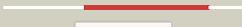
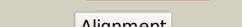
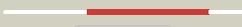


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2847c_cysG_3154664_3155881
Date	Wed Aug 7 12:50:51 BST 2019
Unique Job ID	2416e09ed8ce582b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1pjtB_	 Alignment		100.0	37	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatase for3 siroheme synthesis
2	d1s4da_	 Alignment		100.0	43	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
3	c2yboA_	 Alignment		100.0	43	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
4	c1cbfA_	 Alignment		100.0	31	PDB header: methyltransferase Chain: A: PDB Molecule: cobalt-precorrin-4 transmethylase; PDBTitle: the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
5	d1cbfa_	 Alignment		100.0	31	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
6	c4e16A_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: precorrin-4 c(11)-methyltransferase from clostridium difficile
7	d1pjqa2	 Alignment		100.0	39	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
8	c3ndcB_	 Alignment		100.0	28	PDB header: transferase Chain: B: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
9	c3kwpA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
10	d1va0a1	 Alignment		100.0	43	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
11	d1ve2a1	 Alignment		100.0	41	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase

12	c5hw4C_	Alignment		100.0	21	PDB header: transferase Chain: C: PDB Molecule: ribosomal rna small subunit methyltransferase i; PDBTitle: crystal structure of escherichia coli 16s rrna methyltransferase rsmi2 in complex with adomet
13	c2zvba_	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: precorrin-3 c17-methyltransferase; PDBTitle: crystal structure of tt0207 from thermus thermophilus hb8
14	c3nutC_	Alignment		100.0	22	PDB header: transferase Chain: C: PDB Molecule: precorrin-3 methylase; PDBTitle: crystal structure of the methyltransferase cobj
15	d1wyza1	Alignment		100.0	13	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
16	d2deka1	Alignment		100.0	21	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
17	d1wdea_	Alignment		100.0	18	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
18	c2e0ka_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 c20-methyltransferase; PDBTitle: crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
19	c1kyqC_	Alignment		100.0	20	PDB header: oxidoreductase, lyase Chain: C: PDB Molecule: siroheme biosynthesis protein met8; PDBTitle: met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
20	c2qbuA_	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 methyltransferase; PDBTitle: crystal structure of methanothermobacter thermautotrophicus cbil
21	d1vhva_	Alignment	not modelled	100.0	15	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
22	c5n0sa_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: peptide n-methyltransferase; PDBTitle: crystal structure of opha-deltac6 mutant y98a in complex with sam
23	c3i4ta_	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: diphthine synthase; PDBTitle: crystal structure of putative diphthine synthase from entamoeba2 histolytica
24	c2nnpA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: putative cobalamin synthesis related protein; PDBTitle: crystal structure of putative cobalamin synthesis related protein2 (cobf) from corynebacterium diphtheriae
25	c3nd1B_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: precorrin-6a synthase/cobf protein; PDBTitle: crystal structure of precorrin-6a synthase from rhodobacter capsulatus
26	c3dfzB_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: precorrin-2 dehydrogenase; PDBTitle: sirc, precorrin-2 dehydrogenase
27	c2bb3B_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: cobalamin biosynthesis precorrin-6y methylase (cbie); PDBTitle: crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
28	d2bb3a1	Alignment	not modelled	100.0	17	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase

29	d1kyqa1	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
30	d1pjqa1	Alignment	not modelled	99.9	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
31	c3hh1D	Alignment	not modelled	99.9	23	PDB header: transferase Chain: D: PDB Molecule: tetrapyrrole methylase family protein; PDBTitle: the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum t1s
32	c3fq6A	Alignment	not modelled	99.5	20	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
33	d2jfga1	Alignment	not modelled	98.3	20	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
34	c3d4oA	Alignment	not modelled	98.3	19	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
35	c2rirA	Alignment	not modelled	98.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
36	d1pjqa3	Alignment	not modelled	98.0	22	Fold: Siroheme synthase middle domains-like Superfamily: Siroheme synthase middle domains-like Family: Siroheme synthase middle domains-like
37	c3uagA	Alignment	not modelled	98.0	18	PDB header: ligase Chain: A: PDB Molecule: protein (udp-n-acetylmuramoyl-l-alanine:d- PDBTitle: udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
38	c4p22A	Alignment	not modelled	97.9	22	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme 1; PDBTitle: crystal structure of n-terminal fragments of e1
39	c4d7aA	Alignment	not modelled	97.8	23	PDB header: ligase Chain: A: PDB Molecule: trna threonylcarbamoyladenine dehydratase; PDBTitle: crystal structure of e. coli trna n6-threonylcarbamoyladenine2 dehydratase, tcda, in complex with amp at 1.801 angstrom3 resolution
40	c2g1uA	Alignment	not modelled	97.8	20	PDB header: transport protein Chain: A: PDB Molecule: hypothetical protein tm1088a; PDBTitle: crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
41	d1lssa	Alignment	not modelled	97.8	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
42	c3gvpB	Alignment	not modelled	97.7	25	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
43	c3dhyC	Alignment	not modelled	97.7	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
44	d1li4a1	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
45	c5hm8C	Alignment	not modelled	97.7	26	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad.
46	c1y8qA	Alignment	not modelled	97.7	15	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like 1 activating enzyme e1a; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex
47	c1d4fD	Alignment	not modelled	97.7	22	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
48	c3gucB	Alignment	not modelled	97.6	8	PDB header: transferase Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: human ubiquitin-activating enzyme 5 in complex with amppnp
49	c3oneA	Alignment	not modelled	97.6	22	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
50	c3x2fA	Alignment	not modelled	97.6	22	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
51	d1kyqa2	Alignment	not modelled	97.6	25	Fold: Siroheme synthase middle domains-like Superfamily: Siroheme synthase middle domains-like Family: Siroheme synthase middle domains-like
52	d1jw9b	Alignment	not modelled	97.6	22	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Molybdenum cofactor biosynthesis protein MoeB
53	d1e5qa1	Alignment	not modelled	97.6	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						Fold: NAD(P)-binding Rossmann-fold domains

54	d1v8ba1	Alignment	not modelled	97.6	18	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
55	c1v8bA	Alignment	not modelled	97.6	19	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
56	c1gpiA	Alignment	not modelled	97.6	19	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
57	c5v96A	Alignment	not modelled	97.6	25	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
58	c3n58D	Alignment	not modelled	97.5	23	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
59	c3d64A	Alignment	not modelled	97.5	25	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
60	c6aphA	Alignment	not modelled	97.5	26	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
61	c6f3oC	Alignment	not modelled	97.5	24	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
62	c1zfnA	Alignment	not modelled	97.5	17	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase thif; PDBTitle: structural analysis of escherichia coli thif
63	c3llvA	Alignment	not modelled	97.4	16	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
64	d1ygva1	Alignment	not modelled	97.4	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
65	c2f00A	Alignment	not modelled	97.4	16	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
66	c4g65A	Alignment	not modelled	97.4	16	PDB header: transport protein Chain: A: PDB Molecule: trk system potassium uptake protein trka; PDBTitle: potassium transporter peripheral membrane component (trka) from vibrio2 vulnificus
67	c4j7cA	Alignment	not modelled	97.4	17	PDB header: transport protein Chain: A: PDB Molecule: ktr system potassium uptake protein a; PDBTitle: ktrab potassium transporter from bacillus subtilis
68	c3kydB	Alignment	not modelled	97.4	21	PDB header: ligase Chain: B: PDB Molecule: sumo-activating enzyme subunit 2; PDBTitle: human sumo e1~sumo1-amp tetrahedral intermediate mimic
69	c3eywA	Alignment	not modelled	97.4	21	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
70	c1wwkA	Alignment	not modelled	97.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
71	c1y8qD	Alignment	not modelled	97.3	22	PDB header: ligase Chain: D: PDB Molecule: ubiquitin-like 2 activating enzyme e1b; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex
72	c4g2nA	Alignment	not modelled	97.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; PDBTitle: crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js6 66
73	c6h77B	Alignment	not modelled	97.3	11	PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: e1 enzyme for ubiquitin like protein activation in complex with ubl
74	c3fwzA	Alignment	not modelled	97.3	21	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ybal; PDBTitle: crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
75	c6cauA	Alignment	not modelled	97.3	17	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
76	c2g76A	Alignment	not modelled	97.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
77	d1gdha1	Alignment	not modelled	97.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
78	c3kycB	Alignment	not modelled	97.3	22	PDB header: ligase Chain: B: PDB Molecule: sumo-activating enzyme subunit 2; PDBTitle: human sumo e1 complex with a sumo1-amp mimic

79	d1p3da1	Alignment	not modelled	97.3	10	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
80	c4qvlB	Alignment	not modelled	97.2	19	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: crystal structure of the gsuk rck domain
81	c2nvuB	Alignment	not modelled	97.2	20	PDB header: protein turnover, ligase Chain: B: PDB Molecule: maltose binding protein/nedd8-activating enzyme PDBTitle: structure of appbp1-uba3--nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
82	c3gznB	Alignment	not modelled	97.2	20	PDB header: protein binding/ligase Chain: B: PDB Molecule: nedd8-activating enzyme e1 catalytic subunit; PDBTitle: structure of nedd8-activating enzyme in complex with nedd8 and mln4924
83	c4n7rB	Alignment	not modelled	97.2	23	PDB header: oxidoreductase/protein binding Chain: B: PDB Molecule: glutamyl-trna reductase 1, chloroplastic; PDBTitle: crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
84	c6dc6A	Alignment	not modelled	97.2	18	PDB header: signaling protein/ligase Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme 1; PDBTitle: crystal structure of human ubiquitin activating enzyme e1 (uba1) in2 complex with ubiquitin
85	c3l4bG	Alignment	not modelled	97.2	17	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
86	c5t8xA	Alignment	not modelled	97.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean
87	d1j6ua1	Alignment	not modelled	97.2	16	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
88	c4gx5D	Alignment	not modelled	97.2	15	PDB header: transport protein Chain: D: PDB Molecule: trka domain protein; PDBTitle: gsuk channel
89	c3wwzB	Alignment	not modelled	97.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: d-lactate dehydrogenase (fermentative); PDBTitle: the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
90	c4cukA	Alignment	not modelled	97.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: structure of salmonella d-lactate dehydrogenase in complex2 with nadh
91	d1j4aa1	Alignment	not modelled	97.1	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
92	c2dbqA	Alignment	not modelled	97.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
93	c3ic5A	Alignment	not modelled	97.1	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
94	c3hn7A	Alignment	not modelled	97.1	10	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
95	c2pv7B	Alignment	not modelled	97.1	12	PDB header: isomerase, oxidoreductase Chain: B: PDB Molecule: t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
96	c4plpB	Alignment	not modelled	97.1	19	PDB header: transferase Chain: B: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad
97	d2naca1	Alignment	not modelled	97.1	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
98	d2fy8a1	Alignment	not modelled	97.1	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
99	c4xa8A	Alignment	not modelled	97.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase nad-binding; PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from xanthobacter autotrophicus py2
100	c5vwwA	Alignment	not modelled	97.0	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: structure of murc from pseudomonas aeruginosa
101	c1j4aA	Alignment	not modelled	97.0	19	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
102	c4e5kC	Alignment	not modelled	97.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: phosphite dehydrogenase (thermostable variant); PDBTitle: thermostable phosphite dehydrogenase in complex with nad and sulfite
103	c3cmmA	Alignment	not modelled	97.0	12	PDB header: ligase/protein binding Chain: A: PDB Molecule: ubiquitin-activating enzyme e1 1;

					PDBTitle: crystal structure of the uba1-ubiquitin complex
104	c4gx2B_	Alignment	not modelled	97.0	17 PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: gsuk channel bound to nad
105	d1gpja2	Alignment	not modelled	97.0	18 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
106	c1np3B_	Alignment	not modelled	97.0	26 PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroxidoreductase from <i>Pseudomonas aeruginosa</i>
107	d1mx3a1	Alignment	not modelled	97.0	18 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
108	d1l7da1	Alignment	not modelled	97.0	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
109	c1gdhA_	Alignment	not modelled	97.0	15 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
110	c3h9gA_	Alignment	not modelled	97.0	21 PDB header: transferase/antibiotic Chain: A: PDB Molecule: mccb protein; PDBTitle: crystal structure of e. coli mccb + mcca-n7isoasn
111	c4hy3D_	Alignment	not modelled	97.0	14 PDB header: oxidoreductase Chain: D: PDB Molecule: phosphoglycerate oxidoreductase; PDBTitle: crystal structure of a phosphoglycerate oxidoreductase from <i>Rhizobium etli</i>
112	c4dioB_	Alignment	not modelled	97.0	11 PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha part 1; PDBTitle: the crystal structure of transhydrogenase from <i>Sinorhizobium meliloti</i>
113	c4lswA_	Alignment	not modelled	96.9	12 PDB header: hydrolase Chain: A: PDB Molecule: d-2-hydroxyacid dehydrogenase protein; PDBTitle: crystallization and structural analysis of 2-hydroxyacid dehydrogenase2 from <i>Ketogulonicigenium vulgare</i> y25
114	c2ph5A_	Alignment	not modelled	96.9	19 PDB header: transferase Chain: A: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase hss from <i>Legionella pneumophila</i> in complex with nad, northeast structural genomics target3 lgr54
115	c4zgsE_	Alignment	not modelled	96.9	22 PDB header: oxidoreductase Chain: E: PDB Molecule: putative d-lactate dehydrogenase; PDBTitle: identification of the pyruvate reductase of <i>Chlamydomonas reinhardtii</i>
116	c4ii3A_	Alignment	not modelled	96.9	24 PDB header: ligase Chain: A: PDB Molecule: ubiquitin-activating enzyme e1 1; PDBTitle: crystal structure of s. pombe ubiquitin activating enzyme 1 (uba1) in2 complex with ubiquitin and atp/mg
117	c2eezG_	Alignment	not modelled	96.9	17 PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from <i>Thermophilus</i>
118	c1e5IA_	Alignment	not modelled	96.9	24 PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from <i>Magnaporthe grisea</i>
119	c6ih2B_	Alignment	not modelled	96.9	17 PDB header: oxidoreductase Chain: B: PDB Molecule: phosphite dehydrogenase; PDBTitle: crystal structure of phosphite dehydrogenase from <i>Ralstonia</i> sp. 4506
120	c3wwyA_	Alignment	not modelled	96.9	12 PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: the crystal structure of d-lactate dehydrogenase from <i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i>