Phyre^2

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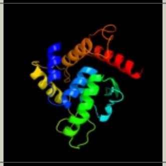
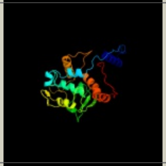
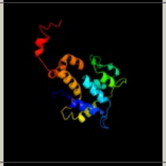
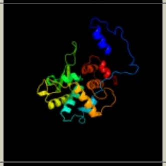
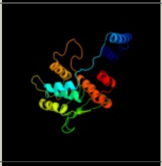
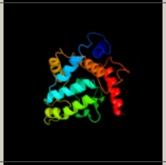
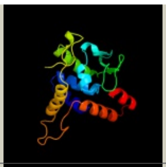
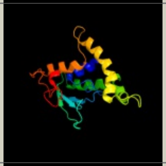
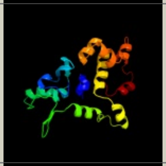
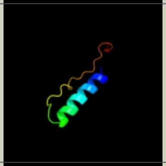
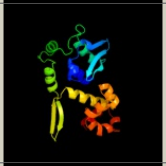
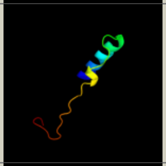
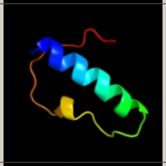
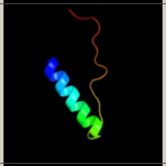
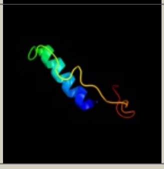
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nkhB_	Alignment		100.0	17	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
2	c1z1bA_	Alignment		99.9	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
3	d1a0pa2	Alignment		99.9	29	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
4	d1f44a2	Alignment		99.9	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
5	d1p7da_	Alignment		99.9	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
6	d1aiha_	Alignment		99.9	17	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
7	c1crxA_	Alignment		99.9	12	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
8	c1ma7A_	Alignment		99.9	11	**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
9	c1a0pA_	Alignment		99.9	23	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd
10	d1ae9a_	Alignment		99.9	18	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
11	c2a3vA_	Alignment		99.9	15	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination

12	d5crxb2_	Alignment		99.8	12	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
13	c2v6eB_	Alignment		96.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
14	c2f4qA_	Alignment		95.4	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
15	c2khqA_	Alignment		88.5	5	**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
16	c2h7fX_	Alignment		87.8	13	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
17	c2kobA_	Alignment		86.4	7	**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
18	c2kkpA_	Alignment		86.1	13	**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).
19	c2kiwA_	Alignment		85.7	17	**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).
20	c2kd1A_	Alignment		83.4	10	**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
21	c2kj5A_	Alignment	not modelled	71.6	12	**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
22	c1p4eB_	Alignment	not modelled	69.5	12	**PDB header:**dna binding protein/recombination/dna **Chain:** B: **PDB Molecule:**recombinase flp protein; **PDBTitle:** flpe w330f mutant-dna holliday junction complex
23	c3lysC_	Alignment	not modelled	68.9	3	**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
24	c2kj8A_	Alignment	not modelled	65.9	5	**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	c2kkvA_	Alignment	not modelled	62.4	10	**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
26	c2kj9A_	Alignment	not modelled	61.2	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
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage integrase;

27	c2keyA_	Alignment	not modelled	57.5	3	**PDBTitle:** solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
28	c2khvA_	Alignment	not modelled	49.0	10	**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.
29	d1p4ea2	Alignment	not modelled	32.0	11	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
30	d1ofcx1	Alignment	not modelled	21.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
31	c2b9sA_	Alignment	not modelled	17.1	14	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
32	d1rr8c1	Alignment	not modelled	16.8	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
33	d1nvpb_	Alignment	not modelled	15.3	26	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
34	c1nvpB_	Alignment	not modelled	15.3	26	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcription initiation factor iia alpha chain; **PDBTitle:** human tfiia/tbp/dna complex
35	d1a41a_	Alignment	not modelled	11.2	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
36	d1k4ta2	Alignment	not modelled	11.2	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
37	d1hvda_	Alignment	not modelled	9.5	12	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
38	d1dwka1	Alignment	not modelled	8.3	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
39	d1nh2b_	Alignment	not modelled	7.5	19	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
40	d1fsea_	Alignment	not modelled	6.9	14	**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)
41	d1bo9a_	Alignment	not modelled	6.7	7	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
42	c1bo9A_	Alignment	not modelled	6.7	7	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein (annexin i); **PDBTitle:** nmr solution structure of domain 1 of human annexin i
43	d1i4aa_	Alignment	not modelled	6.6	8	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
44	c3hh0C_	Alignment	not modelled	6.6	13	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
45	d1m9ia2	Alignment	not modelled	6.5	12	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
46	d1uoua1	Alignment	not modelled	6.2	13	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
47	d1jhfa1	Alignment	not modelled	6.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
48	d1m9ia1	Alignment	not modelled	5.9	12	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
49	d2ie7a1	Alignment	not modelled	5.3	14	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin