Phyre^2

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Description	P25907
Date	Thu Jan 5 11:42:46 GMT 2012
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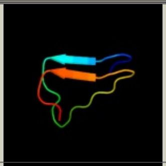
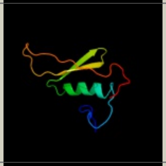
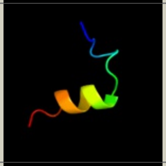
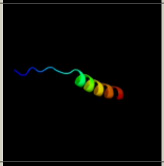
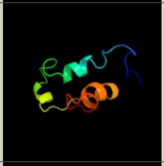
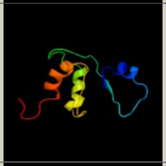
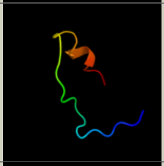
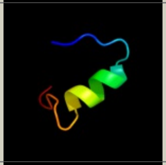
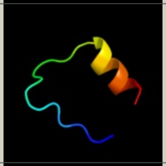
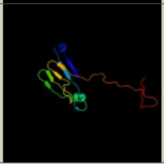
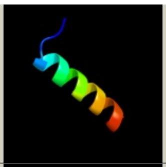
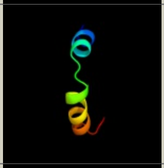
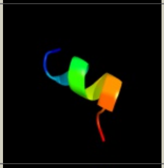
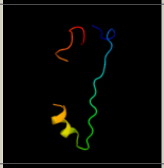
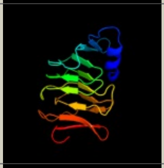
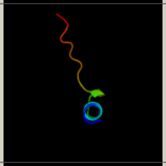
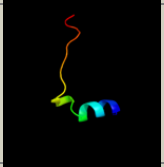
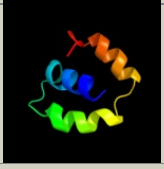
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hf2a1	Alignment		42.4	32	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Cell-division inhibitor MinC, C-terminal domain **Family:**Cell-division inhibitor MinC, C-terminal domain
2	d1jqga1	Alignment		23.7	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases
3	c3st1A_	Alignment		23.4	21	**PDB header:**toxin **Chain:** A: **PDB Molecule:**necrosis-and ethylene-inducing protein; **PDBTitle:** crystal structure of necrosis and ethylene inducing protein 2 from the2 causal agent of cocoa's witches broom disease
4	c3f6oB_	Alignment		22.1	8	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
5	d1vjta1	Alignment		19.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
6	c1bdgA_	Alignment		18.3	20	**PDB header:**hexokinase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** hexokinase from schistosoma mansoni complexed with glucose
7	d1vi1a_	Alignment		17.2	19	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
8	d1w36c1	Alignment		16.3	42	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
9	c2e72A_	Alignment		14.2	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pogo transposable element with znf domain; **PDBTitle:** solution structure of the zinc finger domain of human2 kiaa0461
10	c3u80A_	Alignment		13.3	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase, type ii; **PDBTitle:** 1.60 angstrom resolution crystal structure of a 3-dehydroquinate2 dehydratase-like protein from bifidobacterium longum
11	c2wycB_	Alignment		12.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acyl-homoserine lactone acylase pvdq subunit **PDBTitle:** the quorum quenching n-acyl homoserine lactone acylase pvdq2 in complex with 3-oxo-lauric acid

12	d1ls9a_	Alignment		12.5	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
13	c3bvsA_	Alignment		12.2	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylpurine dna glycosylase alkd; **PDBTitle:** crystal structure of bacillus cereus alkylpurine dna glycosylase alkd
14	d1ef4a_	Alignment		11.5	42	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
15	d2q1ma1	Alignment		10.9	15	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
16	c2ei5B_	Alignment		10.7	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ttha0061; **PDBTitle:** crystal structure of hypothetical protein(ttha0061) from thermus2 thermophilus
17	c1hf2A_	Alignment		10.3	19	**PDB header:**cell division protein **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the bacterial cell-division inhibitor2 minc from t. maritima
18	d2k7ia1	Alignment		10.1	27	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
19	c2k7iB_	Alignment		10.1	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0339 protein atu0232; **PDBTitle:** solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223.
20	d1g3wa2	Alignment		9.7	17	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
21	c1vjtA_	Alignment	not modelled	9.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
22	c3lwzC_	Alignment	not modelled	8.8	32	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
23	c2dxbR_	Alignment	not modelled	8.7	32	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma; **PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
24	c2pmzN_	Alignment	not modelled	8.5	50	**PDB header:**translation, transferase **Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit n; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
25	d1uqra_	Alignment	not modelled	8.4	36	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
26	c3s29C_	Alignment	not modelled	8.4	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sucrose synthase 1; **PDBTitle:** the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
27	d1bu8a1	Alignment	not modelled	8.2	25	**Fold:**Lipase/lipooxygenase domain (PLAT/LH2 domain) **Superfamily:**Lipase/lipooxygenase domain (PLAT/LH2 domain) **Family:**Colipase-binding domain
28	d2fm9a1	Alignment	not modelled	8.1	47	**Fold:**SipA N-terminal domain-like **Superfamily:**SipA N-terminal domain-like **Family:**SipA N-terminal domain-like
						Fold: Peptide deformylase

29	d2defa_	Alignment	not modelled	8.1	19	**Superfamily:**Peptide deformylase **Family:**Peptide deformylase
30	d1twfj_	Alignment	not modelled	8.1	50	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
31	d2isya2	Alignment	not modelled	7.9	11	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
32	c3kipU_	Alignment	not modelled	7.9	32	**PDB header:**lyase **Chain:** U: **PDB Molecule:**3-dehydroquinase, type ii; **PDBTitle:** crystal structure of type-ii 3-dehydroquinase from c. albicans
33	c2odlA_	Alignment	not modelled	7.8	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**adhesin; **PDBTitle:** crystal structure of the hmw1 secretion domain from2 haemophilus influenzae
34	c3on9B_	Alignment	not modelled	7.8	33	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**tumour necrosis factor receptor; **PDBTitle:** the secret domain from ectromelia virus
35	c2w91A_	Alignment	not modelled	7.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-n-acetylglucosaminidase d; **PDBTitle:** structure of a streptococcus pneumoniae family 85 glycoside2 hydrolase, endo-d.
36	c2uygF_	Alignment	not modelled	7.6	23	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallogaphic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
37	d1h05a_	Alignment	not modelled	7.5	23	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
38	d1vi0a1	Alignment	not modelled	7.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
39	c2rngA_	Alignment	not modelled	7.5	100	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**big defensin; **PDBTitle:** solution structure of big defensin
40	d1gmua2	Alignment	not modelled	7.4	47	**Fold:**Ferredoxin-like **Superfamily:**Urease metallochaperone UreE, C-terminal domain **Family:**Urease metallochaperone UreE, C-terminal domain
41	d2p7ja1	Alignment	not modelled	7.3	13	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**YkuI C-terminal domain-like
42	d1s57a_	Alignment	not modelled	7.3	17	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
43	d2k49a1	Alignment	not modelled	7.3	25	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
44	c3n8kG_	Alignment	not modelled	6.9	23	**PDB header:**lyase **Chain:** G: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
45	d1h3ga1	Alignment	not modelled	6.8	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
46	d2fm8c1	Alignment	not modelled	6.8	47	**Fold:**SipA N-terminal domain-like **Superfamily:**SipA N-terminal domain-like **Family:**SipA N-terminal domain-like
47	d1mzha_	Alignment	not modelled	6.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
48	c3gioA_	Alignment	not modelled	6.6	45	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the tnf-alpha inducing protein (tip2 alpha) from helicobacter pylori
49	d2jmua1	Alignment	not modelled	6.6	45	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
50	c3e0zB_	Alignment	not modelled	6.6	23	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**protein of unknown function; **PDBTitle:** crystal structure of a putative imidazole glycerol phosphate synthase2 homolog (eubrec_1070) from eubacterium rectale at 1.75 a resolution
51	c3gdbA_	Alignment	not modelled	6.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein spr0440; **PDBTitle:** crystal structure of spr0440 glycoside hydrolase domain,2 endo-d from streptococcus pneumoniae r6
52	d1sg5a1	Alignment	not modelled	6.5	20	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**Rof-like
53	d1bdga2	Alignment	not modelled	6.5	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
54	c1qhaA_	Alignment	not modelled	6.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hexokinase); **PDBTitle:** human hexokinase type i complexed with atp analogue amp-pnp
55	c2po4A_	Alignment	not modelled	6.4	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**virion rna polymerase; **PDBTitle:** x-ray crystal structure of polymerase domain of the2

						bacteriophage n4 virion rna polymerase
56	c2l5rA_	Alignment	not modelled	6.3	100	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide alyteserin-1c; **PDBTitle:** conformational and membrane interactins studies of antimicrobial2 peptide alyteserin-1c
57	c1s1iA_	Alignment	not modelled	6.3	15	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**60s ribosomal protein l1; **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.
58	c2zkr5_	Alignment	not modelled	6.3	33	**PDB header:**ribosomal protein/rna **Chain:** 5: **PDB Molecule:**60s ribosomal protein l10a; **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
59	d1eara2	Alignment	not modelled	6.3	27	**Fold:**Ferredoxin-like **Superfamily:**Urease metallochaperone UreE, C-terminal domain **Family:**Urease metallochaperone UreE, C-terminal domain
60	d1lmea_	Alignment	not modelled	6.2	26	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
61	d1g47a2	Alignment	not modelled	6.2	32	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
62	d3bbba1	Alignment	not modelled	6.2	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
63	c3sojA_	Alignment	not modelled	6.1	58	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**pile; **PDBTitle:** francisella tularensis pilin pile
64	c2w3tA_	Alignment	not modelled	6.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** chloro complex of the ni-form of e.coli deformylase
65	d2az3a1	Alignment	not modelled	6.0	17	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
66	c3dgpA_	Alignment	not modelled	6.0	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase ii transcription factor b subunit 2; **PDBTitle:** crystal structure of the complex between tfb5 and the c-terminal2 domain of tfb2
67	d1gtza_	Alignment	not modelled	5.8	40	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
68	d1c6ra_	Alignment	not modelled	5.8	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
69	d1txla_	Alignment	not modelled	5.8	21	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Hypothetical protein YodA
70	c1txlA_	Alignment	not modelled	5.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**metal-binding protein yoda; **PDBTitle:** crystal structure of metal-binding protein yoda from e.2 coli, pfam duf149
71	d3bl2a1	Alignment	not modelled	5.7	31	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
72	d1u7na_	Alignment	not modelled	5.7	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
73	d1pd0a1	Alignment	not modelled	5.7	27	**Fold:**ERP29 C domain-like **Superfamily:**Helical domain of Sec23/24 **Family:**Helical domain of Sec23/24
74	d1rlra1	Alignment	not modelled	5.7	16	**Fold:**R1 subunit of ribonucleotide reductase, N-terminal domain **Superfamily:**R1 subunit of ribonucleotide reductase, N-terminal domain **Family:**R1 subunit of ribonucleotide reductase, N-terminal domain
75	c1v4sA_	Alignment	not modelled	5.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase isoform 2; **PDBTitle:** crystal structure of human glucokinase
76	d3c07a1	Alignment	not modelled	5.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
77	d2c4va1	Alignment	not modelled	5.6	25	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
78	c2i5nH_	Alignment	not modelled	5.6	40	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**reaction center protein h chain; **PDBTitle:** 1.96 a x-ray structure of photosynthetic reaction center from2 rhodopseudomonas viridis:crystals grown by microfluidic technique
79	d1rzhh1	Alignment	not modelled	5.5	53	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**Photosynthetic reaction centre, H-chain, cytoplasmic domain
80	c1eysH_	Alignment	not modelled	5.5	24	**PDB header:**electron transport **Chain:** H: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
						PDB header:hydrolase

81	c3i3lA_	Alignment	not modelled	5.5	37	**Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
82	c2ew7A_	Alignment	not modelled	5.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of helicobacter pylori peptide deformylase
83	d1ufya_	Alignment	not modelled	5.5	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
84	d1wlfa1	Alignment	not modelled	5.5	63	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
85	c3h43F_	Alignment	not modelled	5.5	33	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii
86	c3c8iA_	Alignment	not modelled	5.5	27	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** crystal structure of a putative membrane protein from corynebacterium2 diphtheriae
87	c3fk2B_	Alignment	not modelled	5.4	13	**PDB header:**signaling protein, hydrolase activator **Chain:** B: **PDB Molecule:**glucocorticoid receptor dna-binding factor 1; **PDBTitle:** crystal structure of the rhogap domain of human2 glucocorticoid receptor dna-binding factor 1
88	d2ctda1	Alignment	not modelled	5.4	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
89	c3kboB_	Alignment	not modelled	5.4	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate/hydroxypyruvate reductase a; **PDBTitle:** 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from2 salmonella typhimurium in complex with nadp
90	d1t33a1	Alignment	not modelled	5.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
91	d1v0ea2	Alignment	not modelled	5.3	40	**Fold:**Triple-stranded beta-helix **Superfamily:**Phage fibre proteins **Family:**Endo-alpha-sialidase
92	d1l5ja3	Alignment	not modelled	5.3	17	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
93	c3fn2A_	Alignment	not modelled	5.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative sensor histidine kinase domain; **PDBTitle:** crystal structure of a putative sensor histidine kinase domain from2 clostridium symbiosum atcc 14940
94	d1gqoa_	Alignment	not modelled	5.3	27	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
95	d1dwua_	Alignment	not modelled	5.3	23	**Fold:**Ribosomal protein L1 **Superfamily:**Ribosomal protein L1 **Family:**Ribosomal protein L1
96	d2fbqa1	Alignment	not modelled	5.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
97	d1ix1a_	Alignment	not modelled	5.3	23	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
98	d1fqva1	Alignment	not modelled	5.2	55	**Fold:**F-box domain **Superfamily:**F-box domain **Family:**F-box domain
99	c3gnzP_	Alignment	not modelled	5.2	22	**PDB header:**toxin **Chain:** P: **PDB Molecule:**25 kda protein elicitor; **PDBTitle:** toxin fold for microbial attack and plant defense