Phyre^2

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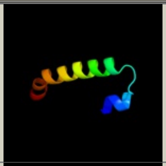
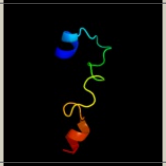
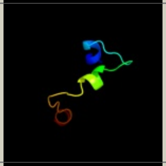
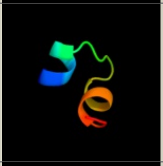
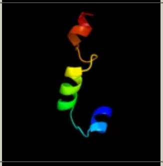
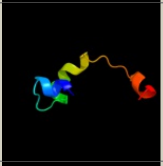
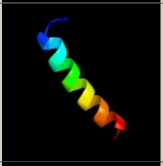
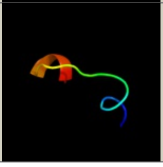
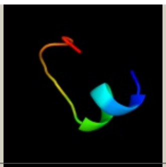
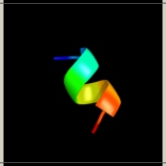
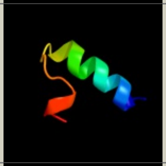
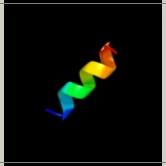
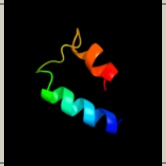
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nkhB_	Alignment		94.2	17	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
2	c1ma7A_	Alignment		72.7	15	**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
3	d1f44a2	Alignment		65.5	12	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
4	c2a3vA_	Alignment		38.4	28	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
5	c1crxA_	Alignment		37.3	15	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
6	d1aiha_	Alignment		35.4	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
7	d1wiia_	Alignment		20.8	33	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
8	d1q46a1	Alignment		13.8	14	**Fold:**SAM domain-like **Superfamily:**eIF2alpha middle domain-like **Family:**eIF2alpha middle domain-like
9	c1z1bA_	Alignment		12.4	0	**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
10	d1v54l_	Alignment		10.4	75	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa) **Family:**Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa)
11	c1a0pA_	Alignment		10.2	19	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd

12	d1p7da_	Alignment		9.6	0	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
13	c2y69Y_	Alignment		9.5	75	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**cytochrome c oxidase subunit 7c; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
14	d1gxha_	Alignment		8.9	26	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
15	c1kzvA_	Alignment		8.4	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpr protein; **PDBTitle:** structure of human immunodeficiency virus type 1 vpr(34-51)2 peptide in chloroform methanol
16	c1kztA_	Alignment		8.4	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpr protein; **PDBTitle:** structure of human immunodeficiency virus type 1 vpr(34-51)2 peptide in dpc micelle containing aqueous solution
17	c1kzsA_	Alignment		8.4	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpr protein; **PDBTitle:** structure of human immunodeficiency virus type 1 vpr(34-51)2 peptide in aqueous tfe solution
18	c1ytrA_	Alignment		7.2	18	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bacteriocin plantaricin a; **PDBTitle:** nmr structure of plantaricin a in dpc micelles, 202 structures
19	d2hi3a1	Alignment		7.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
20	c2k8jX_	Alignment		6.7	57	**PDB header:**viral protein **Chain:** X: **PDB Molecule:**p7tm2; **PDBTitle:** solution structure of hcv p7 tm2
21	d2gy9s1	Alignment	not modelled	6.6	46	**Fold:**Ribosomal protein S19 **Superfamily:**Ribosomal protein S19 **Family:**Ribosomal protein S19
22	d1uhsa_	Alignment	not modelled	6.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
23	c2wl8D_	Alignment	not modelled	6.5	15	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**peroxisomal biogenesis factor 19; **PDBTitle:** x-ray crystal structure of pex19p
24	c1zd1B_	Alignment	not modelled	6.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfotransferase 4a1; **PDBTitle:** human sulfortransferase sult4a1
25	d1f15b_	Alignment	not modelled	5.7	35	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
26	c2wvmA_	Alignment	not modelled	5.7	55	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
27	d1f06a2	Alignment	not modelled	5.6	29	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
28	c1f15C_	Alignment	not modelled	5.6	35	**PDB header:**virus **Chain:** C: **PDB Molecule:**coat protein; **PDBTitle:** cucumber mosaic virus (strain fny)
						PDB header:transcription regulator

29	c2l5gA_	Alignment	not modelled	5.6	29	**Chain:** A: **PDB Molecule:**g protein pathway suppressor 2; **PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
30	d5csma_	Alignment	not modelled	5.5	17	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Allosteric chorismate mutase
31	d1i94m_	Alignment	not modelled	5.4	9	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
32	d2uubs1	Alignment	not modelled	5.2	46	**Fold:**Ribosomal protein S19 **Superfamily:**Ribosomal protein S19 **Family:**Ribosomal protein S19
33	d1ayia_	Alignment	not modelled	5.2	21	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins