Phyre2

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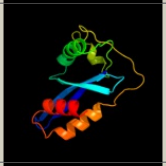
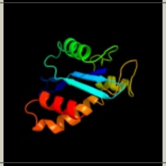
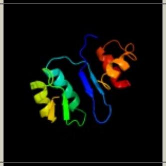
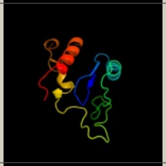
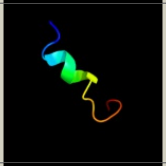
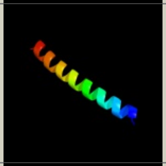
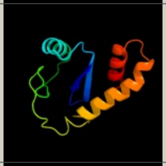
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1cxqa_	Alignment		96.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
2	d1hyva_	Alignment		96.7	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
3	d1exqa_	Alignment		96.5	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
4	d1asua_	Alignment		96.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
5	c1ex4A_	Alignment		94.8	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** hiv-1 integrase catalytic core and c-terminal domain
6	d1c6va_	Alignment		94.2	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
7	c1k6yB_	Alignment		94.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase
8	c3f9kV_	Alignment		93.2	12	**PDB header:**viral protein, recombination **Chain:** V: **PDB Molecule:**integrase; **PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd
9	d1c0ma2	Alignment		93.1	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
10	c3nf9A_	Alignment		92.6	17	**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
11	c1c0mA_	Alignment		89.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase

12	c3dlrA_	Alignment		88.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the catalytic core domain from pfv2 integrase
13	c1bcoA_	Alignment		84.0	10	**PDB header:**transposase **Chain:** A: **PDB Molecule:**bacteriophage mu transposase; **PDBTitle:** bacteriophage mu transposase core domain
14	d1bcoa2	Alignment		69.1	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**mu transposase, core domain
15	c3kksB_	Alignment		66.1	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
16	c2k8fB_	Alignment		45.4	29	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structural basis for the regulation of p53 function by p300
17	c3he5D_	Alignment		36.2	30	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**synzip2; **PDBTitle:** heterospecific coiled-coil pair synzip2:synzip1
18	c3hpgC_	Alignment		34.1	15	**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
19	c1q2iA_	Alignment		20.7	27	**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
20	c3l2tB_	Alignment		18.9	8	**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	d2olua2	Alignment	not modelled	18.4	14	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
22	c2l14B_	Alignment	not modelled	18.0	29	**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
23	d1nvpd2	Alignment	not modelled	16.6	38	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
24	d1st9a_	Alignment	not modelled	16.5	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
25	c3dwkC_	Alignment	not modelled	14.4	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
26	c2glfB_	Alignment	not modelled	13.4	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** crystal structure of aminipeptidase (m18 family) from thermotoga2 maritima
27	d1nh2d2	Alignment	not modelled	12.1	25	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
28	c3dacB_	Alignment	not modelled	10.8	36	**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
						PDB header:cell cycle

29	c3dacP_	Alignment	not modelled	10.7	36	**Chain:** P: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of the human mdmx protein bound to the p53 tumor2 suppressor transactivation domain
30	c2vknA_	Alignment	not modelled	10.4	4	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein ssu81; **PDBTitle:** yeast sho1 sh3 domain complexed with a peptide from pbs2
31	c1nvpD_	Alignment	not modelled	10.3	15	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia gamma chain; **PDBTitle:** human tfiia/tbp/dna complex
32	d1qnta2	Alignment	not modelled	9.8	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Methylated DNA-protein cysteine methyltransferase domain **Family:**Methylated DNA-protein cysteine methyltransferase domain
33	d1e42a2	Alignment	not modelled	9.7	6	**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
34	c3a2aC_	Alignment	not modelled	9.5	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
35	c3bpjD_	Alignment	not modelled	7.6	9	**PDB header:**translation **Chain:** D: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit j; **PDBTitle:** crystal structure of human translation initiation factor 3, subunit 12 alpha
36	c3pp5A_	Alignment	not modelled	7.0	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**brk1; **PDBTitle:** high-resolution structure of the trimeric scar/wave complex precursor2 brk1
37	c2juiA_	Alignment	not modelled	7.0	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**plne; **PDBTitle:** three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaracin ef
38	c3pf6C_	Alignment	not modelled	6.8	29	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein pp-luz7_gp033; **PDBTitle:** the structure of uncharacterized protein pp-luz7_gp033 from2 pseudomonas phage luz7.
39	d1y7ea2	Alignment	not modelled	6.6	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
40	d1v6fa_	Alignment	not modelled	6.4	9	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Cofilin-like
41	d1nc7a_	Alignment	not modelled	6.4	24	**Fold:**Hypothetical protein TM1070 **Superfamily:**Hypothetical protein TM1070 **Family:**Hypothetical protein TM1070
42	d1t1ea2	Alignment	not modelled	6.1	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
43	d2bg1a1	Alignment	not modelled	6.1	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
44	c3p8cE_	Alignment	not modelled	5.9	19	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**probable protein brick1; **PDBTitle:** structure and control of the actin regulatory wave complex
45	c2gljR_	Alignment	not modelled	5.7	11	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:** **PDBTitle:** crystal structure of aminopeptidase i from clostridium2 acetobutylicum
46	d1ce7b2	Alignment	not modelled	5.5	31	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like
47	d2je8a2	Alignment	not modelled	5.4	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain