Phyre2

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Description	P57998
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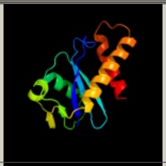
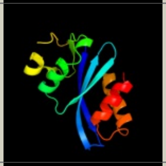
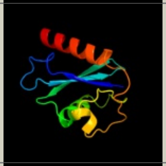
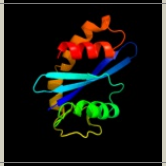
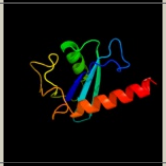
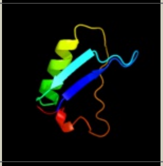
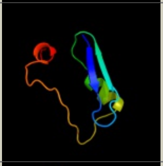
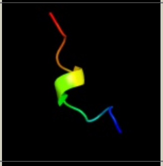
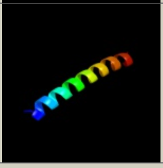
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1cxqa_	Alignment		98.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
2	d1hyva_	Alignment		98.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
3	d1exqa_	Alignment		97.6	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
4	d1asua_	Alignment		97.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
5	c1c0mA_	Alignment		97.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase
6	c1ex4A_	Alignment		97.1	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** hiv-1 integrase catalytic core and c-terminal domain
7	c3nf9A_	Alignment		96.9	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
8	d1c0ma2	Alignment		96.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
9	c3kksB_	Alignment		96.8	21	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of catalytic core domain of biv integrase in crystal2 form ii
10	c3f9kV_	Alignment		96.6	13	**PDB header:**viral protein, recombination **Chain:** V: **PDB Molecule:**integrase; **PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd
11	c1k6yB_	Alignment		96.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase

12	d1c6va_	Alignment		96.4	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
13	c3dlrA_	Alignment		93.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the catalytic core domain from pfv2 integrase
14	c3hpgC_	Alignment		92.7	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
15	c3l2tB_	Alignment		83.4	9	**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)
16	d1bcoa2	Alignment		49.1	4	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**mu transposase, core domain
17	c1bcoA_	Alignment		27.8	4	**PDB header:**transposase **Chain:** A: **PDB Molecule:**bacteriophage mu transposase; **PDBTitle:** bacteriophage mu transposase core domain
18	c1xb4C_	Alignment		27.0	38	**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
19	d1xb4a1	Alignment		24.1	41	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
20	c3he5D_	Alignment		23.2	30	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**synzip2; **PDBTitle:** heterospecific coiled-coil pair synzip2:synzip1
21	c3cuqD_	Alignment	not modelled	21.1	47	**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
22	c2zmeD_	Alignment	not modelled	20.6	47	**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
23	d1baia_	Alignment	not modelled	15.8	33	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Retroviral protease (retropepsin)
24	c2k8fB_	Alignment	not modelled	14.7	29	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structural basis for the regulation of p53 function by p300
25	c3a2aC_	Alignment	not modelled	11.6	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
26	c3e0jG_	Alignment	not modelled	11.5	26	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase subunit delta-2; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
27	c2zkrl_	Alignment	not modelled	10.8	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
						PDB header:hydrolase

28	c3bv6D_	Alignment	not modelled	10.5	11	**Chain:** D: **PDB Molecule:**metal-dependent hydrolase; **PDBTitle:** crystal structure of uncharacterized metallo protein from vibrio2 cholerae with beta-lactamase like fold
29	d1sgua_	Alignment	not modelled	9.8	20	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Retroviral protease (retropepsin)
30	d1v6fa_	Alignment	not modelled	9.3	16	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Cofilin-like
31	d1az5a_	Alignment	not modelled	9.3	20	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Retroviral protease (retropepsin)
32	d1nvpd2	Alignment	not modelled	9.2	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
33	d1gkra1	Alignment	not modelled	9.1	25	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
34	d2rspa_	Alignment	not modelled	9.1	29	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Retroviral protease (retropepsin)
35	d1lyva_	Alignment	not modelled	8.3	33	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
36	d1hvca_	Alignment	not modelled	7.4	30	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Retroviral protease (retropepsin)
37	d2jdid2	Alignment	not modelled	7.0	16	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
38	d2gu3a2	Alignment	not modelled	7.0	16	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**PepSY-like
39	d1mabb2	Alignment	not modelled	6.8	16	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
40	d1nh2d2	Alignment	not modelled	6.5	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
41	c2gu3A_	Alignment	not modelled	6.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ypmb protein; **PDBTitle:** ypmb protein from bacillus subtilis
42	d2bg1a1	Alignment	not modelled	6.4	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
43	d1y7ea2	Alignment	not modelled	6.2	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
44	c3lk3T_	Alignment	not modelled	6.1	38	**PDB header:**protein binding **Chain:** T: **PDB Molecule:**leucine-rich repeat-containing protein 16a; **PDBTitle:** crystal structure of capz bound to the cpi and csi uncapping2 motifs from carmil
45	d3c7bb2	Alignment	not modelled	5.9	36	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
46	d2c5wb1	Alignment	not modelled	5.8	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
47	c2j8oA_	Alignment	not modelled	5.8	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**titin; **PDBTitle:** structure of the immunoglobulin tandem repeat of titin a168-2 a169
48	c3gebC_	Alignment	not modelled	5.6	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**eyes absent homolog 2; **PDBTitle:** crystal structure of edeya2
49	c1tiiC_	Alignment	not modelled	5.5	44	**PDB header:**enterotoxin **Chain:** C: **PDB Molecule:**heat labile enterotoxin type iib; **PDBTitle:** escherichia coli heat labile enterotoxin type iib
50	d1nfga1	Alignment	not modelled	5.5	30	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
51	d2gycj1	Alignment	not modelled	5.4	27	**Fold:**Ribosomal proteins L15p and L18e **Superfamily:**Ribosomal proteins L15p and L18e **Family:**Ribosomal proteins L15p and L18e
52	c3c7bE_	Alignment	not modelled	5.3	40	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
53	d1flga_	Alignment	not modelled	5.2	28	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
54	d4fiva_	Alignment	not modelled	5.2	15	**Fold:**Acid proteases **Superfamily:**Acid proteases

						Family: Retroviral protease (retropepsin)
55	c3t38B_	Alignment	not modelled	5.1	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'