Phyre^2

Email	l.a.kelley@imperial.ac.uk
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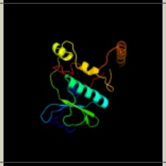
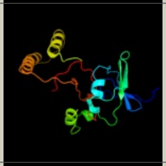
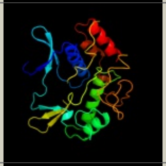
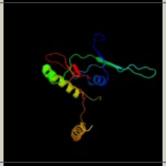
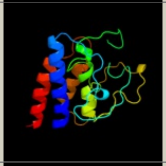
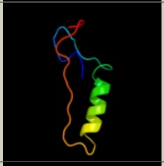
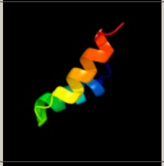
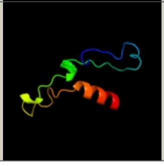
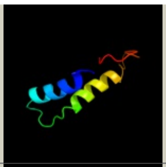
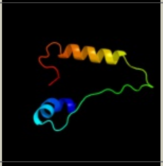
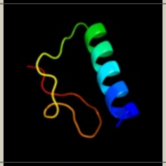
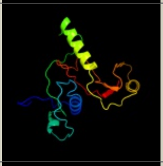
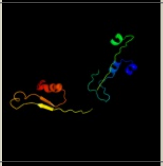
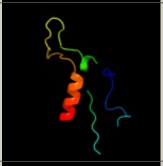
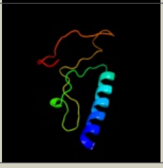
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ppqa1	Alignment		90.7	13	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
2	d1zyla1	Alignment		84.1	10	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
3	c3dxqB_	Alignment		79.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline/ethanolamine kinase family protein; **PDBTitle:** crystal structure of choline/ethanolamine kinase family protein2 (np_106042.1) from mesorhizobium loti at 2.55 a resolution
4	d1nd4a_	Alignment		67.5	15	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
5	c3akjB_	Alignment		58.5	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ctka; **PDBTitle:** crystal structure of a helicobacter pylori proinflammatory kinase ctka
6	c3ovcA_	Alignment		50.2	13	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**hygromycin-b 4-o-kinase; **PDBTitle:** crystal structure of aminoglycoside phosphotransferase aph(4)-ia
7	c2j0kB_	Alignment		47.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**focal adhesion kinase 1; **PDBTitle:** crystal structure of a fragment of focal adhesion kinase2 containing the ferm and kinase domains.
8	c1u0bB_	Alignment		40.6	24	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**cysteinyl trna; **PDBTitle:** crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
9	c1zp9A_	Alignment		40.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rio1 kinase; **PDBTitle:** crystal structure of full-legnth a.fulgidus rio1 serine kinase bound2 to atp and mn2+ ions.
10	c2vzaD_	Alignment		39.6	25	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**cell filamentation protein; **PDBTitle:** type iv secretion system effector protein bepa
11	d1dx4a_	Alignment		39.5	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like

12	c1unhD_	Alignment		37.9	29	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**cyclin-dependent kinase 5 activator 1; **PDBTitle:** structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
13	d1unld_	Alignment		37.6	29	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
14	d2i8da1	Alignment		37.2	13	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
15	d1zara2	Alignment		34.9	18	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**RIO1-like kinases
16	c3dxpA_	Alignment		34.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acyl-coa dehydrogenase; **PDBTitle:** crystal structure of a putative aminoglycoside phosphotransferase2 (reut_a1007) from ralstonia eutropha jmp134 at 2.32 a resolution
17	d1dgja4	Alignment		34.0	23	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
18	d1p0ia_	Alignment		33.0	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
19	d2f2ab1	Alignment		32.3	18	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/GatE C-terminal domain-like
20	c3e7eA_	Alignment		31.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mitotic checkpoint serine/threonine-protein kinase bub1; **PDBTitle:** structure and substrate recruitment of the human spindle checkpoint2 kinase bub
21	c2pm8A_	Alignment	not modelled	31.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cholinesterase; **PDBTitle:** crystal structure of recombinant full length human2 butyrylcholinesterase
22	c1vlbA_	Alignment	not modelled	31.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
23	c3k1sE_	Alignment	not modelled	27.9	23	**PDB header:**transferase **Chain:** E: **PDB Molecule:**pts system, cellobiose-specific iia component; **PDBTitle:** crystal structure of the pts cellobiose specific enzyme iia2 from bacillus anthracis
24	c1q5vB_	Alignment	not modelled	26.5	28	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
25	d1dfoa_	Alignment	not modelled	25.4	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
26	c3l8rA_	Alignment	not modelled	24.1	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative pts system, cellobiose-specific iia **PDBTitle:** the crystal structure of ptca from s. mutans
27	c3eu8D_	Alignment	not modelled	23.5	38	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative glucoamylase; **PDBTitle:** crystal structure of putative glucoamylase (yp_210071.1) from2 bacteroides fragilis nctc 9343 at 2.12 a resolution
28	d1j7la_	Alignment	not modelled	23.2	27	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases

29	c1wcrA_	Alignment	not modelled	23.1	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, n, n'-diacetylchitobiose-specific **PDBTitle:** trimeric structure of the enzyme iia from escherichia coli2 phosphotransferase system specific for n,n'-3 diacetylchitobiose
30	d2e2aa_	Alignment	not modelled	22.5	32	**Fold:**Spectrin repeat-like **Superfamily:**Enzyme IIa from lactose specific PTS, IIa-lac **Family:**Enzyme IIa from lactose specific PTS, IIa-lac
31	d2ha2a1	Alignment	not modelled	22.4	26	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
32	d1vlya1	Alignment	not modelled	22.2	21	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
33	c2zqeA_	Alignment	not modelled	22.0	44	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
34	d1bwva2	Alignment	not modelled	21.9	17	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
35	c2xm5A_	Alignment	not modelled	21.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cloq; **PDBTitle:** structural and mechanistic analysis of the magnesium-2 independent aromatic prenyltransferase cloq from the3 clorobiocin biosynthetic pathway
36	d2burb1	Alignment	not modelled	21.2	25	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
37	d1g8fa3	Alignment	not modelled	21.1	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
38	d1qe3a_	Alignment	not modelled	20.2	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
39	d1wdka2	Alignment	not modelled	20.0	13	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
40	d1f6wa_	Alignment	not modelled	19.4	29	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
41	d1tzva_	Alignment	not modelled	19.3	6	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**Antitermination factor NusB
42	c3f7wA_	Alignment	not modelled	18.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructosamine-3-kinase; **PDBTitle:** crystal structure of putative fructosamine-3-kinase (yp_290396.1) from2 thermobifida fusca yx-er1 at 1.85 a resolution
43	d2oc6a1	Alignment	not modelled	18.8	11	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
44	c3attA_	Alignment	not modelled	18.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rv3168 with atp
45	c3h0mE_	Alignment	not modelled	18.6	12	**PDB header:**ligase **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
46	d2apla1	Alignment	not modelled	18.2	11	**Fold:**PG0816-like **Superfamily:**PG0816-like **Family:**PG0816-like
47	c3al0B_	Alignment	not modelled	18.1	15	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
48	c2ogsA_	Alignment	not modelled	17.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thermostable carboxylesterase est50; **PDBTitle:** crystal structure of the geobacillus stearothermophilus2 carboxylesterase est55 at ph 6.2
49	c3en9B_	Alignment	not modelled	17.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase; **PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
50	c1f8uA_	Alignment	not modelled	17.6	26	**PDB header:**hydrolase/toxin **Chain:** A: **PDB Molecule:**acetylcholinesterase; **PDBTitle:** crystal structure of mutant e202q of human acetylcholinesterase2 complexed with green mamba venom peptide fasciculin-ii
51	d1f8ua_	Alignment	not modelled	17.6	26	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
52	d1s9aa_	Alignment	not modelled	17.6	19	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
53	d2ozla1	Alignment	not modelled	17.6	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module

54	c3csvA_	Alignment	not modelled	16.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminoglycoside phosphotransferase; **PDBTitle:** crystal structure of a putative aminoglycoside phosphotransferase2 (yp_614837.1) from silicibacter sp. tm1040 at 2.15 a resolution
55	d2pyqa1	Alignment	not modelled	16.6	15	**Fold:**Jann4075-like **Superfamily:**Jann4075-like **Family:**Jann4075-like
56	c2g5iB_	Alignment	not modelled	16.3	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
57	d1ug0a_	Alignment	not modelled	16.2	26	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
58	c2w1jB_	Alignment	not modelled	15.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative sortase; **PDBTitle:** crystal structure of sortase c-1 (srtc-1) from2 streptococcus pneumoniae
59	c3ecdC_	Alignment	not modelled	15.3	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase 2; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
60	d3pccm_	Alignment	not modelled	15.2	29	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
61	c2q83A_	Alignment	not modelled	15.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ytaa protein; **PDBTitle:** crystal structure of ytaa (2635576) from bacillus subtilis at 2.50 a2 resolution
62	d2axtf1	Alignment	not modelled	15.1	56	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome b559 subunits **Family:**Cytochrome b559 subunits
63	c1w5cL_	Alignment	not modelled	15.0	56	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**cytochrome b559 beta subunit; **PDBTitle:** photosystem ii from thermosynechococcus elongatus
64	d1xm8a_	Alignment	not modelled	14.9	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
65	d1q7ea_	Alignment	not modelled	14.8	15	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
66	c3izcs_	Alignment	not modelled	14.4	35	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein rpl20 (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
67	c2x1cA_	Alignment	not modelled	13.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl-coenzyme **PDBTitle:** the crystal structure of precursor acyl coenzyme2 a:isopenicillin n acyltransferase from penicillium3 chrysogenum
68	c2v1nA_	Alignment	not modelled	13.9	19	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**protein kin homolog; **PDBTitle:** solution structure of the region 51-160 of human kin172 reveals a winged helix fold
69	c2djcA_	Alignment	not modelled	13.6	40	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**growth-blocking peptide; **PDBTitle:** solution structure of growth-blocking peptide of the2 tobacco cutworm, spodoptera litura
70	c3fc7B_	Alignment	not modelled	13.6	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**htr-like protein; **PDBTitle:** the crystal structure of a domain of htr-like protein from haloarcula2 marismortui atcc 43049
71	c2dzrA_	Alignment	not modelled	13.4	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna
72	c3isyA_	Alignment	not modelled	12.8	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor; **PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
73	c3qd7X_	Alignment	not modelled	12.5	26	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
74	d1ylxa1	Alignment	not modelled	12.5	22	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GK1464-like **Family:**GK1464-like
75	c1irrA_	Alignment	not modelled	12.5	40	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**paralytic peptide; **PDBTitle:** solution structure of paralytic peptide of the silkworm,2 bombyx mori
76	c1zawU_	Alignment	not modelled	12.3	36	**PDB header:**structural protein **Chain:** U: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
77	c1zawW_	Alignment	not modelled	12.3	36	**PDB header:**structural protein **Chain:** W: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
78	c1zawV_	Alignment	not modelled	12.3	36	**PDB header:**structural protein **Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
						PDB header:structural protein

79	c1zaxZ_	Alignment	not modelled	12.1	36	**Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
80	d2d9ia1	Alignment	not modelled	12.1	19	**Fold:**IF3-like **Superfamily:**SMR domain-like **Family:**Smr domain
81	c3o0pA_	Alignment	not modelled	11.9	8	**PDB header:**transferase , hydrolase **Chain:** A: **PDB Molecule:**sortase family protein; **PDBTitle:** pilus-related sortase c of group b streptococcus
82	c2hyiJ_	Alignment	not modelled	11.8	44	**PDB header:**hydrolase/rna binding protein/rna **Chain:** J: **PDB Molecule:**protein casc3; **PDBTitle:** structure of the human exon junction complex with a trapped2 dead-box helicase bound to rna
83	c3i0oA_	Alignment	not modelled	11.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**spectinomycin phosphotransferase; **PDBTitle:** crystal structure of spectinomycin phosphotransferase,2 aph(9)-ia, in complex with adp and spectinomcyin
84	d2pnwa1	Alignment	not modelled	11.7	16	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
85	c3ex7I_	Alignment	not modelled	11.6	40	**PDB header:**hydrolase/rna binding protein/rna **Chain:** I: **PDB Molecule:**protein casc3; **PDBTitle:** the crystal structure of ejc in its transition state
86	c1zaxY_	Alignment	not modelled	11.5	37	**PDB header:**structural protein **Chain:** Y: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
87	c1zaxX_	Alignment	not modelled	11.5	37	**PDB header:**structural protein **Chain:** X: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
88	c1zavY_	Alignment	not modelled	11.5	37	**PDB header:**structural protein **Chain:** Y: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21
89	c1zavX_	Alignment	not modelled	11.5	37	**PDB header:**structural protein **Chain:** X: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21
90	c2dzqA_	Alignment	not modelled	11.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
91	c1zavW_	Alignment	not modelled	11.4	36	**PDB header:**structural protein **Chain:** W: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21
92	c1zaxW_	Alignment	not modelled	11.4	36	**PDB header:**structural protein **Chain:** W: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
93	c1zaxU_	Alignment	not modelled	11.4	36	**PDB header:**structural protein **Chain:** U: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
94	c1zavU_	Alignment	not modelled	11.4	36	**PDB header:**structural protein **Chain:** U: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21
95	d1zavu1	Alignment	not modelled	11.4	36	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
96	c1zavV_	Alignment	not modelled	11.4	36	**PDB header:**structural protein **Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21
97	c1zaxV_	Alignment	not modelled	11.4	36	**PDB header:**structural protein **Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
98	c1dd3C_	Alignment	not modelled	11.2	36	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** crystal structure of ribosomal protein l12 from thermotoga maritima
99	c1dd3D_	Alignment	not modelled	11.2	36	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** crystal structure of ribosomal protein l12 from thermotoga maritima