
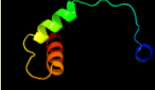







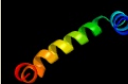

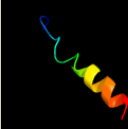



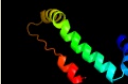



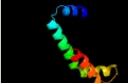


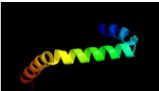










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0741 (-) _832537_832851
Date	Fri Jul 26 01:50:31 BST 2019
Unique Job ID	885fac8db5890d74

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1k6yB_	 Alignment		57.4	14	PDB header: transferase Chain: B; PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
2	d1hyva_	 Alignment		55.1	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
3	c3f9kV_	 Alignment		53.1	15	PDB header: viral protein, recombination Chain: V; PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
4	c4mq3A_	 Alignment		30.8	19	PDB header: viral protein Chain: A; PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
5	c2h5gA_	 Alignment		30.3	18	PDB header: oxidoreductase Chain: A; PDB Molecule: delta 1-pyrroline-5-carboxylate synthetase; PDBTitle: crystal structure of human pyrroline-5-carboxylate synthetase
6	c1ex4A_	 Alignment		29.9	23	PDB header: viral protein Chain: A; PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
7	c2dmnA_	 Alignment		27.8	17	PDB header: transcription Chain: A; PDB Molecule: homeobox protein tgif2lx; PDBTitle: the solution structure of the homeobox domain of human2 homeobox protein tgif2lx
8	d1o20a_	 Alignment		27.8	14	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
9	c3nf9A_	 Alignment		27.4	18	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	c3k9dD_	 Alignment		26.7	9	PDB header: oxidoreductase Chain: D; PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e
11	d1e3oc1	 Alignment		25.7	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain

12	c1vluB	Alignment		25.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: gamma-glutamyl phosphate reductase; PDBTitle: crystal structure of gamma-glutamyl phosphate reductase (yor323c) from2 saccharomyces cerevisiae at 2.40 a resolution
13	c5kw2A	Alignment		25.6	12	PDB header: fatty acid binding protein/hydrolase Chain: A: PDB Molecule: free fatty acid receptor 1,lysozyme,free fatty acid PDBTitle: the extra-helical binding site of gpr40 and the structural basis for2 allosteric agonism and incretin stimulation
14	d1akha	Alignment		25.2	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
15	c2dmpA	Alignment		24.9	15	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
16	c5cz1B	Alignment		24.5	14	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
17	c4jbeA	Alignment		24.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: gamma-glutamyl phosphate reductase; PDBTitle: 1.95 angstrom crystal structure of gamma-glutamyl phosphate reductase2 from saccharomonospora viridis.
18	c5j78B	Alignment		24.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: acetaldehyde dehydrogenase (acetylating); PDBTitle: crystal structure of an acetylating aldehyde dehydrogenase from2 geobacillus thermoglucosidasius
19	d1dl5a2	Alignment		24.1	31	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
20	d1hlva2	Alignment		22.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
21	c2da1A	Alignment	not modelled	22.7	9	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)
22	d1o4xa1	Alignment	not modelled	21.6	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
23	c5ifgC	Alignment	not modelled	21.4	11	PDB header: hydrolase/antitoxin Chain: C: PDB Molecule: mrna interferase higb; PDBTitle: crystal structure of higa-higb complex from e. coli
24	d1vlua	Alignment	not modelled	20.4	12	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
25	c4qgkB	Alignment	not modelled	20.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty aldehyde dehydrogenase; PDBTitle: structure of the human sjogren larsson syndrome enzyme fatty aldehyde2 dehydrogenase (faldh)
26	c2dmqA	Alignment	not modelled	19.9	5	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
27	c2dn0A	Alignment	not modelled	19.3	9	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
28	c3nauA	Alignment	not modelled	19.1	13	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)
						Fold: DNA/RNA-binding 3-helical bundle

29	d1gt0c1	Alignment	not modelled	17.8	9	Superfamily: Homeodomain-like Family: Homeodomain
30	d1asua	Alignment	not modelled	17.8	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
31	c5m0rF	Alignment	not modelled	17.2	18	PDB header: hydrolase Chain: F: PDB Molecule: integrase; PDBTitle: cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
32	c2da7A	Alignment	not modelled	17.1	2	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)
33	c4kkkA	Alignment	not modelled	16.4	38	PDB header: hydrolase Chain: A: PDB Molecule: exoglucanase s; PDBTitle: complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
34	c2dmtA	Alignment	not modelled	16.3	12	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
35	d1cxqa	Alignment	not modelled	15.7	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
36	d1au7a1	Alignment	not modelled	15.7	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
37	c4ghkB	Alignment	not modelled	15.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: gamma-glutamyl phosphate reductase; PDBTitle: x-ray crystal structure of gamma-glutamyl phosphate reductase from2 burkholderia thailandensis
38	d2ecba1	Alignment	not modelled	15.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
39	c5u1cA	Alignment	not modelled	15.1	16	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
40	c2da2A	Alignment	not modelled	14.6	9	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)
41	c2da5A	Alignment	not modelled	14.4	15	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)
42	c4fusA	Alignment	not modelled	14.3	31	PDB header: hydrolase Chain: A: PDB Molecule: rtx toxins and related ca2+-binding protein; PDBTitle: the x-ray structure of hahella chejuensis family 48 glycosyl hydrolase
43	d2ecca1	Alignment	not modelled	14.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
44	d1ad3a	Alignment	not modelled	14.2	20	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
45	c2dmuA	Alignment	not modelled	14.1	11	PDB header: dna binding protein Chain: A: PDB Molecule: homeobox protein gooseoid; PDBTitle: solution structure of the homeobox domain of homeobox2 protein gooseoid
46	c4plaA	Alignment	not modelled	14.1	10	PDB header: transferase,hydrolase Chain: A: PDB Molecule: chimera protein of phosphatidylinositol 4-kinase type 2- PDBTitle: crystal structure of phosphatidyl inositol 4-kinase ii alpha in2 complex with atp
47	c2da3A	Alignment	not modelled	14.0	7	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)
48	d1p7ia	Alignment	not modelled	13.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
49	c3my7A	Alignment	not modelled	13.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase/acetalddehyde dehydrogenase; PDBTitle: the crystal structure of the acdh domain of an alcohol dehydrogenase2 from vibrio parahaemolyticus to 2.25a
50	d1le8a	Alignment	not modelled	12.9	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
51	d1ez0a	Alignment	not modelled	12.5	10	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
52	c3jcaE	Alignment	not modelled	12.3	26	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
53	c5z2tC	Alignment	not modelled	12.1	18	PDB header: dna binding protein/dna Chain: C: PDB Molecule: double homeobox protein 4; PDBTitle: crystal structure of dna-bound dux4-hd2
						PDB header: hydrolase

54	c4jiiA_	Alignment	not modelled	12.0	31	Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of t. fusca gh48 d224n mutant
55	d1exqa_	Alignment	not modelled	12.0	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
56	d1octc1_	Alignment	not modelled	11.9	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
57	c5nnoA_	Alignment	not modelled	11.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of tbalhd3 complexed with nad and an3057 aldehyde
58	c4txyA_	Alignment	not modelled	11.7	7	PDB header: transferase Chain: A: PDB Molecule: cyclic amp-gmp synthase; PDBTitle: crystal structure of vibrio cholerae dncv cyclic amp-gmp synthase, a2 prokaryotic cgas homolog
59	c1l2aD_	Alignment	not modelled	11.6	19	PDB header: hydrolase Chain: D: PDB Molecule: cellobiohydrolase; PDBTitle: the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
60	d1l1ya_	Alignment	not modelled	11.6	19	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
61	c3narA_	Alignment	not modelled	11.5	16	PDB header: transcription Chain: A: PDB Molecule: zinc fingers and homeoboxes protein 1; PDBTitle: crystal structure of zhx1 hd4 (zinc-fingers and homeoboxes protein 1,2 homeodomain 4)
62	d2hddb_	Alignment	not modelled	11.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
63	d1g9ga_	Alignment	not modelled	11.5	31	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
64	c2wwbB_	Alignment	not modelled	11.5	19	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sec61 subunit gamma; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
65	c2mg4B_	Alignment	not modelled	11.5	23	PDB header: de novo protein Chain: B: PDB Molecule: computational designed homodimer; PDBTitle: computational design and experimental verification of a symmetric2 protein homodimer
66	c4el8A_	Alignment	not modelled	11.4	19	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 48; PDBTitle: the unliganded structure of c.bescii cela gh48 module
67	c3pqaA_	Alignment	not modelled	11.3	10	PDB header: oxidoreductase Chain: A: PDB Molecule: lactaldehyde dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
68	c5hodD_	Alignment	not modelled	11.3	7	PDB header: transcription Chain: D: PDB Molecule: lim/homeobox protein lhx4; PDBTitle: structure of lhx4 transcription factor complexed with dna
69	c3dntB_	Alignment	not modelled	11.1	14	PDB header: transferase Chain: B: PDB Molecule: protein hipa; PDBTitle: structures of mdt proteins
70	c2ly9A_	Alignment	not modelled	10.9	9	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
71	c4itaA_	Alignment	not modelled	10.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate-semialdehyde dehydrogenase; PDBTitle: structure of bacterial enzyme in complex with cofactor
72	c2dmsA_	Alignment	not modelled	10.8	14	PDB header: dna binding protein Chain: A: PDB Molecule: homeobox protein otx2; PDBTitle: solution structure of the homeobox domain of homeobox2 protein otx2
73	c2zqeA_	Alignment	not modelled	10.7	18	PDB header: dna binding protein Chain: A: PDB Molecule: smuts2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus muts2
74	c1hf0A_	Alignment	not modelled	10.6	9	PDB header: transcription Chain: A: PDB Molecule: octamer-binding transcription factor 1; PDBTitle: crystal structure of the dna-binding domain of oct-1 bound to dna as a2 dimer
75	c2hjmB_	Alignment	not modelled	10.1	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein pf1176; PDBTitle: crystal structure of a singleton protein pf1176 from p. furiosus
76	c4ochA_	Alignment	not modelled	9.9	21	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease muts2; PDBTitle: apo structure of smr domain of muts2 from deinococcus radiodurans
77	c3qanB_	Alignment	not modelled	9.7	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-pyrroline-5-carboxylate dehydrogenase 1; PDBTitle: crystal structure of 1-pyrroline-5-carboxylate dehydrogenase from2 bacillus halodurans
78	d1yrnb_	Alignment	not modelled	9.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
79	d3d19a2_	Alignment	not modelled	9.4	3	Fold: Bromodomain-like Superfamily: Bacillus cereus metalloprotein-like

						Family: Bacillus cereus metalloprotein-like
80	c2e19A_	Alignment	not modelled	9.4	5	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
81	c3lnsD_	Alignment	not modelled	9.2	13	PDB header: oxidoreductase Chain: D: PDB Molecule: benzaldehyde dehydrogenase; PDBTitle: benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
82	d1f43a_	Alignment	not modelled	9.2	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
83	c1c0mA_	Alignment	not modelled	9.0	20	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
84	c1ezeA_	Alignment	not modelled	9.0	4	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.
85	c4xesA_	Alignment	not modelled	8.9	12	PDB header: signaling protein, hydrolase Chain: A: PDB Molecule: neurotensin receptor type 1, endolysin chimera; PDBTitle: structure of active-like neurotensin receptor
86	c3efvC_	Alignment	not modelled	8.9	5	PDB header: oxidoreductase Chain: C: PDB Molecule: putative succinate-semialdehyde dehydrogenase; PDBTitle: crystal structure of a putative succinate-semialdehyde dehydrogenase2 from salmonella typhimurium lt2 with bound nad
87	d1ocpa_	Alignment	not modelled	8.8	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
88	c4c3sA_	Alignment	not modelled	8.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of a propionaldehyde dehydrogenase from the clostridium2 phytofermentans fucose utilisation bacterial microcompartment
89	d1lvaa4	Alignment	not modelled	8.8	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
90	d1wnda_	Alignment	not modelled	8.8	16	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
91	c2jg7G_	Alignment	not modelled	8.6	7	PDB header: oxidoreductase Chain: G: PDB Molecule: antiquitin; PDBTitle: crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
92	c2pjpA_	Alignment	not modelled	8.6	12	PDB header: translation/rna Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
93	c2d4eB_	Alignment	not modelled	8.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 5-carboxymethyl-2-hydroxyuconate semialdehyde PDBTitle: crystal structure of the hpcc from thermus thermophilus hb8
94	c1t90B_	Alignment	not modelled	8.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: probable methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of methylmalonate semialdehyde dehydrogenase from2 bacillus subtilis
95	c4ohtB_	Alignment	not modelled	8.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate-semialdehyde dehydrogenase; PDBTitle: crystal structure of succinic semialdehyde dehydrogenase from2 streptococcus pyogenes in complex with nadp+ as the cofactor
96	d1a4sa_	Alignment	not modelled	8.4	25	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
97	c3kksB_	Alignment	not modelled	8.2	14	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii
98	c4dalB_	Alignment	not modelled	8.2	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative aldehyde dehydrogenase; PDBTitle: crystal structure of putative aldehyde dehydrogenase from2 sinorhizobium meliloti 1021
99	c5zbqA_	Alignment	not modelled	8.2	12	PDB header: signaling protein Chain: A: PDB Molecule: neuropeptide y receptor type 1,t4 lysozyme; PDBTitle: the crystal structure of human neuropeptide y y1 receptor with ur-2 mk299