Phyre2

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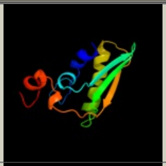
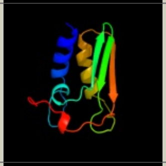
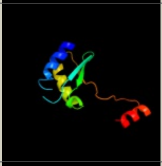
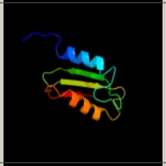
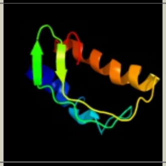
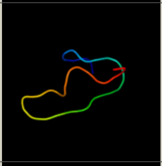
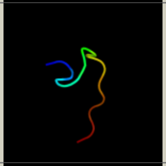
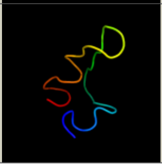
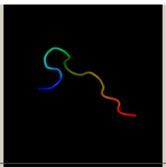
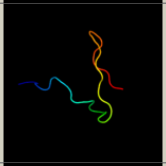
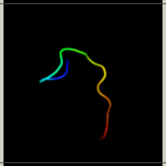
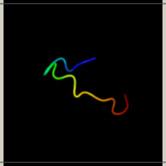
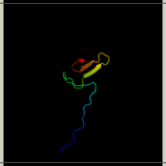
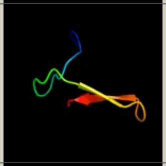
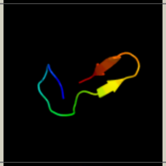
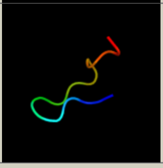
Description	P76080
Date	Thu Jan 5 12:18:21 GMT 2012
Unique Job ID	920232367e88f245

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lnoA_	Alignment		100.0	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of domain of unknown function duf59 from2 bacillus anthracis
2	d1uwda_	Alignment		100.0	27	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
3	d2cu6a1	Alignment		99.9	30	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
4	c2z51A_	Alignment		94.3	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 2, chloroplast; **PDBTitle:** crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis
5	d1xhja_	Alignment		94.1	21	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
6	c2jnvA_	Alignment		94.1	19	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
7	d1veha_	Alignment		89.3	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
8	d1th5a1	Alignment		87.8	13	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
9	c3cw2M_	Alignment		78.7	36	**PDB header:**translation **Chain:** M: **PDB Molecule:**translation initiation factor 2 subunit beta; **PDBTitle:** crystal structure of the intact archaeal translation2 initiation factor 2 from sulfolobus solfataricus .
10	c3a44D_	Alignment		74.0	27	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
11	c1neeA_	Alignment		73.0	32	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 beta **PDBTitle:** structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum

12	d1k81a_	Alignment		72.0	36	**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
13	d1dl6a_	Alignment		70.4	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
14	c2kdxA_	Alignment		69.6	21	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
15	c2aklA_	Alignment		65.1	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
16	d1wiia_	Alignment		61.1	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
17	d1pfta_	Alignment		59.6	26	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
18	d1nuia2	Alignment		58.4	29	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
19	d3bypa1	Alignment		57.8	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
20	c2dcuB_	Alignment		57.1	50	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 beta subunit; **PDBTitle:** crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
21	d2akla2	Alignment	not modelled	55.2	38	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
22	d1hk8a_	Alignment	not modelled	52.0	21	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
23	c1hk8A_	Alignment	not modelled	52.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
24	c2e9hA_	Alignment	not modelled	50.3	43	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
25	d1lv3a_	Alignment	not modelled	49.9	32	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Hypothetical zinc finger protein YacG
26	c3lpeF_	Alignment	not modelled	44.4	40	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
27	c2xigA_	Alignment	not modelled	40.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
28	c3qxbB_	Alignment	not modelled	39.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative xylose isomerase; **PDBTitle:** crystal structure of a putative xylose isomerase

						(yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
29	c1x31D_	Alignment	not modelled	38.6	36	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**sarcosine oxidase delta subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
30	c1qysA_	Alignment	not modelled	37.9	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
31	c1eucB_	Alignment	not modelled	37.4	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**succinyl-coa synthetase, beta chain; **PDBTitle:** crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
32	c2kt2A_	Alignment	not modelled	37.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
33	c2elpA_	Alignment	not modelled	35.3	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
34	c2opfA_	Alignment	not modelled	34.4	30	**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
35	d1atga_	Alignment	not modelled	34.3	24	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
36	c3zyqA_	Alignment	not modelled	33.7	28	**PDB header:**signaling **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
37	d1qupa2	Alignment	not modelled	33.6	9	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
38	c1k82D_	Alignment	not modelled	33.3	20	**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
39	d2fhpa1	Alignment	not modelled	33.2	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
40	d2gnra1	Alignment	not modelled	33.0	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
41	c2jvfA_	Alignment	not modelled	32.7	17	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
42	d1j26a_	Alignment	not modelled	32.0	23	**Fold:**dsRBD-like **Superfamily:**Peptidyl-tRNA hydrolase domain-like **Family:**Peptidyl-tRNA hydrolase domain
43	d1pfva3	Alignment	not modelled	31.6	40	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
44	d2dsxa1	Alignment	not modelled	31.4	14	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
45	c3mv2A_	Alignment	not modelled	30.0	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of a-cop in complex with e-cop
46	d1iloa_	Alignment	not modelled	28.0	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
47	c1nnjA_	Alignment	not modelled	27.8	28	**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
48	c2rrlA_	Alignment	not modelled	27.3	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar hook-length control protein; **PDBTitle:** solution structure of the c-terminal domain of the flik
49	c2fu4B_	Alignment	not modelled	27.2	23	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
50	d2r7ca2	Alignment	not modelled	27.1	71	**Fold:**Rotavirus NSP2 fragment, N-terminal domain **Superfamily:**Rotavirus NSP2 fragment, N-terminal domain **Family:**Rotavirus NSP2 fragment, N-terminal domain
51	c2k2dA_	Alignment	not modelled	26.8	31	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain- **PDBTitle:** solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c
52	c2o03A_	Alignment	not modelled	26.7	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
53	d2fiya1	Alignment	not modelled	26.3	17	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like

54	c2csuB_	Alignment	not modelled	26.0	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
55	d4rxna_	Alignment	not modelled	25.5	15	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
56	c2hk1D_	Alignment	not modelled	25.4	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**d-psicose 3-epimerase; **PDBTitle:** crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
57	d1mzba_	Alignment	not modelled	25.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
58	c2x5cB_	Alignment	not modelled	24.4	33	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hypothetical protein orf131; **PDBTitle:** crystal structure of hypothetical protein orf131 from2 pyrobaculum spherical virus
59	c3jvfC_	Alignment	not modelled	24.4	18	**PDB header:**signaling protein / cytokine **Chain:** C: **PDB Molecule:**interleukin-17 receptor a; **PDBTitle:** crystal structure of an interleukin-17 receptor complex
60	c3eyyA_	Alignment	not modelled	24.4	17	**PDB header:**transport **Chain:** A: **PDB Molecule:**putative iron uptake regulatory protein; **PDBTitle:** structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
61	c2l7xA_	Alignment	not modelled	24.2	60	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** crimean congo hemorrhagic fever gn zinc finger
62	c2w57A_	Alignment	not modelled	24.0	26	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
63	d1r7ha_	Alignment	not modelled	23.9	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
64	c2nu9E_	Alignment	not modelled	23.9	15	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
65	d1xzoa1	Alignment	not modelled	23.2	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
66	c2kn9A_	Alignment	not modelled	23.2	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin; **PDBTitle:** solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
67	d1dx8a_	Alignment	not modelled	23.0	25	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
68	d1h7va_	Alignment	not modelled	22.8	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
69	d1tz9a_	Alignment	not modelled	22.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
70	c1s24A_	Alignment	not modelled	22.6	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
71	d1s24a_	Alignment	not modelled	22.6	17	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
72	c2f5qA_	Alignment	not modelled	22.6	24	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
73	c3mkrB_	Alignment	not modelled	22.5	29	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
74	c2pptA_	Alignment	not modelled	22.2	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
75	d1iroa_	Alignment	not modelled	21.9	15	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
76	d2fu5a1	Alignment	not modelled	21.8	50	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
77	c3ktcB_	Alignment	not modelled	21.7	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
78	d1ee8a3	Alignment	not modelled	21.6	24	**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
79	d2ct1a1	Alignment	not modelled	21.6	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2

80	d1brfa_	Alignment	not modelled	21.4	17	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
81	d1cmca_	Alignment	not modelled	21.3	44	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Met repressor, MetJ (MetR)
82	d1qcva_	Alignment	not modelled	21.2	10	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
83	d1rb9a_	Alignment	not modelled	21.0	14	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
84	d1w4ha1	Alignment	not modelled	20.7	28	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
85	d1vbka2	Alignment	not modelled	20.5	20	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
86	c1jrxA_	Alignment	not modelled	20.3	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
87	c2v3bB_	Alignment	not modelled	20.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
88	d2rdva_	Alignment	not modelled	20.0	17	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
89	c2owoA_	Alignment	not modelled	19.9	17	**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
90	c2r7cA_	Alignment	not modelled	19.7	71	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**non-structural rna-binding protein 35; **PDBTitle:** crystallographic and biochemical analysis of rotavirus nsp22 with nucleotides reveals an ndp kinase like activity
91	d2qifa1	Alignment	not modelled	19.3	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
92	c2v51E_	Alignment	not modelled	19.3	58	**PDB header:**structural protein/contractile protein **Chain:** E: **PDB Molecule:**mkl/myocardin-like protein 1; **PDBTitle:** structure of mal-rpel1 complexed to actin
93	d1hxra_	Alignment	not modelled	19.1	50	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
94	d2fyma1	Alignment	not modelled	19.1	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
95	c3io1B_	Alignment	not modelled	19.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminobenzoyl-glutamate utilization protein; **PDBTitle:** crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
96	c1ee8A_	Alignment	not modelled	18.7	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
97	d1tdza3	Alignment	not modelled	18.6	24	**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
98	c2jvaA_	Alignment	not modelled	18.4	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase domain protein; **PDBTitle:** nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
99	d2gmga1	Alignment	not modelled	18.2	45	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like