxA_	Alignment	not modelled	97.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
120	c3pgjB_	Alignment	not modelled	97.3	13	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate