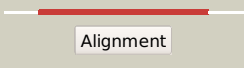

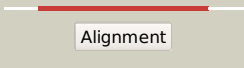

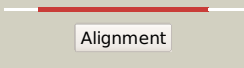

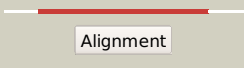
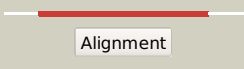

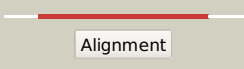

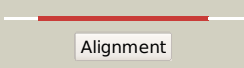

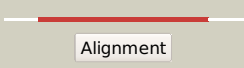
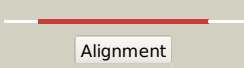

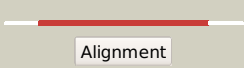

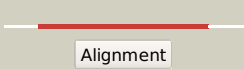












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3712_(-)_4157159_4158400
Date	Fri Aug 9 18:20:40 BST 2019
Unique Job ID	11e26475c54572de

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6gs2B_			100.0	27	PDB header: biosynthetic protein Chain: B: PDB Molecule: sa1708 protein; PDBTitle: crystal structure of the gatd/murt enzyme complex from staphylococcus2 aureus
2	c4qdiA_			100.0	20	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
3	c3lk7A_			100.0	19	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
4	c3uagA_			100.0	22	PDB header: ligase Chain: A: PDB Molecule: protein (udp-n-acetylmuramoyl-l-alanine:d- PDBTitle: udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
5	c4c13A_			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
6	c2xjaD_			100.0	21	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
7	c6fqbd_			100.0	27	PDB header: ligase Chain: D: PDB Molecule: mur ligase family protein; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
8	c1e8cB_			100.0	21	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
9	c2f00A_			100.0	18	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
10	c2am1A_			100.0	17	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine-d-glutamyl-lysine-d-alanyl-d- PDBTitle: sp protein ligand 1
11	c2wtzC_			100.0	23	PDB header: ligase Chain: C: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate- PDBTitle: mure ligase of mycobacterium tuberculosis

12	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
13	c4bucA	Alignment		100.0	15	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
14	c3zl8A	Alignment		100.0	16	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
15	c1gg4A	Alignment		100.0	18	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
16	c4cvkA	Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine PDBTitle: pamurf in complex with udp-murnac-tripeptide (mdap)
17	c1j6uA	Alignment		100.0	21	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
18	c2vosA	Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: folypolyglutamate synthase protein folc; PDBTitle: mycobacterium tuberculosis folypolyglutamate synthase2 complexed with adp
19	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
20	c2qc6A	Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: folypolyglutamate synthase; PDBTitle: s73a mutant of l. casei fpgs
21	c1o5zA	Alignment	not modelled	100.0	17	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
22	c1w78A	Alignment	not modelled	100.0	18	PDB header: synthase Chain: A: PDB Molecule: folc bifunctional protein; PDBTitle: e.coli folc in complex with dhpp and adp
23	c1gqgA	Alignment	not modelled	100.0	18	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
24	c3n2aA	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: bifunctional folypolyglutamate synthase/dihydrofolate PDBTitle: crystal structure of bifunctional folypolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
25	c5vwwA	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: structure of murc from pseudomonas aeruginosa
26	d1p3da3	Alignment	not modelled	100.0	21	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
27	d1e8ca3	Alignment	not modelled	100.0	24	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
28	c3eagA	Alignment	not modelled	100.0	22	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
29	d2gc6a2	Alignment	not modelled	100.0	18	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
30	d2jfga3	Alignment	not modelled	100.0	23	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
31	c6cauA	Alignment	not modelled	100.0	21	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
32	d1j6ua3	Alignment	not modelled	100.0	23	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
33	d1gg4a4	Alignment	not modelled	100.0	19	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
34	d1o5za2	Alignment	not modelled	100.0	16	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
35	d2jfga2	Alignment	not modelled	99.7	15	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
36	d1e8ca2	Alignment	not modelled	99.6	17	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
37	d1p3da2	Alignment	not modelled	99.5	12	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
38	d1gg4a1	Alignment	not modelled	99.4	14	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
39	d1o5za1	Alignment	not modelled	99.3	16	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folylpolyglutamate synthetase, C-terminal domain
40	d1j6ua2	Alignment	not modelled	99.2	14	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
41	d2gc6a1	Alignment	not modelled	99.2	10	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folylpolyglutamate synthetase, C-terminal domain
42	c3mvaA	Alignment	not modelled	99.2	11	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	d1a7ja	Alignment	not modelled	96.7	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
44	c2j37W	Alignment	not modelled	96.3	16	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
45	c3b9qA	Alignment	not modelled	96.0	22	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
46	c3of5A	Alignment	not modelled	96.0	11	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
47	c3fmaA	Alignment	not modelled	95.9	27	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
48	d1byia	Alignment	not modelled	95.5	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
49	c2cnwF	Alignment	not modelled	95.2	15	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
50	c5l3sF	Alignment	not modelled	95.2	19	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
51	c2ph1A	Alignment	not modelled	95.2	18	PDB header: ligand binding protein Chain: A: PDB Molecule: nucleotide-binding protein; PDBTitle: crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
52	c3tqcB	Alignment	not modelled	95.0	28	PDB header: transferase Chain: B: PDB Molecule: pantothenate kinase; PDBTitle: structure of the pantothenate kinase (coaa) from coxiella burnetii
53	c2og2A	Alignment	not modelled	95.0	20	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
						Fold: P-loop containing nucleoside triphosphate hydrolases

54	d1vmaa2	Alignment	not modelled	94.9	23	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
55	c2qy9A	Alignment	not modelled	94.5	21	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
56	c3cioA	Alignment	not modelled	94.4	10	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
57	d2qy9a2	Alignment	not modelled	94.3	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
58	c2iy3A	Alignment	not modelled	94.2	15	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
59	c3dm5A	Alignment	not modelled	94.2	13	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
60	c3c8uA	Alignment	not modelled	94.2	29	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
61	d1rz3a	Alignment	not modelled	94.2	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
62	c2qmoA	Alignment	not modelled	94.0	25	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biob) from helicobacter2 pylori
63	c5l3qB	Alignment	not modelled	94.0	25	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
64	c2v3cC	Alignment	not modelled	93.8	15	PDB header: signaling protein Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
65	c6cy1B	Alignment	not modelled	93.7	28	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
66	c4nkrB	Alignment	not modelled	93.7	23	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
67	c2f1rA	Alignment	not modelled	93.4	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
68	c2vedA	Alignment	not modelled	93.2	28	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
69	c4pfsA	Alignment	not modelled	93.1	37	PDB header: ligase Chain: A: PDB Molecule: cobyrinic acid a,c-diamide synthase; PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
70	c4ru8C	Alignment	not modelled	93.0	34	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with amppnp
71	c3la6P	Alignment	not modelled	92.9	10	PDB header: transferase Chain: P: PDB Molecule: tyrosine-protein kinase wzc; PDBTitle: octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
72	c2bekB	Alignment	not modelled	92.8	32	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
73	d1okkd2	Alignment	not modelled	92.8	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
74	d1ihua2	Alignment	not modelled	92.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
75	c6g2gA	Alignment	not modelled	92.6	29	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
76	c4dzzB	Alignment	not modelled	92.5	18	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
77	d1np6a	Alignment	not modelled	92.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
78	c1hyqA	Alignment	not modelled	92.4	38	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
79	d1hyqa	Alignment	not modelled	92.4	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

						Family: Nitrogenase iron protein-like
80	c2ozeA	Alignment	not modelled	92.4	23	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
81	c3vx3A	Alignment	not modelled	92.3	28	PDB header: adp binding protein Chain: A: PDB Molecule: atpase involved in chromosome partitioning, para/mind PDBTitle: crystal structure of [nife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1
82	c1qzwC	Alignment	not modelled	92.3	12	PDB header: signaling protein/rna Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
83	d1g3qa	Alignment	not modelled	92.3	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
84	c4rz3B	Alignment	not modelled	92.2	38	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
85	d1iona	Alignment	not modelled	92.2	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
86	c511jA	Alignment	not modelled	92.2	36	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
87	c2q9cA	Alignment	not modelled	92.2	17	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmpnp with mgcl complex
88	c4v02B	Alignment	not modelled	92.1	38	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
89	d1sq5a	Alignment	not modelled	91.5	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
90	c1zu4A	Alignment	not modelled	91.4	16	PDB header: protein transport Chain: A: PDB Molecule: ftsyl; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
91	c2xj9B	Alignment	not modelled	91.3	42	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
92	c1vmaA	Alignment	not modelled	91.1	26	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
93	c2yhsA	Alignment	not modelled	90.9	17	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
94	c2gesA	Alignment	not modelled	90.4	33	PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase; PDBTitle: pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
95	c2gksB	Alignment	not modelled	90.3	25	PDB header: transferase Chain: B: PDB Molecule: bifunctional sat/aps kinase; PDBTitle: crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
96	c3q9lB	Alignment	not modelled	90.2	38	PDB header: cell cycle, hydrolase Chain: B: PDB Molecule: septum site-determining protein mind; PDBTitle: the structure of the dimeric e.coli mind-atp complex
97	d1eg7a	Alignment	not modelled	90.1	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
98	c2z0hA	Alignment	not modelled	89.7	29	PDB header: transferase Chain: A: PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of thymidylate kinase in complex with dtdp2 and adp from thermotoga maritima
99	c3endA	Alignment	not modelled	89.4	42	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
100	c2j289	Alignment	not modelled	89.4	16	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
101	c3do6B	Alignment	not modelled	89.3	25	PDB header: ligase Chain: B: PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of putative formyltetrahydrofolate synthetase2 (tm1766) from thermotoga maritima at 1.85 a resolution
102	c2px0D	Alignment	not modelled	88.9	19	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmpnp/mg(2+)
103	d1qzxa3	Alignment	not modelled	88.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
104	c3k9gA	Alignment	not modelled	88.3	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: pf-32 protein; PDBTitle: crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak PDB header: structural genomics, unknown function Chain: A: PDB Molecule: structural genomics, unknown function

105	c3fkqA_	Alignment	not modelled	87.9	24	Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
106	c3ea0B_	Alignment	not modelled	87.7	18	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
107	c5a4jC_	Alignment	not modelled	87.4	31	PDB header: ligase Chain: C: PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of fthfs1 from t.acetoxydans re1
108	d1odfa_	Alignment	not modelled	86.6	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
109	c3zq6D_	Alignment	not modelled	86.5	29	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
110	c6iucC_	Alignment	not modelled	86.5	31	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
111	c3dmdA_	Alignment	not modelled	85.9	18	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
112	c5gafi_	Alignment	not modelled	85.7	15	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: rnc in complex with srp
113	c3hdtB_	Alignment	not modelled	85.3	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative kinase; PDBTitle: crystal structure of putative kinase from clostridium symbiosum atcc2 14940
114	c5f4hF_	Alignment	not modelled	85.3	16	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase
115	d1khta_	Alignment	not modelled	85.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
116	c3ez6B_	Alignment	not modelled	84.9	16	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
117	d1ls1a2	Alignment	not modelled	84.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
118	d1nksa_	Alignment	not modelled	84.2	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
119	d1vcoa2	Alignment	not modelled	84.1	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
120	c3lv8A_	Alignment	not modelled	83.6	24	PDB header: transferase Chain: A: PDB Molecule: thymidylate kinase; PDBTitle: 1.8 angstrom resolution crystal structure of a thymidylate kinase2 (tmk) from vibrio cholerae o1 biovar eltor str. n16961 in complex3 with tmp, thymidine-5'-diphosphate and adp