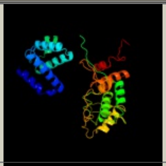
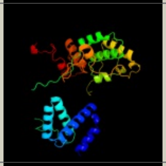
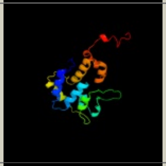
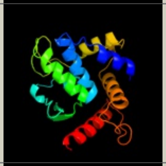
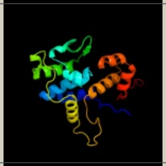
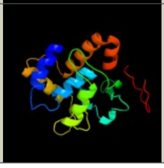
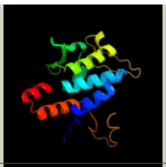
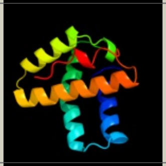
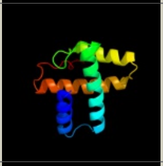
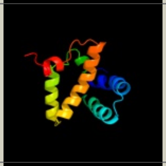
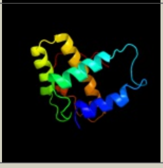
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8P6
Date	Thu Jan 5 11:08:26 GMT 2012
Unique Job ID	941f49b40175366f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c1crxA_	Alignment		100.0	13	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
3	c1a0pA_	Alignment		100.0	34	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd
4	d1p7da_	Alignment		100.0	18	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
5	c2a3vA_	Alignment		100.0	20	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
6	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
7	c3nkhB_	Alignment		99.9	20	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
8	d1aiha_	Alignment		99.9	19	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
9	d1a0pa2	Alignment		99.8	38	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
10	d1f44a2	Alignment		99.8	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
11	d1ae9a_	Alignment		99.7	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core

12	d5crxb2	Alignment		99.5	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
13	c3nrwA_	Alignment		99.5	13	**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
14	c2oxoA_	Alignment		99.2	25	**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	d1f44a1	Alignment		99.1	11	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
16	d1a0pa1	Alignment		99.1	24	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
17	c2khqA_	Alignment		99.1	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
18	c2kd1A_	Alignment		99.0	14	**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
19	c2keyA_	Alignment		99.0	12	**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
20	c2kkpA_	Alignment		98.9	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).
21	c3lysC_	Alignment	not modelled	98.9	8	**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
22	c2kobA_	Alignment	not modelled	98.9	14	**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	c2kiwA_	Alignment	not modelled	98.9	11	**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).
24	c2kj8A_	Alignment	not modelled	98.7	10	**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
25	c2kj9A_	Alignment	not modelled	98.6	12	**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
26	c2kkvA_	Alignment	not modelled	98.6	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
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase;

27	c2khvA_	Alignment	not modelled	98.5	11	**PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
28	c2kj5A_	Alignment	not modelled	98.3	13	**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
29	c2v6eB_	Alignment	not modelled	96.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
30	c3mzyA_	Alignment	not modelled	36.6	11	**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
31	c2f4qA_	Alignment	not modelled	33.3	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
32	c3sqiA_	Alignment	not modelled	27.2	7	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**klla0e03807p; **PDBTitle:** dna binding domain of ndc10
33	c3t79A_	Alignment	not modelled	27.2	7	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**klla0e03807p; **PDBTitle:** ndc10: a platform for inner kinetochore assembly in budding yeast
34	d1s7oa_	Alignment	not modelled	26.2	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
35	c3sohB_	Alignment	not modelled	22.7	14	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** architecture of the flagellar rotor
36	d1trra_	Alignment	not modelled	18.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
37	d1jhga_	Alignment	not modelled	13.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
38	c3hugA_	Alignment	not modelled	12.9	13	**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
39	d2auwa1	Alignment	not modelled	12.1	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
40	c1r71B_	Alignment	not modelled	10.3	14	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in2 complex with the operator dna
41	c2x48B_	Alignment	not modelled	8.6	16	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
42	d1hcra_	Alignment	not modelled	7.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
43	d1ijwc_	Alignment	not modelled	7.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
44	d1fsea_	Alignment	not modelled	7.6	11	**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)
45	c2o8xA_	Alignment	not modelled	7.5	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
46	c2h7fX_	Alignment	not modelled	7.3	17	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
47	d1sf9a_	Alignment	not modelled	7.1	10	**Fold:**SH3-like barrel **Superfamily:**Hypothetical protein YfhH **Family:**Hypothetical protein YfhH
48	d1v2za_	Alignment	not modelled	7.1	11	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
49	d1r8ja1	Alignment	not modelled	6.9	15	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
50	d2g7la1	Alignment	not modelled	6.7	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
51	d1or7a1	Alignment	not modelled	6.7	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
52	c3bhwA_	Alignment	not modelled	6.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from magnetospirillum2 magneticum
						Fold:DNA/RNA-binding 3-helical bundle

53	d1vz0a1	Alignment	not modelled	6.5	17	**Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
54	c2kq6A_	Alignment	not modelled	6.2	28	**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
55	c2q1zA_	Alignment	not modelled	6.1	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rpoe, ecf sige; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
56	d1sv1a_	Alignment	not modelled	5.9	25	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
57	c2kleA_	Alignment	not modelled	5.8	31	**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
58	d2d6ya1	Alignment	not modelled	5.7	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
59	c2rnjA_	Alignment	not modelled	5.6	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
60	d1ofcx1	Alignment	not modelled	5.5	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
61	c2wl8D_	Alignment	not modelled	5.5	19	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**peroxisomal biogenesis factor 19; **PDBTitle:** x-ray crystal structure of pex19p
62	c3frwF_	Alignment	not modelled	5.4	9	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
63	c1x3uA_	Alignment	not modelled	5.4	7	**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
64	d1xsva_	Alignment	not modelled	5.4	2	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
65	c2jpcA_	Alignment	not modelled	5.2	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
66	c2ka4B_	Alignment	not modelled	5.2	83	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** nmr structure of the cbp-taz1/stat2-tad complex
67	d2nvma1	Alignment	not modelled	5.1	7	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
68	d2nlva1	Alignment	not modelled	5.1	7	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like