Phyre^2

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Description	RVBD1263_(amiB2)_1410437_1411825
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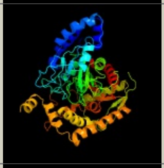
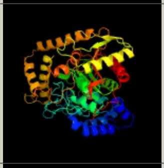
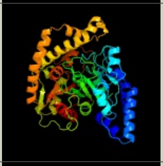
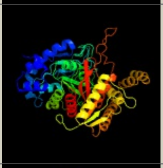
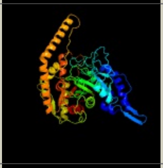
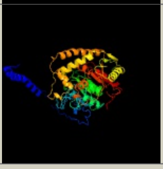
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6diiH_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**fatty acid amide hydrolase; **PDBTitle:** structure of arabidopsis fatty acid amide hydrolase in complex with2 methyl linolenyl fluorophosphonate
2	d2f2aa1	Alignment		100.0	27	**Fold:**Amidase signature (AS) enzymes **Superfamily:**Amidase signature (AS) enzymes **Family:**Amidase signature (AS) enzymes
3	c4wj3A_	Alignment		100.0	33	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit a; **PDBTitle:** crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
4	c4gysA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allophanate hydrolase; **PDBTitle:** granulibacter bethesdensis allophanate hydrolase co-crystallized with2 malonate
5	c3h0rP_	Alignment		100.0	30	**PDB header:**ligase **Chain:** P: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit a; **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
6	c3a2qA_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-aminohexanoate-cyclic-dimer hydrolase; **PDBTitle:** structure of 6-aminohexanoate cyclic dimer hydrolase complexed with2 substrate
7	c4cp8C_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**allophanate hydrolase; **PDBTitle:** structure of the amidase domain of allophanate hydrolase2 from pseudomonas sp strain adp
8	c3kfuE_	Alignment		100.0	33	**PDB header:**ligase/rna **Chain:** E: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit a; **PDBTitle:** crystal structure of the transamidosome
9	c5h6sB_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidase; **PDBTitle:** crystal structure of hydrazidase s179a mutant complexed with a2 substrate
10	c2dc0A_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable amidase; **PDBTitle:** crystal structure of amidase
11	d1m22a_	Alignment		100.0	30	**Fold:**Amidase signature (AS) enzymes **Superfamily:**Amidase signature (AS) enzymes **Family:**Amidase signature (AS) enzymes

12	d1mt5a_	Alignment		100.0	28	**Fold:**Amidase signature (AS) enzymes **Superfamily:**Amidase signature (AS) enzymes **Family:**Amidase signature (AS) enzymes
13	c6c6gA_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**biuret hydrolase; **PDBTitle:** an unexpected vestigial protein complex reveals the evolutionary2 origins of an s-triazine catabolic enzyme. inhibitor bound complex.
14	c5h6tB_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidase; **PDBTitle:** crystal structure of hydrazidase from microbacterium sp. strain hm58-2
15	c4yj6A_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aryl acylamidase; **PDBTitle:** the crystal structure of a bacterial aryl acylamidase belonging to the2 amidase signature (as) enzymes family
16	c2vyaB_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fatty-acid amide hydrolase 1; **PDBTitle:** crystal structure of fatty acid amide hydrolase conjugated2 with the drug-like inhibitor pf-750
17	d2gi3a1	Alignment		100.0	28	**Fold:**Amidase signature (AS) enzymes **Superfamily:**Amidase signature (AS) enzymes **Family:**Amidase signature (AS) enzymes
18	c4issA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allophanate hydrolase; **PDBTitle:** semet-substituted kluyveromyces lactis allophanate hydrolase
19	c5i8iD_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**urea amidolyase; **PDBTitle:** crystal structure of the k. lactis urea amidolyase
20	c3a1iA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidase; **PDBTitle:** crystal structure of rhodococcus sp. n-771 amidase complexed2 with benzamide
21	d1ocka_	Alignment	not modelled	100.0	28	**Fold:**Amidase signature (AS) enzymes **Superfamily:**Amidase signature (AS) enzymes **Family:**Amidase signature (AS) enzymes
22	c5ewqC_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**amidase; **PDBTitle:** the crystal structure of an amidase family protein from bacillus2 anthracis str. ames
23	c4n0hA_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit a, **PDBTitle:** crystal structure of s. cerevisiae mitochondrial gatfab
24	d1w53a_	Alignment	not modelled	44.6	11	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Phosphoserine phosphatase RsbU, N-terminal domain
25	c5y6iB_	Alignment	not modelled	37.4	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator kdgr; **PDBTitle:** crystal structure of pseudomonas aeruginosa hmgr
26	c3izbF_	Alignment	not modelled	25.2	16	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**40s ribosomal protein rps5 (s7p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
27	d1k75a_	Alignment	not modelled	25.0	21	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
28	d1h1js_	Alignment	not modelled	23.8	19	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
						PDB header:regulatory protein

29	c2c4kD_	Alignment	not modelled	23.7	28	**Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase-associated protein **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate synthetase-2 associated protein 39 (pap39)
30	c3r4kD_	Alignment	not modelled	23.6	15	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**transcriptional regulator, iclr family; **PDBTitle:** crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
31	c5tjjA_	Alignment	not modelled	23.6	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, iclr family; **PDBTitle:** crystal structure of icir transcriptional regulator from2 alicyclobacillus acidocaldarius
32	c4g4sP_	Alignment	not modelled	22.8	27	**PDB header:**hydrolase/chaperone **Chain:** P: **PDB Molecule:**proteasome assembly chaperone 2; **PDBTitle:** structure of proteasome-pba1-pba2 complex
33	d2dloa2	Alignment	not modelled	22.7	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
34	c3ilvA_	Alignment	not modelled	19.8	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
35	c4my4A_	Alignment	not modelled	19.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
36	c5xoeA_	Alignment	not modelled	19.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp-dependent 6-phosphofructokinase; **PDBTitle:** crystal structure of the apo staphylococcus aureus phosphofructokinase
37	c2kvuA_	Alignment	not modelled	17.4	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**mkl/myocardin-like protein 1; **PDBTitle:** solution nmr structure of sap domain of mkl/myocardin-like2 protein 1 from h.sapiens, northeast structural genomics3 consortium target target hr4547e
38	d1ggaa2	Alignment	not modelled	17.1	27	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
39	c1ysqA_	Alignment	not modelled	17.1	25	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator yiaj; **PDBTitle:** the crystal structure of transcriptional regulator yaij
40	c3mjdA_	Alignment	not modelled	16.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
41	c6an0A_	Alignment	not modelled	16.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histidinol dehydrogenase; **PDBTitle:** crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
42	d1o98a1	Alignment	not modelled	15.5	5	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
43	c3hgkE_	Alignment	not modelled	15.1	21	**PDB header:**transferase **Chain:** E: **PDB Molecule:**effector protein hopab2; **PDBTitle:** crystal structure of effect protein avrptob complexed with2 kinase pto
44	c2kssA_	Alignment	not modelled	15.0	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**carotenogenesis protein cars; **PDBTitle:** nmr structure of myxococcus xanthus antirepressor cars1
45	c5xyiF_	Alignment	not modelled	13.7	22	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**40s ribosomal protein s5-b, putative; **PDBTitle:** small subunit of trichomonas vaginalis ribosome
46	c2na9A_	Alignment	not modelled	13.5	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytokine receptor common subunit beta; **PDBTitle:** transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta
47	c3dahB_	Alignment	not modelled	13.3	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
48	c3mq0A_	Alignment	not modelled	13.2	14	**PDB header:**transcription repressor **Chain:** A: **PDB Molecule:**transcriptional repressor of the blcabc operon; **PDBTitle:** crystal structure of agobacterium tumefaciens repressor blcr
49	c2jmkA_	Alignment	not modelled	13.2	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical protein ta0956; **PDBTitle:** solution structure of ta0956
50	c2na8A_	Alignment	not modelled	13.1	38	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cytokine receptor common subunit beta; **PDBTitle:** transmembrane structure of the cytokine receptor common subunit beta
51	d1y88a1	Alignment	not modelled	13.0	8	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**Hypothetical protein AF1548, C-terminal domain
52	c2g7uB_	Alignment	not modelled	12.7	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
53	c4uc0A_	Alignment	not modelled	12.2	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of a purine nucleoside phosphorylase

						(psi-nysgrc-2 029736) from agrobacterium vitis
54	c2do1A_	Alignment	not modelled	12.2	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nuclear protein hcc-1; **PDBTitle:** solution structure of the sap domain of human nuclear2 protein hcc-1
55	d1zrja1	Alignment	not modelled	11.6	14	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
56	c1zrjA_	Alignment	not modelled	11.5	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**e1b-55kda-associated protein 5 isoform c; **PDBTitle:** solution structure of the sap domain of human e1b-55kda-2 associated protein 5 isoform c
57	d2do1a1	Alignment	not modelled	11.5	11	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
58	d1tf1a_	Alignment	not modelled	11.0	16	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
59	c4lnaA_	Alignment	not modelled	11.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase i from spirosoma2 linguale dsm 74, nysgrc target 029362
60	c4nsnC_	Alignment	not modelled	10.8	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from2 porphyromonas gingivalis atcc 33277, nysgrc target 030972,3 orthorhombic symmetry
61	c2mfqB_	Alignment	not modelled	10.3	61	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bdnf/nt-3 growth factors receptor; **PDBTitle:** nmr solution structures of frs2a ptb domain with neurotrophin receptor2 trkb
62	c4m1eC_	Alignment	not modelled	10.3	33	**PDB header:**transferase **Chain:** C: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase i from2 planctomyces limnophilus dsm 3776, nysgrc target 029364.
63	d1saza2	Alignment	not modelled	10.1	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
64	d1u9ya2	Alignment	not modelled	9.9	36	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
65	c1o98A_	Alignment	not modelled	9.8	5	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
66	c2yzkC_	Alignment	not modelled	9.7	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
67	d1g99a2	Alignment	not modelled	9.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
68	d2f48a1	Alignment	not modelled	9.5	18	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
69	c5ifkC_	Alignment	not modelled	9.5	38	**PDB header:**transferase **Chain:** C: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** purine nucleoside phosphorylase
70	c1yspA_	Alignment	not modelled	9.5	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator kdgr; **PDBTitle:** crystal structure of the c-terminal domain of e. coli transcriptional2 regulator kdgr.
71	c5kgmA_	Alignment	not modelled	9.3	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** 2.95a resolution structure of apo independent phosphoglycerate mutase2 from c. elegans (monoclinic form)
72	c4l5cE_	Alignment	not modelled	9.1	33	**PDB header:**transferase **Chain:** E: **PDB Molecule:**s-methyl-5'-thioadenosine phosphorylase; **PDBTitle:** methylthioadenosine phosphorylase from schistosoma mansoni in complex2 with adenine in space group p212121
73	c4g07A_	Alignment	not modelled	8.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histidinol dehydrogenase; **PDBTitle:** the crystal structure of the c366s mutant of hdh from brucella suis
74	c3u88M_	Alignment	not modelled	8.7	42	**PDB header:**transcription **Chain:** M: **PDB Molecule:**histone-lysine n-methyltransferase 2a; **PDBTitle:** crystal structure of human menin in complex with mll1 and ledgf
75	c2higA_	Alignment	not modelled	8.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase; **PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
76	d2h5na1	Alignment	not modelled	8.4	27	**Fold:**TerB-like **Superfamily:**TerB-like **Family:**PG1108-like
77	d1h5wa_	Alignment	not modelled	8.3	14	**Fold:**Upper collar protein gp10 (connector protein) **Superfamily:**Upper collar protein gp10 (connector protein) **Family:**Upper collar protein gp10 (connector protein)
78	d1i32a2	Alignment	not modelled	8.1	27	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
79	c3ndqA_	Alignment	not modelled	8.1	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor a protein 1; **PDBTitle:** structure of human tfiis domain ii

80	d2g82a2	Alignment	not modelled	8.0	20	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
81	c1ijgE_	Alignment	not modelled	8.0	14	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**upper collar protein; **PDBTitle:** structure of the bacteriophage phi29 head-tail connector2 protein
82	c2wnsB_	Alignment	not modelled	7.5	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
83	d1mzva_	Alignment	not modelled	7.5	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
84	c1vbiA_	Alignment	not modelled	7.5	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type 2 malate/lactate dehydrogenase; **PDBTitle:** crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
85	c3o8oC_	Alignment	not modelled	7.4	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**6-phosphofructokinase subunit alpha; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
86	c1uasA_	Alignment	not modelled	7.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of rice alpha-galactosidase
87	c2hkeB_	Alignment	not modelled	7.3	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**diphosphomevalonate decarboxylase, putative; **PDBTitle:** mevalonate diphosphate decarboxylase from trypanosoma brucei
88	c4gicB_	Alignment	not modelled	7.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histidinol dehydrogenase; **PDBTitle:** crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
89	c3efhB_	Alignment	not modelled	7.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
90	c3igzB_	Alignment	not modelled	7.0	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
91	c1wtjB_	Alignment	not modelled	6.9	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ureidoglycolate dehydrogenase; **PDBTitle:** crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
92	c3k2qA_	Alignment	not modelled	6.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrophosphate-dependent phosphofructokinase; **PDBTitle:** crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
93	c5ikjB_	Alignment	not modelled	6.8	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cryptic loci regulator protein 1; **PDBTitle:** structure of clr2 bound to the clr1 c-terminus
94	c2xzmG_	Alignment	not modelled	6.8	14	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**ribosomal protein s7 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
95	c3p4iA_	Alignment	not modelled	6.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** crystal structure of acetate kinase from mycobacterium avium
96	d2acfa1	Alignment	not modelled	6.6	38	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
97	c2w0cL_	Alignment	not modelled	6.5	55	**PDB header:**virus **Chain:** L: **PDB Molecule:**protein 2; **PDBTitle:** x-ray structure of the entire lipid-containing bacteriophage pm2
98	c2j6yB_	Alignment	not modelled	6.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphoserine phosphatase rsbu; **PDBTitle:** structural and functional characterisation of partner switching2 regulating the environmental stress response in bacillus subtilis
99	c5khaA_	Alignment	not modelled	6.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad+ synthetase; **PDBTitle:** structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)