Phyre²

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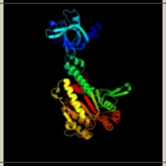
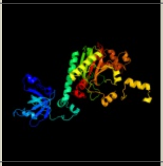
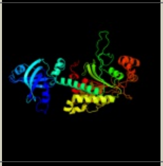
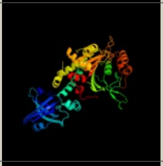
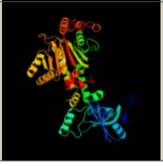
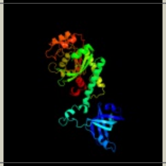
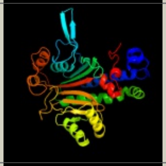
Description	P0A8N5
Date	Thu Jan 5 11:08:20 GMT 2012
Unique Job ID	5e16b5d1001ce66f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1e22A_	Alignment		100.0	100	**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
2	c3bjuB_	Alignment		100.0	45	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
3	c3e9hB_	Alignment		100.0	55	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
4	c1eqrC_	Alignment		100.0	28	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
5	c1efwA_	Alignment		100.0	28	**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
6	c1b8aB_	Alignment		100.0	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
7	c1asyA_	Alignment		100.0	25	**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
8	c1wydB_	Alignment		100.0	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
9	c2xgtB_	Alignment		100.0	19	**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	25	**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	c3i7fA_	Alignment		100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica

12	c3m4qA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
13	c1n9wA_	Alignment		100.0	28	**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	d1l0wa3	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
15	d1c0aa3	Alignment		100.0	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
16	d1eova2	Alignment		100.0	26	**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	26	**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	d1e1oa2	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
19	d1bbua2	Alignment		100.0	91	**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	d1n9wa2	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	d1nnha_	Alignment	not modelled	100.0	25	**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	31	**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	d1e1oa1	Alignment	not modelled	100.0	100	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
24	d1bbua1	Alignment	not modelled	100.0	86	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
25	c2znjB_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pyrrolysyl-trna synthetase from2 desulfitobacterium hafniense
26	c2zimA_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyrrolysyl-trna synthetase; **PDBTitle:** pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
27	d1kmma2	Alignment	not modelled	100.0	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
28	d1h4vb2	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
						PDB header:transferase

29	c1z7nB_	Alignment	not modelled	100.0	14	**Chain:** B: **PDB Molecule:**atp phosphoribosyltransferase regulatory subunit; **PDBTitle:** atp phosphoribosyl transferase (hiszg atp-prtase) from2 lactococcus lactis with bound prpp substrate
30	d1qe0a2	Alignment	not modelled	100.0	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
31	c2rhqA_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
32	d1krta_	Alignment	not modelled	99.9	89	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
33	d1wu7a2	Alignment	not modelled	99.9	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
34	c3racA_	Alignment	not modelled	99.9	15	**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.
35	d1jjca_	Alignment	not modelled	99.9	24	**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	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase; **PDBTitle:** phenylalanyl trna synthetase complexed with phenylalanine
37	d1l0wa1	Alignment	not modelled	99.9	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
38	c3pcoC_	Alignment	not modelled	99.9	21	**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
39	d1b8aa1	Alignment	not modelled	99.9	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
40	d1c0aa1	Alignment	not modelled	99.9	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
41	d1n9wa1	Alignment	not modelled	99.8	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
42	d1eova1	Alignment	not modelled	99.8	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
43	c3l4gI_	Alignment	not modelled	99.7	30	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
44	c1adyA_	Alignment	not modelled	99.7	15	**PDB header:**trna synthetase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase in complex with histidyl-adenylate
45	c2du4B_	Alignment	not modelled	99.7	22	**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
46	c3od1A_	Alignment	not modelled	99.6	14	**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
47	c2du7C_	Alignment	not modelled	99.5	24	**PDB header:**ligase **Chain:** C: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
48	d1z7ma1	Alignment	not modelled	99.5	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
49	c2i4lC_	Alignment	not modelled	99.4	17	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna ligase; **PDBTitle:** rhodopseudomonas palustris prolyl-trna synthetase
50	c1nyqA_	Alignment	not modelled	99.3	16	**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
51	c3cmqA_	Alignment	not modelled	99.3	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial phenylalanine trna2 synthetase
52	c1wu7A_	Alignment	not modelled	99.3	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum
53	c3a32A_	Alignment	not modelled	99.3	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**probable threonyl-trna synthetase 1; **PDBTitle:** crystal structure of putative threonyl-trna synthetase2 thrrs-1 from aeropyrum pernix

54	c2j3mA_	Alignment	not modelled	99.3	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
55	d12asa_	Alignment	not modelled	99.3	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
56	c2el9B_	Alignment	not modelled	99.3	14	**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
57	d1nyra4	Alignment	not modelled	99.3	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
58	c1fyfB_	Alignment	not modelled	99.3	16	**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
59	c3hriF_	Alignment	not modelled	99.2	14	**PDB header:**ligase **Chain:** F: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase (apo) from trypanosoma brucei
60	d1hc7a2	Alignment	not modelled	99.2	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
61	d1qf6a4	Alignment	not modelled	99.1	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
62	c1qf6A_	Alignment	not modelled	99.1	14	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
63	c1h4tD_	Alignment	not modelled	99.1	13	**PDB header:**aminoacyl-trna synthetase **Chain:** D: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
64	c1qe0B_	Alignment	not modelled	99.1	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of apo s. aureus histidyl-trna synthetase
65	c1ggmB_	Alignment	not modelled	99.1	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (glycyl-trna synthetase); **PDBTitle:** glycyl-trna synthetase from thermus thermophilus complexed with2 glycyl-adenylate
66	c1atiA_	Alignment	not modelled	99.0	17	**PDB header:**protein biosynthesis **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** crystal structure of glycyl-trna synthetase from thermus thermophilus
67	d1nj8a3	Alignment	not modelled	99.0	19	**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	c3netB_	Alignment	not modelled	99.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120
69	c1nj2A_	Alignment	not modelled	99.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
70	c1nj8C_	Alignment	not modelled	99.0	20	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii
71	c3ialB_	Alignment	not modelled	99.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** giardia lamblia prolyl-trna synthetase in complex with prolyl-2 adenylate
72	d1nj1a3	Alignment	not modelled	98.9	19	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
73	d1atia2	Alignment	not modelled	98.8	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
74	c3lssA_	Alignment	not modelled	98.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
75	d1b76a2	Alignment	not modelled	98.7	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
76	d1seta2	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
77	c1wleB_	Alignment	not modelled	98.6	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
78	c1sryB_	Alignment	not modelled	98.6	24	**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
79	c2dq0A_	Alignment	not modelled	98.6	17	**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
80	c3qo8A_	Alignment	not modelled	98.6	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
81	c2dq3A_	Alignment	not modelled	98.6	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
82	c3mf2B_	Alignment	not modelled	98.5	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**bll0957 protein; **PDBTitle:** crystal structure of class ii aars homologue (bll0957) complexed with2 amp
83	d1usya_	Alignment	not modelled	98.4	12	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
84	c3errB_	Alignment	not modelled	98.3	21	**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
85	c2cj9A_	Alignment	not modelled	98.2	15	**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	c2pmfA_	Alignment	not modelled	98.1	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** the crystal structure of a human glycyl-trna synthetase mutant
87	c3ikmC_	Alignment	not modelled	98.0	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**dna polymerase subunit gamma-2; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
88	c1g5hA_	Alignment	not modelled	97.9	15	**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
89	c3kf6A_	Alignment	not modelled	97.8	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
90	d1j5wa_	Alignment	not modelled	97.8	19	**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	d1g5ha2	Alignment	not modelled	97.8	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
92	c3e0eA_	Alignment	not modelled	97.8	24	**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 targe mrr110b
93	c3icaB_	Alignment	not modelled	97.5	12	**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
94	c3dm3A_	Alignment	not modelled	97.4	19	**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
95	c3ig2B_	Alignment	not modelled	97.3	12	**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
96	c3l4gL_	Alignment	not modelled	97.1	14	**PDB header:**ligase **Chain:** L: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
97	d2pi2a1	Alignment	not modelled	96.8	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
98	d2g4ca2	Alignment	not modelled	96.8	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
99	d1jjcb5	Alignment	not modelled	96.8	24	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
100	c2k50A_	Alignment	not modelled	96.4	24	**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.
101	d1gm5a2	Alignment	not modelled	96.3	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
102	c3kf8C_	Alignment	not modelled	96.3	14	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
103	c3pcoD_	Alignment	not modelled	95.7	19	**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

104	c2pi2A_	Alignment	not modelled	95.7	13	**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
105	c1yfsB_	Alignment	not modelled	95.6	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
106	c3rf1B_	Alignment	not modelled	95.3	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glycyl-trna synthetase alpha subunit; **PDBTitle:** the crystal structure of glycyl-trna synthetase subunit alpha from2 campylobacter jejuni subsp. jejuni nctc 11168
107	c1ynxA_	Alignment	not modelled	94.7	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication factor-a protein 1; **PDBTitle:** solution structure of dna binding domain a (dbd-a) of2 s.cerevisiae replication protein a (rpa)
108	c2k75A_	Alignment	not modelled	94.7	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ta0387; **PDBTitle:** solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
109	d1nnxa_	Alignment	not modelled	92.7	17	**Fold:**OB-fold **Superfamily:**Hypothetical protein YgiW **Family:**Hypothetical protein YgiW
110	d1jmca1	Alignment	not modelled	92.7	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
111	c1gm5A_	Alignment	not modelled	92.5	19	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
112	d1o7ia_	Alignment	not modelled	92.3	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
113	c2rhsB_	Alignment	not modelled	91.5	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
114	c3hxxA_	Alignment	not modelled	90.6	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
115	c1fguA_	Alignment	not modelled	89.4	17	**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
116	c2kenA_	Alignment	not modelled	88.8	9	**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.
117	c2pqaB_	Alignment	not modelled	87.5	21	**PDB header:**replication **Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit; **PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer
118	c2ztgA_	Alignment	not modelled	86.6	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase lacking the c-terminal dimerization domain in3 complex with ala-sa
119	c3f2cA_	Alignment	not modelled	86.4	14	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
120	c2akwB_	Alignment	not modelled	86.3	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of t.thermophilus phenylalanyl-trna synthetase2 complexed with p-cl-phenylalanine