Phyre^2

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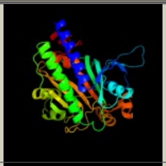
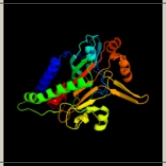
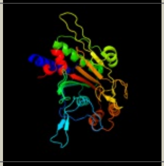
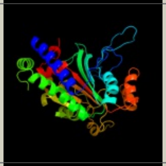
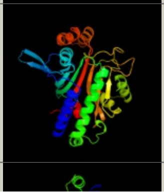
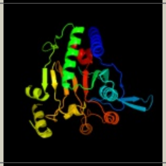
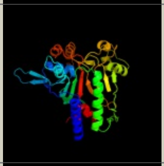
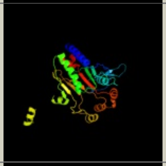
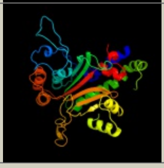
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d12asa_	Alignment		100.0	99	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
2	d1nnha_	Alignment		99.8	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
3	d1l0wa3	Alignment		99.6	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
4	d1c0aa3	Alignment		99.5	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
5	c3g1zB_	Alignment		99.3	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative lysyl-trna synthetase; **PDBTitle:** structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
6	d1bbua2	Alignment		99.3	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
7	c3m4qA_	Alignment		99.3	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
8	c1wydB_	Alignment		99.2	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
9	d1e1oa2	Alignment		99.2	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
10	c2xgtB_	Alignment		99.1	16	**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
11	c1x55A_	Alignment		99.1	19	**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

12	c1asyA_	Alignment		99.0	17	**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
13	c1b8aB_	Alignment		99.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
14	c3e9hB_	Alignment		99.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
15	c1e22A_	Alignment		98.9	20	**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
16	c3bjuB_	Alignment		98.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
17	c3i7fA_	Alignment		98.9	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
18	d1b8aa2	Alignment		98.8	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
19	c1eqrC_	Alignment		98.7	22	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
20	d1eova2	Alignment		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
21	c1n9wA_	Alignment	not modelled	98.6	20	**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
22	d1n9wa2	Alignment	not modelled	98.6	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
23	c1efwA_	Alignment	not modelled	98.1	26	**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
24	c2znjB_	Alignment	not modelled	95.1	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pyrrolysyl-trna synthetase from2 desulfitobacterium hafniense
25	c1b70A_	Alignment	not modelled	94.1	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase; **PDBTitle:** phenylalanyl trna synthetase complexed with phenylalanine
26	d1jjca_	Alignment	not modelled	93.3	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
27	c3l4gI_	Alignment	not modelled	92.2	24	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
28	c3mf2B_	Alignment	not modelled	87.5	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**bll0957 protein; **PDBTitle:** crystal structure of class ii aars homologue (bll0957) complexed with2 amp
						Fold: Class II aaRS and biotin synthetases

29	d1kmma2	Alignment	not modelled	83.4	19	**Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
30	d1h4vb2	Alignment	not modelled	72.6	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
31	d1p3qq_	Alignment	not modelled	69.1	32	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
32	c3qo8A_	Alignment	not modelled	67.6	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
33	c2du7C_	Alignment	not modelled	65.4	14	**PDB header:**ligase **Chain:** C: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
34	c2zimA_	Alignment	not modelled	62.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyrrolysyl-trna synthetase; **PDBTitle:** pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
35	c3pcoC_	Alignment	not modelled	62.4	24	**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
36	d1qe0a2	Alignment	not modelled	58.2	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
37	c2rhqA_	Alignment	not modelled	54.1	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
38	d2a7va1	Alignment	not modelled	52.7	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
39	c2a7vA_	Alignment	not modelled	52.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** human mitochondrial serine hydroxymethyltransferase 2
40	c3racA_	Alignment	not modelled	52.3	16	**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.
41	c3lm3A_	Alignment	not modelled	42.6	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative glycoside hydrolase/deacetylase2 (bdi_3119) from parabacteroides distasonis at 1.44 a resolution
42	c2du4B_	Alignment	not modelled	41.6	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
43	c2dq3A_	Alignment	not modelled	37.5	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
44	c3errB_	Alignment	not modelled	35.0	25	**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
45	d1ir1s_	Alignment	not modelled	34.9	23	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
46	c1wleB_	Alignment	not modelled	32.8	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
47	c1sryB_	Alignment	not modelled	32.2	25	**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
48	c2dq0A_	Alignment	not modelled	32.0	25	**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
49	d1gk8i_	Alignment	not modelled	31.2	27	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
50	d2v6ai1	Alignment	not modelled	28.5	26	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
51	d1ej7s_	Alignment	not modelled	28.3	19	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
52	d1unda_	Alignment	not modelled	27.1	21	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
53	d1unca_	Alignment	not modelled	26.8	36	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
54	d1yu8x1	Alignment	not modelled	26.7	36	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain

55	d1uzdc1	Alignment	not modelled	26.4	26	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
56	d8ruci_	Alignment	not modelled	26.2	23	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
57	d1wdds_	Alignment	not modelled	25.4	23	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
58	d1qzpa_	Alignment	not modelled	23.4	43	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
59	d1ny722	Alignment	not modelled	23.3	70	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
60	c2l3xA_	Alignment	not modelled	23.3	43	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ablim2 protein; **PDBTitle:** villin head piece domain of human ablim2
61	d1ujsa_	Alignment	not modelled	23.2	43	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
62	d1seta2	Alignment	not modelled	22.4	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
63	c2k6nA_	Alignment	not modelled	22.4	29	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**supervillin; **PDBTitle:** solution structure of human supervillin headpiece, minimized2 average
64	d1pgl22	Alignment	not modelled	20.9	70	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
65	d1uj8a1	Alignment	not modelled	20.7	47	**Fold:**Another 3-helical bundle **Superfamily:**IscX-like **Family:**IscX-like
66	d1yu5x1	Alignment	not modelled	20.4	36	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
67	d2fnoa2	Alignment	not modelled	20.1	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
68	c1jvnB_	Alignment	not modelled	19.6	67	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hishf; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
69	c2k29A_	Alignment	not modelled	18.3	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
70	c2z4tA_	Alignment	not modelled	17.9	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-galactoside alpha-2,6-sialyltransferase; **PDBTitle:** crystal structure of vibrionaceae photobacterium sp. jt-ish-224 2,6-2 sialyltransferase in a ternary complex with donor product cmp and3 accepter substrate lactose
71	d1htwa_	Alignment	not modelled	17.3	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**YjeE-like
72	d1uzhc1	Alignment	not modelled	17.2	26	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
73	c2zwiA_	Alignment	not modelled	17.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-/beta-galactoside alpha-2,3-sialyltransferase; **PDBTitle:** crystal structure of alpha/beta-galactoside alpha-2,3-2 sialyltransferase from a luminous marine bacterium, *photobacterium3 phosphoreum*
74	d1p3qr_	Alignment	not modelled	14.5	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
75	c1z7nB_	Alignment	not modelled	13.1	12	**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
76	c1xahA_	Alignment	not modelled	12.8	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of staphlyococcus aureus 3-dehydroquinate2 synthase (dhqs) in complex with zn2+ and nad+
77	d2cbpa_	Alignment	not modelled	12.1	41	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
78	c2pmfA_	Alignment	not modelled	11.9	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** the crystal structure of a human glycyl-trna synthetase mutant
79	c2bfuL_	Alignment	not modelled	11.6	64	**PDB header:**virus **Chain:** L: **PDB Molecule:**cowpea mosaic virus, large (l) subunit; **PDBTitle:** x-ray structure of cpmv top component
						PDB header:ligase

80	c2j3mA_	Alignment	not modelled	10.6	25	**Chain:** A: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
81	d1vqoi1	Alignment	not modelled	9.9	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
82	c1vq8I_	Alignment	not modelled	9.9	29	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**50s ribosomal protein l11p; **PDBTitle:** the structure of ccda-phe-cap-bio and the antibiotic sparsomycin bound2 to the large ribosomal subunit of haloarcula marismortui
83	c2flyA_	Alignment	not modelled	9.7	20	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**proadrenomedullin n-20 terminal peptide; **PDBTitle:** proadrenomedullin n-terminal 20 peptide
84	c3uhjE_	Alignment	not modelled	9.5	35	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**probable glycerol dehydrogenase; **PDBTitle:** crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
85	d2gycg1	Alignment	not modelled	9.4	57	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
86	c2zkri_	Alignment	not modelled	9.3	57	**PDB header:**ribosomal protein/rna **Chain:** I: **PDB Molecule:**rna expansion segment es15 part i; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
87	d1hc8a_	Alignment	not modelled	9.2	71	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
88	c2dzlA_	Alignment	not modelled	9.1	37	**PDB header:**structural genomics unknown function **Chain:** A: **PDB Molecule:**protein fam100b; **PDBTitle:** solution structure of the uba domain in human protein2 fam100b
89	d1rw3a_	Alignment	not modelled	9.0	11	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
90	d2ga1a1	Alignment	not modelled	8.7	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Alr1493-like
91	c2vacA_	Alignment	not modelled	8.4	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**twinfilin-2; **PDBTitle:** structure of n-terminal actin depolymerizing factor2 homology (adf-h) domain of human twinfilin-2
92	c2nysA_	Alignment	not modelled	8.4	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**agr_c_3712p; **PDBTitle:** x-ray crystal structure of protein agr_c_3712 from2 agrobacterium tumefaciens. northeast structural genomics3 consortium target atr88.
93	d2nysa1	Alignment	not modelled	8.4	28	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**AGR C 3712p-like
94	d2pkqo2	Alignment	not modelled	8.3	23	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
95	c1zzgB_	Alignment	not modelled	8.0	33	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
96	c2l0gA_	Alignment	not modelled	8.0	83	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** solution nmr structure of ubiquitin-binding motif (ubm2) of human2 polymerase iota
97	d1obfo2	Alignment	not modelled	8.0	23	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
98	d1gsua2	Alignment	not modelled	7.8	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
99	c2khuA_	Alignment	not modelled	7.5	83	**PDB header:**transferase/protein binding **Chain:** A: **PDB Molecule:**immunoglobulin g-binding protein g, dna **PDBTitle:** solution structure of the ubiquitin-binding motif of human2 polymerase iota