

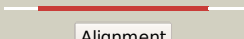

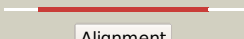




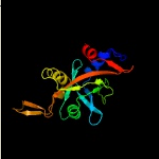

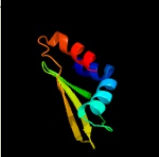







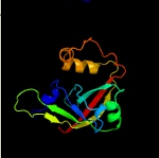




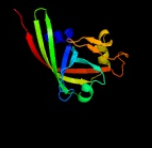



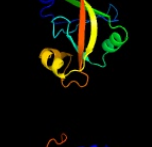

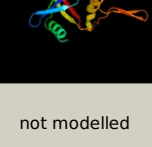


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3839_(- )_4312943_4313719
Date	Sat Aug 10 22:05:02 BST 2019
Unique Job ID	77134819dd2f8aab

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5bncB_</a>	 Alignment		100.0	18	<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
2	<a href="#">c4n7rD_</a>	 Alignment		100.0	16	<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
3	<a href="#">d2arza1</a>	 Alignment		100.0	17	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
4	<a href="#">c3dnhB_</a>	 Alignment		100.0	14	<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
5	<a href="#">d1xha1</a>	 Alignment		100.0	17	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
6	<a href="#">c3gasA_</a>	 Alignment		99.8	15	<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
7	<a href="#">d1vl7a_</a>	 Alignment		99.5	9	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
8	<a href="#">c3tgvD_</a>	 Alignment		99.4	8	<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 storsge protein from vibrio2 cholerae
9	<a href="#">c2iabB_</a>	 Alignment		98.5	22	<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
10	<a href="#">c3f7eB_</a>	 Alignment		98.5	13	<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
11	<a href="#">c3db0B_</a>	 Alignment		98.2	10	<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

12	<a href="#">d2fhqa1</a>	Alignment		98.1	10	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
13	<a href="#">c3ec6A</a>	Alignment		98.1	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
14	<a href="#">c3u34D</a>	Alignment		98.0	11	<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
15	<a href="#">d1rfea</a>	Alignment		98.0	8	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
16	<a href="#">d1w9aa</a>	Alignment		98.0	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
17	<a href="#">c2re7A</a>	Alignment		98.0	10	<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
18	<a href="#">d2i02a1</a>	Alignment		97.9	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
19	<a href="#">c3u0iA</a>	Alignment		97.9	21	<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
20	<a href="#">c4zkyB</a>	Alignment		97.9	16	<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
21	<a href="#">c2ig6B</a>	Alignment	not modelled	97.8	10	<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
22	<a href="#">c2qeaB</a>	Alignment	not modelled	97.8	9	<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
23	<a href="#">d2asfa1</a>	Alignment	not modelled	97.7	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
24	<a href="#">c3dmbA</a>	Alignment	not modelled	97.7	11	<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
25	<a href="#">c3fkhB</a>	Alignment	not modelled	97.6	13	<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
26	<a href="#">d2htia1</a>	Alignment	not modelled	97.5	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
27	<a href="#">c2htiA</a>	Alignment	not modelled	97.5	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
						<b>Fold:</b> Split barrel-like

28	<a href="#">d2hq7a1</a>	Alignment	not modelled	97.5	9	<b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
29	<a href="#">d2hq9a1</a>	Alignment	not modelled	97.4	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
30	<a href="#">c3cp3A</a>	Alignment	not modelled	97.4	19	<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
31	<a href="#">c2hhzA</a>	Alignment	not modelled	97.3	9	<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
32	<a href="#">d2fg9a1</a>	Alignment	not modelled	97.2	15	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
33	<a href="#">c6eciQ</a>	Alignment	not modelled	97.0	14	<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 msmeg_5243 from mycobacterium2 smegmatis
34	<a href="#">c2ou5B</a>	Alignment	not modelled	96.3	14	<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
35	<a href="#">d2fura1</a>	Alignment	not modelled	96.3	10	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
36	<a href="#">d1flma</a>	Alignment	not modelled	95.8	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
37	<a href="#">c2q9ka</a>	Alignment	not modelled	95.7	13	<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="#">c4ybnB</a>	Alignment	not modelled	95.7	13	<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 msmeg_4975 from2 mycobacterium smegmatis
39	<a href="#">c1nrgA</a>	Alignment	not modelled	95.6	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
40	<a href="#">d1nrga</a>	Alignment	not modelled	95.6	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
41	<a href="#">d1t9ma</a>	Alignment	not modelled	95.2	16	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
42	<a href="#">d1dnla</a>	Alignment	not modelled	95.0	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
43	<a href="#">c5escD</a>	Alignment	not modelled	95.0	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
44	<a href="#">d1ty9a</a>	Alignment	not modelled	94.5	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
45	<a href="#">d2vpaa1</a>	Alignment	not modelled	93.2	15	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
46	<a href="#">c2a2jA</a>	Alignment	not modelled	93.2	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
47	<a href="#">c2htdB</a>	Alignment	not modelled	91.6	13	<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
48	<a href="#">d2a2ja1</a>	Alignment	not modelled	89.9	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
49	<a href="#">c4hmbW</a>	Alignment	not modelled	86.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of phz3 from burkholderia lata 383
50	<a href="#">c6rk0A</a>	Alignment	not modelled	73.0	12	<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
51	<a href="#">c2ol5B</a>	Alignment	not modelled	58.6	10	<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
52	<a href="#">d1ci0a</a>	Alignment	not modelled	39.6	10	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
						<b>PDB header:</b> oxidoreductase

53	<a href="#">c3r5wO_</a>	Alignment	not modelled	36.4	16	<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
54	<a href="#">c3r5yC_</a>	Alignment	not modelled	32.9	16	<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
55	<a href="#">c2i51B_</a>	Alignment	not modelled	31.5	15	<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
56	<a href="#">d1fx0a1</a>	Alignment	not modelled	21.5	13	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
57	<a href="#">d1skyb1</a>	Alignment	not modelled	20.3	10	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
58	<a href="#">d2glia1</a>	Alignment	not modelled	15.6	27	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
59	<a href="#">c3r5zB_</a>	Alignment	not modelled	13.0	14	<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
60	<a href="#">d2f43a1</a>	Alignment	not modelled	12.0	27	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
61	<a href="#">c5c6uA_</a>	Alignment	not modelled	10.2	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> rv3722c aminotransferase from mycobacterium tuberculosis
62	<a href="#">c3zmnA_</a>	Alignment	not modelled	9.5	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vp17; <b>PDBTitle:</b> vp17, a capsid protein of bacteriophage p23-77
63	<a href="#">d1v86a_</a>	Alignment	not modelled	8.6	25	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
64	<a href="#">c4y9iA_</a>	Alignment	not modelled	8.5	13	<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) msmeg_2027
65	<a href="#">c2dzmA_</a>	Alignment	not modelled	8.4	23	<b>PDB header:</b> structural genomics unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> fas-associated factor 1; <b>PDBTitle:</b> solution structure of the ubiquitin-like domain in human2 fas-associated factor 1 (hfaf1)
66	<a href="#">d2jdia1</a>	Alignment	not modelled	7.8	19	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
67	<a href="#">c2rfeF_</a>	Alignment	not modelled	7.4	55	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> erbb receptor feedback inhibitor 1; <b>PDBTitle:</b> crystal structure of the complex between the egfr kinase domain and a2 mig6 peptide
68	<a href="#">c2rf9C_</a>	Alignment	not modelled	7.3	55	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> erbb receptor feedback inhibitor 1; <b>PDBTitle:</b> crystal structure of the complex between the egfr kinase domain and a2 mig6 peptide
69	<a href="#">c2rf9D_</a>	Alignment	not modelled	7.3	55	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> erbb receptor feedback inhibitor 1; <b>PDBTitle:</b> crystal structure of the complex between the egfr kinase domain and a2 mig6 peptide
70	<a href="#">c4i21D_</a>	Alignment	not modelled	7.3	55	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> erbb receptor feedback inhibitor 1; <b>PDBTitle:</b> crystal structure of l858r + t790m egfr kinase domain in complex with2 mig6 peptide
71	<a href="#">c2rfeE_</a>	Alignment	not modelled	7.3	55	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> erbb receptor feedback inhibitor 1; <b>PDBTitle:</b> crystal structure of the complex between the egfr kinase domain and a2 mig6 peptide
72	<a href="#">c2vsfA_</a>	Alignment	not modelled	7.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair helicase rad3 related protein; <b>PDBTitle:</b> structure of xpd from thermoplasma acidophilum
73	<a href="#">c5igwA_</a>	Alignment	not modelled	7.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide 2'-phosphotransferase ii; <b>PDBTitle:</b> macrolide 2'-phosphotransferase type ii - complex with gdp and2 clarithromycin
74	<a href="#">c5z6pB_</a>	Alignment	not modelled	6.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> b-agarase; <b>PDBTitle:</b> the crystal structure of an agarase, agwh50c
75	<a href="#">c5iy8W_</a>	Alignment	not modelled	6.2	10	<b>PDB header:</b> transcription, transferase/dna <b>Chain:</b> W: <b>PDB Molecule:</b> tfiih basal transcription factor complex helicase xpd <b>PDBTitle:</b> human holo-pic in the initial transcribing state
76	<a href="#">c4o5oA_</a>	Alignment	not modelled	6.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> x-ray crystal structure of a 3-hydroxyacyl-coa dehydrogenase from2 brucella suis
						<b>PDB header:</b> transferase

77	<a href="#">c3pplB_</a>	Alignment	not modelled	5.9	21	<b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
78	<a href="#">c2q6mA_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> cholix toxin; <b>PDBTitle:</b> catalytic fragment of cholix toxin from vibrio cholerae in complex2 with the pj34 inhibitor
79	<a href="#">c4i21C_</a>	Alignment	not modelled	5.7	55	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> erbb receptor feedback inhibitor 1; <b>PDBTitle:</b> crystal structure of l858r + t790m egfr kinase domain in complex with2 mig6 peptide
80	<a href="#">d1ib8a1</a>	Alignment	not modelled	5.7	7	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> YhbC-like, C-terminal domain <b>Family:</b> YhbC-like, C-terminal domain
81	<a href="#">d1tf3a3</a>	Alignment	not modelled	5.6	25	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
82	<a href="#">d2o23a1</a>	Alignment	not modelled	5.4	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
83	<a href="#">c4bq3A_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> b-agarase; <b>PDBTitle:</b> structural analysis of an exo-beta-agarase
84	<a href="#">c6em5v_</a>	Alignment	not modelled	5.3	22	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 60s ribosomal protein l23-a; <b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes