Phyre2

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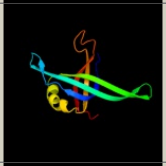
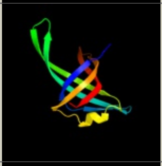
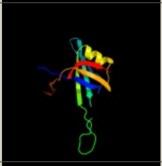
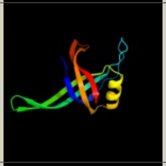
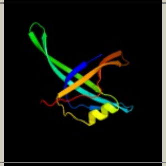
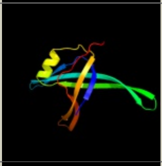
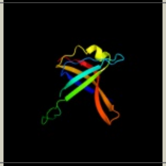
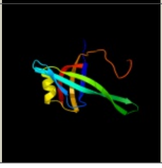
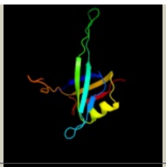
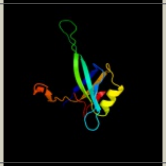
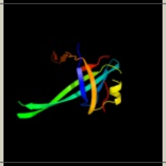
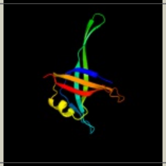
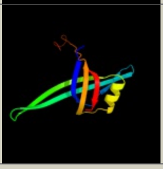
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v1qa_	Alignment		100.0	99	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
2	c3k8aA_	Alignment		100.0	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative primosomal replication protein; **PDBTitle:** neisseria gonorrhoeae prib
3	c3fhwB_	Alignment		100.0	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**primosomal replication protein n; **PDBTitle:** crystal structure of the protein prib from bordetella parapertussis.2 northeast structural genomics consortium target bpr162.
4	d1txya_	Alignment		99.9	99	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
5	c2vw9B_	Alignment		99.9	18	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**single-stranded dna binding protein; **PDBTitle:** single stranded dna binding protein complex from2 helicobacter pylori
6	c3en2A_	Alignment		99.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable primosomal replication protein n; **PDBTitle:** three-dimensional structure of the protein prib from2 ralstonia solanacearum at the resolution 2.3a. northeast3 structural genomics consortium target rsr213c.
7	c1se8A_	Alignment		99.9	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** structure of single-stranded dna-binding protein (ssb) from d.2 radiodurans
8	d1se8a_	Alignment		99.9	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
9	c2ihfA_	Alignment		99.9	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus
10	c2iheA_	Alignment		99.9	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
11	c3tqyA_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** structure of a single-stranded dna-binding protein (ssb), from2 coxiella burnetii

12	d1qvca_	Alignment		99.9	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
13	c1z9fA_	Alignment		99.9	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution
14	d1eyga_	Alignment		99.9	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
15	c3pgzB_	Alignment		99.9	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of a single strand binding protein (ssb) from2 bartonella henselae
16	c3lgjA_	Alignment		99.9	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae
17	d3ulla_	Alignment		99.8	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
18	c1eqqD_	Alignment		99.8	15	**PDB header:**replication/rna **Chain:** D: **PDB Molecule:**single stranded dna binding protein; **PDBTitle:** single stranded dna binding protein and ssdna complex
19	c3kojA_	Alignment		99.8	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ycf41; **PDBTitle:** crystal structure of the ssb domain of q5n255_synp6 protein2 from synechococcus sp. northeast structural genomics3 consortium target snr59a.
20	d1ue1a_	Alignment		99.8	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
21	c3eivB_	Alignment	not modelled	99.8	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**single-stranded dna-binding protein 2; **PDBTitle:** crystal structure of single-stranded dna-binding protein2 from streptomyces coelicolor
22	c1ue7A_	Alignment	not modelled	99.8	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** crystal structure of the single-stranded dna-binding2 protein from mycobacterium tuberculosis
23	c3e0eA_	Alignment	not modelled	97.3	12	**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
24	c3k81D_	Alignment	not modelled	96.9	17	**PDB header:**immune system, rna binding protein **Chain:** D: **PDB Molecule:**mp18 rna editing complex protein; **PDBTitle:** structure of the central interaction protein from the trypanosoma2 brucei editosome in complex with single domain antibodies
25	c3stbC_	Alignment	not modelled	96.9	17	**PDB header:**rna binding protein/immune system **Chain:** C: **PDB Molecule:**rna-editing complex protein mp42; **PDBTitle:** a complex of two editosome proteins and two nanobodies
26	c3dm3A_	Alignment	not modelled	96.8	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
27	c2k50A_	Alignment	not modelled	96.4	10	**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.
						PDB header:transferase/dna

