Phyre2

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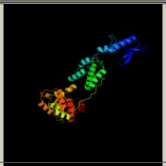
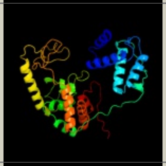
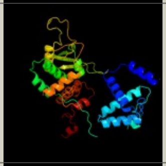
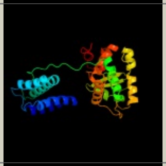
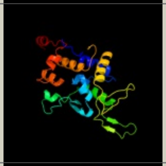
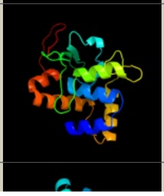
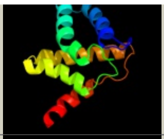
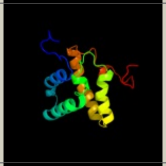
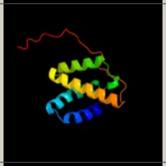
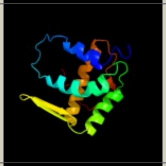
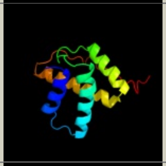
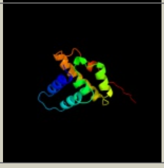
Description	P76056
Date	Wed Jan 25 15:21:05 GMT 2012
Unique Job ID	9c64ce4caf48a439

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z1bA_	Alignment		100.0	17	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a lambda integrase dimer bound to a2 coc' core site
2	c2a3vA_	Alignment		100.0	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
3	c1ma7A_	Alignment		100.0	14	**PDB header:**hydrolase, ligase/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** crystal structure of cre site-specific recombinase2 complexed with a mutant dna substrate, loxp-a8/t27
4	c1crxA_	Alignment		99.9	12	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
5	d1p7da_	Alignment		99.9	17	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
6	c3nkhB_	Alignment		99.9	21	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
7	c1a0pA_	Alignment		99.9	16	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd
8	d1aiha_	Alignment		99.7	18	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
9	d1f44a2	Alignment		99.7	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
10	d1a0pa2	Alignment		99.5	22	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
11	d1ae9a_	Alignment		99.4	18	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
						

12	c2kj8A_	Alignment		99.4	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative prophage cps-53 integrase; **PDBTitle:** nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
13	c2kd1A_	Alignment		99.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dna integration/recombination/invertion protein; **PDBTitle:** solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f
14	c2kj9A_	Alignment		99.4	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e
15	c2kiwA_	Alignment		99.4	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**int protein; **PDBTitle:** solution nmr structure of the domain n-terminal to the2 integrase domain of sh1003 from staphylococcus3 haemolyticus. northeast structural genomics consortium4 target shr105f (64-166).
16	c2kkvA_	Alignment		99.4	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of an integrase domain from protein2 spa4288 from salmonella enterica, northeast structural3 genomics consortium target slr105h
17	c2kkpA_	Alignment		99.4	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
18	c3lysC_	Alignment		99.3	13	**PDB header:**recombination **Chain:** C: **PDB Molecule:**prophage pi2 protein 01, integrase; **PDBTitle:** crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f
19	c2khqA_	Alignment		99.3	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
20	c2kobA_	Alignment		99.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of clolep_01837 (fragment 61-160)2 from clostridium leptum. northeast structural genomics3 consortium target qlr8a
21	c2oxoA_	Alignment	not modelled	99.3	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
22	d5crxb2	Alignment	not modelled	99.2	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
23	c2khvA_	Alignment	not modelled	99.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
24	c2kj5A_	Alignment	not modelled	99.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of a domain from a putative phage2 integrase protein nmul_a0064 from nitrosospira multiformis,3 northeast structural genomics consortium target nmr46c
25	c2keyA_	Alignment	not modelled	99.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage integrase; **PDBTitle:** solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
26	c3nrwA_	Alignment	not modelled	99.0	14	**PDB header:**recombination **Chain:** A: **PDB Molecule:**phage integrase/site-specific recombinase; **PDBTitle:** crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
27	c3ju0A_	Alignment	not modelled	98.1	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7

						integrase
28	d1a0pa1	Alignment	not modelled	97.9	12	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
29	c3jtzA_	Alignment	not modelled	97.6	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structure of the arm-type binding domain of hpi integrase
30	d1f44a1	Alignment	not modelled	96.4	14	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
31	c2v6eB_	Alignment	not modelled	95.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
32	c2f4qA_	Alignment	not modelled	80.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
33	c2h7fX_	Alignment	not modelled	61.6	12	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
34	c3igmA_	Alignment	not modelled	40.7	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pf14_0633 protein; **PDBTitle:** a 2.2a crystal structure of the ap2 domain of pf14_0633 from p.2 falciparum, bound as a domain-swapped dimer to its cognate dna
35	d1trra_	Alignment	not modelled	40.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
36	d1jhga_	Alignment	not modelled	31.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
37	d1gcca_	Alignment	not modelled	30.9	17	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**GCC-box binding domain
38	d2iw5b1	Alignment	not modelled	28.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
39	d1xc5a1	Alignment	not modelled	27.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
40	d2auwa1	Alignment	not modelled	23.8	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
41	d1hcra_	Alignment	not modelled	23.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
42	d1l8qa1	Alignment	not modelled	23.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
43	d1ijwc_	Alignment	not modelled	23.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
44	c2eqrA_	Alignment	not modelled	22.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear receptor corepressor 1; **PDBTitle:** solution structure of the first sant domain from human2 nuclear receptor corepressor 1
45	c3lsgD_	Alignment	not modelled	21.3	16	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**two-component response regulator yesn; **PDBTitle:** the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
46	c2yqkA_	Alignment	not modelled	19.5	21	**PDB header:**transcription/apoptosis **Chain:** A: **PDB Molecule:**arginine-glutamic acid dipeptide repeats protein; **PDBTitle:** solution structure of the sant domain in arginine-glutamic2 acid dipeptide (re) repeats
47	d1whna_	Alignment	not modelled	18.3	17	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
48	c1x3uA_	Alignment	not modelled	18.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj; **PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
49	d2crga1	Alignment	not modelled	17.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
50	d1fsea_	Alignment	not modelled	17.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
51	d1a41a_	Alignment	not modelled	17.1	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
52	c2iw5B_	Alignment	not modelled	17.1	11	**PDB header:**oxidoreductase/transcription regulator **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** structural basis for corest-dependent demethylation of2 nucleosomes by the human lsd1 histone demethylase
53	c2x0lB_	Alignment	not modelled	17.1	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** crystal structure of a neuro-specific splicing variant of2 human histone lysine demethylase lsd1.

54	c2xajB_	Alignment	not modelled	17.1	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** crystal structure of lsd1-corest in complex with (-)-trans-2 2-phenylcyclopropyl-1-amine
55	c2v1dB_	Alignment	not modelled	17.1	11	**PDB header:**oxidoreductase/repressor **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
56	d1a04a1	Alignment	not modelled	16.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
57	c2krfB_	Alignment	not modelled	15.4	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
58	d2aq0a1	Alignment	not modelled	15.2	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
59	c4a69C_	Alignment	not modelled	15.2	21	**PDB header:**transcription **Chain:** C: **PDB Molecule:**nuclear receptor corepressor 2; **PDBTitle:** structure of hdac3 bound to corepressor and inositol tetraphosphate
60	d1k78a1	Alignment	not modelled	14.6	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
61	d1yioa1	Alignment	not modelled	14.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
62	c2rnjA_	Alignment	not modelled	12.7	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
63	d1qu6a2	Alignment	not modelled	11.8	15	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
64	c2jpcA_	Alignment	not modelled	11.8	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
65	c2auwB_	Alignment	not modelled	11.4	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
66	d1kwga1	Alignment	not modelled	10.6	28	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
67	c1u78A_	Alignment	not modelled	10.3	0	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
68	d1k4ta2	Alignment	not modelled	10.2	11	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
69	d1pdnc_	Alignment	not modelled	9.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
70	c1zljE_	Alignment	not modelled	9.3	19	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
71	d1x48a1	Alignment	not modelled	9.2	9	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
72	c3sohB_	Alignment	not modelled	9.1	12	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** architecture of the flagellar rotor
73	d2csba1	Alignment	not modelled	8.8	15	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
74	c2ef8A_	Alignment	not modelled	8.7	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
75	c2x48B_	Alignment	not modelled	8.3	26	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
76	d1uxca_	Alignment	not modelled	8.0	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
77	c3frwF_	Alignment	not modelled	7.8	11	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
78	d1p4wa_	Alignment	not modelled	7.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
79	d1bl0a2	Alignment	not modelled	7.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
80	d2b7ta1	Alignment	not modelled	7.5	19	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)

81	d1dwka1	Alignment	not modelled	7.5	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
82	d6paxa1	Alignment	not modelled	7.4	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
83	d1l3la1	Alignment	not modelled	7.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
84	d1rr8c1	Alignment	not modelled	7.4	11	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
85	c3korD_	Alignment	not modelled	7.1	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**possible trp repressor; **PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus
86	d1rkta1	Alignment	not modelled	7.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
87	c1f8aB_	Alignment	not modelled	6.8	27	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima- **PDBTitle:** structural basis for the phosphoserine-proline recognition2 by group iv ww domains
88	c3oouA_	Alignment	not modelled	6.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
89	d1d5ya2	Alignment	not modelled	6.7	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
90	c2khxA_	Alignment	not modelled	6.6	21	**PDB header:**gene regulation,nuclear protein **Chain:** A: **PDB Molecule:**ribonuclease 3; **PDBTitle:** drosha double-stranded rna binding motif
91	c3mzyA_	Alignment	not modelled	6.5	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna polymerase sigma-h factor; **PDBTitle:** the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
92	d1x47a1	Alignment	not modelled	6.5	22	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
93	d2gf5a1	Alignment	not modelled	6.4	12	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
94	d1rp3a2	Alignment	not modelled	6.4	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
95	c3b7hA_	Alignment	not modelled	6.3	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
96	d1z91a1	Alignment	not modelled	6.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
97	c2l2nA_	Alignment	not modelled	6.2	17	**PDB header:**rna binding protein, plant protein **Chain:** A: **PDB Molecule:**hyponastic leave 1; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for the first2 dsrbd of protein hyl1
98	c3adiC_	Alignment	not modelled	6.2	17	**PDB header:**gene regulation/rna **Chain:** C: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
99	c3hugA_	Alignment	not modelled	6.2	14	**PDB header:**transcription/membrane protein **Chain:** A: **PDB Molecule:**rna polymerase sigma factor; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl