
















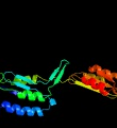






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1836c (-) _2082610_2084643
Date	Fri Aug 2 13:30:44 BST 2019
Unique Job ID	c64e94ce4f377506

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fx5A_	 Alignment		100.0	12	PDB header: blood clotting Chain: A: PDB Molecule: von willebrand factor type a; PDBTitle: von willebrand factor type a from catenulispora acidiphila
2	c6fpzA_	 Alignment		99.9	13	PDB header: structural protein Chain: A: PDB Molecule: inter-alpha-trypsin inhibitor heavy chain h1; PDBTitle: inter-alpha-inhibitor heavy chain 1, d298a
3	c5a8jA_	 Alignment		99.9	13	PDB header: transcription Chain: A: PDB Molecule: vwa2; PDBTitle: crystal structure of the arnb paralog vwa2 from2 sulfobolus acidocaldarius
4	c6nmiE_	 Alignment		99.9	17	PDB header: transcription Chain: E: PDB Molecule: general transcription factor iih subunit 2, p44; PDBTitle: cryo-em structure of the human tfiih core complex
5	c6o9l6_	 Alignment		99.8	17	PDB header: transcription/dna Chain: 6: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
6	c3ibsA_	 Alignment		99.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein batb; PDBTitle: crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron
7	c5iy70_	 Alignment		99.8	17	PDB header: transcription, transferase/dna Chain: 0: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the open state
8	c1rs0A_	 Alignment		99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: complement factor b; PDBTitle: crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
9	c4rckB_	 Alignment		99.8	16	PDB header: membrane protein Chain: B: PDB Molecule: hypothetical membrane spanning protein; PDBTitle: crystal structure of uncharacterized membrane spanning protein from2 vibrio fischeri
10	c3jbrF_	 Alignment		99.8	13	PDB header: membrane protein Chain: F: PDB Molecule: voltage-dependent calcium channel subunit alpha-2/delta-1; PDBTitle: cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
11	c4b4tW_	 Alignment		99.8	17	PDB header: hydrolase Chain: W: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome

12	c4wfgA_	Alignment		99.8	15	PDB header: transcription Chain: A: PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: crystal structure of tfiih subunit
13	c2x5nA_	Alignment		99.8	15	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: crystal structure of the sprpn10 vwa domain
14	c5gjfF_	Alignment		99.8	13	PDB header: membrane protein Chain: F: PDB Molecule: voltage-dependent calcium channel subunit alpha-2/delta-1; PDBTitle: structure of the mammalian voltage-gated calcium channel cav1.12 complex at near atomic resolution
15	c2x31F_	Alignment		99.8	17	PDB header: ligase Chain: F: PDB Molecule: magnesium-chelatase 60 kda subunit; PDBTitle: modelling of the complex between subunits bchi and bchd of magnesium2 chelatase based on single-particle cryo-em reconstruction at 7.5 ang
16	c5oqj6_	Alignment		99.7	15	PDB header: transcription Chain: 6: PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
17	c2ok5A_	Alignment		99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: complement factor b; PDBTitle: human complement factor b
18	d2ok5a1	Alignment		99.7	12	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
19	d1sbpa_	Alignment		99.7	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
20	c6ddnB_	Alignment		99.7	23	PDB header: transport protein Chain: B: PDB Molecule: probable sulfate-binding lipoprotein subi; PDBTitle: the sulfate-binding protein subi from mycobacterium tuberculosis h37rv
21	c4hqnb_	Alignment	not modelled	99.7	11	PDB header: cell adhesion Chain: B: PDB Molecule: sporozoite surface protein 2; PDBTitle: crystal structure of manganese-loaded plasmodium vivax trap protein
22	c5gjqW_	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: W: PDB Molecule: 26s proteasome non-atpase regulatory subunit 4; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
23	c2i6sA_	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
24	d1q0pa_	Alignment	not modelled	99.6	17	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
25	c4rxIA_	Alignment	not modelled	99.6	21	PDB header: transport protein Chain: A: PDB Molecule: molybdenum abc transporter, periplasmic molybdenum-binding PDBTitle: crystal structure of molybdenum abc transporter solute binding protein2 vc_a0726 from vibrio cholerae, target efi-510913, in complex with3 tungstate
26	d1pd0a3	Alignment	not modelled	99.6	12	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
27	d1amfa_	Alignment	not modelled	99.6	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
28	d1jeyb2	Alignment	not modelled	99.6	10	Fold: vWA-like Superfamily: vWA-like

						Family: Ku80 subunit N-terminal domain
29	c4hqfA_	Alignment	not modelled	99.5	10	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-related anonymous protein, trap; PDBTitle: crystal structure of plasmodium falciparum trap, i4 form
30	c2iueA_	Alignment	not modelled	99.5	14	PDB header: membrane protein Chain: A: PDB Molecule: pactolus i-domain; PDBTitle: pactolus i-domain: functional switching of the rossmann2 fold
31	c5um2A_	Alignment	not modelled	99.5	14	PDB header: transport protein Chain: A: PDB Molecule: abc transporter sulfate binding protein; PDBTitle: functional and structural characterization of a sulfate-binding2 protein (sbp) from xanthomonas citri
32	d1jeya2	Alignment	not modelled	99.5	6	Fold: vWA-like Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
33	c3n2nC_	Alignment	not modelled	99.5	11	PDB header: toxin receptor Chain: C: PDB Molecule: anthrax toxin receptor 1; PDBTitle: the crystal structure of tumor endothelial marker 8 (tem8)2 extracellular domain
34	d1shux_	Alignment	not modelled	99.5	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
35	d1ijba_	Alignment	not modelled	99.5	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
36	d1atza_	Alignment	not modelled	99.5	17	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
37	c2b2xB_	Alignment	not modelled	99.5	15	PDB header: immune system Chain: B: PDB Molecule: integrin alpha-1; PDBTitle: vla1 rdeltah i-domain complexed with a quadruple mutant of the aqc22 fab
38	d1u0oc1	Alignment	not modelled	99.5	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
39	c2h5yC_	Alignment	not modelled	99.5	19	PDB header: metal transport Chain: C: PDB Molecule: molybdate-binding periplasmic protein; PDBTitle: crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate
40	c4cnbA_	Alignment	not modelled	99.5	11	PDB header: structural protein Chain: A: PDB Molecule: proximal thread matrix protein 1; PDBTitle: structure of proximal thread matrix protein 1 (ptmp1) from the2 mussel byssus - crystal form 2
41	d1atga_	Alignment	not modelled	99.4	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
42	d1n3ya_	Alignment	not modelled	99.4	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
43	c4okuA_	Alignment	not modelled	99.4	13	PDB header: cell adhesion Chain: A: PDB Molecule: micronemal protein mic2; PDBTitle: structure of toxoplasma gondii promic2
44	c3txaA_	Alignment	not modelled	99.4	16	PDB header: cell adhesion Chain: A: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae
45	c4kd5A_	Alignment	not modelled	99.4	14	PDB header: transport protein Chain: A: PDB Molecule: abc-type transport system, molybdenum-specific PDBTitle: substrate binding domain of putative molybdenum abc transporter from2 clostridium difficile
46	c5e6rA_	Alignment	not modelled	99.4	19	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-I; PDBTitle: structures of leukocyte integrin alb2: the ai domain, the headpiece,2 and the pocket for the internal ligand
47	c3gxbB_	Alignment	not modelled	99.4	13	PDB header: cell adhesion Chain: B: PDB Molecule: von willebrand factor; PDBTitle: crystal structure of vwf a2 domain
48	d1yvra2	Alignment	not modelled	99.3	11	Fold: vWA-like Superfamily: vWA-like Family: RoRNP C-terminal domain-like
49	c5my5A_	Alignment	not modelled	99.3	9	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic substrate-binding protein; PDBTitle: tungstate binding protein - tupa - from desulfovibrio alaskensis g20
50	d1ck4a_	Alignment	not modelled	99.3	17	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
51	d1mf7a_	Alignment	not modelled	99.3	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
52	c2xggB_	Alignment	not modelled	99.3	12	PDB header: hydrolase Chain: B: PDB Molecule: microneme protein 2; PDBTitle: structure of toxoplasma gondii micronemal protein 2 a_i2 domain
53	c2nvoA_	Alignment	not modelled	99.3	15	PDB header: rna binding protein Chain: A: PDB Molecule: ro sixty-related protein, rsr; PDBTitle: crystal structure of deinococcus radiodurans ro (rsr) protein
54	d1v7pc_	Alignment	not modelled	99.3	16	Fold: vWA-like Superfamily: vWA-like

						Family: Integrin A (or I) domain
55	c4ihkA_	Alignment	not modelled	99.2	14	PDB header: cell adhesion Chain: A: PDB Molecule: collagen alpha3(vi); PDBTitle: crystal structure of the collagen vi alpha3 n5 domain r1061q
56	c3tw0D_	Alignment	not modelled	99.2	13	PDB header: cell adhesion Chain: D: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae
57	d1pt6a_	Alignment	not modelled	99.2	15	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
58	c1jeyB_	Alignment	not modelled	99.1	10	PDB header: dna binding protein/dna Chain: B: PDB Molecule: ku80; PDBTitle: crystal structure of the ku heterodimer bound to dna
59	d1mjna_	Alignment	not modelled	99.1	20	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
60	c3fj7A_	Alignment	not modelled	98.9	13	PDB header: protein binding Chain: A: PDB Molecule: major antigenic peptide peb3; PDBTitle: crystal structure of l-phospholactate bound peb3
61	c3muqB_	Alignment	not modelled	98.9	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
62	d1tyeb2	Alignment	not modelled	98.8	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
63	c3cfxA_	Alignment	not modelled	98.8	14	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein ma_0280; PDBTitle: crystal structure of m. acetivorans periplasmic binding protein2 moda/wtpa with bound tungstate
64	c4jb7A_	Alignment	not modelled	98.7	13	PDB header: cell invasion Chain: A: PDB Molecule: accessory colonization factor acfc; PDBTitle: 1.42 angstrom resolution crystal structure of accessory colonization2 factor acfc (acfc) in complex with d-aspartic acid
65	c6nmiF_	Alignment	not modelled	98.7	14	PDB header: transcription Chain: F: PDB Molecule: general transcription factor iih subunit 3, p34; PDBTitle: cryo-em structure of the human tfiih core complex
66	c4jwoA_	Alignment	not modelled	98.7	10	PDB header: phosphate binding protein Chain: A: PDB Molecule: phosphate binding protein; PDBTitle: the crystal structure of a possible phosphate binding protein from2 planctomyces limnophilus dsm 3776
67	d2onsa1	Alignment	not modelled	98.6	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
68	c3cvgD_	Alignment	not modelled	98.6	15	PDB header: metal binding protein Chain: D: PDB Molecule: putative metal binding protein; PDBTitle: crystal structure of a periplasmic putative metal binding protein
69	c3c9hB_	Alignment	not modelled	98.6	11	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of the substrate binding protein of the abc2 transporter from agrobacterium tumefaciens
70	c6bxjA_	Alignment	not modelled	98.5	15	PDB header: cell adhesion Chain: A: PDB Molecule: chimera protein of integrin beta-3 and integrin alpha-I; PDBTitle: structure of a single-chain beta3 integrin
71	c4n13A_	Alignment	not modelled	98.5	10	PDB header: transport protein Chain: A: PDB Molecule: phosphate abc transporter, periplasmic phosphate-binding PDBTitle: crystal structure of psts (bb_0215) from borrelia burgdorferi
72	c4ombB_	Alignment	not modelled	98.5	9	PDB header: transport protein Chain: B: PDB Molecule: phosphate binding protein; PDBTitle: phosphate binding protein
73	c3cg3A_	Alignment	not modelled	98.5	13	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein ph0151; PDBTitle: crystal structure of p. horikoshii periplasmic binding2 protein moda/wtpa with bound tungstate
74	c4gd5B_	Alignment	not modelled	98.5	11	PDB header: transport protein Chain: B: PDB Molecule: phosphate abc transporter, phosphate-binding protein; PDBTitle: x-ray crystal structure of a putative phosphate abc transporter2 substrate-binding protein with bound phosphate from clostridium3 perfringens
75	c5t1pB_	Alignment	not modelled	98.5	12	PDB header: hydrolase Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of the putative periplasmic solute-binding protein2 from campylobacter jejuni
76	c3kn3C_	Alignment	not modelled	98.5	10	PDB header: transcription Chain: C: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinnella succinogenes
77	c3lr1A_	Alignment	not modelled	98.5	9	PDB header: transport protein Chain: A: PDB Molecule: tungstate abc transporter, periplasmic tungstate- PDBTitle: the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
78	c6bxfA_	Alignment	not modelled	98.5	15	PDB header: cell adhesion Chain: A: PDB Molecule: chimera protein of integrin beta-3 and integrin alpha-I; PDBTitle: crystal structure of an extended b3 integrin I33
79	d2qtva3	Alignment	not modelled	98.5	13	Fold: vWA-like Superfamily: vWA-like

				Family:Trunk domain of Sec23/24		
80	c3cg1A	Alignment	not modelled	98.4	14	PDB header: transport protein Chain: A: PDB Molecule: cupf0100 protein pf0080; PDBTitle: crystal structure of p. furiosus periplasmic binding protein2 moda/wtpa with bound tungstate
81	c1pd0A	Alignment	not modelled	98.4	12	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the copii coat subunit, sec24.2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
82	c6djpB	Alignment	not modelled	98.4	14	PDB header: membrane protein Chain: B: PDB Molecule: integrin beta-8; PDBTitle: integrin alpha-v beta-8 in complex with the fabs 8b8 and 68
83	c2qryD	Alignment	not modelled	98.4	10	PDB header: transport protein Chain: D: PDB Molecule: thiamine-binding periplasmic protein; PDBTitle: periplasmic thiamin binding protein
84	c3k6wA	Alignment	not modelled	98.3	13	PDB header: transport protein Chain: A: PDB Molecule: solute-binding protein ma_0280; PDBTitle: apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans
85	c4um9D	Alignment	not modelled	98.3	13	PDB header: immune system Chain: D: PDB Molecule: integrin beta-6; PDBTitle: crystal structure of alpha v beta 6 with peptide
86	c3ragA	Alignment	not modelled	98.3	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
87	c3eg9B	Alignment	not modelled	98.3	18	PDB header: protein transport Chain: B: PDB Molecule: sec24 related gene family, member d; PDBTitle: crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin
88	c3eh2B	Alignment	not modelled	98.3	19	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24c; PDBTitle: crystal structure of the human copii-coat protein sec24c
89	c4r73B	Alignment	not modelled	98.2	13	PDB header: transport protein Chain: B: PDB Molecule: abc-type fe3+ transport system, periplasmic component; PDBTitle: structure of the periplasmic binding protein afua from actinobacillus2 pleuropneumoniae (endogenous glucose-6-phosphate and mannose-6-3 phosphate bound)
90	c3eg9A	Alignment	not modelled	98.2	15	PDB header: protein transport Chain: A: PDB Molecule: protein transport protein sec23a; PDBTitle: crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin
91	c1twyG	Alignment	not modelled	98.2	12	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
92	c4ecfA	Alignment	not modelled	98.2	14	PDB header: phosphate-binding protein Chain: A: PDB Molecule: abc-type phosphate transport system, periplasmic component; PDBTitle: crystal structure of an abc-type phosphate transport system,2 periplasmic component (lvis_0633) from lactobacillus brevis atcc 3673 at 1.55 a resolution
93	d1twya	Alignment	not modelled	98.2	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
94	c1jeqA	Alignment	not modelled	98.2	7	PDB header: dna binding protein Chain: A: PDB Molecule: ku70; PDBTitle: crystal structure of the ku heterodimer
95	c4exlD	Alignment	not modelled	98.2	10	PDB header: transport protein Chain: D: PDB Molecule: phosphate-binding protein psts 1; PDBTitle: crystal structure of phosphate abc transporter, periplasmic phosphate-2 binding protein psts 1 (pbp1) from streptococcus pneumoniae canada3 mdr_19a
96	c6fjID	Alignment	not modelled	98.1	17	PDB header: metal binding protein Chain: D: PDB Molecule: abc-type fe3+ transport system, periplasmic component; PDBTitle: structure of ibps from dickeya dadantii
97	c3vi3D	Alignment	not modelled	98.1	12	PDB header: cell adhesion/immune system Chain: D: PDB Molecule: integrin beta-1; PDBTitle: crystal structure of alpha5beta1 integrin headpiece (ligand-free form)
98	c1u8cB	Alignment	not modelled	98.1	12	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: a novel adaptation of the integrin psi domain revealed from its2 crystal structure
99	c1m2vB	Alignment	not modelled	98.0	13	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
100	c3v4pB	Alignment	not modelled	97.9	12	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-7; PDBTitle: crystal structure of a4b7 headpiece complexed with fab act-1
101	c1m2oA	Alignment	not modelled	97.8	14	PDB header: protein transport/signaling protein Chain: A: PDB Molecule: protein transport protein sec23; PDBTitle: crystal structure of the sec23-sar1 complex
102	c3k71G	Alignment	not modelled	97.8	15	PDB header: cell adhesion Chain: G: PDB Molecule: integrin alpha-x; PDBTitle: structure of integrin alphax beta2 ectodomain
103	c4eloD	Alignment	not modelled	97.8	11	PDB header: metal transport Chain: D: PDB Molecule: iron abc transporter, periplasmic iron-binding protein; PDBTitle: ferric binding protein in apo form 1 PDB header: protein binding

104	c3ijeB_	Alignment	not modelled	97.7	12	Chain: B: PDB Molecule: integrin beta-3; PDBTitle: crystal structure of the complete integrin alphavbeta3 ectodomain plus2 an alpha/beta transmembrane fragment
105	c3egxB_	Alignment	not modelled	97.7	17	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24a; PDBTitle: crystal structure of the mammalian copii-coat protein sec23a/24a2 complexed with the snare protein sec22b and bound to the transport3 signal sequence of the snare protein bet1
106	c3fcuB_	Alignment	not modelled	97.6	13	PDB header: cell adhesion/blood clotting Chain: B: PDB Molecule: integrin beta-3; PDBTitle: structure of headpiece of integrin aiiib3 in open conformation
107	c5y58E_	Alignment	not modelled	97.5	14	PDB header: rna binding protein Chain: E: PDB Molecule: atp-dependent dna helicase ii subunit 1; PDBTitle: crystal structure of ku70/80 and tlc1
108	d1xvxa_	Alignment	not modelled	97.4	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
109	d1xc1a_	Alignment	not modelled	97.3	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
110	c1yvra_	Alignment	not modelled	97.3	14	PDB header: rna binding protein Chain: A: PDB Molecule: 60-kda ss-a/ro ribonucleoprotein; PDBTitle: ro autoantigen
111	c4r6yA_	Alignment	not modelled	97.3	12	PDB header: transport protein Chain: A: PDB Molecule: putative 2-aminoethylphosphonate-binding periplasmic PDBTitle: crystal structure of solute-binding protein stm0429 from salmonella2 enterica subsp. enterica serovar typhimurium str. lt2, target efi-3 510776, a closed conformation, in complex with glycerol and acetate
112	c3k6sB_	Alignment	not modelled	97.2	14	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-2; PDBTitle: structure of integrin alphaxbeta2 ectodomain
113	d1y9ua_	Alignment	not modelled	97.2	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
114	d1xvya_	Alignment	not modelled	97.1	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
115	c5y58D_	Alignment	not modelled	97.1	10	PDB header: rna binding protein Chain: D: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku70/80 and tlc1
116	c6nlpA_	Alignment	not modelled	97.1	13	PDB header: transport protein Chain: A: PDB Molecule: bacterial extracellular solute-binding family protein; PDBTitle: the crystal structure of an abc transporter periplasmic binding2 protein ydcs from escherichia coli bw25113
117	d1y4ta_	Alignment	not modelled	97.1	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
118	c2pt1A_	Alignment	not modelled	97.0	9	PDB header: metal transport Chain: A: PDB Molecule: iron transport protein; PDBTitle: futa1 synechocystis pcc 6803
119	c3cfzA_	Alignment	not modelled	96.9	17	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein mj1186; PDBTitle: crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate
120	c4i1dB_	Alignment	not modelled	96.6	11	PDB header: transport protein Chain: B: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: the crystal structure of an abc transporter substrate-binding protein2 from bradyrhizobium japonicum usda 110