28	c3f2cA_	Alignment	not modelled	94.7	18	**Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
29	c1fguA_	Alignment	not modelled	93.9	11	**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
30	c1ynxA_	Alignment	not modelled	92.5	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)
31	d1jmca1	Alignment	not modelled	91.5	6	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
32	d1c0aa1	Alignment	not modelled	90.0	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
33	c2k75A_	Alignment	not modelled	88.3	16	**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.
34	d1l0wa1	Alignment	not modelled	88.1	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
35	d1b8aa1	Alignment	not modelled	86.6	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
36	c2hqlB_	Alignment	not modelled	85.3	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hypothetical protein mg376 homolog; **PDBTitle:** crystal structure of a small single-stranded dna binding2 protein from mycoplasma pneumoniae
37	d1e1oa1	Alignment	not modelled	85.0	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
38	d1o7ia_	Alignment	not modelled	80.2	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
39	d1gm5a2	Alignment	not modelled	79.8	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
40	d1bbua1	Alignment	not modelled	76.9	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
41	d1jmca2	Alignment	not modelled	75.7	4	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
42	c3kf6A_	Alignment	not modelled	70.2	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
43	d1krta_	Alignment	not modelled	69.0	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
44	d1eova1	Alignment	not modelled	65.3	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
45	c3i7fA_	Alignment	not modelled	55.7	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
46	d1n9wa1	Alignment	not modelled	53.0	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
47	d1wjja_	Alignment	not modelled	52.1	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
48	c1e22A_	Alignment	not modelled	51.6	14	**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
49	c2kenA_	Alignment	not modelled	51.2	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.
50	c2xgtB_	Alignment	not modelled	50.9	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
51	d1ltla_	Alignment	not modelled	45.4	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
52	c1eqrC_	Alignment	not modelled	42.8	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
53	c3bjuB_	Alignment	not modelled	42.2	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase

54	c1wydB_	Alignment	not modelled	41.7	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
55	c3e9hB_	Alignment	not modelled	40.3	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
56	c3m4qA_	Alignment	not modelled	38.2	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
57	c1ltlE_	Alignment	not modelled	37.5	12	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
58	c1b8aB_	Alignment	not modelled	36.5	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
59	c1x55A_	Alignment	not modelled	33.8	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
60	d1xjva2	Alignment	not modelled	30.6	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
61	c1efwA_	Alignment	not modelled	30.0	14	**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
62	c1gm5A_	Alignment	not modelled	22.9	12	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
63	d2zjrg1	Alignment	not modelled	20.5	25	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
64	c3cf5G_	Alignment	not modelled	20.5	25	**PDB header:**ribosome/antibiotic **Chain:** G: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans
65	c1n9wA_	Alignment	not modelled	20.4	18	**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
66	d1xjva1	Alignment	not modelled	19.3	8	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
67	c2pi2A_	Alignment	not modelled	17.6	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
68	d1vqoj1	Alignment	not modelled	17.5	15	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
69	c2vl6C_	Alignment	not modelled	16.6	16	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain
70	d1qr0a1	Alignment	not modelled	16.6	16	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**4'-Phosphopantetheinyl transferase SFP
71	d2nn6g1	Alignment	not modelled	16.1	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
72	d1nnxa_	Alignment	not modelled	15.8	15	**Fold:**OB-fold **Superfamily:**Hypothetical protein YgiW **Family:**Hypothetical protein YgiW
73	c2zkrj_	Alignment	not modelled	15.1	16	**PDB header:**ribosomal protein/rna **Chain:** J: **PDB Molecule:**rna expansion segment es15 part ii; **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
74	c1asyA_	Alignment	not modelled	14.9	19	**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
75	d1j3aa_	Alignment	not modelled	14.5	11	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
76	d2j01n1	Alignment	not modelled	14.1	26	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
77	c3d5bN_	Alignment	not modelled	13.7	26	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
78	c3kzeA_	Alignment	not modelled	13.1	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**t-lymphoma invasion and metastasis-inducing protein 1; **PDBTitle:** crystal structure of t-cell lymphoma invasion and

						metastasis-1 pdz in2 complex with ssrkeyya peptide
79	c2ja9A_	Alignment	not modelled	12.7	9	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the n-terminal deletion of yeast exosome2 component rrp40
80	c2ftcH_	Alignment	not modelled	12.6	11	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**39s ribosomal protein l13, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
81	c2k4mA_	Alignment	not modelled	12.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0146 protein mth_1000; **PDBTitle:** solution nmr structure of m. thermoautotrophicum protein2 mth_1000, northeast structural genomics consortium target3 tr8
82	c4a1aI_	Alignment	not modelled	12.0	25	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l13a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
83	d2ja9a1	Alignment	not modelled	11.8	7	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
84	c1xjvA_	Alignment	not modelled	11.6	8	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protection of telomeres 1; **PDBTitle:** crystal structure of human pot1 bound to telomeric single-2 stranded dna (ttagggttag)
85	c3jywM_	Alignment	not modelled	11.0	20	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l16(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
86	d2b3ga1	Alignment	not modelled	10.8	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
87	c3izcK_	Alignment	not modelled	10.6	20	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein rpl16 (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
88	c3bboL_	Alignment	not modelled	10.3	32	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**ribosomal protein l13; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
89	c1krhA_	Alignment	not modelled	10.3	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
90	d2pi2a1	Alignment	not modelled	10.1	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
91	c3kf8C_	Alignment	not modelled	10.0	14	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
92	d1vk3a3	Alignment	not modelled	9.0	11	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
93	d1htwa_	Alignment	not modelled	8.8	5	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**YjeE-like
94	d1qfza1	Alignment	not modelled	8.7	14	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
95	c3nklA_	Alignment	not modelled	8.7	14	**PDB header:**oxidoreductase/lyase **Chain:** A: **PDB Molecule:**udp-d-quinovosamine 4-dehydrogenase; **PDBTitle:** crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
96	d1fnda1	Alignment	not modelled	7.1	9	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
97	d1krha1	Alignment	not modelled	7.0	9	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
98	c2nn6G_	Alignment	not modelled	7.0	12	**PDB header:**hydrolase/transferase **Chain:** G: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
99	c1ph4A_	Alignment	not modelled	6.9	9	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggttttggcg