Phyre^2

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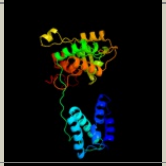
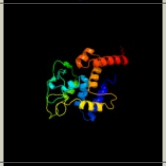
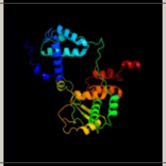
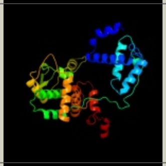
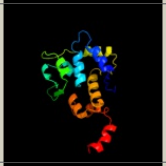
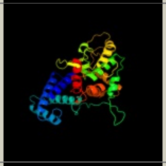
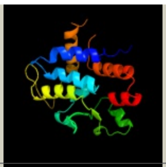
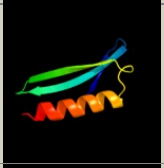
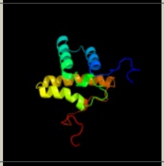
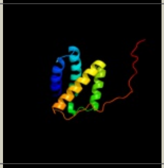
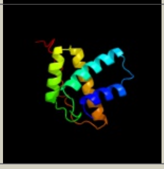
Description	P39347
Date	Thu Jan 5 11:59:37 GMT 2012
Unique Job ID	93f1c47d6d5ae2b4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z1bA_	Alignment		100.0	16	**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	d1p7da_	Alignment		99.9	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
3	c3nkhB_	Alignment		99.9	22	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
4	c1ma7A_	Alignment		99.9	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
5	c1crxA_	Alignment		99.9	13	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
6	d1aiha_	Alignment		99.9	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
7	c1a0pA_	Alignment		99.9	16	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd
8	c2a3vA_	Alignment		99.9	14	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
9	d1a0pa2	Alignment		99.8	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
10	d1f44a2	Alignment		99.8	12	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
11	d1ae9a_	Alignment		99.8	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core

12	d5crxb2_	Alignment		99.6	12	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
13	c3ju0A_	Alignment		99.4	68	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7 integrase
14	c3jtzA_	Alignment		99.2	51	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structure of the arm-type binding domain of hpi integrase
15	c2kkvA_	Alignment		98.7	53	**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
16	c2kj9A_	Alignment		98.6	45	**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
17	c2kiwA_	Alignment		98.5	16	**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).
18	c2kj5A_	Alignment		98.4	22	**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
19	c2kj8A_	Alignment		98.4	27	**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
20	c2khqA_	Alignment		98.2	12	**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
21	c2kkpA_	Alignment	not modelled	98.2	15	**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).
22	c3lysC_	Alignment	not modelled	98.2	9	**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
23	c2oxoA_	Alignment	not modelled	98.1	13	**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
24	c2khvA_	Alignment	not modelled	98.1	17	**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.
25	c2kd1A_	Alignment	not modelled	98.1	12	**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
26	c2kobA_	Alignment	not modelled	97.9	17	**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
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage integrase;

27	c2keyA_	Alignment	not modelled	97.3	15	**PDBTitle:** solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
28	c2v6eB_	Alignment	not modelled	97.2	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
29	c3nrwA_	Alignment	not modelled	96.7	9	**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
30	c2f4qA_	Alignment	not modelled	96.4	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
31	c2h7fX_	Alignment	not modelled	94.6	17	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
32	c2b9sA_	Alignment	not modelled	93.0	19	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
33	d1k4ta2	Alignment	not modelled	90.9	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
34	d1rr8c1	Alignment	not modelled	90.6	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
35	d1a41a_	Alignment	not modelled	89.0	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
36	c1a31A_	Alignment	not modelled	86.2	17	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**protein (topoisomerase i); **PDBTitle:** human reconstituted dna topoisomerase i in covalent complex2 with a 22 base pair dna duplex
37	c3igmA_	Alignment	not modelled	81.9	11	**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
38	d1a0pa1	Alignment	not modelled	79.7	15	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
39	c1nh3A_	Alignment	not modelled	74.9	17	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** human topoisomerase i ara-c complex
40	d1gcca_	Alignment	not modelled	66.8	25	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**GCC-box binding domain
41	d1z1ba1	Alignment	not modelled	66.7	28	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**lambda integrase N-terminal domain
42	c1kjkA_	Alignment	not modelled	65.9	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution structure of the lambda integrase amino-terminal2 domain
43	d1qu6a2	Alignment	not modelled	55.4	13	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
44	d1x48a1	Alignment	not modelled	45.4	11	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
45	c1p4eB_	Alignment	not modelled	32.5	10	**PDB header:**dna binding protein/recombination/dna **Chain:** B: **PDB Molecule:**recombinase flp protein; **PDBTitle:** flpe w330f mutant-dna holliday junction complex
46	d1x49a1	Alignment	not modelled	23.8	16	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
47	d1qu6a1	Alignment	not modelled	23.6	14	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
48	c2khxA_	Alignment	not modelled	21.6	14	**PDB header:**gene regulation,nuclear protein **Chain:** A: **PDB Molecule:**ribonuclease 3; **PDBTitle:** drosha double-stranded rna binding motif
49	d1f44a1	Alignment	not modelled	20.6	11	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
50	d1x47a1	Alignment	not modelled	19.5	9	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
51	d1o0wa2	Alignment	not modelled	18.7	19	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
52	c3adjA_	Alignment	not modelled	16.5	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
						PDB header:gene regulation/rna

53	c3adiC_	Alignment	not modelled	15.2	12	**Chain:** C: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
54	d2b7ta1	Alignment	not modelled	12.1	19	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
55	c1or7A_	Alignment	not modelled	11.9	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-e factor; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
56	c3llhB_	Alignment	not modelled	11.9	15	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**risc-loading complex subunit tarbp2; **PDBTitle:** crystal structure of the first dsrbd of tar rna-binding protein 2
57	c2l33A_	Alignment	not modelled	11.2	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**interleukin enhancer-binding factor 3; **PDBTitle:** solution nmr structure of drbm 2 domain of interleukin enhancer-2 binding factor 3 from homo sapiens, northeast structural genomics3 consortium target hr4527e
58	d2b7va1	Alignment	not modelled	10.5	14	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
59	d1d4aa_	Alignment	not modelled	10.0	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
60	c2l2nA_	Alignment	not modelled	10.0	11	**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
61	c2yt4A_	Alignment	not modelled	9.9	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein dgcr8; **PDBTitle:** crystal structure of human dgcr8 core
62	d2dmya1	Alignment	not modelled	9.7	16	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
63	c3pmrB_	Alignment	not modelled	9.4	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**amyloid-like protein 1; **PDBTitle:** crystal structure of e2 domain of human amyloid precursor-like protein2 1
64	c3kmpA_	Alignment	not modelled	9.0	18	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**smad1-mh1; **PDBTitle:** crystal structure of smad1-mh1/dna complex
65	d1sfka_	Alignment	not modelled	8.5	12	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
66	d1bb8a_	Alignment	not modelled	7.8	23	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**DNA-binding domain from tn916 integrase
67	d1tf5a2	Alignment	not modelled	7.5	8	**Fold:**Helical scaffold and wing domains of SecA **Superfamily:**Helical scaffold and wing domains of SecA **Family:**Helical scaffold and wing domains of SecA
68	c2ka4B_	Alignment	not modelled	7.4	33	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** nmr structure of the cbp-taz1/stat2-tad complex
69	d1nkta2	Alignment	not modelled	7.4	17	**Fold:**Helical scaffold and wing domains of SecA **Superfamily:**Helical scaffold and wing domains of SecA **Family:**Helical scaffold and wing domains of SecA
70	c2l3jA_	Alignment	not modelled	7.4	20	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**double-stranded rna-specific editase 1; **PDBTitle:** the solution structure of the adar2 dsrbm-rna complex reveals a2 sequence-specific read out of the minor groove
71	d1u5ta1	Alignment	not modelled	7.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
72	c1f8aB_	Alignment	not modelled	7.2	19	**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
73	d1sfkb_	Alignment	not modelled	7.1	12	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
74	d1r6ra_	Alignment	not modelled	7.0	16	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
75	c1r6rA_	Alignment	not modelled	7.0	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** solution structure of dengue virus capsid protein reveals a2 new fold
76	c3cuqA_	Alignment	not modelled	6.9	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
77	d1j2oa2	Alignment	not modelled	6.7	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
78	d2gf5a1	Alignment	not modelled	6.7	13	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
79	d1di2a_	Alignment	not modelled	6.6	18	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)

80	d1kwga1	Alignment	not modelled	6.4	20	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
81	c2zmeA_	Alignment	not modelled	6.4	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
82	d1uila_	Alignment	not modelled	6.2	14	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
83	d1e6vc_	Alignment	not modelled	6.1	31	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase gamma chain
84	d2dgxa1	Alignment	not modelled	6.0	20	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
85	c2eqrA_	Alignment	not modelled	5.9	3	**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
86	d2csba1	Alignment	not modelled	5.9	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
87	c2kpqA_	Alignment	not modelled	5.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of agrobacterium tumefaciens protein atu1219:2 northeast structural genomics consortium target att14
88	c2zhhA_	Alignment	not modelled	5.6	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
89	d1xc5a1	Alignment	not modelled	5.6	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
90	c1qu6A_	Alignment	not modelled	5.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase pkr; **PDBTitle:** structure of the double-stranded rna-binding domain of the2 protein kinase pkr reveals the molecular basis of its3 dsrna-mediated activation
91	d1rw6a_	Alignment	not modelled	5.5	19	**Fold:**STAT-like **Superfamily:**CAPPD, an extracellular domain of amyloid beta A4 protein **Family:**CAPPD, an extracellular domain of amyloid beta A4 protein
92	c2ljhA_	Alignment	not modelled	5.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**double-stranded rna-specific editase adar; **PDBTitle:** nmr structure of double-stranded rna-specific editase adar
93	d1q08a_	Alignment	not modelled	5.4	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
94	d1dwka1	Alignment	not modelled	5.4	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
95	c2gf5A_	Alignment	not modelled	5.3	13	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fadd protein; **PDBTitle:** structure of intact fadd (mort1)
96	d1hbnc_	Alignment	not modelled	5.3	25	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase gamma chain
97	c2jzvA_	Alignment	not modelled	5.2	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** solution structure of s. aureus prsa-ppiase
98	c2nogA_	Alignment	not modelled	5.1	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**iswi protein; **PDBTitle:** sant domain structure of xenopus remodeling factor iswi
99	c1u5tA_	Alignment	not modelled	5.1	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex