Phyre^2

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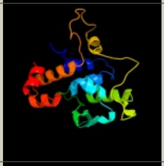
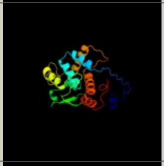
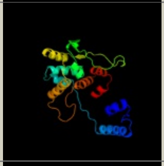
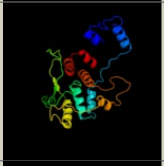
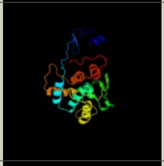
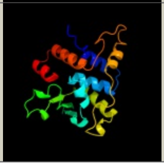
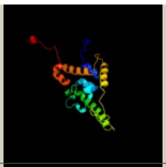
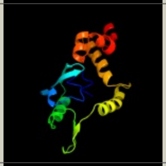
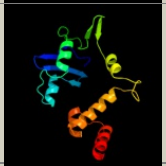
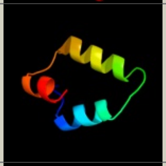
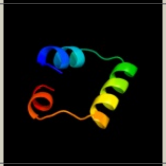
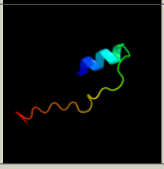
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nkhB_	Alignment		100.0	19	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
2	d1a0pa2	Alignment		99.9	19	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
3	d1aiha_	Alignment		99.9	17	**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	d1ae9a_	Alignment		99.9	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
6	c1z1bA_	Alignment		99.9	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
7	c1crxA_	Alignment		99.9	13	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
8	c1ma7A_	Alignment		99.9	10	**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	d1p7da_	Alignment		99.9	11	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
10	c1a0pA_	Alignment		99.9	20	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd
11	d5crxb2	Alignment		99.8	11	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core

12	c2a3vA_	Alignment		99.7	18	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
13	c2v6eB_	Alignment		95.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
14	c2f4qA_	Alignment		89.9	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
15	c2h7fX_	Alignment		66.3	11	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
16	d1khda1	Alignment		35.9	15	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
17	d1a41a_	Alignment		33.4	10	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
18	d2tpta1	Alignment		26.5	18	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
19	d1uoua1	Alignment		25.8	13	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
20	c2khqA_	Alignment		21.9	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
21	d1v8ga1	Alignment	not modelled	21.8	23	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
22	d1ynra1	Alignment	not modelled	21.5	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
23	c2kkvA_	Alignment	not modelled	20.5	15	**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
24	d1p4ea2	Alignment	not modelled	19.6	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
25	c2kkpA_	Alignment	not modelled	18.3	9	**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).
26	c1otpA_	Alignment	not modelled	17.9	18	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
27	c3h5qA_	Alignment	not modelled	16.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
						PDB header:dna binding protein/recombination/dna

28	c1p4eB_	Alignment	not modelled	15.9	13	**Chain:** B: **PDB Molecule:**recombinase flp protein; **PDBTitle:** flpe w330f mutant-dna holliday junction complex
29	c2kobA_	Alignment	not modelled	15.8	4	**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
30	c2j0fC_	Alignment	not modelled	15.4	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
31	c2dsjA_	Alignment	not modelled	15.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
32	d1cc5a_	Alignment	not modelled	15.0	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
33	c2kj8A_	Alignment	not modelled	14.7	17	**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
34	d1ofcx1	Alignment	not modelled	14.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
35	d1brwa1	Alignment	not modelled	14.6	23	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
36	c1w2lA_	Alignment	not modelled	13.7	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome oxidase subunit ii; **PDBTitle:** cytochrome c domain of caa3 oxygen oxidoreductase
37	d1sxea_	Alignment	not modelled	12.8	15	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
38	c2kiwA_	Alignment	not modelled	12.6	6	**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).
39	c2bpqB_	Alignment	not modelled	11.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
40	c1brwB_	Alignment	not modelled	11.3	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
41	c2d0sA_	Alignment	not modelled	10.5	0	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
42	c2w9kA_	Alignment	not modelled	10.3	12	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crithidia fasciculata cytochrome c
43	d1hroa_	Alignment	not modelled	10.0	6	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
44	c1vquB_	Alignment	not modelled	9.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
45	d1cora_	Alignment	not modelled	9.7	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
46	d1a56a_	Alignment	not modelled	9.7	12	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
47	d1sv0c_	Alignment	not modelled	9.2	9	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
48	c3oa8B_	Alignment	not modelled	8.6	18	**PDB header:**heme-binding protein/heme-binding protei **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** diheme soxax
49	c2kd1A_	Alignment	not modelled	8.4	3	**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
50	c1khdD_	Alignment	not modelled	8.2	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum)
51	d1ijwc_	Alignment	not modelled	8.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
						PDB header:isomerase/dna

52	c2b9sA_	Alignment	not modelled	7.9	13	**Chain:** A: **PDB Molecule:**topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
53	d1hcra_	Alignment	not modelled	7.8	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
54	c2kj5A_	Alignment	not modelled	7.6	9	**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
55	d351ca_	Alignment	not modelled	7.6	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
56	d1sfka_	Alignment	not modelled	7.4	20	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
57	d1fi3a_	Alignment	not modelled	7.2	12	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
58	d1ccra_	Alignment	not modelled	6.9	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
59	c2zzsW_	Alignment	not modelled	6.8	19	**PDB header:**electron transport **Chain:** W: **PDB Molecule:** **PDBTitle:** crystal structure of cytochrome c554 from vibrio2 parahaemolyticus strain rimd2210633
60	d1m70a1	Alignment	not modelled	6.8	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
61	c2dkxA_	Alignment	not modelled	6.6	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam pointed domain-containing ets transcription **PDBTitle:** solution structure of the sam_pnt-domain of ets2 transcription factor pdef (prostate ets)
62	d1o17a1	Alignment	not modelled	6.6	18	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
63	c2juhA_	Alignment	not modelled	6.2	13	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**telomere binding protein tbp1; **PDBTitle:** solution structure of dna binding domain of ngtrf1
64	d1h1oa1	Alignment	not modelled	6.2	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
65	d1dvha_	Alignment	not modelled	6.2	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
66	d1dvva_	Alignment	not modelled	6.1	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
67	c2hjhB_	Alignment	not modelled	5.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
68	d1m70a2	Alignment	not modelled	5.9	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
69	d1c53a_	Alignment	not modelled	5.9	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
70	d3c2ca_	Alignment	not modelled	5.6	12	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
71	c3mk7F_	Alignment	not modelled	5.6	35	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
72	d1sfkb_	Alignment	not modelled	5.4	20	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C