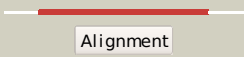

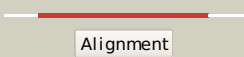

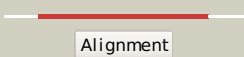

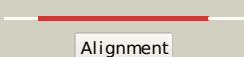

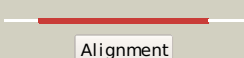

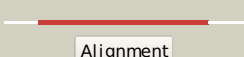

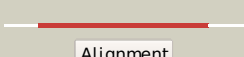

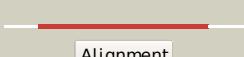

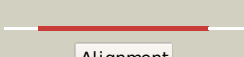

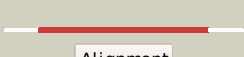














#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	cleqrC_	 Alignment		100.0	100	PDB header: ligase Chain: C: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of free aspartyl-trna synthetase from2 escherichia coli
2	clefwA_	 Alignment		100.0	50	PDB header: ligase/rna Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
3	cle22A_	 Alignment		100.0	28	PDB header: ligase Chain: A: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
4	c1wydB_	 Alignment		100.0	31	PDB header: ligase Chain: B: PDB Molecule: hypothetical aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
5	c3e9hB_	 Alignment		100.0	27	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
6	c3bjub_	 Alignment		100.0	26	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna2 synthetase
7	c1b8aB_	 Alignment		100.0	31	PDB header: ligase Chain: B: PDB Molecule: protein (aspartyl-trna synthetase); PDBTitle: aspartyl-trna synthetase
8	clasYA_	 Alignment		100.0	26	PDB header: complex (aminoacyl-trna synthase/trna) Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
9	c2xgtB_	 Alignment		100.0	25	PDB header: ligase Chain: B: PDB Molecule: asparaginyl-trna synthetase, cytoplasmic; PDBTitle: asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
10	c1x55A_	 Alignment		100.0	27	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase; PDBTitle: crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
11	c3m4qA_	 Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase, putative; PDBTitle: entamoeba histolytica asparaginyl-trna synthetase (asnrs)

12	c3i7fA_	Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: aspartyl trna synthetase from entamoeba histolytica
13	c1n9wA_	Alignment		100.0	37	PDB header: biosynthetic protein Chain: A: PDB Molecule: aspartyl-trna synthetase 2; PDBTitle: crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
14	d1c0aa3	Alignment		100.0	100	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
15	d1l0wa3	Alignment		100.0	57	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
16	d1eova2	Alignment		100.0	28	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
17	d1b8aa2	Alignment		100.0	30	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
18	d1n9wa2	Alignment		100.0	32	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
19	d1nnha_	Alignment		100.0	28	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
20	d1e1oa2	Alignment		100.0	29	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
21	d1bbua2	Alignment	not modelled	100.0	30	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
22	c3g1zB_	Alignment	not modelled	100.0	29	PDB header: ligase Chain: B: PDB Molecule: putative lysyl-trna synthetase; PDBTitle: structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
23	c2znjB_	Alignment	not modelled	100.0	27	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pyrrolysyl-trna synthetase from2 desulfitobacterium hafniense
24	d1c0aa1	Alignment	not modelled	100.0	100	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
25	c2zimA_	Alignment	not modelled	100.0	27	PDB header: ligase Chain: A: PDB Molecule: pyrrolysyl-trna synthetase; PDBTitle: pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
26	d1kmma2	Alignment	not modelled	100.0	18	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
27	d1l0wa1	Alignment	not modelled	100.0	50	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
28	c1z7nB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase regulatory subunit; PDBTitle: atp phosphoribosyl transferase (hiszg atp-prtase) from2 lactococcus lactis with bound prpp substrate

29	d1h4vb2	Alignment	not modelled	100.0	20	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
30	c2rhqA	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
31	d1b8aa1	Alignment	not modelled	100.0	35	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
32	d1qe0a2	Alignment	not modelled	100.0	14	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
33	d1bbua1	Alignment	not modelled	99.9	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
34	d1e1oa1	Alignment	not modelled	99.9	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
35	d1wu7a2	Alignment	not modelled	99.9	20	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
36	c1b70A	Alignment	not modelled	99.9	32	PDB header: ligase Chain: A: PDB Molecule: phenylalanyl-trna synthetase; PDBTitle: phenylalanyl trna synthetase complexed with phenylalanine
37	d1jjca	Alignment	not modelled	99.9	31	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
38	c3racA	Alignment	not modelled	99.9	21	PDB header: ligase Chain: A: PDB Molecule: histidine-trna ligase; PDBTitle: crystal strucutre of histidine--trna ligase subunit from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446.
39	d1n9wa1	Alignment	not modelled	99.9	40	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
40	d1eova1	Alignment	not modelled	99.9	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
41	d1krta	Alignment	not modelled	99.9	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
42	c3pcoC	Alignment	not modelled	99.9	23	PDB header: ligase Chain: C: PDB Molecule: phenylalanyl-trna synthetase, alpha subunit; PDBTitle: crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
43	c3l4gl	Alignment	not modelled	99.8	37	PDB header: ligase Chain: I: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
44	c2du4B	Alignment	not modelled	99.7	19	PDB header: ligase/rna Chain: B: PDB Molecule: o-phosphoseryl-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys
45	c2du7C	Alignment	not modelled	99.6	20	PDB header: ligase Chain: C: PDB Molecule: o-phosphoseryl-trna synthetase; PDBTitle: crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
46	d1c0aa2	Alignment	not modelled	99.5	100	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
47	c3od1A	Alignment	not modelled	99.5	17	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase regulatory subunit; PDBTitle: the crystal structure of an atp phosphoribosyltransferase regulatory2 subunit/histidyl-trna synthetase from bacillus halodurans c
48	d1z7ma1	Alignment	not modelled	99.4	17	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
49	c3cmqA	Alignment	not modelled	99.4	21	PDB header: ligase Chain: A: PDB Molecule: phenylalanyl-trna synthetase, mitochondrial; PDBTitle: crystal structure of human mitochondrial phenylalanine trna2 synthetase
50	c1wu7A	Alignment	not modelled	99.3	19	PDB header: ligase Chain: A: PDB Molecule: histidyl-trna synthetase; PDBTitle: crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum
51	c1adyA	Alignment	not modelled	99.3	17	PDB header: trna synthetase Chain: A: PDB Molecule: histidyl-trna synthetase; PDBTitle: histidyl-trna synthetase in complex with histidyl-adenylate
52	c1nyqA	Alignment	not modelled	99.2	18	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase 1; PDBTitle: structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
53	d1nyra4	Alignment	not modelled	99.2	18	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain

54	c2i4lC_	Alignment	not modelled	99.2	18	PDB header: ligase Chain: C: PDB Molecule: proline-trna ligase; PDBTitle: rhodopseudomonas palustris prolyl-trna synthetase
55	c2el9B_	Alignment	not modelled	99.2	16	PDB header: ligase Chain: B: PDB Molecule: histidyl-trna synthetase; PDBTitle: crystal structure of e.coli histidyl-trna synthetase2 complexed with a histidyl-adenylate analogue
56	d1l0wa2	Alignment	not modelled	99.1	40	Fold: DcoH-like Superfamily: GAD domain-like Family: GAD domain
57	c2j3mA_	Alignment	not modelled	99.1	14	PDB header: ligase Chain: A: PDB Molecule: prolyl-trna synthetase; PDBTitle: prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
58	c3a32A_	Alignment	not modelled	99.1	15	PDB header: ligase Chain: A: PDB Molecule: probable threonyl-trna synthetase 1; PDBTitle: crystal structure of putative threonyl-trna synthetase2 thrss-1 from aeropyrum pernix
59	d1hc7a2	Alignment	not modelled	99.0	13	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
60	d12asa_	Alignment	not modelled	99.0	21	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
61	c1fyfB_	Alignment	not modelled	99.0	15	PDB header: ligase Chain: B: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of a truncated form of threonyl-trna2 synthetase complexed with a seryl adenylate analog
62	d1qf6a4	Alignment	not modelled	99.0	18	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
63	c3hriF_	Alignment	not modelled	99.0	12	PDB header: ligase Chain: F: PDB Molecule: histidyl-trna synthetase; PDBTitle: histidyl-trna synthetase (apo) from trypanosoma brucei
64	c1qf6A_	Alignment	not modelled	99.0	17	PDB header: ligase/rna Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
65	c1h4tD_	Alignment	not modelled	98.9	13	PDB header: aminoacyl-trna synthetase Chain: D: PDB Molecule: prolyl-trna synthetase; PDBTitle: prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
66	c3lssA_	Alignment	not modelled	98.9	15	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: trypanosoma brucei seryl-trna synthetase in complex with atp
67	d1nj8a3	Alignment	not modelled	98.9	22	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
68	c3ialB_	Alignment	not modelled	98.9	14	PDB header: ligase Chain: B: PDB Molecule: prolyl-trna synthetase; PDBTitle: giardia lamblia prolyl-trna synthetase in complex with prolyl-2 adenylate
69	c1ggmB_	Alignment	not modelled	98.9	21	PDB header: ligase Chain: B: PDB Molecule: protein (glycyl-trna synthetase); PDBTitle: glycyl-trna synthetase from thermus thermophilus complexed with2 glycyl-adenylate
70	c1nj8C_	Alignment	not modelled	98.8	22	PDB header: ligase Chain: C: PDB Molecule: proline-trna synthetase; PDBTitle: crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii
71	c1atiA_	Alignment	not modelled	98.8	20	PDB header: protein biosynthesis Chain: A: PDB Molecule: glycyl-trna synthetase; PDBTitle: crystal structure of glycyl-trna synthetase from thermus thermophilus
72	c3netB_	Alignment	not modelled	98.8	21	PDB header: ligase Chain: B: PDB Molecule: histidyl-trna synthetase; PDBTitle: crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120
73	d1nj1a3	Alignment	not modelled	98.7	23	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
74	d1atia2	Alignment	not modelled	98.6	18	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
75	c1qe0B_	Alignment	not modelled	98.6	18	PDB header: ligase Chain: B: PDB Molecule: histidyl-trna synthetase; PDBTitle: crystal structure of apo s. aureus histidyl-trna synthetase
76	c1nj2A_	Alignment	not modelled	98.6	22	PDB header: ligase Chain: A: PDB Molecule: proline-trna synthetase; PDBTitle: crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
77	d1b76a2	Alignment	not modelled	98.5	22	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
78	c3qo8A_	Alignment	not modelled	98.5	15	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase, cytoplasmic; PDBTitle: crystal structure of seryl-trna synthetase from candida albicans
79	c1sryB_	Alignment	not modelled	98.5	16	PDB header: ligase(synthetase) Chain: B: PDB Molecule: seryl-trna synthetase; PDBTitle: refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution

80	c1wleB_	Alignment	not modelled	98.5	15	PDB header: ligase Chain: B: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
81	d1seta2	Alignment	not modelled	98.4	15	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
82	c2dq0A_	Alignment	not modelled	98.4	12	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
83	c3errB_	Alignment	not modelled	98.3	15	PDB header: ligase Chain: B: PDB Molecule: fusion protein of microtubule binding domain from PDBTitle: microtubule binding domain from mouse cytoplasmic dynein as2 a fusion with seryl-trna synthetase
84	c2dq3A_	Alignment	not modelled	98.3	14	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
85	c2cj9A_	Alignment	not modelled	98.2	11	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of methanosarcina barkeri seryl-trna2 synthetase complexed with an analog of seryladenylate
86	c3mf2B_	Alignment	not modelled	98.2	13	PDB header: ligase Chain: B: PDB Molecule: blt0957 protein; PDBTitle: crystal structure of class ii aars homologue (blt0957) complexed with2 amp
87	c3kf6A_	Alignment	not modelled	98.0	21	PDB header: structural protein Chain: A: PDB Molecule: protein stn1; PDBTitle: crystal structure of s. pombe stn1-ten1 complex
88	c3e0eA_	Alignment	not modelled	97.8	21	PDB header: replication Chain: A: PDB Molecule: replication protein a; PDBTitle: crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 target mrr110b
89	d1usya_	Alignment	not modelled	97.8	15	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
90	d1g5ha2	Alignment	not modelled	97.7	14	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
91	c2pmfA_	Alignment	not modelled	97.6	27	PDB header: ligase Chain: A: PDB Molecule: glycyl-trna synthetase; PDBTitle: the crystal structure of a human glycyl-trna synthetase mutant
92	c3ikmC_	Alignment	not modelled	97.6	12	PDB header: transferase Chain: C: PDB Molecule: dna polymerase subunit gamma-2; PDBTitle: crystal structure of human mitochondrial dna polymerase2 holoenzyme
93	c3dm3A_	Alignment	not modelled	97.3	25	PDB header: replication Chain: A: PDB Molecule: replication factor a; PDBTitle: crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e
94	c3l4gL_	Alignment	not modelled	97.3	12	PDB header: ligase Chain: L: PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
95	d2pi2a1	Alignment	not modelled	97.2	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
96	c2k50A_	Alignment	not modelled	97.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: replication factor a related protein; PDBTitle: solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
97	c3ig2B_	Alignment	not modelled	97.0	15	PDB header: ligase Chain: B: PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: the crystal structure of a putative phenylalanyl-trna synthetase2 (phers) beta chain domain from bacteroides fragilis to 2.1a
98	c1g5hA_	Alignment	not modelled	96.9	24	PDB header: dna binding protein Chain: A: PDB Molecule: mitochondrial dna polymerase accessory subunit; PDBTitle: crystal structure of the accessory subunit of murine mitochondrial2 polymerase gamma
99	c2pi2A_	Alignment	not modelled	96.5	19	PDB header: replication, dna binding protein Chain: A: PDB Molecule: replication protein a 32 kda subunit; PDBTitle: full-length replication protein a subunits rpa14 and rpa32
100	c3icaB_	Alignment	not modelled	96.4	14	PDB header: ligase Chain: B: PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: the crystal structure of the beta subunit of a phenylalanyl-trna2 synthetase from porphyromonas gingivalis w83
101	d1jcb5	Alignment	not modelled	96.2	16	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
102	d1nnxa_	Alignment	not modelled	96.2	16	Fold: OB-fold Superfamily: Hypothetical protein YgiW Family: Hypothetical protein YgiW
103	c2pqaB_	Alignment	not modelled	96.1	12	PDB header: replication Chain: B: PDB Molecule: replication protein a 14 kda subunit; PDBTitle: crystal structure of full-length human rpa 14/32 heterodimer
104	c1vnx4	Alignment	not modelled	95.9	17	PDB header: dna binding protein Chain: A: PDB Molecule: replication factor-a protein 1;

104	c1ynA	Alignment	not modelled	95.9	17	PDBTitle: solution structure of dna binding domain a (dbd-a) of 2 s.cerevisiae replication protein a (rpa)
105	c3kf8C	Alignment	not modelled	95.9	12	PDB header: structural protein Chain: C: PDB Molecule: protein stn1; PDBTitle: crystal structure of c. tropicalis stn1-ten1 complex
106	d1gm5a2	Alignment	not modelled	95.9	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain
107	d2pi2e1	Alignment	not modelled	95.7	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
108	d1jmca1	Alignment	not modelled	95.1	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
109	c3f2cA	Alignment	not modelled	94.7	18	PDB header: transferase/dna Chain: A: PDB Molecule: geobacillus kaustophilus dna polc; PDBTitle: dna polymerase polc from geobacillus kaustophilus complex with dna, 2 dgtg and mn
110	c1fguA	Alignment	not modelled	94.5	13	PDB header: replication Chain: A: PDB Molecule: replication protein a 70 kda dna-binding subunit; PDBTitle: ssdna-binding domain of the large subunit of replication2 protein a
111	c2k75A	Alignment	not modelled	94.4	12	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein ta0387; PDBTitle: solution nmr structure of the ob domain of ta0387 from 2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
112	d2g4ca2	Alignment	not modelled	93.5	14	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
113	c3pcoD	Alignment	not modelled	92.5	9	PDB header: ligase Chain: D: PDB Molecule: phenylalanyl-trna synthetase, beta chain; PDBTitle: crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
114	c1gm5A	Alignment	not modelled	90.8	22	PDB header: helicase Chain: A: PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
115	d1j5wa	Alignment	not modelled	89.7	27	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
116	c1z9fA	Alignment	not modelled	89.6	18	PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of single stranded dna-binding protein (tm0604) from 2 thermotoga maritima at 2.60 a resolution
117	c3rf1B	Alignment	not modelled	89.2	27	PDB header: ligase Chain: B: PDB Molecule: glycyl-trna synthetase alpha subunit; PDBTitle: the crystal structure of glycyl-trna synthetase subunit alpha from 2 campylobacter jejuni subsp. jejuni nctc 11168
118	c2rhsB	Alignment	not modelled	89.0	16	PDB header: ligase Chain: B: PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
119	c2kenA	Alignment	not modelled	86.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazei. northeast structural3 genomics consortium target mar214a.
120	d3ulla	Alignment	not modelled	85.8	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB