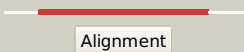

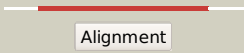



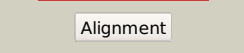



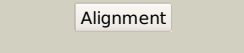

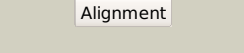



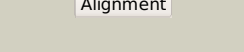

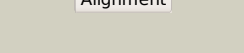

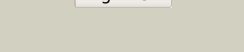



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2155c_(murD)_2414942_2416402
Date	Mon Aug 5 13:25:27 BST 2019
Unique Job ID	691d945dc8ebbc90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3uagA_	 Alignment		100.0	32	PDB header: ligase Chain: A: PDB Molecule: protein (udp-n-acetylmuramoyl-l-alanine:d- PDBTitle: udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
2	c3lk7A_	 Alignment		100.0	30	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d- glutamate ligase; PDBTitle: the crystal structure of udp-n-acetylmuramoylalanine-d- glutamate2 (murD) ligase from streptococcus agalactiae to 1.5a
3	c4bucA_	 Alignment		100.0	27	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d- glutamate ligase; PDBTitle: crystal structure of murD ligase from thermotoga maritima in apo form
4	c2f00A_	 Alignment		100.0	20	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murC
5	c3hn7A_	 Alignment		100.0	17	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
6	c1j6uA_	 Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
7	c1gqgA_	 Alignment		100.0	20	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus influenzae
8	c5vvwA_	 Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: structure of murc from pseudomonas aeruginosa
9	c2xjaD_	 Alignment		100.0	27	PDB header: ligase Chain: D: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d- glutamate--2,6- PDBTitle: structure of mure from m.tuberculosis with dipeptide and adp
10	c4qdiA_	 Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-tripeptide--d- alanyl-d-alanine ligase; PDBTitle: crystal structure ii of murf from acinetobacter baumannii
11	c3eagA_	 Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d- glutamyl-meso- PDBTitle: the crystal structure of udp-n-acetylmuramate:l-alanyl- gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides

12	c6cauA	Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with amppnp
13	c2am1A	Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine-d-glutamyl-lysine-d-alanyl-d- PDBTitle: sp protein ligand 1
14	c4c13A	Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--l-lysine ligase; PDBTitle: x-ray crystal structure of staphylococcus aureus mure with udp-murnac-2 ala-glu-lys
15	c1e8cB	Alignment		100.0	24	PDB header: ligase Chain: B: PDB Molecule: udp-n-acetylmuramoylalanyl-d-glutamate-2,6-diaminopimelate PDBTitle: structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli
16	c4bubA	Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--ld-lysine PDBTitle: crystal structure of mure ligase from thermotoga maritima2 in complex with adp
17	c4cvkA	Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine PDBTitle: pamurf in complex with udp-murnac-tripeptide (mdap)
18	c2wtzC	Alignment		100.0	30	PDB header: ligase Chain: C: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate- PDBTitle: mure ligase of mycobacterium tuberculosis
19	c1gg4A	Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanyl-d-glutamyl-2,6-diaminopimelate- PDBTitle: crystal structure of escherichia coli udpmurnac-tripeptide d-alanyl-d-2 alanine-adding enzyme (murf) at 2.3 angstrom resolution
20	c3zl8A	Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine PDBTitle: crystal structure of murf ligase from thermotoga maritima2 in complex with adp
21	c2vosA	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: folypolyglutamate synthase protein folc; PDBTitle: mycobacterium tuberculosis folypolyglutamate synthase2 complexed with adp
22	c2gc6A	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: folypolyglutamate synthase; PDBTitle: s73a mutant of l. casei fpgs
23	c1w78A	Alignment	not modelled	100.0	26	PDB header: synthase Chain: A: PDB Molecule: folc bifunctional protein; PDBTitle: e.coli folc in complex with dhpp and adp
24	c1o5zA	Alignment	not modelled	100.0	15	PDB header: ligase Chain: A: PDB Molecule: folypolyglutamate synthase/dihydrofolate synthase; PDBTitle: crystal structure of folypolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
25	c6gs2B	Alignment	not modelled	100.0	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: sa1708 protein; PDBTitle: crystal structure of the gatd/murt enzyme complex from staphylococcus2 aureus
26	c3n2aA	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: bifunctional folypolyglutamate synthase/dihydrofolate PDBTitle: crystal structure of bifunctional folypolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
27	d2jfga3	Alignment	not modelled	100.0	31	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
28	c6fqbdD	Alignment	not modelled	100.0	19	PDB header: ligase Chain: D: PDB Molecule: mur ligase family protein; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from

					streptococcus2 pneumoniae r6
29	d1p3da3	Alignment	not modelled	100.0	22 Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
30	d1e8ca3	Alignment	not modelled	100.0	27 Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
31	d2gc6a2	Alignment	not modelled	100.0	16 Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
32	d1j6ua3	Alignment	not modelled	100.0	21 Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
33	d1gg4a4	Alignment	not modelled	100.0	23 Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
34	d2jfga2	Alignment	not modelled	100.0	33 Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
35	d1o5za2	Alignment	not modelled	100.0	14 Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
36	d1p3da1	Alignment	not modelled	99.7	16 Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
37	d1j6ua1	Alignment	not modelled	99.7	15 Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
38	d2jfga1	Alignment	not modelled	99.7	30 Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
39	d1p3da2	Alignment	not modelled	99.6	13 Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
40	d1e8ca2	Alignment	not modelled	99.6	22 Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
41	d1gg4a1	Alignment	not modelled	99.6	22 Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
42	c3mvnA	Alignment	not modelled	99.5	24 PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate: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
43	d1j6ua2	Alignment	not modelled	99.2	20 Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
44	d1o5za1	Alignment	not modelled	99.0	16 Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folylpolyglutamate synthetase, C-terminal domain
45	d2gc6a1	Alignment	not modelled	98.9	25 Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folylpolyglutamate synthetase, C-terminal domain
46	d1pjqa1	Alignment	not modelled	98.3	18 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
47	c4wb1B	Alignment	not modelled	98.2	22 PDB header: oxidoreductase Chain: B: PDB Molecule: calS8; PDBTitle: crystal structure of calS8 from micromonospora echinospora (p294s2 mutant)
48	c3d4oA	Alignment	not modelled	98.1	22 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
49	c1mv8A	Alignment	not modelled	98.1	15 PDB header: oxidoreductase Chain: A: PDB Molecule: gdp-mannose 6-dehydrogenase; PDBTitle: 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
50	c3gg2B	Alignment	not modelled	98.0	16 PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose dehydrogenase PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from porphyromonas2 gingivalis bound to product udp-glucuronate
51	c3cumA	Alignment	not modelled	98.0	20 PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
52	c4a7pA	Alignment	not modelled	98.0	17 PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized ugdg, udp-glucose dehydrogenase from sphingomonas2 elodea
53	c2rirA	Alignment	not modelled	98.0	21 PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
54	c4r16A	Alignment	not modelled	98.0	17 PDB header: oxidoreductase Chain: A: PDB Molecule: 418aa long hypothetical udp-n-acetyl-d-mannosaminuronic

						PDBTitle: structure of udp-d-mannac dehydrogenase from pyrococcus horikoshii
55	c3vtfA_	Alignment	not modelled	98.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum
56	c6aqjB_	Alignment	not modelled	97.9	18	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadh+); PDBTitle: crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that3 have biocidal activity.
57	c4xdzB_	Alignment	not modelled	97.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
58	c4dioB_	Alignment	not modelled	97.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha part 1; PDBTitle: the crystal structure of transhydrogenase from sinorhizobium melloti
59	c2o3jC_	Alignment	not modelled	97.9	21	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
60	c5g6sD_	Alignment	not modelled	97.9	21	PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
61	d3cuma2	Alignment	not modelled	97.9	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
62	c2y0dB_	Alignment	not modelled	97.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
63	c3ojlA_	Alignment	not modelled	97.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: cap5o; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
64	d1l7da1	Alignment	not modelled	97.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
65	c4oqzA_	Alignment	not modelled	97.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase
66	c6jczL_	Alignment	not modelled	97.9	17	PDB header: isomerase Chain: L: PDB Molecule: putative ketol-acid reductoisomerase 2; PDBTitle: cryo-em structure of sulfolobus solfataricus ketol-acid2 reductoisomerase (sso-kari) in complex with mg2+, nadp, and cpd at3 ph7.5
67	c3g79A_	Alignment	not modelled	97.9	19	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
68	d1li4a1	Alignment	not modelled	97.8	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
69	c5ocmA_	Alignment	not modelled	97.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nad_gly3p_dh, nad-dependent glycerol-3-phosphate PDBTitle: imine reductase from streptosporangium roseum in complex with nadp+2 and 2,2,2-trifluoroacetophenone hydrate
70	c3prjB_	Alignment	not modelled	97.8	14	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.
71	c5b37A_	Alignment	not modelled	97.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan dehydrogenase; PDBTitle: crystal structure of l-tryptophan dehydrogenase from nostoc2 punctiforme
72	d1bg6a2	Alignment	not modelled	97.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
73	c4kqxB_	Alignment	not modelled	97.8	19	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: mutant slackia exigua kari ddv in complex with nad and an inhibitor
74	c2g5cD_	Alignment	not modelled	97.8	16	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
75	c3w6uA_	Alignment	not modelled	97.8	18	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
76	c4ypoB_	Alignment	not modelled	97.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
77	c3x2fA_	Alignment	not modelled	97.8	24	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
78	c3ktdC_	Alignment	not modelled	97.7	16	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution

79	c4d3fB_	Alignment	not modelled	97.7	21	PDB header: oxidoreductase Chain: B: PDB Molecule: imine reductase; PDBTitle: bcsired from bacillus cereus in complex with nadph
80	c5a9tA_	Alignment	not modelled	97.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisquinoline
81	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 isomeroreductase from2 pseudomonas aeruginosa
82	c1bg6A_	Alignment	not modelled	97.7	16	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
83	d1a4ia1	Alignment	not modelled	97.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
84	c4oqyA_	Alignment	not modelled	97.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: (s)-imine reductase; PDBTitle: streptomyces sp. gf3546 imine reductase
85	c5butG_	Alignment	not modelled	97.7	14	PDB header: membrane protein Chain: G: PDB Molecule: ktr system potassium uptake protein a,ktr system potassium PDBTitle: crystal structure of inactive conformation of ktrab k+ transporter
86	c5u5gC_	Alignment	not modelled	97.7	18	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: psf3 in complex with nadp+ and 2-opp
87	c4tskA_	Alignment	not modelled	97.7	12	PDB header: oxidoreductase,isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
88	c5yeqB_	Alignment	not modelled	97.7	17	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp+); PDBTitle: the structure of sac-kari protein
89	d1luxja1	Alignment	not modelled	97.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
90	c3g0oA_	Alignment	not modelled	97.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
91	c3gvpB_	Alignment	not modelled	97.7	19	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
92	d1v8ba1	Alignment	not modelled	97.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
93	c3pefA_	Alignment	not modelled	97.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, nad-binding; PDBTitle: crystal structure of ketol-gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
94	c4gbjB_	Alignment	not modelled	97.7	21	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
95	d1e5qa1	Alignment	not modelled	97.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	c3l6dB_	Alignment	not modelled	97.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
97	c3dhyC_	Alignment	not modelled	97.6	22	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
98	d1mv8a2	Alignment	not modelled	97.6	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
99	c4e21B_	Alignment	not modelled	97.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase (decarboxylating); PDBTitle: the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
100	c5v96A_	Alignment	not modelled	97.6	20	PDB header: hydrolase Chain: A: PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
101	c1e51A_	Alignment	not modelled	97.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
102	c2hk8B_	Alignment	not modelled	97.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
103	c1d4fD_	Alignment	not modelled	97.6	23	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-

						2 adenosylhomocysteine hydrolase PDB header: hydrolase
104	c3d64A_	Alignment	not modelled	97.6	26	Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
105	d2cvza2	Alignment	not modelled	97.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
106	c4dllB_	Alignment	not modelled	97.6	17	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
107	d1vpda2	Alignment	not modelled	97.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
108	c2f1kD_	Alignment	not modelled	97.6	13	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
109	d1f0ya2	Alignment	not modelled	97.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
110	c2q3eH_	Alignment	not modelled	97.6	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
111	c1vpdA_	Alignment	not modelled	97.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
112	c3b1fA_	Alignment	not modelled	97.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
113	c6grlA_	Alignment	not modelled	97.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: beta-hydroxyacid dehydrogenase, 3-hydroxyisobutyrate PDBTitle: structure of imine reductase (apo form) at 1.6 a resolution from2 saccharomonospora xinjiangensis
114	c6f3oC_	Alignment	not modelled	97.6	20	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
115	d1np3a2	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
116	d2naca1	Alignment	not modelled	97.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
117	c3n58D_	Alignment	not modelled	97.6	26	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
118	c6apeA_	Alignment	not modelled	97.6	23	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional protein fold from helicobacter2 pylori
119	c6aphA_	Alignment	not modelled	97.6	23	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
120	c3k96B_	Alignment	not modelled	97.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii