

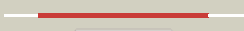






























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1a0pA_</a>	 Alignment		100.0	97	<b>PDB header:</b> dna recombination <b>Chain:</b> A: <b>PDB Molecule:</b> site-specific recombinase xerd; <b>PDBTitle:</b> site-specific recombinase, xerd
2	<a href="#">c1ma7A_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase, ligase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> cre recombinase; <b>PDBTitle:</b> crystal structure of cre site-specific recombinase2 complexed with a mutant dna substrate, loxp-a8/t27
3	<a href="#">c1crxA_</a>	 Alignment		100.0	14	<b>PDB header:</b> replication/dna <b>Chain:</b> A: <b>PDB Molecule:</b> cre recombinase; <b>PDBTitle:</b> cre recombinase/dna complex reaction intermediate i
4	<a href="#">d1p7da_</a>	 Alignment		100.0	16	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
5	<a href="#">c2a3vA_</a>	 Alignment		100.0	21	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> site-specific recombinase inti4; <b>PDBTitle:</b> structural basis for broad dna-specificity in integron2 recombination
6	<a href="#">c1z1bA_</a>	 Alignment		100.0	16	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of a lambda integrase dimer bound to a2 coc' core site
7	<a href="#">d1a0pa2</a>	 Alignment		99.9	98	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
8	<a href="#">c3nkhB_</a>	 Alignment		99.9	18	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of integrase from mrsa strain staphylococcus aureus
9	<a href="#">d1aiha_</a>	 Alignment		99.9	24	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
10	<a href="#">d1f44a2</a>	 Alignment		99.8	15	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
11	<a href="#">d1ae9a_</a>	 Alignment		99.8	15	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core

12	<a href="#">d5crxb2</a>	Alignment		99.6	18	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
13	<a href="#">d1a0pa1</a>	Alignment		99.4	97	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> lambda integrase-like, N-terminal domain <b>Family:</b> lambda integrase-like, N-terminal domain
14	<a href="#">c3nrwA</a>	Alignment		99.3	15	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase/site-specific recombinase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
15	<a href="#">d1f44a1</a>	Alignment		99.3	10	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> lambda integrase-like, N-terminal domain <b>Family:</b> lambda integrase-like, N-terminal domain
16	<a href="#">c2oxoA</a>	Alignment		99.1	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
17	<a href="#">c2khqA</a>	Alignment		99.0	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
18	<a href="#">c2keyA</a>	Alignment		99.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative phage integrase; <b>PDBTitle:</b> solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
19	<a href="#">c2kd1A</a>	Alignment		98.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dna integration/recombination/inversion protein; <b>PDBTitle:</b> solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f
20	<a href="#">c3lysC</a>	Alignment		98.9	15	<b>PDB header:</b> recombination <b>Chain:</b> C: <b>PDB Molecule:</b> prophage pi2 protein 01, integrase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f
21	<a href="#">c2kiwA</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> int protein; <b>PDBTitle:</b> 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).
22	<a href="#">c2kkaA</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase; <b>PDBTitle:</b> 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	<a href="#">c2kobA</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of clolep_01837 (fragment 61-160)2 from clostridium leptum. northeast structural genomics3 consortium target qlr8a
24	<a href="#">c2kj8A</a>	Alignment	not modelled	98.5	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative prophage cps-53 integrase; <b>PDBTitle:</b> nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
25	<a href="#">c2kj9A</a>	Alignment	not modelled	98.4	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e
26	<a href="#">c2kkaA</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> solution nmr structure of an integrase domain from protein2 spa4288 from salmonella enterica, northeast structural3 genomics consortium target slr105h
						<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase;

27	<a href="#">c2khvA</a>	Alignment	not modelled	98.0	11	<b>PDBTitle:</b> solution nmr structure of protein nmul_a0922 from2 nitrospira multiformis. northeast structural genomics3 consortium target nmr38b.
28	<a href="#">c2kj5A</a>	Alignment	not modelled	97.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phage integrase; <b>PDBTitle:</b> solution nmr structure of a domain from a putative phage2 integrase protein nmul_a0064 from nitrospira multiformis,3 northeast structural genomics consortium target nmr46c
29	<a href="#">c2v6eB</a>	Alignment	not modelled	97.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protelemorase; <b>PDBTitle:</b> protelomerase telk complexed with substrate dna
30	<a href="#">c3sqiA</a>	Alignment	not modelled	71.9	25	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> klla0e03807p; <b>PDBTitle:</b> dna binding domain of ndc10
31	<a href="#">c3t79A</a>	Alignment	not modelled	71.1	25	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> klla0e03807p; <b>PDBTitle:</b> ndc10: a platform for inner kinetochore assembly in budding yeast
32	<a href="#">c3mzyA</a>	Alignment	not modelled	40.1	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
33	<a href="#">d1s7oa</a>	Alignment	not modelled	29.5	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
34	<a href="#">d1r8ja1</a>	Alignment	not modelled	24.9	24	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Circadian clock protein KaiA, C-terminal domain
35	<a href="#">d1sv1a</a>	Alignment	not modelled	23.5	27	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Circadian clock protein KaiA, C-terminal domain
36	<a href="#">d1trra</a>	Alignment	not modelled	22.5	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
37	<a href="#">d1v2za</a>	Alignment	not modelled	21.2	27	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Circadian clock protein KaiA, C-terminal domain
38	<a href="#">d1jhga</a>	Alignment	not modelled	16.3	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
39	<a href="#">c3sohB</a>	Alignment	not modelled	14.3	10	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar motor switch protein flag; <b>PDBTitle:</b> architecture of the flagellar rotor
40	<a href="#">d2auwa1</a>	Alignment	not modelled	13.8	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE0471 C-terminal domain-like
41	<a href="#">d1vz0a1</a>	Alignment	not modelled	13.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
42	<a href="#">c1r71B</a>	Alignment	not modelled	12.9	12	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor protein korb; <b>PDBTitle:</b> crystal structure of the dna binding domain of korb in2 complex with the operator dna
43	<a href="#">c2f4qA</a>	Alignment	not modelled	11.6	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> type i topoisomerase, putative; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans topoisomerase ib
44	<a href="#">c3hugA</a>	Alignment	not modelled	11.5	22	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigl
45	<a href="#">c2o8xA</a>	Alignment	not modelled	9.3	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
46	<a href="#">c2x48B</a>	Alignment	not modelled	8.6	19	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> cag38821; <b>PDBTitle:</b> orf 55 from sulfolobus islandicus rudivirus 1
47	<a href="#">d1fsea</a>	Alignment	not modelled	7.9	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
48	<a href="#">d1xsva</a>	Alignment	not modelled	7.6	2	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
49	<a href="#">d1r71a</a>	Alignment	not modelled	7.6	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
50	<a href="#">d2o3la1</a>	Alignment	not modelled	7.6	11	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> BH3980-like <b>Family:</b> BH3980-like
51	<a href="#">c3d7qB</a>	Alignment	not modelled	7.0	22	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> xisi protein-like; <b>PDBTitle:</b> crystal structure of a xisi-like protein (npun_ar114) from nostoc punctiforme pcc 73102 at 2.30 a resolution
52	<a href="#">d2o4ta1</a>	Alignment	not modelled	6.8	10	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> BH3980-like <b>Family:</b> BH3980-like
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

53	<a href="#">d1or7a1</a>	Alignment	not modelled	6.7	14	<b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
54	<a href="#">d1ldda_</a>	Alignment	not modelled	6.3	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> SCF ubiquitin ligase complex WHB domain
55	<a href="#">d1ofcx1</a>	Alignment	not modelled	5.8	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Myb/SANT domain
56	<a href="#">c2rnjA_</a>	Alignment	not modelled	5.6	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vrrA; <b>PDBTitle:</b> nmr structure of the s. aureus vrrA dna binding domain
57	<a href="#">d1umqa_</a>	Alignment	not modelled	5.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
58	<a href="#">c1umqA_</a>	Alignment	not modelled	5.5	10	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prrA(regA) from r. sphaeroides:3 insights into dna binding specificity
59	<a href="#">d2g7la1</a>	Alignment	not modelled	5.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
60	<a href="#">c2kq6A_</a>	Alignment	not modelled	5.3	28	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> polycystin-2; <b>PDBTitle:</b> the structure of the ef-hand domain of polycystin-2 suggests a2 mechanism for ca2+-dependent regulation of polycystin-2 channel3 activity
61	<a href="#">d1ijwc_</a>	Alignment	not modelled	5.2	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
62	<a href="#">d1q08a_</a>	Alignment	not modelled	5.1	32	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
63	<a href="#">d1hcra_</a>	Alignment	not modelled	5.1	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
64	<a href="#">c2jpcA_</a>	Alignment	not modelled	5.0	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrB; <b>PDBTitle:</b> ssrB dna binding protein