
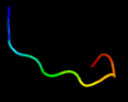
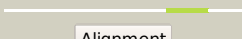
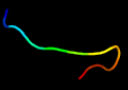
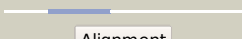

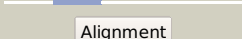
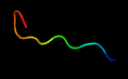
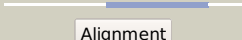

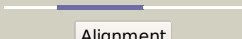
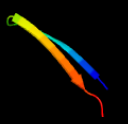
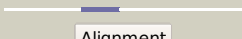

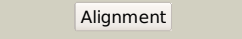

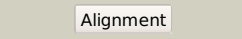

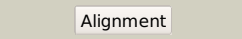
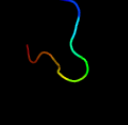
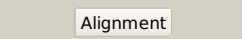



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0186Ac_(RVBD0186Ac)_218388_218549
 Date Tue Jul 23 14:50:24 BST 2019
 Unique Job ID 5580cb336215e297

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xknE_	 Alignment		60.7	55	PDB header: transferase/signaling protein Chain: E; PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complex with epfl4
2	c5xknF_	 Alignment		60.7	55	PDB header: transferase/signaling protein Chain: F; PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complex with epfl4
3	c2mw0A_	 Alignment		27.8	60	PDB header: protein binding Chain: A; PDB Molecule: kalata b7; PDBTitle: kalata b7 ser mutant
4	c2elnA_	 Alignment		27.4	50	PDB header: transcription Chain: A; PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 11th c2h2 zinc finger of human2 zinc finger protein 406
5	d1bx7a_	 Alignment		22.4	28	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Leech antihemostatic proteins Family: Huristasin-like
6	c3zxaA_	 Alignment		19.5	20	PDB header: transferase Chain: A; PDB Molecule: hypoxia sensor histidine kinase response regulator dost; PDBTitle: crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
7	d2j7ja2	 Alignment		19.0	60	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
8	d1ddza2	 Alignment		16.9	40	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
9	d1ddza1	 Alignment		16.4	60	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
10	d1ejab_	 Alignment		16.2	45	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Leech antihemostatic proteins Family: Huristasin-like
11	c5ztpB_	 Alignment		15.4	27	PDB header: lyase Chain: B; PDB Molecule: carbonic anhydrase; PDBTitle: carbonic anhydrase from glaciozyma antarctica

12	c3lasA_	Alignment		15.4	20	PDB header: lyase Chain: A: PDB Molecule: putative carbonic anhydrase; PDBTitle: crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
13	c2a8cE_	Alignment		15.1	40	PDB header: lyase Chain: E: PDB Molecule: carbonic anhydrase 2; PDBTitle: haemophilus influenzae beta-carbonic anhydrase
14	c3j0cH_	Alignment		15.0	32	PDB header: virus Chain: H: PDB Molecule: e2 envelope glycoprotein; PDBTitle: models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map
15	c1ylkA_	Alignment		14.9	20	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein rv1284/mt1322; PDBTitle: crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
16	d1dx5i1	Alignment		14.8	36	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
17	c4o1jB_	Alignment		14.8	40	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
18	d1i6pa_	Alignment		14.3	50	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
19	c1ddzA_	Alignment		14.1	60	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
20	c2w3nA_	Alignment		13.8	40	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase 2; PDBTitle: structure and inhibition of the co2-sensing carbonic anhydrase can22 from the pathogenic fungus cryptococcus neoformans
21	c2a5vB_	Alignment	not modelled	13.5	30	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase (carbonate dehydratase) (carbonic PDBTitle: crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
22	c2fynO_	Alignment	not modelled	13.3	35	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
23	c5cxkG_	Alignment	not modelled	13.3	50	PDB header: lyase Chain: G: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of beta carbonic anhydrase from vibrio cholerae
24	c3eyxB_	Alignment	not modelled	13.1	40	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
25	c4o1kA_	Alignment	not modelled	12.6	50	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
26	d1g5ca_	Alignment	not modelled	12.5	27	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
27	c3tenD_	Alignment	not modelled	11.9	30	PDB header: hydrolase Chain: D: PDB Molecule: cs2 hydrolase; PDBTitle: holo form of carbon disulfide hydrolase
						PDB header: transferase

28	c4biyD_	Alignment	not modelled	11.8	25	Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
29	c3ucoB_	Alignment	not modelled	11.8	50	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: coccomyxa beta-carbonic anhydrase in complex with iodide
30	d1ekja_	Alignment	not modelled	11.6	27	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
31	c5swcE_	Alignment	not modelled	11.5	40	PDB header: lyase Chain: E: PDB Molecule: carbonic anhydrase; PDBTitle: the structure of the beta-carbonic anhydrase ccaa
32	c3vrkA_	Alignment	not modelled	11.1	27	PDB header: hydrolase Chain: A: PDB Molecule: carbonyl sulfide hydrolase; PDBTitle: crystal structure of thiobacillus thioparus thi115 carbonyl sulfide2 hydrolase / thiocyanate complex
33	c2xfbl_	Alignment	not modelled	11.0	32	PDB header: virus Chain: I: PDB Molecule: e2 envelope glycoprotein; PDBTitle: the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map
34	c3n43B_	Alignment	not modelled	10.9	32	PDB header: viral protein Chain: B: PDB Molecule: e2 envelope glycoprotein; PDBTitle: crystal structures of the mature envelope glycoprotein complex2 (trypsin cleavage) of chikungunya virus.
35	c6gwuB_	Alignment	not modelled	10.9	36	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: carbonic anhydrase cance103p from candida albicans
36	c2e76D_	Alignment	not modelled	10.9	35	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
37	c6avjB_	Alignment	not modelled	10.5	70	PDB header: metal binding protein Chain: B: PDB Molecule: cdgsh iron-sulfur domain-containing protein 3, PDBTitle: crystal structure of human mitochondrial inner neet protein (mint)2 /cisd3
38	d2i9wa3	Alignment	not modelled	10.5	47	Fold: Sec-C motif Superfamily: Sec-C motif Family: Sec-C motif
39	c4rxyA_	Alignment	not modelled	10.5	50	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of the beta carbonic anhydrase psca3 isolated from2 pseudomonas aeruginosa
40	c3q7tB_	Alignment	not modelled	10.1	42	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein; PDBTitle: 2.15a resolution structure (i41 form) of the chxr receiver domain from2 chlamydia trachomatis
41	c6atyA_	Alignment	not modelled	9.6	80	PDB header: toxin Chain: A: PDB Molecule: venom protein 51.1; PDBTitle: exploring cystine dense peptide space to open a unique molecular2 toolbox
42	c6hwhB_	Alignment	not modelled	9.3	53	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
43	c5xjoF_	Alignment	not modelled	9.2	46	PDB header: transferase/membrane protein Chain: F: PDB Molecule: protein epidermal patterning factor 1; PDBTitle: plant receptor erl1-tmm in complex with peptide epf1
44	d2akla2	Alignment	not modelled	9.0	55	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
45	c2xpoB_	Alignment	not modelled	8.9	57	PDB header: transcription Chain: B: PDB Molecule: chromatin structure modulator; PDBTitle: crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form ii
46	c2xpoD_	Alignment	not modelled	8.8	57	PDB header: transcription Chain: D: PDB Molecule: chromatin structure modulator; PDBTitle: crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form ii
47	c5xkjF_	Alignment	not modelled	8.6	46	PDB header: transferase/membrane protein/hormone Chain: F: PDB Molecule: protein epidermal patterning factor 2; PDBTitle: crystal structure of plant receptor erl1-tmm in complex with epf2
48	d1omba_	Alignment	not modelled	8.4	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
49	d2bz1a1	Alignment	not modelled	8.0	33	Fold: RibA-like Superfamily: RibA-like Family: RibA-like
50	d2g45a1	Alignment	not modelled	7.9	44	Fold: RING/U-box Superfamily: RING/U-box Family: Zf-UBP
51	c1g9il_	Alignment	not modelled	7.8	44	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: bowman-birk type trypsin inhibitor; PDBTitle: crystal structure of beta-trypsin complex in cyclohexane
52	c1p84E_	Alignment	not modelled	7.6	35	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
53	c2jr7A_	Alignment	not modelled	7.5	50	PDB header: metal binding protein Chain: A: PDB Molecule: dph3 homolog; PDBTitle: solution structure of human desr1

54	d1agga_	Alignment	not modelled	7.3	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
55	d1ywsa1	Alignment	not modelled	7.3	71	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
56	c3n40P_	Alignment	not modelled	7.1	32	PDB header: viral protein Chain: P: PDB Molecule: p62 envelope glycoprotein; PDBTitle: crystal structure of the immature envelope glycoprotein complex of f2 chikungunya virus.
57	d3cx5e1	Alignment	not modelled	7.1	27	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
58	c3zxoB_	Alignment	not modelled	7.0	30	PDB header: transferase Chain: B: PDB Molecule: redox sensor histidine kinase response regulator devs; PDBTitle: crystal structure of the mutant atp-binding domain of f2 mycobacterium tuberculosis doss
59	c2xppB_	Alignment	not modelled	6.9	57	PDB header: transcription Chain: B: PDB Molecule: chromatin structure modulator; PDBTitle: crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form iii
60	c2xpnB_	Alignment	not modelled	6.8	57	PDB header: transcription Chain: B: PDB Molecule: chromatin structure modulator; PDBTitle: crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form i
61	d2qlia3	Alignment	not modelled	6.8	57	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
62	c4ri4B_	Alignment	not modelled	6.6	33	PDB header: hydrolase Chain: B: PDB Molecule: gtp cyclohydrolase-2; PDBTitle: crystal structure of gtp cyclohydrolase ii from helicobacter pylori2 26695
63	d1wgea1	Alignment	not modelled	6.5	71	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
64	c2yrtA_	Alignment	not modelled	6.3	46	PDB header: transcription Chain: A: PDB Molecule: chord containing protein-1; PDBTitle: solution structure of the chord domain of human chord-2 containing protein 1
65	c1bi6H_	Alignment	not modelled	6.2	44	PDB header: cysteine protease inhibitor Chain: H: PDB Molecule: bromelain inhibitor vi; PDBTitle: nmr structure of bromelain inhibitor vi from pineapple stem
66	c2bi6H_	Alignment	not modelled	6.0	44	PDB header: cysteine protease inhibitor Chain: H: PDB Molecule: bromelain inhibitor vi; PDBTitle: nmr study of bromelain inhibitor vi from pineapple stem
67	d1x3ca1	Alignment	not modelled	6.0	67	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
68	d1a1ia1	Alignment	not modelled	5.8	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
69	d1jm1a_	Alignment	not modelled	5.8	45	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
70	c1sx0A_	Alignment	not modelled	5.8	47	PDB header: protein transport Chain: A: PDB Molecule: seca; PDBTitle: solution nmr structure and x-ray absorption analysis of the2 c-terminal zinc-binding domain of the seca atpase
71	c1sx1A_	Alignment	not modelled	5.7	47	PDB header: protein transport Chain: A: PDB Molecule: seca; PDBTitle: solution nmr structure and x-ray absorption analysis of the2 c-terminal zinc-binding domain of the seca atpase
72	d1bdsa_	Alignment	not modelled	5.6	67	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
73	c1bdsA_	Alignment	not modelled	5.6	67	PDB header: anti-hypertensive, anti-viral protein Chain: A: PDB Molecule: bds-i; PDBTitle: determination of the three-dimensional solution structure of the2 antihypertensive and antiviral protein bds-i from the sea anemone3 anemonia sulcata. a study using nuclear magnetic resonance and hybrid4 distance geometry-dynamical simulated annealing
74	c4mi0A_	Alignment	not modelled	5.6	25	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase ezh2; PDBTitle: human enhancer of zeste (drosophila) homolog 2(ezh2)
75	d1gtra2	Alignment	not modelled	5.5	33	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
76	d1nzza_	Alignment	not modelled	5.5	42	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
77	c1sbwl_	Alignment	not modelled	5.3	30	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: protein (mung bean inhibitor lysin active PDBTitle: crystal structure of mung bean inhibitor lysine active2 fragment complex with bovine beta-trypsin at 1.8a3 resolution
78	d1tf3a2	Alignment	not modelled	5.3	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
79	c2odxA_	Alignment	not modelled	5.3	44	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c oxidase polypeptide iv; PDBTitle: solution structure of zn(ii)cox4

80	c6mwcN_	Alignment	not modelled	5.3	46	PDB header: virus/immune system Chain: N: PDB Molecule: e2; PDBTitle: cryoem structure of chimeric eastern equine encephalitis virus with2 fab of eeev-5 antibody
81	d1ozbi_	Alignment	not modelled	5.3	38	Fold: Sec-C motif Superfamily: Sec-C motif Family: Sec-C motif
82	c1ozbl_	Alignment	not modelled	5.3	38	PDB header: protein transport Chain: I: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of secb complexed with seca c-terminus
83	c1ozbj_	Alignment	not modelled	5.2	38	PDB header: protein transport Chain: J: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of secb complexed with seca c-terminus
84	d1iarb1	Alignment	not modelled	5.1	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
85	c4g6zA_	Alignment	not modelled	5.1	25	PDB header: ligase Chain: A: PDB Molecule: glutamate-trna ligase; PDBTitle: crystal structure of a glutamyl-trna synthetase glurs from2 burkholderia thailandensis bound to l-glutamate
86	c4kp4B_	Alignment	not modelled	5.1	30	PDB header: transferase/signaling protein Chain: B: PDB Molecule: osmolarity sensor protein envz, histidine kinase; PDBTitle: deciphering cis-trans directionality and visualizing2 autophosphorylation in histidine kinases.