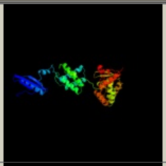
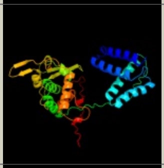
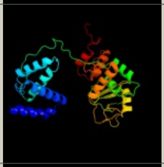
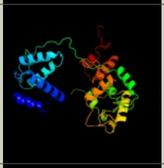
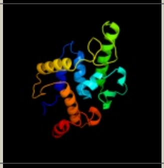
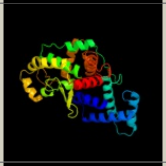
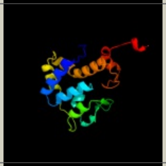
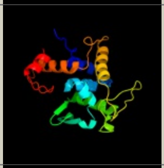
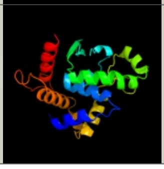
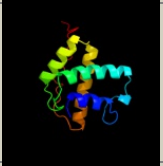
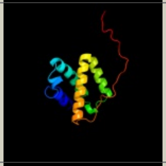
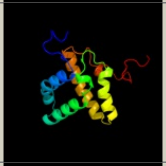
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P75969
Date	Thu Jan 5 12:16:36 GMT 2012
Unique Job ID	7f2cf0187faa8c67

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z1bA_	Alignment		100.0	33	**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	36	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
3	c1ma7A_	Alignment		100.0	12	**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		100.0	11	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
5	c2a3vA_	Alignment		100.0	17	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
6	c3nkhB_	Alignment		100.0	17	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
7	c1a0pA_	Alignment		100.0	16	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd
8	d1ae9a_	Alignment		99.9	36	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
9	d1aiha_	Alignment		99.9	17	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
10	d1f44a2	Alignment		99.9	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
11	d1a0pa2	Alignment		99.9	17	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core

12	d5crxb2	Alignment		99.8	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
13	c2khqA_	Alignment		99.1	14	**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
14	c2oxoA_	Alignment		99.1	28	**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
15	c2kiwA_	Alignment		99.0	13	**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	c3lysC_	Alignment		99.0	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
17	c2kj8A_	Alignment		98.8	15	**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
18	c2kkvA_	Alignment		98.8	12	**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
19	c2kj9A_	Alignment		98.8	11	**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
20	c2kobA_	Alignment		98.7	9	**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	c2kd1A_	Alignment	not modelled	98.6	5	**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
22	c2kkpA_	Alignment	not modelled	98.6	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).
23	c2khvA_	Alignment	not modelled	98.6	16	**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	98.5	15	**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	98.4	10	**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	c2v6eB_	Alignment	not modelled	98.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
						Fold:DNA-binding domain

27	d1z1ba1	Alignment	not modelled	98.1	41	**Superfamily:**DNA-binding domain **Family:**lambda integrase N-terminal domain
28	c3nrwA_	Alignment	not modelled	98.1	12	**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	c1kjkA_	Alignment	not modelled	98.1	41	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution structure of the lambda integrase amino-terminal2 domain
30	c3ju0A_	Alignment	not modelled	97.9	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7 integrase
31	c3jtzA_	Alignment	not modelled	97.5	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structure of the arm-type binding domain of hpi integrase
32	d1a0pa1	Alignment	not modelled	96.9	14	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
33	d1f44a1	Alignment	not modelled	95.0	12	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
34	c2b9sA_	Alignment	not modelled	77.9	16	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
35	c1a31A_	Alignment	not modelled	77.2	16	**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
36	d1p4ea2	Alignment	not modelled	74.6	17	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
37	d1k4ta2	Alignment	not modelled	74.2	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
38	c1p4eB_	Alignment	not modelled	72.8	17	**PDB header:**dna binding protein/recombination/dna **Chain:** B: **PDB Molecule:**recombinase flp protein; **PDBTitle:** flpe w330f mutant-dna holliday junction complex
39	d1rr8c1	Alignment	not modelled	69.9	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
40	c2f4qA_	Alignment	not modelled	47.3	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
41	c1nh3A_	Alignment	not modelled	35.5	16	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** human topoisomerase i ara-c complex
42	c2h7fX_	Alignment	not modelled	28.3	15	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
43	c2k49A_	Alignment	not modelled	14.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein so_3888; **PDBTitle:** solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
44	d2csba5	Alignment	not modelled	14.4	27	**Fold:**Topoisomerase V catalytic domain-like **Superfamily:**Topoisomerase V catalytic domain-like **Family:**Topoisomerase V catalytic domain-like
45	c3m6zA_	Alignment	not modelled	12.0	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of an n-terminal 44 kda fragment of topoisomerase v2 in the presence of guanidium hydrochloride
46	c3igmA_	Alignment	not modelled	11.4	6	**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
47	d1tc3c_	Alignment	not modelled	10.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
48	c2k8eA_	Alignment	not modelled	10.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein yegp; **PDBTitle:** solution nmr structure of protein of unknown function yegp from e.2 coli. ontario center for structural proteomics target ec0640_1_1233 northeast structural genomics consortium target et102.
49	c2csdB_	Alignment	not modelled	10.0	27	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
50	d2k49a2	Alignment	not modelled	7.8	11	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
51	d2k8ea1	Alignment	not modelled	7.5	11	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
						PDB header:hormone

52	c2rrhA_	Alignment	not modelled	7.4	30	**Chain:** A: **PDB Molecule:**vip peptides; **PDBTitle:** nmr structure of vasoactive intestinal peptide in methanol
53	d1o66a_	Alignment	not modelled	7.1	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
54	c2ka4B_	Alignment	not modelled	6.4	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
55	c2d2pA_	Alignment	not modelled	6.4	30	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**pituitary adenylate cyclase activating **PDBTitle:** the solution structure of micelle-bound peptide
56	c1yd6A_	Alignment	not modelled	6.2	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrc; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease2 domain of uvrc from bacillus caldotenax
57	d2al3a1	Alignment	not modelled	5.9	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
58	c2kvvA_	Alignment	not modelled	5.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative excisionase; **PDBTitle:** solution nmr of putative excisionase from klebsiella pneumoniae,2 northeast structural genomics consortium target target kpr49
59	d1ug2a_	Alignment	not modelled	5.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
60	d1j6xa_	Alignment	not modelled	5.3	16	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
61	d2bgxa2	Alignment	not modelled	5.2	8	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
62	d1d1da2	Alignment	not modelled	5.1	18	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
63	c2kgfA_	Alignment	not modelled	5.1	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein p27; **PDBTitle:** n-terminal domain of capsid protein from the mason-pfizer2 monkey virus
64	d1j2oa2	Alignment	not modelled	5.1	44	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain