Phyre^2

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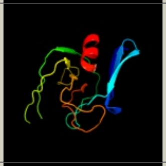
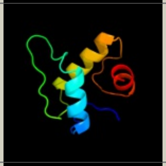
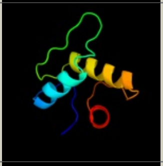
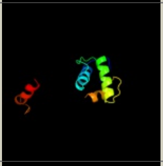
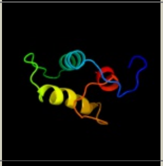
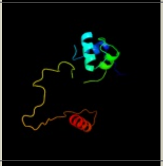
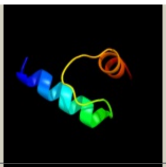
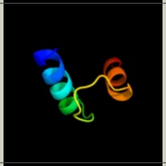
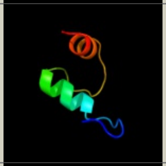
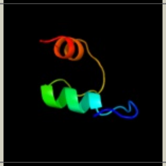
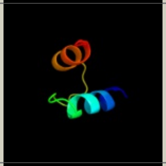
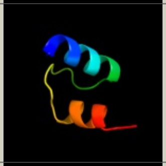
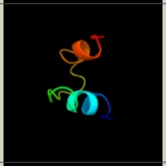
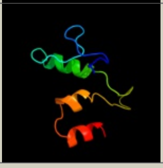
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hklB_	Alignment		99.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l,d-transpeptidase; **PDBTitle:** crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant
2	d1zata1	Alignment		99.5	24	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
3	d1lbua1	Alignment		99.2	34	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD
4	c1y7mB_	Alignment		99.2	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14040; **PDBTitle:** crystal structure of the b. subtilis ykud protein at 2 a2 resolution
5	c1lbuA_	Alignment		99.1	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**muramoyl-pentapeptide carboxypeptidase; **PDBTitle:** hydrolase metallo (zn) dd-peptidase
6	c3bkhA_	Alignment		99.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
7	d1y7ma1	Alignment		99.1	30	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
8	c2bh7A_	Alignment		98.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
9	c1l6jA_	Alignment		97.3	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
10	d1eaka1	Alignment		97.1	16	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
11	d2ikba1	Alignment		97.0	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like

12	d1slma1	Alignment		97.0	18	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
13	c1slmA_	Alignment		97.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
14	d1su3a1	Alignment		96.8	22	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
15	c1su3A_	Alignment		96.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
16	c1eakA_	Alignment		96.5	22	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
17	d2nr7a1	Alignment		96.3	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
18	d1l6ja1	Alignment		96.2	23	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
19	c1gxdA_	Alignment		93.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
20	c3a05A_	Alignment		74.1	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
21	d2bgxa1	Alignment	not modelled	67.0	20	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD
22	d2oo3a1	Alignment	not modelled	49.4	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**LPG1296-like
23	c2rjbD_	Alignment	not modelled	45.2	23	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein ydcj (sf1787)2 from shigella flexneri which includes domain duf1338.3 northeast structural genomics consortium target sfr276
24	c2juoA_	Alignment	not modelled	40.4	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ga-binding protein alpha chain; **PDBTitle:** gabpa ost domain
25	c3n9iA_	Alignment	not modelled	38.2	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
26	c1wsuA_	Alignment	not modelled	35.6	12	**PDB header:**translation/rna **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** c-terminal domain of elongation factor selb complexed with2 secis rna
27	d2ns0a1	Alignment	not modelled	34.4	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
28	d1r1ga_	Alignment	not modelled	30.2	67	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins

29	c1r1gB_	Alignment	not modelled	30.2	67	**PDB header:**toxin **Chain:** B: **PDB Molecule:**neurotoxin bmk37; **PDBTitle:** crystal structure of the scorpion toxin bmbkttx1
30	c1r1gA_	Alignment	not modelled	30.2	67	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin bmk37; **PDBTitle:** crystal structure of the scorpion toxin bmbkttx1
31	d2d69a1	Alignment	not modelled	29.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
32	c2d69B_	Alignment	not modelled	25.9	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ribulose bisphosphate carboxylase; **PDBTitle:** crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
33	c2r5kE_	Alignment	not modelled	25.8	27	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**major capsid protein l1; **PDBTitle:** pentamer structure of major capsid protein l1 of human2 papilloma virus type 11
34	c3phuA_	Alignment	not modelled	24.5	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase l; **PDBTitle:** otu domain of crimean congo hemorrhagic fever virus
35	c2r5iL_	Alignment	not modelled	23.8	24	**PDB header:**viral protein **Chain:** L: **PDB Molecule:**l1 protein; **PDBTitle:** pentamer structure of major capsid protein l1 of human2 papilloma virus type 18
36	c3pt2A_	Alignment	not modelled	23.4	30	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**rna polymerase; **PDBTitle:** structure of a viral otu domain protease bound to ubiquitin
37	c1dzlA_	Alignment	not modelled	23.1	27	**PDB header:**virus **Chain:** A: **PDB Molecule:**late major capsid protein l1; **PDBTitle:** l1 protein of human papillomavirus 16
38	d1dzla_	Alignment	not modelled	23.1	27	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group I dsDNA viruses **Family:**Papovaviridae-like VP
39	c3qm2A_	Alignment	not modelled	22.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
40	c3jxeB_	Alignment	not modelled	22.1	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
41	c3hv0A_	Alignment	not modelled	21.6	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
42	c2yy5C_	Alignment	not modelled	21.4	19	**PDB header:**ligase **Chain:** C: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
43	d1i6la_	Alignment	not modelled	20.8	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
44	c2lafA_	Alignment	not modelled	20.4	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lipoprotein 34; **PDBTitle:** nmr solution structure of the n-terminal domain of the e. coli2 lipoprotein bamc
45	c2zviB_	Alignment	not modelled	20.2	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-diketo-5-methylthiopentyl-1-phosphate **PDBTitle:** crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
46	d1ykwa1	Alignment	not modelled	20.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
47	d2p0la1	Alignment	not modelled	19.5	20	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
48	c3iyjE_	Alignment	not modelled	19.2	18	**PDB header:**virus **Chain:** E: **PDB Molecule:**major capsid protein l1; **PDBTitle:** bovine papillomavirus type 1 outer capsid
49	d1ej7l1	Alignment	not modelled	18.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
50	c2qygC_	Alignment	not modelled	17.8	16	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**ribulose bisphosphate carboxylase-like protein 2; **PDBTitle:** crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
51	c2j5bA_	Alignment	not modelled	17.6	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosynol
52	c2ip1A_	Alignment	not modelled	17.2	34	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
53	c3elyA_	Alignment	not modelled	17.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** wesselsbron virus methyltransferase in complex with adohcy
						PDB header:lyase **Chain:** E: **PDB Molecule:**ribulose-1,5-bisphosphate

54	c1gehE_	Alignment	not modelled	16.7	12	carboxylase/oxygenase; **PDBTitle:** crystal structure of archaeal rubisco (ribulose 1,5-bisphosphate2 carboxylase/oxygenase)
55	d3ci0j1	Alignment	not modelled	16.5	19	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**EpsJ-like
56	c2xvsA_	Alignment	not modelled	16.4	21	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**tetratricopeptide repeat protein 5; **PDBTitle:** crystal structure of human ttc5 (strap) c-terminal ob2 domain
57	c1telA_	Alignment	not modelled	16.4	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase, large subunit; **PDBTitle:** crystal structure of a rubisco-like protein from chlorobium2 tepidum
58	c2oxtC_	Alignment	not modelled	16.2	28	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**nucleoside-2'-o-methyltransferase; **PDBTitle:** crystal structure of meaban virus nucleoside-2'-o-2 methyltransferase
59	d1geha1	Alignment	not modelled	16.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
60	d1wuua1	Alignment	not modelled	16.0	26	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
61	c2plyB_	Alignment	not modelled	15.8	12	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
62	d1rbla1	Alignment	not modelled	15.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
63	d1pgsa2	Alignment	not modelled	15.4	26	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**PHM/PNGase F **Family:**Glycosyl-asparaginase
64	d1iufa2	Alignment	not modelled	14.4	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
65	c2i6oA_	Alignment	not modelled	14.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfolobus solfataricus protein tyrosine **PDBTitle:** crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
66	d1vlra2	Alignment	not modelled	13.5	24	**Fold:**mRNA decapping enzyme DcpS N-terminal domain **Superfamily:**mRNA decapping enzyme DcpS N-terminal domain **Family:**mRNA decapping enzyme DcpS N-terminal domain
67	c1zswA_	Alignment	not modelled	13.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of bacillus cereus metallo protein from glyoxalase2 family
68	c3nwrA_	Alignment	not modelled	13.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**a rubisco-like protein; **PDBTitle:** crystal structure of a rubisco-like protein from burkholderia fungorum
69	c3nk4B_	Alignment	not modelled	12.8	25	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**zona pellucida 3; **PDBTitle:** crystal structure of full-length sperm receptor zp3 at 2.0 a2 resolution
70	c2quiB_	Alignment	not modelled	12.3	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp
71	c3hzrD_	Alignment	not modelled	12.1	26	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase homolog from entamoeba histolytica
72	c1r6uB_	Alignment	not modelled	11.9	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
73	d2p5ia1	Alignment	not modelled	11.8	19	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
74	d2z15a1	Alignment	not modelled	11.7	16	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
75	d8ruca1	Alignment	not modelled	11.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
76	d3bl9a2	Alignment	not modelled	11.4	25	**Fold:**mRNA decapping enzyme DcpS N-terminal domain **Superfamily:**mRNA decapping enzyme DcpS N-terminal domain **Family:**mRNA decapping enzyme DcpS N-terminal domain
77	c2gezE_	Alignment	not modelled	11.4	11	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
78	c3sz3A_	Alignment	not modelled	11.3	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
79	d3e9va1	Alignment	not modelled	11.1	23	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like

80	c3focB_	Alignment	not modelled	11.1	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from giardia lamblia
81	c1rcxH_	Alignment	not modelled	11.0	17	**PDB header:**lyase (carbon-carbon) **Chain:** H: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase; **PDBTitle:** non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
82	d1atga_	Alignment	not modelled	10.7	15	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
83	c1vqzA_	Alignment	not modelled	10.7	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoate-protein ligase, putative; **PDBTitle:** crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
84	d1bwva1	Alignment	not modelled	10.5	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
85	c2yfnA_	Alignment	not modelled	10.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
86	c1bqfA_	Alignment	not modelled	10.0	57	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**protein (growth-blocking peptide); **PDBTitle:** growth-blocking peptide (gbp) from pseudaletia separata
87	c2kimA_	Alignment	not modelled	9.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o6-methylguanine-dna methyltransferase; **PDBTitle:** 1.7-mm microcryoprobe solution nmr structure of an o6-2 methylguanine dna methyltransferase family protein from3 vibrio parahaemolyticus. northeast structural genomics4 consortium target vpr247.
88	c3qfwB_	Alignment	not modelled	9.6	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ribulose-1,5-bisphosphate carboxylase/oxygenase large **PDBTitle:** crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
89	c3prhB_	Alignment	not modelled	8.5	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase val144pro mutant from b. subtilis
90	c1iufA_	Alignment	not modelled	8.5	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**centromere abp1 protein; **PDBTitle:** low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
91	d1vqza2	Alignment	not modelled	8.4	15	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
92	d1vlya2	Alignment	not modelled	8.1	11	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain
93	c3tgoD_	Alignment	not modelled	7.9	13	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**lipoprotein 34; **PDBTitle:** crystal structure of the e. coli bamcd complex
94	c3e4wB_	Alignment	not modelled	7.9	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a 33kda catalase-related protein from2 mycobacterium avium subsp. paratuberculosis. p2(1)2(1)2(1) crystal3 form.
95	c1sghA_	Alignment	not modelled	7.8	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin ferm domain bound to ebp50 c-terminal peptide
96	c3m5wB_	Alignment	not modelled	7.8	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 campylobacter jejuni
97	d2ibaa2	Alignment	not modelled	7.7	8	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
98	d1dgsa1	Alignment	not modelled	7.5	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
99	d1r8se_	Alignment	not modelled	7.3	22	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain