Phyre2

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Description	P45771
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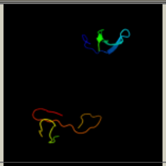
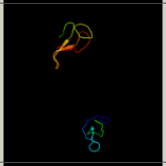
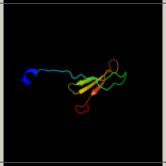
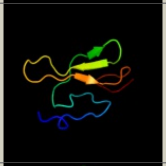
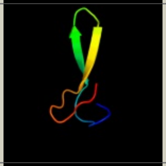
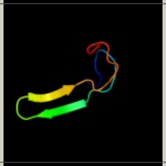
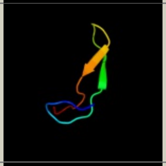
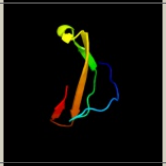
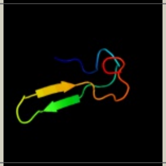
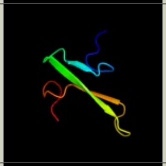
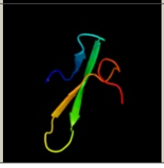
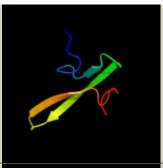
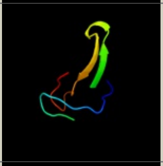
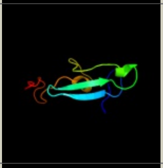
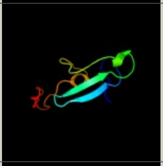
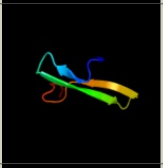
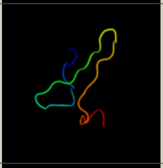
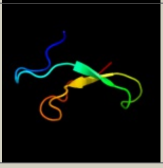
Unique Job ID	b901e41347191060

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1i3ql_	Alignment		97.0	18	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii 14.2kd **PDBTitle:** rna polymerase ii crystal form i at 3.1 a resolution
2	c3h0gI_	Alignment		96.3	17	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
3	c2gajA_	Alignment		95.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
4	d2fiya1	Alignment		94.5	24	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
5	d1pvma3	Alignment		93.8	27	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein Ta0289 C-terminal domain **Family:**Hypothetical protein Ta0289 C-terminal domain
6	c1dgsB_	Alignment		90.9	34	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
7	d1dgsa1	Alignment		89.0	50	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
8	d1twfi2	Alignment		88.9	23	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
9	c1v9pB_	Alignment		87.2	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
10	d1tdza3	Alignment		85.2	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
11	c1nnjA_	Alignment		85.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna

12	c1k82D_	Alignment		84.5	29	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
13	d1qypa_	Alignment		83.9	29	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
14	d1k3xa3	Alignment		83.8	13	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
15	c2jneA_	Alignment		83.3	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein yfgj; **PDBTitle:** nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317.
16	d2jnea1	Alignment		83.3	27	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
17	c2opfA_	Alignment		83.3	15	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
18	d1yuaa1	Alignment		82.3	29	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment
19	c2owoA_	Alignment		81.2	18	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
20	c1yuaA_	Alignment		80.3	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**topoisomerase i; **PDBTitle:** c-terminal domain of escherichia coli topoisomerase i
21	c2js4A_	Alignment	not modelled	79.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
22	d1l1ta3	Alignment	not modelled	79.3	15	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
23	d1ee8a3	Alignment	not modelled	79.1	16	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
24	d1k82a3	Alignment	not modelled	77.4	16	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
25	c1yuzB_	Alignment	not modelled	77.2	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
26	d1r2za3	Alignment	not modelled	76.9	13	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
27	c2jvnA_	Alignment	not modelled	76.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
28	c2jr6A_	Alignment	not modelled	75.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein nma0874; **PDBTitle:** solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32

29	c2f5qA_	Alignment	not modelled	75.3	21	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
30	d2hf1a1	Alignment	not modelled	75.2	24	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
31	d2jnya1	Alignment	not modelled	75.1	12	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
32	d1nuia2	Alignment	not modelled	74.4	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
33	c2jrpA_	Alignment	not modelled	73.4	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
34	c1ee8A_	Alignment	not modelled	72.2	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
35	c2hr5B_	Alignment	not modelled	71.1	25	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
36	d2pk7a1	Alignment	not modelled	70.9	17	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
37	c2riqA_	Alignment	not modelled	69.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** crystal structure of the third zinc-binding domain of human parp-1
38	d1pfta_	Alignment	not modelled	67.9	34	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
39	d1weoa_	Alignment	not modelled	67.7	18	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
40	c2lcqA_	Alignment	not modelled	67.5	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
41	c2kdxA_	Alignment	not modelled	67.3	21	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
42	c1dvbA_	Alignment	not modelled	66.6	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
43	c2kpiA_	Alignment	not modelled	66.4	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco3027; **PDBTitle:** solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
44	d1wd2a_	Alignment	not modelled	64.1	25	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
45	c2odxA_	Alignment	not modelled	63.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c oxidase polypeptide iv; **PDBTitle:** solution structure of zn(ii)cox4
46	d1tfia_	Alignment	not modelled	62.0	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
47	d1lkoa2	Alignment	not modelled	57.7	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
48	d1odha_	Alignment	not modelled	56.1	26	**Fold:**GCM domain **Superfamily:**GCM domain **Family:**GCM domain
49	d1xm0a1	Alignment	not modelled	55.0	13	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**SelR domain
50	d1dl6a_	Alignment	not modelled	51.1	33	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
51	d1zina2	Alignment	not modelled	50.6	23	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
52	d1p3ja2	Alignment	not modelled	49.3	19	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
53	d1nnqa2	Alignment	not modelled	48.8	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
54	d1s3ga2	Alignment	not modelled	47.8	19	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger"

						domain
55	d2akla2	Alignment	not modelled	45.3	24	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
56	c2zkrz_	Alignment	not modelled	45.3	28	**PDB header:**ribosomal protein/rna **Chain:** Z: **PDB Molecule:**e site t-rna; **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
57	d1yuza2	Alignment	not modelled	44.8	31	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
58	c1yshD_	Alignment	not modelled	44.6	28	**PDB header:**structural protein/rna **Chain:** D: **PDB Molecule:**ribosomal protein l37a; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
59	c3tsuA_	Alignment	not modelled	44.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
60	d1vqoz1	Alignment	not modelled	43.8	24	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
61	c2y69S_	Alignment	not modelled	42.9	22	**PDB header:**electron transport **Chain:** S: **PDB Molecule:**cytochrome c oxidase subunit 5b; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
62	d1jj2y_	Alignment	not modelled	42.5	31	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
63	c3cc4Z_	Alignment	not modelled	41.9	48	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
64	c3lpeF_	Alignment	not modelled	41.7	30	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
65	d2ak3a2	Alignment	not modelled	41.6	23	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
66	d1akya2	Alignment	not modelled	40.8	12	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
67	c4a17Y_	Alignment	not modelled	40.4	33	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rpl37a; **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 2.
68	d1v54f_	Alignment	not modelled	39.9	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Cytochrome c oxidase Subunit F
69	d1e4va2	Alignment	not modelled	38.8	12	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
70	c3hcjB_	Alignment	not modelled	38.7	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** structure of msrb from xanthomonas campestris (oxidized2 form)
71	c3a44D_	Alignment	not modelled	38.6	26	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
72	c3cngC_	Alignment	not modelled	36.1	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
73	c3cezA_	Alignment	not modelled	33.8	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
74	d1ffkw_	Alignment	not modelled	33.0	24	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
75	c2qa4Z_	Alignment	not modelled	32.6	39	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
76	c1s1i9_	Alignment	not modelled	31.7	24	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
77	c3f2cA_	Alignment	not modelled	31.1	21	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
78	d2k4xa1	Alignment	not modelled	30.9	22	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
						Fold: Rubredoxin-like

79	d1dfxa2	Alignment	not modelled	29.8	29	**Superfamily:**Rubredoxin-like **Family:**Desulforedoxin
80	d1k81a_	Alignment	not modelled	29.0	29	**Fold:**Zinc-binding domain of translation initiation factor 2 beta **Superfamily:**Zinc-binding domain of translation initiation factor 2 beta **Family:**Zinc-binding domain of translation initiation factor 2 beta
81	c3ld0Q_	Alignment	not modelled	27.9	46	**PDB header:**gene regulation **Chain:** Q: **PDB Molecule:**inhibitor of trap, regulated by t-box (trp) sequence rtpa; **PDBTitle:** crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
82	d1p91a_	Alignment	not modelled	27.4	32	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
83	d1l1da_	Alignment	not modelled	26.4	13	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**SelR domain
84	d6rxna_	Alignment	not modelled	26.3	20	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
85	d2cona1	Alignment	not modelled	25.2	17	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
86	c3jyw9_	Alignment	not modelled	25.1	30	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
87	d1vzia2	Alignment	not modelled	24.5	17	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Desulforedoxin
88	d2dkta1	Alignment	not modelled	24.3	18	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
89	d1lv3a_	Alignment	not modelled	23.9	16	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Hypothetical zinc finger protein YacG
90	c2gb5B_	Alignment	not modelled	23.8	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
91	d1x4la2	Alignment	not modelled	21.9	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
92	c2l1uA_	Alignment	not modelled	21.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b2, mitochondrial; **PDBTitle:** structure-functional analysis of mammalian msrb2 protein
93	c2kaoA_	Alignment	not modelled	21.4	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b1; **PDBTitle:** structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
94	d2cu8a1	Alignment	not modelled	21.3	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
95	c2hu9B_	Alignment	not modelled	20.5	39	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**mercuric transport protein periplasmic component; **PDBTitle:** x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
96	c2k5rA_	Alignment	not modelled	19.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein xf2673; **PDBTitle:** solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
97	d2qam01	Alignment	not modelled	19.3	17	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
98	d1imla1	Alignment	not modelled	19.1	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
99	c1xwhA_	Alignment	not modelled	18.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**autoimmune regulator; **PDBTitle:** nmr structure of the first phd finger of autoimmune2 regulator protein (aire1): insights into apeced