

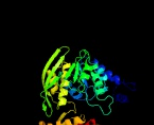








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2152c_murC_2410646_2412130
Date	Mon Aug 5 13:25:27 BST 2019
Unique Job ID	aa93366c022cf3c1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2f00A_</a>	Alignment		100.0	35	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc
2	<a href="#">c1j6uA_</a>	Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramate-alanine ligase murc; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
3	<a href="#">c3hn7A_</a>	Alignment		100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramate-l-alanine ligase; <b>PDBTitle:</b> crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
4	<a href="#">c1gqqA_</a>	Alignment		100.0	36	<b>PDB header:</b> cell wall biosynthesis <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramate-l-alanine ligase; <b>PDBTitle:</b> murc - crystal structure of the apo-enzyme from haemophilus influenzae
5	<a href="#">c3uagA_</a>	Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (udp-n-acetylmuramoyl-l-alanine:d- <b>PDBTitle:</b> udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
6	<a href="#">c4bucA_</a>	Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine--d-glutamate ligase; <b>PDBTitle:</b> crystal structure of murd ligase from thermotoga maritima in apo form
7	<a href="#">c3lk7A_</a>	Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine--d-glutamate ligase; <b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramoylalanine-d-glutamate2 (murd) ligase from streptococcus agalactiae to 1.5a
8	<a href="#">c5vwwA_</a>	Alignment		100.0	40	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> structure of murc from pseudomonas aeruginosa
9	<a href="#">c6cauA_</a>	Alignment		100.0	37	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with amppnp
10	<a href="#">c3eagA_</a>	Alignment		100.0	29	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- <b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
11	<a href="#">c4c13A_</a>	Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--l-lysine ligase; <b>PDBTitle:</b> x-ray crystal structure of staphylococcus aureus mure with udp-murnac-2 ala-glu-lys

12	<a href="#">c4bubA</a>	Alignment		100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--ld-lysine <b>PDBTitle:</b> crystal structure of mure ligase from thermotoga maritima2 in complex with adp
13	<a href="#">c2xjaD</a>	Alignment		100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- <b>PDBTitle:</b> structure of mure from m.tuberculosis with dipeptide and adp
14	<a href="#">c4qdiA</a>	Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine ligase; <b>PDBTitle:</b> crystal structure ii of murf from acinetobacter baumannii
15	<a href="#">c1e8cB</a>	Alignment		100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanyl-d-glutamate-2,6-diaminopimelate <b>PDBTitle:</b> structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli
16	<a href="#">c2wtzC</a>	Alignment		100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate- <b>PDBTitle:</b> mure ligase of mycobacterium tuberculosis
17	<a href="#">c2am1A</a>	Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine-d-glutamyl-lysine-d-alanyl-d- <b>PDBTitle:</b> sp protein ligand 1
18	<a href="#">c2vosA</a>	Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folypolyglutamate synthase protein folc; <b>PDBTitle:</b> mycobacterium tuberculosis folypolyglutamate synthase2 complexed with adp
19	<a href="#">c3z18A</a>	Alignment		100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine <b>PDBTitle:</b> crystal structure of murf ligase from thermotoga maritima2 in complex with adp
20	<a href="#">c1gg4A</a>	Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanyl-d-glutamyl-2,6-diaminopimelate- <b>PDBTitle:</b> crystal structure of escherichia coli udpmurnac-tripeptide d-alanyl-d-2 alanine-adding enzyme (murf) at 2.3 angstrom resolution
21	<a href="#">c4cvkA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine <b>PDBTitle:</b> pamurf in complex with udp-murnac-tripeptide (mdap)
22	<a href="#">c1w78A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> synthase <b>Chain:</b> A: <b>PDB Molecule:</b> folc bifunctional protein; <b>PDBTitle:</b> e.coli folc in complex with dhpp and adp
23	<a href="#">c2gc6A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folypolyglutamate synthase; <b>PDBTitle:</b> s73a mutant of l. casei fpgs
24	<a href="#">c1o5zA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folypolyglutamate synthase/dihydrofolate synthase; <b>PDBTitle:</b> crystal structure of folypolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
25	<a href="#">c3n2aA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional folypolyglutamate synthase/dihydrofolate <b>PDBTitle:</b> crystal structure of bifunctional folypolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
26	<a href="#">c6gs2B</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> sa1708 protein; <b>PDBTitle:</b> crystal structure of the gatd/murt enzyme complex from staphylococcus2 aureus
27	<a href="#">c6fqbD</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> mur ligase family protein; <b>PDBTitle:</b> murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
28	<a href="#">d1p3da3</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF

29	<a href="#">d2jfga3</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
30	<a href="#">d1j6ua3</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
31	<a href="#">d1e8ca3</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
32	<a href="#">d2gc6a2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> Folylpolyglutamate synthetase
33	<a href="#">d1gg4a4</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
34	<a href="#">d1o5za2</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> Folylpolyglutamate synthetase
35	<a href="#">d1p3da2</a>	Alignment	not modelled	99.9	35	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
36	<a href="#">d1p3da1</a>	Alignment	not modelled	99.8	42	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
37	<a href="#">d1j6ua1</a>	Alignment	not modelled	99.8	33	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
38	<a href="#">d1j6ua2</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
39	<a href="#">c3mvaA</a>	Alignment	not modelled	99.8	33	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- <b>PDBTitle:</b> crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
40	<a href="#">d1e8ca2</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
41	<a href="#">d2jfga2</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
42	<a href="#">d2jfga1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
43	<a href="#">d1gg4a1</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
44	<a href="#">d1o5za1</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> Folylpolyglutamate synthetase, C-terminal domain
45	<a href="#">d2gc6a1</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> Folylpolyglutamate synthetase, C-terminal domain
46	<a href="#">d1pjqa1</a>	Alignment	not modelled	98.1	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
47	<a href="#">c4wb1B</a>	Alignment	not modelled	97.9	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cals8; <b>PDBTitle:</b> crystal structure of cals8 from micromonospora echinospora (p294s2 mutant)
48	<a href="#">d1a4ia1</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
49	<a href="#">c3g79A</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; <b>PDBTitle:</b> crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1
50	<a href="#">c3ojlA</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cap5o; <b>PDBTitle:</b> native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
51	<a href="#">c4r16A</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 418aa long hypothetical udp-n-acetyl-d-mannosaminuronic <b>PDBTitle:</b> structure of udp-d-mannac dehdrogeanse from pyrococcus horikoshii
52	<a href="#">c3cumA</a>	Alignment	not modelled	97.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
53	<a href="#">c3gg2B</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar dehydrogenase, udp-glucose/gdp-mannose dehydrogenase <b>PDBTitle:</b> crystal structure of udp-glucose 6-dehydrogenase from porphyromonas2 gingivalis bound to product udp-glucuronate
54	<a href="#">d1uxja1</a>	Alignment	not modelled	97.6	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like

55	<a href="#">d1b0aa1</a>	Alignment	not modelled	97.6	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
56	<a href="#">c2y0dB</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
57	<a href="#">c2o3jC</a>	Alignment	not modelled	97.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of caenorhabditis elegans udp-glucose dehydrogenase
58	<a href="#">d1l7da1</a>	Alignment	not modelled	97.5	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
59	<a href="#">c5butG</a>	Alignment	not modelled	97.5	20	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> ktr system potassium uptake protein a,ktr system potassium <b>PDBTitle:</b> crystal structure of inactive conformation of ktrab k+ transporter
60	<a href="#">c3vtfA</a>	Alignment	not modelled	97.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum
61	<a href="#">c1mv8A</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose 6-dehydrogenase; <b>PDBTitle:</b> 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from pseudomonas aeruginosa
62	<a href="#">c4a7pA</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> se-met derivatized ugdg, udp-glucose dehydrogenase from sphingomonas2 elodea
63	<a href="#">c3d4oA</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
64	<a href="#">d1e5qa1</a>	Alignment	not modelled	97.4	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	<a href="#">c1djnB</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trimethylamine dehydrogenase; <b>PDBTitle:</b> structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
66	<a href="#">c4gjbB</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase nad-binding; <b>PDBTitle:</b> crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
67	<a href="#">c6apeA</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of bifunctional protein fold from helicobacter2 pylori
68	<a href="#">c6qkqB</a>	Alignment	not modelled	97.3	21	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> ncr a; <b>PDBTitle:</b> 2-naphthoyl-coa reductase(ncr)
69	<a href="#">c3l07B</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
70	<a href="#">c3hn2A</a>	Alignment	not modelled	97.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
71	<a href="#">d1bg6a2</a>	Alignment	not modelled	97.3	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
72	<a href="#">c5g6sD</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> imine reductase; <b>PDBTitle:</b> imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
73	<a href="#">c3ghyA</a>	Alignment	not modelled	97.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ketopantoate reductase protein; <b>PDBTitle:</b> crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
74	<a href="#">c3ktdC</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative prephenate dehydrogenase (cg10226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
75	<a href="#">c2ev9B</a>	Alignment	not modelled	97.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate 5-dehydrogenase (aroe) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate
76	<a href="#">c2g5cD</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from aquifex aeolicus
77	<a href="#">d3cuma2</a>	Alignment	not modelled	97.3	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
78	<a href="#">c3l6dB</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
						<b>PDB header:</b> isomerase, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> t-protein [includes: chorismate mutase (ec

79	<a href="#">c2pv7B_</a>	Alignment	not modelled	97.3	23	5.4.99.5) (cm) <b>PDBTitle:</b> crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
80	<a href="#">c5je8A_</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> the crystal structure of bacillus cereus 3-hydroxyisobutyrate2 dehydrogenase in complex with nad
81	<a href="#">c3ggpA_</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
82	<a href="#">c4wjiA_</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cyclohexadienyl dehydrogenase and adh prephenate <b>PDBTitle:</b> crystal structure of cyclohexadienyl dehydrogenase from sinorhizobium2 meliloti in complex with nadp and tyrosine
83	<a href="#">c4oqyA_</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-imine reductase; <b>PDBTitle:</b> streptomyces sp. gf3546 imine reductase
84	<a href="#">c1ps9A_</a>	Alignment	not modelled	97.2	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
85	<a href="#">c1b0aA_</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (fold bifunctional protein); <b>PDBTitle:</b> 5,10, methylene-tetrahydrofolate2 dehydrogenase/cyclohydrolase from e. coli.
86	<a href="#">c1pjtB_</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> transferase/oxidoreductase/lyase <b>Chain:</b> B: <b>PDB Molecule:</b> siroheme synthase; <b>PDBTitle:</b> the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatae for3 siroheme synthesis
87	<a href="#">c5a9tA_</a>	Alignment	not modelled	97.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
88	<a href="#">c5nhsB_</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> the crystal structure of xanthomonas albilineans n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
89	<a href="#">c3ax6C_</a>	Alignment	not modelled	97.2	14	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima
90	<a href="#">d2pv7a2</a>	Alignment	not modelled	97.2	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
91	<a href="#">c3prjB_</a>	Alignment	not modelled	97.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
92	<a href="#">c3k30B_</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> histamine dehydrogenase from nocardioes simplex
93	<a href="#">c4j0eB_</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable 3-hydroxyacyl-coa dehydrogenase f54c8.1; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase from2 caenorhadbitis elegans in p1 space group
94	<a href="#">d1nyta1</a>	Alignment	not modelled	97.1	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
95	<a href="#">c1vpdA_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tartronate semialdehyde reductase; <b>PDBTitle:</b> x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
96	<a href="#">d1vpda2</a>	Alignment	not modelled	97.1	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
97	<a href="#">c1npyA_</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical shikimate 5-dehydrogenase-like protein hi0607; <b>PDBTitle:</b> structure of shikimate 5-dehydrogenase-like protein hi0607
98	<a href="#">c6fqzB_</a>	Alignment	not modelled	97.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> plasmodium falciparum 6-phosphogluconate dehydrogenase in its apo2 form, in complex with its cofactor nadp+ and in complex with its3 substrate 6-phosphogluconate
99	<a href="#">c2dwcB_</a>	Alignment	not modelled	97.1	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 433aa long hypothetical phosphoribosylglycinamide formyl <b>PDBTitle:</b> crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
100	<a href="#">c4oqzA_</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase yfjr; <b>PDBTitle:</b> streptomyces aurantiacus imine reductase
101	<a href="#">d1ps9a3</a>	Alignment	not modelled	97.1	25	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
102	<a href="#">c2q3eH_</a>	Alignment	not modelled	97.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of human udp-glucose dehydrogenase

						complexed with nadh and2 udp-glucose
103	<a href="#">c3w6uA_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, nad-binding protein; <b>PDBTitle:</b> crystal structure of nadp bound l-serine 3-dehydrogenase from2 hyperthermophilic archaeon pyrobaculum caldifontis
104	<a href="#">c3hwrA_</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution
105	<a href="#">c4dioB_</a>	Alignment	not modelled	97.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha part 1; <b>PDBTitle:</b> the crystal structure of transhydrogenase from sinorhizobium melloti
106	<a href="#">c3qhaB_</a>	Alignment	not modelled	97.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
107	<a href="#">c1e5IA_</a>	Alignment	not modelled	97.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
108	<a href="#">c5u5gC_</a>	Alignment	not modelled	97.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> psf3 in complex with nadp+ and 2-opp
109	<a href="#">c5y8mA_</a>	Alignment	not modelled	97.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
110	<a href="#">c3p2oB_</a>	Alignment	not modelled	97.0	16	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
111	<a href="#">c2uyyD_</a>	Alignment	not modelled	97.0	19	<b>PDB header:</b> cytokine <b>Chain:</b> D: <b>PDB Molecule:</b> n-pac protein; <b>PDBTitle:</b> structure of the cytokine-like nuclear factor n-pac
112	<a href="#">c3ic5A_</a>	Alignment	not modelled	97.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
113	<a href="#">d2pgda2</a>	Alignment	not modelled	97.0	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
114	<a href="#">c1np3B_</a>	Alignment	not modelled	97.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
115	<a href="#">c4a26B_</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative c-1-tetrahydrofolate synthase, cytoplasmic; <b>PDBTitle:</b> the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
116	<a href="#">c5nmwA_</a>	Alignment	not modelled	97.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> crystal structure of the pyrrolizidine alkaloid n-oxygenase from2 zonocerus variegatus in complex with fad
117	<a href="#">d1i36a2</a>	Alignment	not modelled	97.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
118	<a href="#">c4a5oB_</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
119	<a href="#">c1nytC_</a>	Alignment	not modelled	97.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> shikimate dehydrogenase aroe complexed with nadp+
120	<a href="#">c1bg6A_</a>	Alignment	not modelled	97.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; <b>PDBTitle:</b> crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c