Phyre^2

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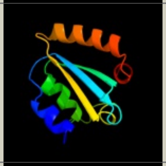
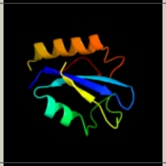
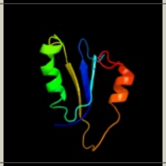
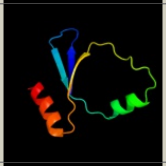
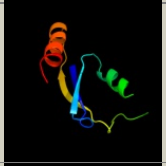
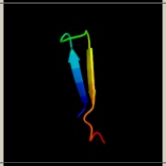
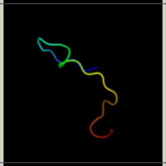
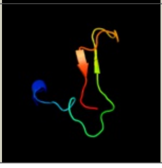
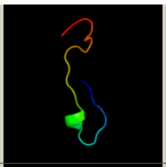
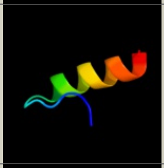
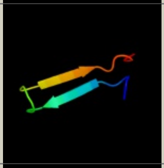
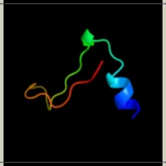
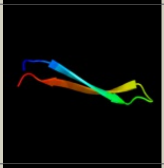
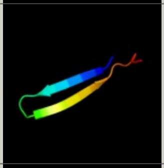
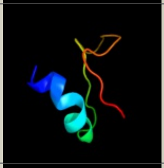
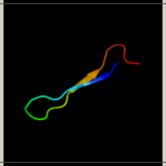
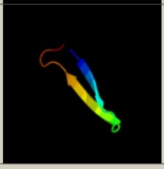
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yd2A_	Alignment		99.9	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease domain of2 uvrc from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation
2	c1yd6A_	Alignment		99.9	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrc; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease2 domain of uvrc from bacillus caldotenax
3	c2wshC_	Alignment		99.9	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endonuclease ii; **PDBTitle:** structure of bacteriophage t4 endoii e118a mutant
4	d1mk0a_	Alignment		98.6	15	**Fold:**GIY-YIG endonuclease **Superfamily:**GIY-YIG endonuclease **Family:**GIY-YIG endonuclease
5	c3nicA_	Alignment		96.8	26	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**eco29kir; **PDBTitle:** dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
6	c1zg2A_	Alignment		94.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0213 protein bh0048; **PDBTitle:** solution nmr structure of the upf0213 protein bh0048 from2 bacillus halodurans. northeast structural genomics target3 bhr2.
7	c1ywlA_	Alignment		93.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0213 protein ef2693; **PDBTitle:** solution nmr structure of the protein ef2693 from e.2 faecalis: northeast structural genomics consortium target3 efr36
8	d1pd0a4	Alignment		68.5	25	**Fold:**Gelsolin-like **Superfamily:**C-terminal, gelsolin-like domain of Sec23/24 **Family:**C-terminal, gelsolin-like domain of Sec23/24
9	d1utaa_	Alignment		41.4	14	**Fold:**Ferredoxin-like **Superfamily:**Sporulation related repeat **Family:**Sporulation related repeat
10	d1xdpa4	Alignment		38.0	33	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
11	c2gj3A_	Alignment		37.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nitrogen fixation regulatory protein; **PDBTitle:** crystal structure of the fad-containing pas domain of the2 protein nifl from azotobacter vinelandii.

12	d2o8ra4	Alignment		36.6	21	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
13	c1x60A_	Alignment		34.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sporulation-specific n-acetylmuramoyl-l-alanine **PDBTitle:** solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
14	c1pd0A_	Alignment		32.7	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
15	c2qkpD_	Alignment		31.8	28	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
16	c2rivB_	Alignment		30.7	33	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**thyroxine-binding globulin; **PDBTitle:** crystal structure of the reactive loop cleaved human thyroxine binding2 globulin
17	c3egxB_	Alignment		28.2	25	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1
18	c3luqC_	Alignment		27.4	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of a pas domain from a sensory box2 histidine kinase regulator from geobacter sulfurreducens to3 2.5a
19	c3eh2B_	Alignment		27.2	30	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24c; **PDBTitle:** crystal structure of the human copii-coat protein sec24c
20	c1m2vB_	Alignment		26.8	25	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the yeast sec23/24 heterodimer
21	c3eg9B_	Alignment	not modelled	26.5	30	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**sec24 related gene family, member d; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
22	c1hleB_	Alignment	not modelled	25.4	13	**PDB header:**hydrolase inhibitor(serine proteinase) **Chain:** B: **PDB Molecule:**horse leukocyte elastase inhibitor; **PDBTitle:** crystal structure of cleaved equine leucocyte elastase2 inhibitor determined at 1.95 angstroms resolution
23	c1xdoB_	Alignment	not modelled	23.0	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of escherichia coli polyphosphate kinase
24	d1gcca_	Alignment	not modelled	20.8	33	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**GCC-box binding domain
25	c2o8rA_	Alignment	not modelled	20.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
26	c3mxqC_	Alignment	not modelled	20.1	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
27	c3mr0B_	Alignment	not modelled	20.1	10	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**sensory box histidine kinase/response regulator; **PDBTitle:** crystal structure of sensory box histidine kinase/response regulator2 from burkholderia thailandensis e264
28	d1g1pa_	Alignment	not modelled	19.7	71	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Conotoxin

29	c1jjoE_	Alignment	not modelled	18.7	25	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**neuroserpin; **PDBTitle:** crystal structure of mouse neuroserpin (cleaved form)
30	c2jheB_	Alignment	not modelled	18.6	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription regulator tyrr; **PDBTitle:** n-terminal domain of tyrr transcription factor (residues 1 -2 190)
31	d1nwza_	Alignment	not modelled	17.8	15	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
32	d1lkta_	Alignment	not modelled	17.6	29	**Fold:**Head-binding domain of phage P22 tailspike protein **Superfamily:**Head-binding domain of phage P22 tailspike protein **Family:**Head-binding domain of phage P22 tailspike protein
33	c2w0nA_	Alignment	not modelled	17.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein dcus; **PDBTitle:** plasticity of pas domain and potential role for signal2 transduction in the histidine-kinase dcus
34	c3f02C_	Alignment	not modelled	16.9	17	**PDB header:**hydrolase inhibitor **Chain:** C: **PDB Molecule:**neuroserpin; **PDBTitle:** cleaved human neuroserpin
35	c3mfxA_	Alignment	not modelled	16.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sensory box/ggdef family protein; **PDBTitle:** crystal structure of the sensory box domain of the sensory-2 box/ggdef protein so_1695 from shewanella oneidensis,3 northeast structural genomics consortium target sor288b
36	c2h4qB_	Alignment	not modelled	15.8	13	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**heterochromatin-associated protein ment; **PDBTitle:** crystal structure of a m-loop deletion variant of ment in2 the cleaved conformation
37	c9paiB_	Alignment	not modelled	15.3	19	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**protein (plasminogen activator inhibitor-1) residues 365- **PDBTitle:** cleaved substrate variant of plasminogen activator inhibitor-1
38	d1v9ya_	Alignment	not modelled	15.0	19	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
39	c1v9yA_	Alignment	not modelled	15.0	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**heme pas sensor protein; **PDBTitle:** crystal structure of the heme pas sensor domain of ec dos (ferric2 form)
40	c1f0cB_	Alignment	not modelled	15.0	20	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**ice inhibitor; **PDBTitle:** structure of the viral serpin crma
41	d2gjva1	Alignment	not modelled	14.8	27	**Fold:**Phage tail protein-like **Superfamily:**Phage tail protein-like **Family:**STM4215-like
42	c3gr1A_	Alignment	not modelled	14.4	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
43	c2gjvF_	Alignment	not modelled	13.8	27	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** crystal structure of a protein of unknown function from salmonella2 typhimurium
44	c1yylM_	Alignment	not modelled	13.8	56	**PDB header:**viral protein/immune system **Chain:** M: **PDB Molecule:**cd4m33, scorpion-toxin mimic of cd4; **PDBTitle:** crystal structure of cd4m33, a scorpion-toxin mimic of cd4, in complex2 with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-1 antibody3 17b
45	c1yylS_	Alignment	not modelled	13.7	56	**PDB header:**viral protein/immune system **Chain:** S: **PDB Molecule:**cd4m33, scorpion-toxin mimic of cd4; **PDBTitle:** crystal structure of cd4m33, a scorpion-toxin mimic of cd4, in complex2 with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-1 antibody3 17b
46	c2r78D_	Alignment	not modelled	13.2	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of a domain of the sensory box sensor2 histidine kinase/response regulator from geobacter3 sulfurreducens
47	c7apiB_	Alignment	not modelled	12.9	33	**PDB header:**proteinase inhibitor **Chain:** B: **PDB Molecule:**alpha 1-antitrypsin; **PDBTitle:** the s variant of human alpha1-antitrypsin, structure and implications2 for function and metabolism
48	c3eg9A_	Alignment	not modelled	12.4	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec23a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
49	c2vkyB_	Alignment	not modelled	12.2	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**tail protein, piigcn4; **PDBTitle:** headbinding domain of phage p22 tailspike c-terminally2 fused to isoleucine zipper piigcn4 (chimera i)
50	c3mjqB_	Alignment	not modelled	12.1	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the pas domain of q24qt8_deshy protein from2 desulfitobacterium hafniense. northeast structural genomics3 consortium target dhr85c.
51	d2fcja1	Alignment	not modelled	11.8	16	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
52	d1d0na6	Alignment	not modelled	11.1	19	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
53	c2i9nA_	Alignment	not modelled	9.8	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**mhb4a peptide; **PDBTitle:** design of bivalent miniprotein consisting of two2

						independent elements, a b-hairpin peptide and a-helix3 peptide, tethered by four glycines
54	d2omoa1	Alignment	not modelled	9.6	9	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
55	d1svya_	Alignment	not modelled	9.1	10	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
56	c3c7tB_	Alignment	not modelled	9.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ecdysteroid-phosphate phosphatase; **PDBTitle:** crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
57	c2dnaA_	Alignment	not modelled	9.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
58	c3ll4B_	Alignment	not modelled	9.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein ykr043c; **PDBTitle:** structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
59	d2axtb1	Alignment	not modelled	8.9	20	**Fold:**Photosystem II antenna protein-like **Superfamily:**Photosystem II antenna protein-like **Family:**Photosystem II antenna protein-like
60	c2i9oA_	Alignment	not modelled	8.8	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**mhb8a peptide; **PDBTitle:** design of bivalent miniprotein consisting of two2 independent elements, a b-hairpin peptide and a-helix3 peptide, tethered by eight glycines
61	c1vddC_	Alignment	not modelled	8.6	39	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
62	c3eehA_	Alignment	not modelled	8.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative light and redox sensing histidine kinase; **PDBTitle:** the crystal structure of the domain of the putative light and redox2 sensing histidine kinase from haloarcula marismortui
63	d2fh1a3	Alignment	not modelled	8.4	13	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
64	c3d4iD_	Alignment	not modelled	7.9	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sts-2 protein; **PDBTitle:** crystal structure of the 2h-phosphatase domain of sts-2
65	d1jr3d2	Alignment	not modelled	7.9	43	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
66	c3q5dA_	Alignment	not modelled	7.9	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atlastin-1; **PDBTitle:** crystal structure of human atlastin-1 (residues 1-447) bound to gdp,2 crystal form 1
67	d1oj4a2	Alignment	not modelled	7.8	18	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
68	d1cuoa_	Alignment	not modelled	7.8	9	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
69	c1m1jA_	Alignment	not modelled	7.7	21	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
70	d2axwa1	Alignment	not modelled	7.5	14	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
71	c3caxA_	Alignment	not modelled	7.5	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf0695; **PDBTitle:** crystal structure of uncharacterized protein pf0695
72	c2ikqA_	Alignment	not modelled	7.4	15	**PDB header:**signaling protein, immune system **Chain:** A: **PDB Molecule:**suppressor of t-cell receptor signaling 1; **PDBTitle:** crystal structure of mouse sts-1 pgm domain in complex with phosphate
73	d1b2pa_	Alignment	not modelled	7.4	25	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
74	d2ga9d1	Alignment	not modelled	7.3	21	**Fold:**Poly(A) polymerase catalytic subunit-like **Superfamily:**Poly(A) polymerase catalytic subunit-like **Family:**Poxvirus poly(A) polymerase catalytic subunit-like
75	d1mbya_	Alignment	not modelled	7.2	29	**Fold:**Polo-box domain **Superfamily:**Polo-box domain **Family:**Swapped Polo-box domain
76	c3knuD_	Alignment	not modelled	7.1	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
77	d1x6va1	Alignment	not modelled	7.1	24	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
78	c3quvB_	Alignment	not modelled	7.0	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a trna-guanine-n1-methyltransferase from2 mycobacterium abscessus
79	d1p9pa_	Alignment	not modelled	7.0	29	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot

						Family:tRNA(m1G37)-methyltransferase TrmD
80	d1fzta_	Alignment	not modelled	7.0	18	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
81	d2pp4a1	Alignment	not modelled	6.9	17	**Fold:**TAFH domain-like **Superfamily:**TAFH domain-like **Family:**TAFH domain-like
82	d2cvba1	Alignment	not modelled	6.8	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
83	d1uala_	Alignment	not modelled	6.8	36	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
84	d1pvda1	Alignment	not modelled	6.7	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
85	c2hpwA_	Alignment	not modelled	6.6	26	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**green fluorescent protein; **PDBTitle:** green fluorescent protein from clytia gregaria
86	c2fvnA_	Alignment	not modelled	6.4	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein afad; **PDBTitle:** the fibrillar tip complex of the afa/dr adhesins from2 pathogen e. coli displays synergistic binding to 5 1 and v3 3 integrins
87	c2kvcA_	Alignment	not modelled	6.4	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
88	c2kpmA_	Alignment	not modelled	6.3	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein from gene2 locus ne0665 of nitrosomonas europaea. northeast structural3 genomics target ner103a
89	c2c9wA_	Alignment	not modelled	6.2	33	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**suppressor of cytokine signaling 2; **PDBTitle:** crystal structure of socs-2 in complex with elongin-b and2 elongin-c at 1.9a resolution
90	c3ky7A_	Alignment	not modelled	6.2	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252
91	d1sq5a_	Alignment	not modelled	6.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
92	c2kpqA_	Alignment	not modelled	6.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of agrobacterium tumefaciens protein atu1219:2 northeast structural genomics consortium target att14
93	d2fe0a1	Alignment	not modelled	5.8	28	**Fold:**Smp-1-like **Superfamily:**Smp-1-like **Family:**Smp-1-like
94	d1udsa2	Alignment	not modelled	5.7	30	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
95	c3p3dA_	Alignment	not modelled	5.6	14	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleoporin 53; **PDBTitle:** crystal structure of the nup53 rrm domain from pichia guilliermondii
96	d2bw0a1	Alignment	not modelled	5.6	14	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
97	d1npha2	Alignment	not modelled	5.5	7	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
98	d1bifa2	Alignment	not modelled	5.5	29	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
99	d1vdda_	Alignment	not modelled	5.4	39	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR