Phyre^2

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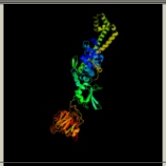
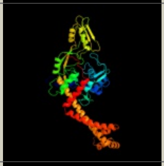
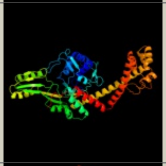
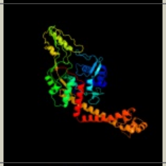
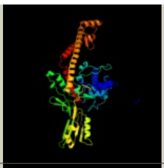
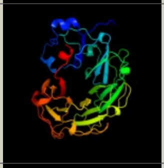
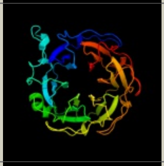
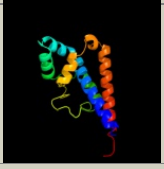
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zvuA_	Alignment		100.0	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit a; **PDBTitle:** structure of the full-length e. coli parc subunit
2	c2wl2B_	Alignment		100.0	99	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
3	c2xcsD_	Alignment		100.0	60	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna
4	c3ifzA_	Alignment		100.0	52	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
5	d1ab4a_	Alignment		100.0	98	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
6	c2xcqA_	Alignment		100.0	60	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
7	c3ilwA_	Alignment		100.0	51	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** structure of dna gyrase subunit a n-terminal domain
8	c2xkjE_	Alignment		100.0	41	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**topoisomerase iv; **PDBTitle:** crystal structure of catalytic core of a. baumannii topo iv2 (pare-parc fusion truncate)
9	c2inrA_	Alignment		100.0	50	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
10	c2novD_	Alignment		100.0	47	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** breakage-reunion domain of s.pneumoniae topo iv: crystal2 structure of a gram-positive quinolone target
11	c3qx3B_	Alignment		100.0	25	**PDB header:**isomerase/dna/isomerase inhibitor **Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta; **PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide

12	c1bjtA_	Alignment		100.0	21	**PDB header:**topoisomerase **Chain:** A: **PDB Molecule:**topoisomerase ii; **PDBTitle:** topoisomerase ii residues 409-1201
13	d1bjta_	Alignment		100.0	21	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
14	c3l6vA_	Alignment		100.0	59	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of the xanthomonas campestris gyrase a c-2 terminal domain
15	d1wp5a_	Alignment		100.0	31	**Fold:**6-bladed beta-propeller **Superfamily:**GyrA/ParC C-terminal domain-like **Family:**GyrA/ParC C-terminal domain-like
16	d1suua_	Alignment		100.0	28	**Fold:**6-bladed beta-propeller **Superfamily:**GyrA/ParC C-terminal domain-like **Family:**GyrA/ParC C-terminal domain-like
17	c1zi0A_	Alignment		100.0	99	**PDB header:**isomerase, dna bindng protein **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** a superhelical spiral in escherichia coli dna gyrase a c-2 terminal domain imparts unidirectional supercoiling bias
18	c3no0B_	Alignment		100.0	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** aquifex aeolicus type iia topoisomerase c-terminal domain
19	c1zvtA_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit a; **PDBTitle:** structure of the e. coli parc c-terminal domain
20	c3ku8A_	Alignment		100.0	100	**PDB header:**toxin/isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** ccdbvfi:gyra14ec
21	d1x75a1	Alignment	not modelled	100.0	94	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
22	c2oajA_	Alignment	not modelled	86.9	12	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**protein sni1; **PDBTitle:** crystal structure of sro7 from s. cerevisiae
23	c3dm0A_	Alignment	not modelled	73.6	15	**PDB header:**sugar binding protein,signaling protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein fused with **PDBTitle:** maltose binding protein fusion with rack1 from a. thaliana
24	c1t3jA_	Alignment	not modelled	72.3	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitofusin 1; **PDBTitle:** mitofusin domain hr2 v686m/i708m mutant
25	c2q6tB_	Alignment	not modelled	61.6	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
26	c3jroA_	Alignment	not modelled	58.2	13	**PDB header:**transport protein, structural protein **Chain:** A: **PDB Molecule:**fusion protein of protein transport protein sec13 **PDBTitle:** nup84-nup145c-sec13 edge element of the npc lattice
27	c1c9lA_	Alignment	not modelled	56.3	13	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**clathrin; **PDBTitle:** peptide-in-groove interactions link target proteins to the2 b-propeller of clathrin
28	d2g0da1	Alignment	not modelled	56.2	16	**Fold:**alpha/alpha toroid **Superfamily:**LanC-like **Family:**LanC-like

29	d1jwea_	Alignment	not modelled	54.0	16	**Fold:**N-terminal domain of DnaB helicase **Superfamily:**N-terminal domain of DnaB helicase **Family:**N-terminal domain of DnaB helicase
30	c3fokH_	Alignment	not modelled	53.6	17	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**uncharacterized protein cgl0159; **PDBTitle:** crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
31	c3a7pB_	Alignment	not modelled	53.5	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
32	c2vyeA_	Alignment	not modelled	50.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
33	c3lssA_	Alignment	not modelled	48.2	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
34	d2v8qb1	Alignment	not modelled	47.9	22	**Fold:**AMPKBI-like **Superfamily:**AMPKBI-like **Family:**AMPKBI-like
35	c1q1hA_	Alignment	not modelled	40.7	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor e; **PDBTitle:** an extended winged helix domain in general transcription2 factor e/iie alpha
36	d1q1ha_	Alignment	not modelled	40.7	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcription factor E/IIe-alpha, N-terminal domain
37	c3gndC_	Alignment	not modelled	38.8	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
38	d1b79a_	Alignment	not modelled	35.4	17	**Fold:**N-terminal domain of DnaB helicase **Superfamily:**N-terminal domain of DnaB helicase **Family:**N-terminal domain of DnaB helicase
39	c1dpuA_	Alignment	not modelled	35.3	36	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
40	d1dpua_	Alignment	not modelled	35.3	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
41	d2ayua1	Alignment	not modelled	34.1	15	**Fold:**NAP-like **Superfamily:**NAP-like **Family:**NAP-like
42	c2ayuA_	Alignment	not modelled	34.1	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**nucleosome assembly protein; **PDBTitle:** the structure of nucleosome assembly protein suggests a mechanism for2 histone binding and shuttling
43	c2qjhH_	Alignment	not modelled	33.8	19	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
44	c3mkqA_	Alignment	not modelled	33.5	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**coatomer beta'-subunit; **PDBTitle:** crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat
45	c3a7mA_	Alignment	not modelled	29.6	13	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**flagellar protein flit; **PDBTitle:** structure of flit, the flagellar type iii chaperone for flid
46	d2qrdb1	Alignment	not modelled	29.1	15	**Fold:**AMPKBI-like **Superfamily:**AMPKBI-like **Family:**AMPKBI-like
47	c2h47F_	Alignment	not modelled	28.6	10	**PDB header:**oxidoreductase/electron transport **Chain:** F: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of an electron transfer complex between2 aromatic amine dephydrogenase and azurin from alcaligenes3 faecalis (form 1)
48	c2jesG_	Alignment	not modelled	28.4	12	**PDB header:**viral protein **Chain:** G: **PDB Molecule:**portal protein; **PDBTitle:** portal protein from bacteriophage spp1
49	c2b5nD_	Alignment	not modelled	28.0	12	**PDB header:**dna binding protein/protein binding **Chain:** D: **PDB Molecule:**damage-specific dna binding protein 1; **PDBTitle:** crystal structure of the ddb1 bpb domain
50	d2dloa1	Alignment	not modelled	27.5	71	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
51	d1ivsa1	Alignment	not modelled	27.3	27	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
52	c1ce0B_	Alignment	not modelled	27.2	31	**PDB header:**hiv-1 envelope protein **Chain:** B: **PDB Molecule:**protein (leucine zipper model h38-p1); **PDBTitle:** trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
53	c2pqaB_	Alignment	not modelled	26.5	29	**PDB header:**replication **Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit; **PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer
54	c3ushB_	Alignment	not modelled	26.5	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q2s0r5 protein from salinibacter ruber,2 northeast structural genomics consortium target srr207

55	d1k32a3	Alignment	not modelled	24.8	10	**Fold:**7-bladed beta-propeller **Superfamily:**Tricorn protease domain 2 **Family:**Tricorn protease domain 2
56	d1iwpa_	Alignment	not modelled	24.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Diol dehydratase, alpha subunit
57	d1a06a_	Alignment	not modelled	23.9	30	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
58	c2p9mD_	Alignment	not modelled	23.7	15	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0922; **PDBTitle:** crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
59	d2pi2e1	Alignment	not modelled	23.0	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
60	c3so4C_	Alignment	not modelled	22.3	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**methionine-adenosyltransferase; **PDBTitle:** methionine-adenosyltransferase from entamoeba histolytica
61	c2zezC_	Alignment	not modelled	21.9	41	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**s-layer associated multidomain endoglucanase; **PDBTitle:** family 16 carbohydrate binding module-2
62	c3ocmB_	Alignment	not modelled	21.0	8	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
63	c1ztaA_	Alignment	not modelled	20.6	34	**PDB header:**dna-binding motif **Chain:** A: **PDB Molecule:**leucine zipper monomer; **PDBTitle:** the solution structure of a leucine-zipper motif peptide
64	c3ol2B_	Alignment	not modelled	20.4	18	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**plexin-b1; **PDBTitle:** receptor-ligand structure of human semaphorin 4d with plexin b1.
65	d1mlda2	Alignment	not modelled	19.4	18	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
66	c3izcR_	Alignment	not modelled	18.9	8	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**60s ribosomal protein rpl18 (l18e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
67	c2dfdD_	Alignment	not modelled	18.4	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of human malate dehydrogenase type 2
68	d2f2ac1	Alignment	not modelled	18.1	16	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Glu-tRNAGln amidotransferase C subunit **Family:**Glu-tRNAGln amidotransferase C subunit
69	c3e5zA_	Alignment	not modelled	18.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative gluconolactonase; **PDBTitle:** x-ray structure of the putative gluconolactonase in protein family2 pf08450. northeast structural genomics consortium target drr130.
70	c2hpcF_	Alignment	not modelled	17.7	17	**PDB header:**blood clotting **Chain:** F: **PDB Molecule:**fibrinogen, gamma polypeptide; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
71	c1u0iA_	Alignment	not modelled	17.6	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**iaal-e3; **PDBTitle:** iaal-e3/k3 heterodimer
72	c2lmiA_	Alignment	not modelled	17.5	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**g-rich sequence factor 1; **PDBTitle:** nmr structure of the protein bc040485 from homo sapiens
73	c2xzrA_	Alignment	not modelled	17.1	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
74	c3czoD_	Alignment	not modelled	17.0	24	**PDB header:**lyase **Chain:** D: **PDB Molecule:**histidine ammonia-lyase; **PDBTitle:** crystal structure of double mutant phenylalanine ammonia-2 lyase from anabaena variabilis
75	c2a5wC_	Alignment	not modelled	16.6	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfite reductase, desulfoviridin-type subunit gamma **PDBTitle:** crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrc) from archaeoglobus fulgidus
76	c3kpbA_	Alignment	not modelled	16.5	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0100; **PDBTitle:** crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
77	c1mldA_	Alignment	not modelled	16.4	18	**PDB header:**oxidoreductase(nad(a)-choh(d)) **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases
78	c2jjmH_	Alignment	not modelled	16.1	22	**PDB header:**transferase **Chain:** H: **PDB Molecule:**glycosyl transferase, group 1 family protein; **PDBTitle:** crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
79	c2pwzG_	Alignment	not modelled	15.8	18	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of the apo form of e.coli malate dehydrogenase

80	c2pfiA_	Alignment	not modelled	15.7	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**chloride channel protein clc-ka; **PDBTitle:** crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
81	d1y5ha3	Alignment	not modelled	15.6	3	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
82	c2oszA_	Alignment	not modelled	15.4	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin p58/p45; **PDBTitle:** structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
83	c1yx3A_	Alignment	not modelled	15.2	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
84	c2v8kA_	Alignment	not modelled	15.0	35	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pectate lyase; **PDBTitle:** structure of a family 2 pectate lyase in complex with2 trigalacturonic acid
85	c2r60A_	Alignment	not modelled	14.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
86	c3ltjA_	Alignment	not modelled	14.6	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**alpharep-4; **PDBTitle:** structure of a new family of artificial alpha helicoidal repeat2 proteins (alpha-rep) based on thermostable heat-like repeats
87	c3m9bK_	Alignment	not modelled	14.5	20	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
88	c3somO_	Alignment	not modelled	14.5	23	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**methylmalonic aciduria and homocystinuria type c protein; **PDBTitle:** crystal structure of human mmachc
89	c3ue3A_	Alignment	not modelled	14.3	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**septum formation, penicillin binding protein 3, **PDBTitle:** crystal structure of acinetobacter baumanni pbp3
90	c3idwA_	Alignment	not modelled	13.9	20	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
91	c3l31B_	Alignment	not modelled	13.8	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable manganase-dependent inorganic **PDBTitle:** crystal structure of the cbs and drtgg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
92	c2d4zB_	Alignment	not modelled	13.8	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride channel protein; **PDBTitle:** crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
93	c2qh1B_	Alignment	not modelled	13.7	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ta0289; **PDBTitle:** structure of ta289, a cbs-rubredoxin-like protein, in its fe+2-bound2 state
94	d1rp3a2	Alignment	not modelled	13.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
95	d1o50a3	Alignment	not modelled	13.2	15	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
96	d1wi9a_	Alignment	not modelled	12.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
97	c3kfuJ_	Alignment	not modelled	12.9	26	**PDB header:**ligase/rna **Chain:** J: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c; **PDBTitle:** crystal structure of the transamidosome
98	d1n0ua3	Alignment	not modelled	12.8	26	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
99	d2ca1a1	Alignment	not modelled	12.7	21	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein