Phyre^2

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Description	P0CF27
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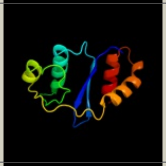
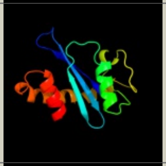
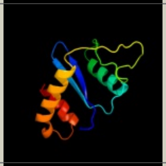
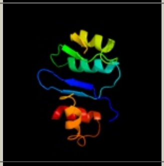
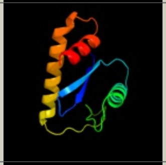
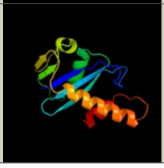
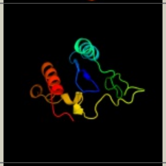
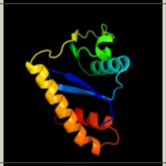
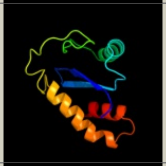
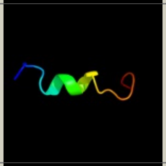
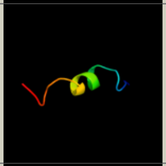
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hyva_	Alignment		97.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
2	d1cxqa_	Alignment		96.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
3	d1exqa_	Alignment		96.2	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
4	c1ex4A_	Alignment		95.0	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** hiv-1 integrase catalytic core and c-terminal domain
5	c1k6yB_	Alignment		95.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase
6	c3f9kV_	Alignment		94.3	14	**PDB header:**viral protein, recombination **Chain:** V: **PDB Molecule:**integrase; **PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd
7	d1asua_	Alignment		93.8	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
8	d1c6va_	Alignment		93.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
9	c3nf9A_	Alignment		91.1	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
10	c1c0mA_	Alignment		90.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase
11	d1c0ma2	Alignment		90.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain

12	c3dlrA_	Alignment		89.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the catalytic core domain from pfv2 integrase
13	c1bcoA_	Alignment		80.3	10	**PDB header:**transposase **Chain:** A: **PDB Molecule:**bacteriophage mu transposase; **PDBTitle:** bacteriophage mu transposase core domain
14	c3kksB_	Alignment		69.6	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of catalytic core domain of biv integrase in crystal2 form ii
15	d1bcoa2	Alignment		60.2	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**mu transposase, core domain
16	c3hpgC_	Alignment		47.7	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**integrase; **PDBTitle:** visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
17	c2k8fB_	Alignment		42.7	26	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structural basis for the regulation of p53 function by p300
18	c3he5D_	Alignment		31.1	30	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**synzip2; **PDBTitle:** heterospecific coiled-coil pair synzip2:synzip1
19	c2l14B_	Alignment		17.5	26	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of cbp nuclear coactivator binding domain in complex with2 p53 tad
20	c3l2tB_	Alignment		13.3	11	**PDB header:**recombination/dna **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
21	c1q2iA_	Alignment	not modelled	13.3	21	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**pnc27; **PDBTitle:** nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
22	c3dacB_	Alignment	not modelled	9.6	33	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of the human mdmx protein bound to the p53 tumor2 suppressor transactivation domain
23	c2glfB_	Alignment	not modelled	9.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** crystal structure of aminipeptidase (m18 family) from thermotoga2 maritima
24	c3dacP_	Alignment	not modelled	9.4	33	**PDB header:**cell cycle **Chain:** P: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of the human mdmx protein bound to the p53 tumor2 suppressor transactivation domain
25	d1v6fa_	Alignment	not modelled	9.4	9	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Cofilin-like
26	c3a2aC_	Alignment	not modelled	9.3	69	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**voltage-gated hydrogen channel 1; **PDBTitle:** the structure of the carboxyl-terminal domain of the human voltage-2 gated proton channel hv1
27	d1flga_	Alignment	not modelled	7.8	23	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
28	d1xb4a1	Alignment	not modelled	7.7	43	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain

29	d1e42a2	Alignment	not modelled	7.4	5	**Fold:**Subdomain of clathrin and coatomer appendage domain **Superfamily:**Subdomain of clathrin and coatomer appendage domain **Family:**Clathrin adaptor appendage, alpha and beta chain-specific domain
30	c1xb4C_	Alignment	not modelled	7.1	43	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**hypothetical 23.6 kda protein in yuh1-ura8 **PDBTitle:** crystal structure of subunit vps25 of the endosomal2 trafficking complex escrt-ii
31	c2obnA_	Alignment	not modelled	7.1	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
32	d2bg1a1	Alignment	not modelled	7.0	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
33	d1lyva_	Alignment	not modelled	6.6	22	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
34	c3t38B_	Alignment	not modelled	6.5	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
35	d1ce7b2	Alignment	not modelled	6.4	31	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like
36	c2zmeD_	Alignment	not modelled	6.2	43	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vacuolar protein-sorting-associated protein 25; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
37	c1o7dE_	Alignment	not modelled	6.1	31	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
38	d1y7ea2	Alignment	not modelled	6.1	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
39	c3cuqD_	Alignment	not modelled	6.0	43	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vacuolar protein-sorting-associated protein 25; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
40	c2zkrl_	Alignment	not modelled	5.9	16	**PDB header:**ribosomal protein/rna **Chain:** L: **PDB Molecule:**rna expansion segment es20; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
41	d2c5wb1	Alignment	not modelled	5.7	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
42	c3aa0C_	Alignment	not modelled	5.6	63	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**21mer peptide from leucine-rich repeat-containing protein **PDBTitle:** crystal structure of actin capping protein in complex with the cp-2 binding motif derived from carmil
43	c2wmyH_	Alignment	not modelled	5.4	19	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**putative acid phosphatase wzb; **PDBTitle:** crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
44	c3lk2T_	Alignment	not modelled	5.2	63	**PDB header:**protein binding **Chain:** T: **PDB Molecule:**leucine-rich repeat-containing protein 16a; **PDBTitle:** crystal structure of capz bound to the uncapping motif from carmil
45	d1vqqa3	Alignment	not modelled	5.2	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
46	c3pp5A_	Alignment	not modelled	5.1	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**brk1; **PDBTitle:** high-resolution structure of the trimeric scar/wave complex precursor2 brk1
47	d2olua2	Alignment	not modelled	5.1	24	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase