



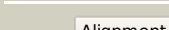

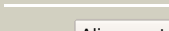
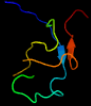



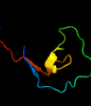

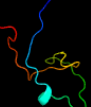


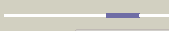


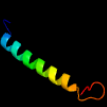

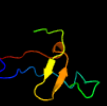


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0235c_(-)_281166_282614
Date	Tue Jul 23 14:50:29 BST 2019
Unique Job ID	1280c3245bfd239

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dmoA_	 Alignment		35.4	28	PDB header: signaling protein Chain: A: PDB Molecule: neutrophil cytosol factor 2; PDBTitle: refined solution structure of the 1st sh3 domain from human2 neutrophil cytosol factor 2 (ncf-2)
2	c4rdbA_	 Alignment		28.2	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: immunoreactive 32 kda antigen pg49; PDBTitle: crystal structure of an immunoreactive 32 kda antigen pg49 (pg_0181)2 from porphyromonas gingivalis w83 at 1.45 a resolution (psi community3 target, nakayama)
3	d1tvxA_	 Alignment		25.9	17	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
4	c2eqiA_	 Alignment		24.0	30	PDB header: immune system, hydrolase Chain: A: PDB Molecule: phospholipase c, gamma 2; PDBTitle: solution structure of the sh3 domain from phospholipase c,2 gamma 2
5	c3hx6A_	 Alignment		21.6	21	PDB header: cell adhesion Chain: A: PDB Molecule: type 4 fimbrial biogenesis protein pily1; PDBTitle: crystal structure of pseudomonas aeruginosa pily1 c-terminal2 domain
6	d1ue9a_	 Alignment		21.5	27	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
7	c2dbkA_	 Alignment		20.6	20	PDB header: signaling protein Chain: A: PDB Molecule: crk-like protein; PDBTitle: solution structures of the sh3 domain of human crk-like2 protein
8	d1tvxB_	 Alignment		20.0	17	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
9	c3wmmY_	 Alignment		18.8	23	PDB header: photosynthesis Chain: Y: PDB Molecule: lh1 alpha polypeptide; PDBTitle: crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
10	c6et5b_	 Alignment		18.8	17	PDB header: photosynthesis Chain: B: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
11	c2d8hA_	 Alignment		16.9	24	PDB header: unknown function Chain: A: PDB Molecule: sh3yl1 protein; PDBTitle: solution structure of the sh3 domain of hypothetical2 protein sh3yl1

12	c3h35B_	Alignment		16.8	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein abo_0056; PDBTitle: structure of the uncharacterized protein abo_0056 from the2 hydrocarbon-degrading marine bacterium alcanivorax borkumensis sk2.
13	c2eyxA_	Alignment		16.8	25	PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog PDBTitle: c-terminal sh3 domain of ct10-regulated kinase
14	c1xrdA_	Alignment		16.8	28	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, alpha chain; PDBTitle: light-harvesting complex 1 alfa subunit from wild-type2 rhodospirillum rubrum
15	d1xrdA1	Alignment		16.8	28	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
16	d1w7ca2	Alignment		16.5	32	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
17	c4z8aA_	Alignment		15.9	27	PDB header: rim-binding protein Chain: A: PDB Molecule: rim-binding protein, isoform f; PDBTitle: sh3-iii of drosophila rim-binding protein bound to a cacophony derived2 peptide
18	c2k2mA_	Alignment		15.6	27	PDB header: signaling protein Chain: A: PDB Molecule: eps8-like protein 1; PDBTitle: structural basis of pxxdy motif recognition in sh3 binding
19	c4d11B_	Alignment		14.4	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase, putative, bgl35a; PDBTitle: the structure of the gh35 beta-galactosidase bgl35a from2 cellvibrio japonicus
20	c4zadB_	Alignment		14.2	19	PDB header: lyase Chain: B: PDB Molecule: fdc1; PDBTitle: structure of c. dubliensis fdc1 with the prenylated-flavin cofactor in2 the iminium form.
21	c4lmgD_	Alignment	not modelled	13.6	41	PDB header: transcription activator/dna Chain: D: PDB Molecule: iron-regulated transcriptional activator aft2; PDBTitle: crystal structure of aft2 in complex with dna
22	d111ca_	Alignment	not modelled	13.0	39	Fold: GroES-like Superfamily: SacY-like RNA-binding domain Family: BglG-like antiterminator proteins
23	c3jtzA_	Alignment	not modelled	12.0	21	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: structure of the arm-type binding domain of hpi integrase
24	c4tkrB_	Alignment	not modelled	11.9	5	PDB header: membrane protein Chain: B: PDB Molecule: thiamine transporter thia; PDBTitle: native-sad phasing for thit from listeria monocytogenes serovar.
25	c5douC_	Alignment	not modelled	11.9	24	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
26	c2eyyA_	Alignment	not modelled	11.4	19	PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog PDBTitle: ct10-regulated kinase isoform i
27	d1f9pa_	Alignment	not modelled	11.2	17	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
28	c3j8eG_	Alignment	not modelled	10.8	23	PDB header: transport protein/isomerase Chain: G: PDB Molecule: ryanodine receptor 1; PDBTitle: cryo-em structure of ryanodine receptor/calstabin-2 complex
						PDB header: lyase Chain: A: PDB Molecule: ...

29	c4za5A_	Alignment	not modelled	10.5	22	Chain: A; PDB Molecule: 1tdc1; PDBTitle: structure of a. niger fdc1 with the prenylated-flavin cofactor in the2 iminium and ketimine forms.
30	c2dl3A_	Alignment	not modelled	10.0	28	PDB header: cell adhesion, signaling protein Chain: A; PDB Molecule: sorbin and sh3 domain-containing protein 1; PDBTitle: solution structure of the first sh3 domain of human sorbin2 and sh3 domain-containing protein 1
31	c3ju0A_	Alignment	not modelled	9.9	19	PDB header: dna binding protein Chain: A; PDB Molecule: phage integrase; PDBTitle: structure of the arm-type binding domain of hai7 integrase
32	c5lxyH_	Alignment	not modelled	9.9	25	PDB header: rna binding protein Chain: H; PDB Molecule: zinc finger cchc domain-containing protein 8; PDBTitle: structure of the minimal rbm7 - zcchc8 complex
33	c5kp0A_	Alignment	not modelled	9.5	20	PDB header: chaperone Chain: A; PDB Molecule: flagellar protein flit,flagellum-specific atp synthase; PDBTitle: recognition and targeting mechanisms by chaperones in flagella2 assembly and operation
34	c5zwo0_	Alignment	not modelled	9.3	21	PDB header: splicing Chain: 0; PDB Molecule: pre-mrna-splicing factor 38; PDBTitle: cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
35	d1plfa_	Alignment	not modelled	8.9	24	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
36	c2rvbA_	Alignment	not modelled	8.0	25	PDB header: dna binding protein/transcription Chain: A; PDB Molecule: dna repair protein complementing xpc-c cells; PDBTitle: solution structure of the complex between xpc acidic domain and tfih2 p62 ph domain
37	c6hu9U_	Alignment	not modelled	7.8	26	PDB header: oxidoreductase/electron transport Chain: U; PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
38	c2okmA_	Alignment	not modelled	7.7	36	PDB header: cell adhesion Chain: A; PDB Molecule: collagen adhesin; PDBTitle: crystal structure of ace19, the collagen binding subdomain2 of enterococcus faecalis surface protein ace
39	c5k4bA_	Alignment	not modelled	7.7	26	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 3 subunit d; PDBTitle: structure of eukaryotic translation initiation factor 3 subunit d2 (eif3d) cap binding domain from nasonia vitripennis, crystal form 1
40	c1wxtA_	Alignment	not modelled	7.4	28	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein flj21522; PDBTitle: solution structure of the sh3 domain of human hypothetical2 protein flj21522
41	d1sq4a_	Alignment	not modelled	7.4	23	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ylba-like
42	c2i0nA_	Alignment	not modelled	7.3	18	PDB header: structural protein Chain: A; PDB Molecule: class vii unconventional myosin; PDBTitle: structure of dictyostelium discoideum myosin vii sh3 domain2 with adjacent proline rich region
43	d1oqya3	Alignment	not modelled	7.2	17	Fold: XPC-binding domain Superfamily: XPC-binding domain Family: XPC-binding domain
44	c5eykD_	Alignment	not modelled	7.2	44	PDB header: transferase Chain: D; PDB Molecule: inner centromere protein a; PDBTitle: crystal structure of aurora b in complex with bi 847325
45	c4rz9A_	Alignment	not modelled	7.2	17	PDB header: rna binding protein Chain: A; PDB Molecule: pre-mrna-splicing factor 38a; PDBTitle: pre-mrna-splicing factor 38a as 1-179
46	c2js0A_	Alignment	not modelled	7.1	15	PDB header: signaling protein Chain: A; PDB Molecule: cytoplasmic protein nck1; PDBTitle: solution structure of second sh3 domain of adaptor nck
47	c5muul_	Alignment	not modelled	7.0	26	PDB header: virus Chain: I; PDB Molecule: major outer capsid protein; PDBTitle: dsrna bacteriophage phi6 nucleocapsid
48	c5l2xA_	Alignment	not modelled	6.9	43	PDB header: transferase/dna Chain: A; PDB Molecule: dna-directed primase/polymerase protein; PDBTitle: crystal structure of human primpol ternary complex
49	c6h6vF_	Alignment	not modelled	6.9	29	PDB header: flavoprotein Chain: F; PDB Molecule: 3-polyprenyl-4-hydroxybenzoate decarboxylase and related PDBTitle: structure of the ubid-class enzyme hmff from pelotomaculum2 thermopropionicum in complex with fmn
50	c2ed1A_	Alignment	not modelled	6.8	20	PDB header: signaling protein Chain: A; PDB Molecule: 130 kda phosphatidylinositol 4,5-biphosphate- PDBTitle: solution structure of the sh3 domain of 130 kda2 phosphatidylinositol 4,5-biphosphate-dependent arf1 gtpase-3 activating protein
51	c2z2sD_	Alignment	not modelled	6.5	25	PDB header: transcription Chain: D; PDB Molecule: anti-sigma factor chrr, transcriptional activator chrr; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
52	d1iowa1	Alignment	not modelled	6.4	25	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
53	c4qpwA_	Alignment	not modelled	6.4	26	PDB header: hydrolase Chain: A; PDB Molecule: glycosyl hydrolase family 10;

						PDBTitle: bixyn10a cbm1 with xylohexaose bound
54	d1pfma_	Alignment	not modelled	6.0	18	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
55	c3h3pT_	Alignment	not modelled	6.0	20	PDB header: immune system Chain: T: PDB Molecule: 4e10_s0_1tjlc_004_n; PDBTitle: crystal structure of hiv epitope-scaffold 4e10 fv complex
56	d1pvea_	Alignment	not modelled	6.0	17	Fold: XPC-binding domain Superfamily: XPC-binding domain Family: XPC-binding domain
57	d2nn6g3	Alignment	not modelled	6.0	17	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
58	c3qc7A_	Alignment	not modelled	5.8	42	PDB header: viral protein Chain: A: PDB Molecule: head fiber protein; PDBTitle: the structure of bacteriophage phi29 head fibers has a supercoiled2 triple repeating helix-turn-helix motif
59	d1roda_	Alignment	not modelled	5.8	20	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
60	c3dwmA_	Alignment	not modelled	5.8	13	PDB header: transferase Chain: A: PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
61	d1ofcx3	Alignment	not modelled	5.8	25	Fold: HAND domain of the nucleosome remodeling ATPase ISWI Superfamily: HAND domain of the nucleosome remodeling ATPase ISWI Family: HAND domain of the nucleosome remodeling ATPase ISWI
62	d1f9ra_	Alignment	not modelled	5.8	18	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
63	c3h3mB_	Alignment	not modelled	5.8	35	PDB header: structural genomics Chain: B: PDB Molecule: flagellar protein flit; PDBTitle: crystal structure of flagellar protein flit from bordetella2 bronchiseptica
64	d2f4mb1	Alignment	not modelled	5.7	17	Fold: XPC-binding domain Superfamily: XPC-binding domain Family: XPC-binding domain
65	c4hi2B_	Alignment	not modelled	5.7	35	PDB header: hydrolase Chain: B: PDB Molecule: acylphosphatase; PDBTitle: crystal structure of an acylphosphatase protein cage
66	c2l9dA_	Alignment	not modelled	5.6	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the protein yp_546394.1, the first structural2 representative of the pfam family pf12112
67	c2kc1A_	Alignment	not modelled	5.6	13	PDB header: structural protein Chain: A: PDB Molecule: mkiaa1027 protein; PDBTitle: nmr structure of the f0 domain (residues 0-85) of the talin2 ferm domain
68	c1xtcC_	Alignment	not modelled	5.5	24	PDB header: toxin Chain: C: PDB Molecule: cholera toxin; PDBTitle: cholera toxin
69	c2p4gA_	Alignment	not modelled	5.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a pyrimidine reductase-like protein (dip1392)2 from corynebacterium diphtheriae nctc at 2.30 a resolution
70	c3vzaE_	Alignment	not modelled	5.5	33	PDB header: cell cycle Chain: E: PDB Molecule: centromere protein t; PDBTitle: crystal structure of the chicken spc24-spc25 globular domain in2 complex with cenp-t peptide
71	c3vzaF_	Alignment	not modelled	5.5	33	PDB header: cell cycle Chain: F: PDB Molecule: centromere protein t; PDBTitle: crystal structure of the chicken spc24-spc25 globular domain in2 complex with cenp-t peptide
72	c2krnA_	Alignment	not modelled	5.4	27	PDB header: signaling protein Chain: A: PDB Molecule: cd2-associated protein; PDBTitle: high resolution structure of the second sh3 domain of cd2ap
73	c3cw4A_	Alignment	not modelled	5.4	26	PDB header: transferase Chain: A: PDB Molecule: polymerase basic protein 2; PDBTitle: large c-terminal domain of influenza a virus rna-dependent polymerase2 pb2
74	c4fe9A_	Alignment	not modelled	5.4	14	PDB header: carbohydrate-binding protein Chain: A: PDB Molecule: outer membrane protein susf; PDBTitle: crystal structure of susf from bacteroides thetaiotaomicron
75	c5n2hA_	Alignment	not modelled	5.4	16	PDB header: transferase Chain: A: PDB Molecule: dna polymerase; PDBTitle: structure of the e9 dna polymerase exonuclease deficient mutant2 (d166a+e168a) from vaccinia virus
76	c3nkzD_	Alignment	not modelled	5.2	25	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: flagellar protein flit; PDBTitle: the crystal structure of a flagella protein from yersinia2 enterocolitica subsp. enterocolitica 8081
77	d1f9qa_	Alignment	not modelled	5.2	18	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
78	c5a4pA_	Alignment	not modelled	5.1	15	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2 z; PDBTitle: structure of ube2z provides functional insight into2 specificity in the fat10 conjugation machinery
79	d1auua_	Alignment	not modelled	5.1	28	Fold: GroES-like Superfamily: SacY-like RNA-binding domain Family: BglG-like antiterminator proteins

80	c6giyC_	Alignment	not modelled	5.1	31	PDB header: structural protein Chain: C: PDB Molecule: tssg; PDBTitle: the baseplate complex from the type vi secretion system
81	c4s13D_	Alignment	not modelled	5.1	19	PDB header: lyase Chain: D: PDB Molecule: ferulic acid decarboxylase 1; PDBTitle: ferulic acid decarboxylase (fdc1)
82	c5j4aA_	Alignment	not modelled	5.1	21	PDB header: toxin Chain: A: PDB Molecule: trna nuclease cdia; PDBTitle: cdia-ct toxin from burkholderia pseudomallei e479 in complex with2 cognate cdii immunity protein
83	d1guqa1	Alignment	not modelled	5.0	19	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase