

# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3178 (-)_3546435_3546794
Date	Thu Aug 8 16:20:36 BST 2019
Unique Job ID	ec0e6a6e1aa1b9a0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3r5zB_</a>	Alignment		100.0	29	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
2	<a href="#">c3r5yC_</a>	Alignment		100.0	31	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
3	<a href="#">c3h96B_</a>	Alignment		100.0	31	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> f420-h2 dependent reductase a; <b>PDBTitle:</b> msmeq_3358 f420 reductase
4	<a href="#">c4y9iA_</a>	Alignment		100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterium tuberculosis paralogous family 11; <b>PDBTitle:</b> structure of f420-h2 dependent reductase (fdr-a) msmeq_2027
5	<a href="#">c3r5wO_</a>	Alignment		100.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> deazaflavin-dependent nitroreductase; <b>PDBTitle:</b> structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420
6	<a href="#">c3f7eB_</a>	Alignment		98.9	17	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn- <b>PDBTitle:</b> msmeq_3380 f420 reductase
7	<a href="#">c2iabB_</a>	Alignment		98.8	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a protein with fmn-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution
8	<a href="#">d1rfea_</a>	Alignment		98.6	17	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
9	<a href="#">d2asfa1</a>	Alignment		98.6	18	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
10	<a href="#">c3tgvD_</a>	Alignment		98.5	21	<b>PDB header:</b> heme binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> heme-binding protein hutz; <b>PDBTitle:</b> crystal structure of hutz, the heme storage protein from vibrio2 cholerae
11	<a href="#">d1w9aa_</a>	Alignment		98.5	19	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like

12	<a href="#">c4zkyB_</a>	Alignment		98.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5-phosphate oxidase; <b>PDBTitle:</b> structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis
13	<a href="#">d1vl7a_</a>	Alignment		98.3	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
14	<a href="#">c3db0B_</a>	Alignment		98.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lin2891 protein; <b>PDBTitle:</b> crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution
15	<a href="#">d2i02a1</a>	Alignment		98.2	9	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
16	<a href="#">c2htiA_</a>	Alignment		98.1	13	<b>PDB header:</b> fmn-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bh0577 protein; <b>PDBTitle:</b> crystal structure of a flavin-nucleotide-binding protein (bh_0577)2 from bacillus halodurans at 2.50 a resolution
17	<a href="#">d2htia1</a>	Alignment		98.1	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
18	<a href="#">d2fg9a1</a>	Alignment		98.1	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
19	<a href="#">c2hhzA_</a>	Alignment		98.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
20	<a href="#">c3ec6A_</a>	Alignment		98.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> general stress protein 26; <b>PDBTitle:</b> crystal structure of the general stress protein 26 from bacillus2 anthracis str. Sterne
21	<a href="#">d2hq9a1</a>	Alignment	not modelled	98.0	16	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
22	<a href="#">c2ig6B_</a>	Alignment	not modelled	98.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nimc/nima family protein; <b>PDBTitle:</b> crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution
23	<a href="#">c5bncB_</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> heme binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> heme binding protein msmeg_6519; <b>PDBTitle:</b> structure of heme binding protein msmeg_6519 from mycobacterium2 smegmatis
24	<a href="#">c2re7A_</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase related2 protein (psyc_0186) from psychrobacter arcticus 273-4 at 2.50 a3 resolution
25	<a href="#">c3dnhB_</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein atu2129; <b>PDBTitle:</b> the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58
26	<a href="#">c3gasA_</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> heme oxygenase; <b>PDBTitle:</b> crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
27	<a href="#">d2arza1</a>	Alignment	not modelled	97.8	19	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
28	<a href="#">d2hq7a1</a>	Alignment	not modelled	97.8	7	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like

29	<a href="#">d2fhqa1</a>	Alignment	not modelled	97.6	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
30	<a href="#">d2fura1</a>	Alignment	not modelled	97.6	17	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
31	<a href="#">c6eciQ_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> fad-binding protein <b>Chain:</b> Q: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn-binding <b>PDBTitle:</b> structure of the fad binding protein msmeq_5243 from mycobacterium2 smegmatis
32	<a href="#">c3u0iA_</a>	Alignment	not modelled	97.6	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable fad-binding, putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a probable fad-binding, putative uncharacterized2 protein from brucella melitensis
33	<a href="#">d1t9ma_</a>	Alignment	not modelled	97.6	17	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
34	<a href="#">c3fkbB_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution
35	<a href="#">c4ybnB_</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavin-nucleotide-binding protein; <b>PDBTitle:</b> structure of the fad and heme binding protein msmeq_4975 from2 mycobacterium smegmatis
36	<a href="#">c5escD_</a>	Alignment	not modelled	97.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> hupz; <b>PDBTitle:</b> crystal structure of group a streptococcus hupz
37	<a href="#">c2q9kA_</a>	Alignment	not modelled	97.5	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution
38	<a href="#">c1nrgA_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxine 5'-phosphate oxidase; <b>PDBTitle:</b> structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
39	<a href="#">d1nrga_</a>	Alignment	not modelled	97.4	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
40	<a href="#">c3cp3A_</a>	Alignment	not modelled	97.3	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae
41	<a href="#">d1ty9a_</a>	Alignment	not modelled	97.3	18	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
42	<a href="#">d2a2ja1</a>	Alignment	not modelled	97.3	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
43	<a href="#">c3u34D_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> general stress protein; <b>PDBTitle:</b> crystal structure of the general stress fmn/fad binding protein from2 the phytopathogen xanthomonas citri
44	<a href="#">c2a2iA_</a>	Alignment	not modelled	97.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
45	<a href="#">c3dmbA_</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative general stress protein 26 with a pnp-oxidase like <b>PDBTitle:</b> crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
46	<a href="#">c2htdB_</a>	Alignment	not modelled	97.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted flavin-nucleotide-binding protein from cog3576 <b>PDBTitle:</b> crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (ldb0262) from lactobacillus delbrueckii subsp. at 1.60 a resolution
47	<a href="#">c2qeaB_</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative general stress protein 26; <b>PDBTitle:</b> crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
48	<a href="#">c4hmwB_</a>	Alignment	not modelled	96.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of phzq from burkholderia lata 383
49	<a href="#">d1ci0a_</a>	Alignment	not modelled	96.6	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
50	<a href="#">d1dnla_</a>	Alignment	not modelled	96.5	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
51	<a href="#">d1xhna1</a>	Alignment	not modelled	96.3	15	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
52	<a href="#">c6rk0A_</a>	Alignment	not modelled	96.0	20	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of the flavocytochrome anf3 from azotobacter vinelandii
53	<a href="#">d2vpaa1</a>	Alignment	not modelled	95.4	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel

						<b>Family:</b> PNP-oxidase like
54	<a href="#">d1flma_</a>	Alignment	not modelled	95.4	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
55	<a href="#">c2ol5B_</a>	Alignment	not modelled	91.0	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> pai 2 protein; <b>PDBTitle:</b> crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearothermophilus
56	<a href="#">c2ptfB_</a>	Alignment	not modelled	90.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mth_863; <b>PDBTitle:</b> crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn
57	<a href="#">c2i51B_</a>	Alignment	not modelled	86.9	14	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein of cog5135; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related, fmn2 binding protein (npun_f5749) from nostoc punctiforme pcc 73102 at3 1.40 a resolution
58	<a href="#">c2ou5B_</a>	Alignment	not modelled	81.9	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn-binding; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related fmn-2 binding protein (jann_0254) from jannaschia sp. ccs1 at 1.60 a3 resolution
59	<a href="#">c4n7rD_</a>	Alignment	not modelled	72.4	10	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> genomic dna, chromosome 3, p1 clone: mxl8; <b>PDBTitle:</b> crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
60	<a href="#">d2ptfa1</a>	Alignment	not modelled	64.0	10	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
61	<a href="#">d2imla1</a>	Alignment	not modelled	40.5	19	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
62	<a href="#">d2nr4a1</a>	Alignment	not modelled	32.3	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
63	<a href="#">c4wt5A_</a>	Alignment	not modelled	15.4	10	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco accumulation factor 1, isoform 2; <b>PDBTitle:</b> the c-terminal domain of rubisco accumulation factor 1 from2 arabidopsis thaliana, crystal form ii
64	<a href="#">d1k3ra1</a>	Alignment	not modelled	15.4	14	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Hypothetical protein MTH1 (MT0001), insert domain
65	<a href="#">c4a2nB_</a>	Alignment	not modelled	14.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> isoprenylcysteine carboxyl methyltransferase; <b>PDBTitle:</b> crystal structure of ma-icmt
66	<a href="#">c3fgeA_</a>	Alignment	not modelled	12.4	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavin reductase with split barrel domain; <b>PDBTitle:</b> crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
67	<a href="#">c5v7pA_</a>	Alignment	not modelled	12.1	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-s-isoprenylcysteine o-methyltransferase; <b>PDBTitle:</b> atomic structure of the eukaryotic intramembrane ras methyltransferase2 icmt (isoprenylcysteine carboxyl methyltransferase), in complex with3 a monobody
68	<a href="#">c3gr1A_</a>	Alignment	not modelled	11.4	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein prgh; <b>PDBTitle:</b> periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-392)
69	<a href="#">c3b5mD_</a>	Alignment	not modelled	10.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
70	<a href="#">c2levA_</a>	Alignment	not modelled	10.6	24	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ler; <b>PDBTitle:</b> structure of the dna complex of the c-terminal domain of ler
71	<a href="#">d1dgsa3</a>	Alignment	not modelled	10.6	21	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> Adenylation domain of NAD+-dependent DNA ligase
72	<a href="#">c6mk1V_</a>	Alignment	not modelled	8.7	50	<b>PDB header:</b> protein fibril <b>Chain:</b> V: <b>PDB Molecule:</b> <b>PDBTitle:</b> cryo-em of self-assembly peptide filament heat_r1
73	<a href="#">d1zq1c1</a>	Alignment	not modelled	8.5	36	<b>Fold:</b> GatB/YqeY motif <b>Superfamily:</b> GatB/YqeY motif <b>Family:</b> GatB/GatE C-terminal domain-like
74	<a href="#">c3bpkB_</a>	Alignment	not modelled	7.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrilotriacetate monooxygenase component b; <b>PDBTitle:</b> crystal structure of nitrilotriacetate monooxygenase component b from2 bacillus cereus
75	<a href="#">c3jslA_</a>	Alignment	not modelled	7.8	9	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> crystal structure of the adenylation domain of nad+-2 dependent dna ligase from staphylococcus aureus
76	<a href="#">d1c9ka_</a>	Alignment	not modelled	7.7	33	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
77	<a href="#">c4yd8A_</a>	Alignment	not modelled	7.5	27	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein pthb1;

						<b>PDBTitle:</b> bardet-biedl syndrome 9 protein (aa1-407), homo sapiens
78	<a href="#">d1ta8a_</a>	Alignment	not modelled	7.5	21	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> Adenylation domain of NAD <sup>+</sup> -dependent DNA ligase
79	<a href="#">c5aj1A_</a>	Alignment	not modelled	7.3	19	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> swi/snf-related matrix-associated actin-dependent regulator <b>PDBTitle:</b> solution structure of the smarc domain
80	<a href="#">c3pn1A_</a>	Alignment	not modelled	7.3	13	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> novel bacterial nad <sup>+</sup> -dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
81	<a href="#">c1zauA_</a>	Alignment	not modelled	7.2	15	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> adenylation domain of nad <sup>+</sup> dependent dna ligase from m.tuberculosis
82	<a href="#">c3zfnA_</a>	Alignment	not modelled	6.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> n-terminal protease npro; <b>PDBTitle:</b> crystal structure of product-like, processed n-terminal protease npro
83	<a href="#">c1ztnA_</a>	Alignment	not modelled	6.8	71	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily c member 4; <b>PDBTitle:</b> inactivation gate of potassium channel raw3, nmr, 8 structures
84	<a href="#">d1v9pa3</a>	Alignment	not modelled	6.7	21	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> Adenylation domain of NAD <sup>+</sup> -dependent DNA ligase
85	<a href="#">c4fprC_</a>	Alignment	not modelled	6.7	29	<b>PDB header:</b> protein binding <b>Chain:</b> C; <b>PDB Molecule:</b> avirulence effector avrlm4-7; <b>PDBTitle:</b> structure of a fungal protein
86	<a href="#">c2dhyA_</a>	Alignment	not modelled	6.6	12	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> cue domain-containing protein 1; <b>PDBTitle:</b> solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
87	<a href="#">d1b04a_</a>	Alignment	not modelled	6.5	13	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> Adenylation domain of NAD <sup>+</sup> -dependent DNA ligase
88	<a href="#">c3qrgA_</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein tthb192; <b>PDBTitle:</b> structure of thermus thermophilus cse3 bound to an rna representing a2 pre-cleavage complex
89	<a href="#">c1cpbA_</a>	Alignment	not modelled	6.3	15	<b>PDB header:</b> hydrolase (c-terminal peptidase) <b>Chain:</b> A; <b>PDB Molecule:</b> carboxypeptidase b; <b>PDBTitle:</b> structure of carboxypeptidase b at 2.8 angstroms resolution
90	<a href="#">d1mg4a_</a>	Alignment	not modelled	6.1	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Doublecortin (DC) <b>Family:</b> Doublecortin (DC)
91	<a href="#">c1v9pB_</a>	Alignment	not modelled	5.9	21	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> crystal structure of nad <sup>+</sup> -dependent dna ligase
92	<a href="#">c1dgsB_</a>	Alignment	not modelled	5.8	21	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> crystal structure of nad <sup>+</sup> -dependent dna ligase from t.2 filiformis
93	<a href="#">c5jzB_</a>	Alignment	not modelled	5.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein yhfg; <b>PDBTitle:</b> e. coli ecfct in complex with ecfca mutant e28g
94	<a href="#">c6d10A_</a>	Alignment	not modelled	5.3	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> alginate biosynthesis protein algf; <b>PDBTitle:</b> cs-rosetta determined structures of the c-terminal domain of algf from2 p. aeruginosa
95	<a href="#">c4u65A_</a>	Alignment	not modelled	5.3	24	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> two component histidine kinase, ggdef domain protein/eal <b>PDBTitle:</b> structure of the periplasmic output domain of the legionella2 pneumophila lapd ortholog cdgs9 in complex with pseudomonas3 fluorescens lapg
96	<a href="#">c5a15A_</a>	Alignment	not modelled	5.3	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> btb/poz domain-containing protein kctd16; <b>PDBTitle:</b> crystal structure of the btb domain of human kctd16
97	<a href="#">d2k49a1</a>	Alignment	not modelled	5.3	36	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
98	<a href="#">c5jzF_</a>	Alignment	not modelled	5.2	18	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> uncharacterized protein yhfg; <b>PDBTitle:</b> e. coli ecfct in complex with ecfca mutant e28g
99	<a href="#">d1hnra_</a>	Alignment	not modelled	5.0	18	<b>Fold:</b> H-NS histone-like proteins <b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins