Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2810c_(-)_3115751_3116149
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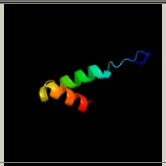
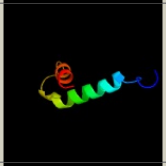
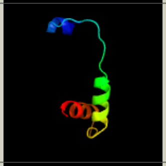
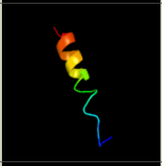
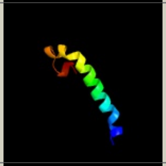
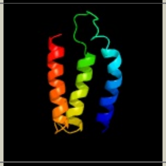
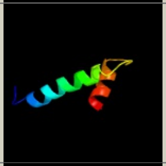
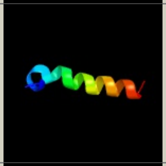
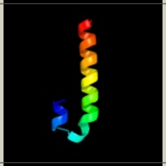
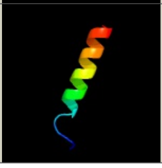
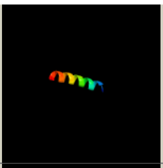
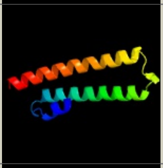
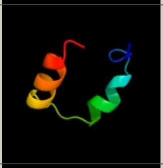
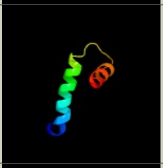
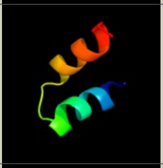
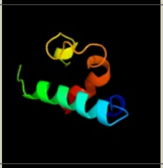
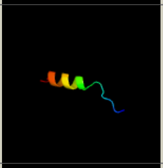
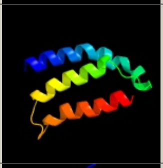
Unique Job ID	bdb6a67ca11041a3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hyva_	Alignment		64.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
2	c3f9kV_	Alignment		52.3	18	**PDB header:**viral protein, recombination **Chain:** V: **PDB Molecule:**integrase; **PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd
3	c1k6yB_	Alignment		46.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase
4	c1ex4A_	Alignment		35.5	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** hiv-1 integrase catalytic core and c-terminal domain
5	c5cz1B_	Alignment		32.3	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of the catalytic core domain of mmtv integrase
6	c3nf9A_	Alignment		28.9	15	**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
7	d1st6a4	Alignment		25.1	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
8	c4mq3A_	Alignment		24.8	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** the 1.1 angstrom structure of catalytic core domain of fiv integrase
9	c5u1cA_	Alignment		24.6	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hiv-1 integrase, sso7d chimera; **PDBTitle:** structure of tetrameric hiv-1 strand transfer complex intasome
10	d2oc5a1	Alignment		23.3	29	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**PMT1231-like
11	d1asua_	Alignment		20.9	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain

12	c5m0rF_	Alignment		19.8	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**integrase; **PDBTitle:** cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
13	d3d19a2	Alignment		19.7	4	**Fold:**Bromodomain-like **Superfamily:**Bacillus cereus metalloprotein-like **Family:**Bacillus cereus metalloprotein-like
14	d1t06a_	Alignment		18.6	7	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**BC3264-like
15	c3jcaE_	Alignment		17.5	13	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**integrase; **PDBTitle:** core model of the mouse mammary tumor virus intasome
16	c2da7A_	Alignment		16.2	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc finger homeobox protein 1b; **PDBTitle:** solution structure of the homeobox domain of zinc finger2 homeobox protein 1b (smad interacting protein 1)
17	c6ivuB_	Alignment		15.6	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rna polymerase sigma factor sigi1; **PDBTitle:** solution structure of the sigma-anti-sigma factor complex rsgi1n-2 sigi1c from clostridium thermocellum
18	d1cxqa_	Alignment		15.1	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
19	d1st6a3	Alignment		15.0	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
20	d1k8ba_	Alignment		13.6	18	**Fold:**Ribosome binding domain-like **Superfamily:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain **Family:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain
21	c2dn0A_	Alignment	not modelled	12.3	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3; **PDBTitle:** solution structure of the second homeobox domain of human2 zinc fingers and homeoboxes protein 3
22	c5uwzA_	Alignment	not modelled	12.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldehyde decarbonylase; **PDBTitle:** protein 12 with aldehyde deformylating oxygenase activity from2 gloeobacter violaceus
23	c2e19A_	Alignment	not modelled	11.6	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor 8; **PDBTitle:** solution structure of the homeobox domain from human nil-2-2 a zinc finger protein, transcription factor 8
24	c1c0mA_	Alignment	not modelled	10.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase
25	c2e9hA_	Alignment	not modelled	9.4	24	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
26	c3kksB_	Alignment	not modelled	8.9	18	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of catalytic core domain of biv integrase in crystal2 form ii
27	c2da2A_	Alignment	not modelled	8.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
28	d1exqa_	Alignment	not modelled	8.7	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain

29	c4quwA_	Alignment	not modelled	8.6	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldehyde decarbonylase; **PDBTitle:** crystal structure of the apo form of cyanobacterial aldehyde-2 deformylating oxygenase
30	c3nauA_	Alignment	not modelled	8.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 2; **PDBTitle:** crystal structure of zhx2 hd2 (zinc-fingers and homeoboxes protein 2,2 homeodomain 2)
31	c2vlaA_	Alignment	not modelled	8.3	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease r.bpuji; **PDBTitle:** crystal structure of restriction endonuclease bpuji recognition domain2 in complex with cognate dna
32	d1e3oc2	Alignment	not modelled	8.2	39	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
33	d1au7a1	Alignment	not modelled	8.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
34	d2ecba1	Alignment	not modelled	8.2	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
35	c2dmqA_	Alignment	not modelled	8.2	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**lim/homeobox protein lhx9; **PDBTitle:** solution structure of the homeobox domain of lim/homeobox2 protein lhx9
36	d1au7a2	Alignment	not modelled	8.0	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
37	d1dl5a2	Alignment	not modelled	7.5	23	**Fold:**Protein-L-isoaspartyl O-methyltransferase, C-terminal domain **Superfamily:**Protein-L-isoaspartyl O-methyltransferase, C-terminal domain **Family:**Protein-L-isoaspartyl O-methyltransferase, C-terminal domain
38	d1gt0c1	Alignment	not modelled	7.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
39	d1o4xa1	Alignment	not modelled	7.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
40	c2da1A_	Alignment	not modelled	7.4	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
41	d2gtsa1	Alignment	not modelled	7.4	16	**Fold:**Ferritin-like **Superfamily:**HP0062-like **Family:**HP0062-like
42	c2dmuA_	Alignment	not modelled	7.3	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein goosecoid; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein goosecoid
43	c3cqxD_	Alignment	not modelled	7.0	19	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**bag family molecular chaperone regulator 2; **PDBTitle:** chaperone complex
44	c1lv4A_	Alignment	not modelled	6.9	57	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**catestatin; **PDBTitle:** human catestatin 21-mer
45	c2dmpA_	Alignment	not modelled	6.9	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 2; **PDBTitle:** solution structure of the third homeobox domain of zinc2 fingers and homeoboxes protein 2
46	c3n5nX_	Alignment	not modelled	6.8	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**a/g-specific adenine dna glycosylase; **PDBTitle:** crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
47	c3l1pA_	Alignment	not modelled	6.8	24	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pou domain, class 5, transcription factor 1; **PDBTitle:** pou protein:dna complex
48	d1c0ma2	Alignment	not modelled	6.8	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
49	d1du0a_	Alignment	not modelled	6.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
50	c1au7B_	Alignment	not modelled	6.7	13	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**protein pit-1; **PDBTitle:** pit-1 mutant/dna complex
51	c2ly9A_	Alignment	not modelled	6.7	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** solution nmr structure of homeobox 2 domain from human zhx1 repressor,2 northeast structural genomics consortium (nesg) target hr7907f
52	c3d1nK_	Alignment	not modelled	6.6	12	**PDB header:**transcription regulator/dna **Chain:** K: **PDB Molecule:**pou domain, class 6, transcription factor 1; **PDBTitle:** structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
53	c2dmsA_	Alignment	not modelled	6.6	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein otx2; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein otx2
54	d1ig7a_	Alignment	not modelled	6.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain

55	c2da3A_	Alignment	not modelled	6.4	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the third homeobox domain of at-2 binding transcription factor 1 (atbf1)
56	c3aq3A_	Alignment	not modelled	6.4	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**6b protein; **PDBTitle:** molecular insights into plant cell proliferation disturbance by2 agrobacterium protein 6b
57	d2craa1	Alignment	not modelled	6.3	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
58	d1e3oc1	Alignment	not modelled	6.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
59	d1octc1	Alignment	not modelled	6.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
60	c3a32A_	Alignment	not modelled	6.1	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**probable threonyl-trna synthetase 1; **PDBTitle:** crystal structure of putative threonyl-trna synthetase thrrs-1 from2 aeropyrum pernix
61	d1x2ma1	Alignment	not modelled	6.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
62	d2awia1	Alignment	not modelled	6.0	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**PrgX N-terminal domain-like
63	d1s7ea1	Alignment	not modelled	6.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
64	d2ecca1	Alignment	not modelled	5.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
65	c2vi6F_	Alignment	not modelled	5.8	19	**PDB header:**transcription **Chain:** F: **PDB Molecule:**homeobox protein nanog; **PDBTitle:** crystal structure of the nanog homeodomain
66	d1p7ia_	Alignment	not modelled	5.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
67	c3a03A_	Alignment	not modelled	5.7	22	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**t-cell leukemia homeobox protein 2; **PDBTitle:** crystal structure of hox11l1 homeodomain
68	d1uhsa_	Alignment	not modelled	5.6	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
69	c2da5A_	Alignment	not modelled	5.4	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3; **PDBTitle:** solution structure of the second homeobox domain of zinc2 fingers and homeoboxes protein 3 (triple homeobox 13 protein)
70	c2dmtA_	Alignment	not modelled	5.3	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein barh-like 1; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein barh-like 1
71	c2l9rA_	Alignment	not modelled	5.3	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein nkx-3.1; **PDBTitle:** solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
72	c2mg4B_	Alignment	not modelled	5.3	15	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**computational designed homodimer; **PDBTitle:** computational design and experimental verification of a symmetric2 protein homodimer
73	d1aepa_	Alignment	not modelled	5.2	25	**Fold:**Apolipophorin-III **Superfamily:**Apolipophorin-III **Family:**Apolipophorin-III
74	c1ezeA_	Alignment	not modelled	5.2	26	**PDB header:**transferase inhibitor **Chain:** A: **PDB Molecule:**cholesteryl ester transferase inhibitor protein; **PDBTitle:** structural studies of a baboon (papio sp.) plasma protein2 inhibitor of cholesteryl ester transferase.
75	d9anta_	Alignment	not modelled	5.1	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
76	d1fngb2	Alignment	not modelled	5.1	21	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain