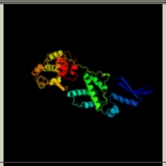
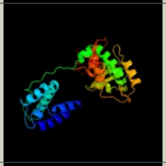
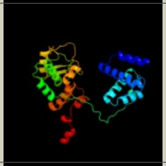
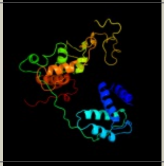
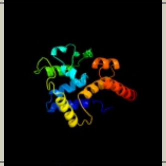
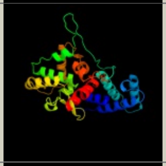
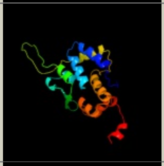
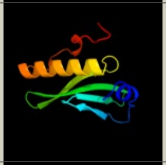
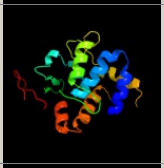
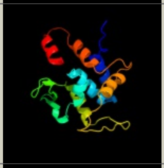
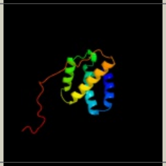
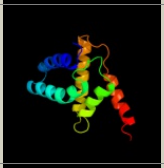
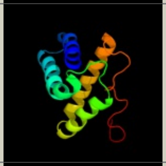
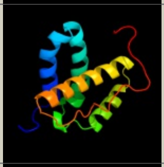
Email	l.a.kelley@imperial.ac.uk
Description	P76542
Date	Thu Jan 5 12:24:15 GMT 2012
Unique Job ID	fe095f5ae688cad8

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	d1p7da_	Alignment		100.0	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
3	c1ma7A_	Alignment		99.9	16	**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	15	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
5	c2a3vA_	Alignment		99.9	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
6	c3nkhB_	Alignment		99.9	15	**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		99.9	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
9	c3ju0A_	Alignment		99.8	43	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7 integrase
10	d1f44a2	Alignment		99.8	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
11	d1a0pa2	Alignment		99.8	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core

12	c3jtzA_	Alignment		99.8	41	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structure of the arm-type binding domain of hpi integrase
13	d1ae9a_	Alignment		99.8	18	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
14	d5crxb2	Alignment		99.6	17	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
15	c2kiwA_	Alignment		98.9	18	**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	c2kj8A_	Alignment		98.9	31	**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
17	c2kj9A_	Alignment		98.8	30	**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
18	c2khvA_	Alignment		98.8	20	**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.
19	c2kd1A_	Alignment		98.8	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
20	c2kkvA_	Alignment		98.8	24	**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
21	c2khqA_	Alignment	not modelled	98.7	22	**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
22	c2kobA_	Alignment	not modelled	98.7	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
23	c2kkpA_	Alignment	not modelled	98.7	16	**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).
24	c3lysC_	Alignment	not modelled	98.6	15	**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
25	c2kj5A_	Alignment	not modelled	98.6	24	**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
26	c2oxoA_	Alignment	not modelled	98.6	19	**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
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage integrase;

27	c2keyA_	Alignment	not modelled	98.3	13	**PDBTitle:** solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
28	c3nrwA_	Alignment	not modelled	97.9	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
29	c2v6eB_	Alignment	not modelled	97.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
30	d1a0pa1	Alignment	not modelled	96.2	16	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
31	c2f4qA_	Alignment	not modelled	96.2	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
32	c2h7fX_	Alignment	not modelled	94.2	15	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
33	c2b9sA_	Alignment	not modelled	92.9	24	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
34	d1k4ta2	Alignment	not modelled	92.4	27	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
35	d1rr8c1	Alignment	not modelled	90.7	27	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
36	c3igmA_	Alignment	not modelled	86.7	15	**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
37	c1a31A_	Alignment	not modelled	83.4	26	**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
38	c1nh3A_	Alignment	not modelled	80.3	27	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** human topoisomerase i ara-c complex
39	d1a41a_	Alignment	not modelled	78.9	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
40	d1f44a1	Alignment	not modelled	77.1	14	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
41	d1gcca_	Alignment	not modelled	74.2	14	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**GCC-box binding domain
42	d1z1ba1	Alignment	not modelled	64.5	22	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**lambda integrase N-terminal domain
43	c1kjkA_	Alignment	not modelled	64.5	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution structure of the lambda integrase amino-terminal2 domain
44	d1qu6a2	Alignment	not modelled	44.2	18	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
45	d1x48a1	Alignment	not modelled	35.0	15	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
46	d2gf5a1	Alignment	not modelled	30.9	11	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
47	d1x49a1	Alignment	not modelled	26.0	26	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
48	c2khxA_	Alignment	not modelled	23.6	14	**PDB header:**gene regulation,nuclear protein **Chain:** A: **PDB Molecule:**ribonuclease 3; **PDBTitle:** drosha double-stranded rna binding motif
49	c2kq6A_	Alignment	not modelled	18.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**polycystin-2; **PDBTitle:** the structure of the ef-hand domain of polycystin-2 suggests a2 mechanism for ca2+-dependent regulation of polycystin-2 channel3 activity
50	d1qu6a1	Alignment	not modelled	17.6	27	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
51	c3epsB_	Alignment	not modelled	16.6	24	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase kinase/phosphatase; **PDBTitle:** the crystal structure of isocitrate dehydrogenase kinase/phosphatase2 from e. coli
52	d1x47a1	Alignment	not modelled	16.0	11	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like

						Family: Double-stranded RNA-binding domain (dsRBD)
53	d1o0wa2	Alignment	not modelled	13.7	22	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
54	d1bb8a_	Alignment	not modelled	13.4	19	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**DNA-binding domain from tn916 integrase
55	c2kleA_	Alignment	not modelled	12.6	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**polycystin-2; **PDBTitle:** isic refined solution structure of the calcium binding2 domain of the c-terminal cytosolic domain of polycystin-2
56	c3adjA_	Alignment	not modelled	11.2	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
57	c3adiC_	Alignment	not modelled	11.2	16	**PDB header:**gene regulation/rna **Chain:** C: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
58	d1woqa2	Alignment	not modelled	10.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
59	c2yt4A_	Alignment	not modelled	9.6	10	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein dgcr8; **PDBTitle:** crystal structure of human dgcr8 core
60	d2b7va1	Alignment	not modelled	9.4	21	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
61	d2b7ta1	Alignment	not modelled	8.9	24	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
62	d1uxca_	Alignment	not modelled	8.9	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
63	d1wjwa_	Alignment	not modelled	8.4	17	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
64	c2zhhA_	Alignment	not modelled	7.8	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
65	c3oouA_	Alignment	not modelled	7.6	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
66	d1r8da_	Alignment	not modelled	7.5	20	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
67	d2dmya1	Alignment	not modelled	7.5	15	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
68	c2l8nA_	Alignment	not modelled	7.4	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
69	c2ae3A_	Alignment	not modelled	6.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaryl 7-aminocephalosporanic acid acylase; **PDBTitle:** glutaryl 7-aminocephalosporanic acid acylase: mutational study of2 activation mechanism
70	d2g3ba1	Alignment	not modelled	6.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
71	c3ol0C_	Alignment	not modelled	6.7	31	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
72	d2csba1	Alignment	not modelled	6.4	35	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
73	d2g39a2	Alignment	not modelled	6.3	26	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
74	c2k9sA_	Alignment	not modelled	6.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
75	c3llhB_	Alignment	not modelled	6.3	23	**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
76	d1uxda_	Alignment	not modelled	6.2	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
77	c3mxnA_	Alignment	not modelled	6.1	2	**PDB header:**replication **Chain:** A: **PDB Molecule:**recq-mediated genome instability protein 1; **PDBTitle:** crystal structure of the rmi core complex
78	c2gf5A_	Alignment	not modelled	6.1	8	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fadd protein; **PDBTitle:** structure of intact fadd (mort1)

79	d1rkta1	Alignment	not modelled	6.0	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
80	c2yqfA_	Alignment	not modelled	6.0	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** solution structure of the death domain of ankyrin-1
81	d1u4ga_	Alignment	not modelled	5.9	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
82	d1j6xa_	Alignment	not modelled	5.9	25	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
83	d1zk8a1	Alignment	not modelled	5.9	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
84	d1bh9b_	Alignment	not modelled	5.7	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
85	c2rrhA_	Alignment	not modelled	5.7	24	**PDB header:**hormone **Chain:** A: **PDB Molecule:**vip peptides; **PDBTitle:** nmr structure of vasoactive intestinal peptide in methanol
86	d1fada_	Alignment	not modelled	5.5	9	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
87	d2nlva1	Alignment	not modelled	5.5	24	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
88	d1vjea_	Alignment	not modelled	5.5	29	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
89	c2l2nA_	Alignment	not modelled	5.4	16	**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
90	d1j6wa_	Alignment	not modelled	5.3	24	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
91	c2ka4B_	Alignment	not modelled	5.3	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
92	c1o0wB_	Alignment	not modelled	5.2	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease iii; **PDBTitle:** crystal structure of ribonuclease iii (tm1102) from2 thermotoga maritima at 2.0 a resolution
93	d2oi8a1	Alignment	not modelled	5.2	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
94	d1lcda_	Alignment	not modelled	5.1	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator