Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P71298
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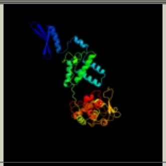
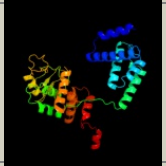
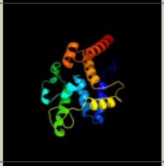
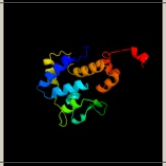
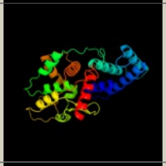
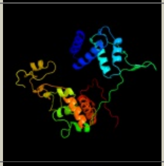
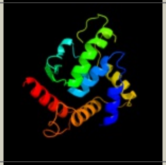
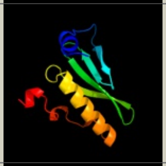
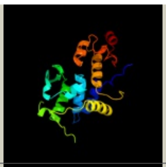
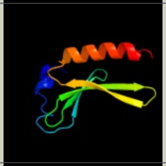
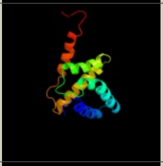
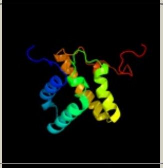
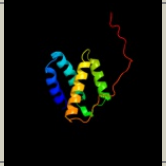
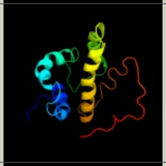
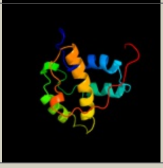
Unique Job ID	e643feabdf2c74b4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z1bA_	Alignment		100.0	14	**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	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
3	c1ma7A_	Alignment		100.0	13	**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	c3nkhB_	Alignment		100.0	18	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
5	c1crxA_	Alignment		100.0	13	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
6	d1aiha_	Alignment		99.9	17	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
7	c1a0pA_	Alignment		99.9	22	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd
8	c2a3vA_	Alignment		99.9	19	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
9	d1a0pa2	Alignment		99.9	21	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
10	c3ju0A_	Alignment		99.9	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7 integrase
11	d1ae9a_	Alignment		99.9	12	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core

12	d1f44a2	Alignment		99.9	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
13	c3jtzA_	Alignment		99.8	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structure of the arm-type binding domain of hpi integrase
14	d5crxb2	Alignment		99.8	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
15	c2khvA_	Alignment		99.3	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.
16	c2kj8A_	Alignment		99.2	11	**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		99.2	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
18	c2kiwA_	Alignment		99.1	10	**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).
19	c2kkvA_	Alignment		99.1	8	**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
20	c2kj5A_	Alignment		99.1	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
21	c2oxoA_	Alignment	not modelled	99.0	15	**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	c2khqA_	Alignment	not modelled	98.9	7	**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
23	c2kd1A_	Alignment	not modelled	98.9	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
24	c2kobA_	Alignment	not modelled	98.9	11	**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
25	c3lysC_	Alignment	not modelled	98.8	19	**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
26	c2kkpA_	Alignment	not modelled	98.8	12	**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).
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage integrase;

27	c2keyA_	Alignment	not modelled	98.2	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	98.1	11	**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	97.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
30	c2f4qA_	Alignment	not modelled	95.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
31	d1a0pa1	Alignment	not modelled	95.0	17	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
32	c2h7fX_	Alignment	not modelled	89.6	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	73.1	15	**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	c3igmA_	Alignment	not modelled	71.0	10	**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	d1k4ta2	Alignment	not modelled	49.3	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
36	d1a41a_	Alignment	not modelled	47.4	18	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
37	d1rr8c1	Alignment	not modelled	36.6	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
38	d1f44a1	Alignment	not modelled	29.1	12	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
39	d2auwa1	Alignment	not modelled	28.2	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
40	c1a31A_	Alignment	not modelled	25.2	13	**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
41	d2csba1	Alignment	not modelled	22.7	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
42	d1j6xa_	Alignment	not modelled	20.7	17	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
43	d1e43a1	Alignment	not modelled	16.5	34	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
44	c3sy3D_	Alignment	not modelled	15.0	7	**PDB header:**lyase **Chain:** D: **PDB Molecule:**gbaa_1210 protein; **PDBTitle:** gbaa_1210 protein, a putative adenylate cyclase, from bacillus2 anthracis
45	c3mxnA_	Alignment	not modelled	14.5	6	**PDB header:**replication **Chain:** A: **PDB Molecule:**recq-mediated genome instability protein 1; **PDBTitle:** crystal structure of the rmi core complex
46	d1uxca_	Alignment	not modelled	12.4	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
47	d1vjea_	Alignment	not modelled	12.2	33	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
48	d1j6wa_	Alignment	not modelled	11.9	19	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
49	c2j5dA_	Alignment	not modelled	11.6	45	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles
50	d1khda1	Alignment	not modelled	11.5	29	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
51	c1nh3A_	Alignment	not modelled	11.2	16	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** human topoisomerase i ara-c complex
52	c3hshA_	Alignment	not modelled	11.2	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**collagen alpha-1(xviii) chain;

						PDBTitle: crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form)
53	c3lsoA_	Alignment	not modelled	11.1	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative membrane anchored protein; **PDBTitle:** crystal structure of putative membrane anchored protein from2 corynebacterium diphtheriae
54	c2l8nA_	Alignment	not modelled	10.9	17	**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
55	c2i3eA_	Alignment	not modelled	10.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**g-rich; **PDBTitle:** solution structure of catalytic domain of goldfish rich2 protein
56	c2zcyM_	Alignment	not modelled	9.5	7	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**proteasome component pre4; **PDBTitle:** yeast 20s proteasome:syringolin a-complex
57	c1q7lB_	Alignment	not modelled	9.3	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
58	c2bpqB_	Alignment	not modelled	9.3	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
59	c2auwB_	Alignment	not modelled	8.8	17	**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
60	d1uxda_	Alignment	not modelled	8.6	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
61	d1m5ya3	Alignment	not modelled	8.1	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
62	d2d3na1	Alignment	not modelled	8.0	24	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
63	d2cqra1	Alignment	not modelled	7.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
64	d1okia2	Alignment	not modelled	7.8	19	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
65	c2ka2B_	Alignment	not modelled	6.9	42	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
66	c2ka2A_	Alignment	not modelled	6.9	42	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
67	c2ka1A_	Alignment	not modelled	6.9	42	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
68	c2ka1B_	Alignment	not modelled	6.9	42	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
69	d1x48a1	Alignment	not modelled	6.9	11	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
70	d2gf5a1	Alignment	not modelled	6.6	17	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
71	d1lcda_	Alignment	not modelled	6.5	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
72	d1ryp2_	Alignment	not modelled	6.4	7	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
73	d2izva1	Alignment	not modelled	6.4	27	**Fold:**SOCS box-like **Superfamily:**SOCS box-like **Family:**SOCS box-like
74	d2i2la1	Alignment	not modelled	6.4	24	**Fold:**YopX-like **Superfamily:**YopX-like **Family:**YopX-like
75	d1v8ga1	Alignment	not modelled	6.2	27	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
76	d2gjpa1	Alignment	not modelled	5.9	22	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
						Fold: Barrel-sandwich hybrid

77	d1vkza1	Alignment	not modelled	5.8	24	**Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
78	c2jzvA_	Alignment	not modelled	5.6	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** solution structure of s. aureus prsa-ppiase
79	c2bgcA_	Alignment	not modelled	5.5	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prfa; **PDBTitle:** prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
80	d1j98a_	Alignment	not modelled	5.5	16	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
81	d1qpza1	Alignment	not modelled	5.3	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
82	c2lcvA_	Alignment	not modelled	5.3	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
83	d2bjca1	Alignment	not modelled	5.1	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
84	c2nogA_	Alignment	not modelled	5.1	8	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**iswi protein; **PDBTitle:** sant domain structure of xenopus remodeling factor iswi
85	d1xg1a1	Alignment	not modelled	5.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of telomeric protein
86	d1gsoa1	Alignment	not modelled	5.0	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like