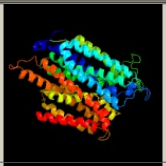
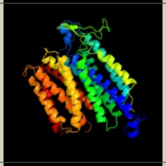
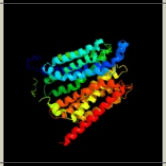
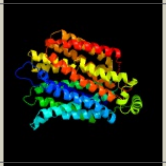
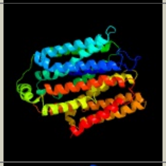
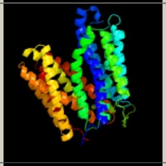
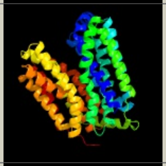
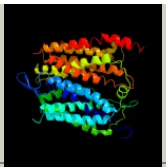
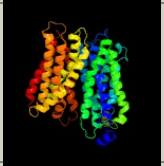
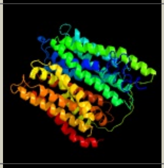
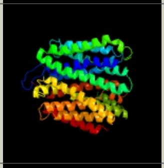
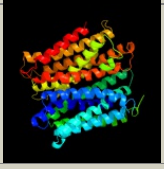
Phyre^2

Email	mdejesus@rockefeller.edu
Description	RVBD0267_(narU)_321331_322722
Date	Tue Jul 23 14:50:33 BST 2019
Unique Job ID	5f256144a3d6e7c1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4iu8A_	Alignment		100.0	33	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrite extrusion protein 2; **PDBTitle:** crystal structure of a membrane transporter (selenomethionine2 derivative)
2	c4iu9A_	Alignment		100.0	34	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrite extrusion protein 2; **PDBTitle:** crystal structure of a membrane transporter
3	c6e9oA_	Alignment		100.0	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**d-galactonate transport; **PDBTitle:** e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
4	d1pw4a_	Alignment		100.0	12	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
5	c4zp0A_	Alignment		100.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multidrug transporter mdfa; **PDBTitle:** crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
6	c6h7dA_	Alignment		100.0	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sugar transport protein 10; **PDBTitle:** crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state
7	c4ldsB_	Alignment		100.0	12	**PDB header:**transport protein, membrane protein **Chain:** B: **PDB Molecule:**bicyclomycin resistance protein tcab; **PDBTitle:** the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
8	c3wdoA_	Alignment		100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**mfs transporter; **PDBTitle:** structure of e. coli yajr transporter
9	c6g9xB_	Alignment		100.0	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**major facilitator superfamily mfs_1; **PDBTitle:** crystal structure of a mfs transporter at 2.54 angstroem resolution
10	c4ybqB_	Alignment		100.0	12	**PDB header:**transport protein/immune system **Chain:** B: **PDB Molecule:**solute carrier family 2, facilitated glucose transporter **PDBTitle:** rat glut5 with fv in the outward-open form
11	c4j05A_	Alignment		100.0	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**phosphate transporter; **PDBTitle:** crystal structure of a eukaryotic phosphate transporter

12	c4cl5B_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**nitrate transporter 1.1; **PDBTitle:** crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
13	c5c65A_	Alignment		100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute carrier family 2, facilitated glucose transporter **PDBTitle:** structure of the human glucose transporter glut3 / slc2a3
14	c6exsA_	Alignment		100.0	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**peptide abc transporter permease; **PDBTitle:** crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
15	c3o7pA_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
16	c4ikyA_	Alignment		100.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**di-tripeptide abc transporter (permease); **PDBTitle:** crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
17	c4w6vA_	Alignment		100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**di-/tripeptide transporter; **PDBTitle:** crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
18	c6gs7A_	Alignment		100.0	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dipeptide and tripeptide permease a; **PDBTitle:** crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
19	c6ei3A_	Alignment		100.0	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**proton-dependent oligopeptide transporter family protein; **PDBTitle:** crystal structure of auto inhibited pot family peptide transporter
20	c4apsB_	Alignment		100.0	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**di-or tripeptide h+ symporter; **PDBTitle:** crystal structure of a pot family peptide transporter in an inward2 open conformation.
21	d1pv7a_	Alignment	not modelled	99.9	8	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
22	c1pv7B_	Alignment	not modelled	99.9	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**lactose permease; **PDBTitle:** crystal structure of lactose permease with tdg
23	c4pypA_	Alignment	not modelled	99.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute carrier family 2, facilitated glucose transporter **PDBTitle:** crystal structure of the human glucose transporter glut1
24	c2gfpA_	Alignment	not modelled	99.9	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
25	c4q65A_	Alignment	not modelled	99.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**dipeptide permease d; **PDBTitle:** structure of the e. coli peptide transporter ybgh
26	c2xutC_	Alignment	not modelled	99.9	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
27	c4lepB_	Alignment	not modelled	99.9	8	**PDB header:**membrane protein, tranport protein **Chain:** B: **PDB Molecule:**proton:oligopeptide symporter pot family; **PDBTitle:** structural insights into substrate recognition in proton dependent2 oligopeptide transporters
28	c4gbzA_	Alignment	not modelled	99.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**d-xylose-proton symporter; **PDBTitle:** the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose
						PDB header:transport protein

29	c5aynA_	Alignment	not modelled	99.9	9	**Chain:** A: **PDB Molecule:**solute carrier family 39 (iron-regulated transporter); **PDBTitle:** crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
30	c5aymA_	Alignment	not modelled	99.8	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute carrier family 39 (iron-regulated transporter); **PDBTitle:** crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
31	c4m64D_	Alignment	not modelled	99.7	12	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**melibiose carrier protein; **PDBTitle:** 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium
32	c6ob7A_	Alignment	not modelled	99.5	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**equilibrative nucleoside transporter 1; **PDBTitle:** human equilibrative nucleoside transporter-1, dilazep bound
33	c6cc4A_	Alignment	not modelled	38.3	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**soluble cytochrome b562, lipid ii flippase murj chimera; **PDBTitle:** structure of murj from escherichia coli
34	c5m73H_	Alignment	not modelled	31.5	30	**PDB header:**rna binding protein **Chain:** H: **PDB Molecule:**signal recognition particle subunit srp72; **PDBTitle:** structure of the human srp s domain with srp72 rna-binding domain
35	c6en3A_	Alignment	not modelled	26.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-n-acetylglucosaminidase f2,multifunctional- **PDBTitle:** crystal structure of full length endos from streptococcus pyogenes in2 complex with g2 oligosaccharide.
36	c4r0cB_	Alignment	not modelled	26.3	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**abgt putative transporter family; **PDBTitle:** crystal structure of the alcanivorax borkumensis ydah transporter2 reveals an unusual topology
37	d1y60a_	Alignment	not modelled	23.8	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Formaldehyde-activating enzyme, FAE
38	c6r8fG_	Alignment	not modelled	20.6	22	**PDB header:**signaling protein **Chain:** G: **PDB Molecule:**brisc and brca1-a complex member 2,brcc45 (bre, brisc and **PDBTitle:** cryo-em structure of the human brisc-shmt2 complex
39	c6r8fE_	Alignment	not modelled	20.6	22	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**brisc and brca1-a complex member 2,brcc45 (bre, brisc and **PDBTitle:** cryo-em structure of the human brisc-shmt2 complex
40	c3p4rM_	Alignment	not modelled	19.2	30	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**fumarate reductase flavoprotein subunit; **PDBTitle:** crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
41	c1yr2A_	Alignment	not modelled	16.8	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl oligopeptidase; **PDBTitle:** structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
42	d2hg7a1	Alignment	not modelled	16.6	15	**Fold:**gpW/XkdW-like **Superfamily:**XkdW-like **Family:**XkdW-like
43	c2hg7A_	Alignment	not modelled	16.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage-like element pbsx protein xkdw; **PDBTitle:** solution nmr structure of phage-like element pbsx protein2 xkdw, northeast structural genomics consortium target sr355
44	c6b9mC_	Alignment	not modelled	16.2	29	**PDB header:**transferase **Chain:** C: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of uhrf1 ttd domain in complex with the polybasic2 region
45	d1sv0c_	Alignment	not modelled	15.7	27	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
46	d1tqza1	Alignment	not modelled	15.6	23	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Necap1 N-terminal domain-like
47	c2g9pA_	Alignment	not modelled	15.5	21	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
48	c1kf6A_	Alignment	not modelled	14.7	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase flavoprotein; **PDBTitle:** e. coli quinol-fumarate reductase with bound inhibitor hqno
49	c3db3A_	Alignment	not modelled	14.3	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the tandem tudor domains of the e3 ubiquitin-2 protein ligase uhrf1 in complex with trimethylated histone h3-k93 peptide
50	c3vvpA_	Alignment	not modelled	14.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of mate in complex with br-nrf
51	d1vqqa1	Alignment	not modelled	13.8	29	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain
52	c5uw7B_	Alignment	not modelled	13.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**peptide cyclase 1; **PDBTitle:** pcy1 y481f variant in complex with follower peptide
53	c4hvtA_	Alignment	not modelled	13.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**post-proline cleaving enzyme; **PDBTitle:** structure of a post-proline cleaving enzyme from rickettsia typhi

54	d1sxda_	Alignment	not modelled	13.4	50	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
55	c4mhvB_	Alignment	not modelled	13.1	30	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protein c-ets-2; **PDBTitle:** crystal structure of the pnt domain of human ets2
56	c3askC_	Alignment	not modelled	12.8	14	**PDB header:**ligase/dna binding protein **Chain:** C: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** structure of uhrf1 in complex with histone tail
57	d1fe8h2	Alignment	not modelled	12.6	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
58	c5azdA_	Alignment	not modelled	12.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**bacteriorhodopsin; **PDBTitle:** crystal structure of thermophilic rhodopsin.
59	c2l92A_	Alignment	not modelled	11.7	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**histone family protein nucleoid-structuring protein h-ns; **PDBTitle:** solution structure of the c-terminal domain of h-ns like protein bv3f
60	c6gjeA_	Alignment	not modelled	11.5	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein amnionless; **PDBTitle:** structure of the amnionless(20-357)-cubilin(36-135) complex
61	c3jcuz_	Alignment	not modelled	10.5	15	**PDB header:**membrane protein **Chain:** Z: **PDB Molecule:**photosystem ii reaction center protein z; **PDBTitle:** cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
62	c2yvxD_	Alignment	not modelled	10.2	8	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
63	c6oh2A_	Alignment	not modelled	10.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cmp-sialic acid transporter; **PDBTitle:** x-ray crystal structure of the mouse cmp-sialic acid transporter in2 complex with cmp, by lipidic cubic phase
64	d2axtz1	Alignment	not modelled	10.0	16	**Fold:**Transmembrane helix hairpin **Superfamily:**PsbZ-like **Family:**PsbZ-like
65	c6bx3N_	Alignment	not modelled	9.9	35	**PDB header:**gene regulation/transferase **Chain:** N: **PDB Molecule:**compass component sdc1; **PDBTitle:** structure of histone h3k4 methyltransferase
66	c2rqmA_	Alignment	not modelled	9.9	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mesoderm development candidate 2; **PDBTitle:** nmr solution structure of mesoderm development (mesd) - open2 conformation
67	c2e8pA_	Alignment	not modelled	9.7	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**elf3 protein; **PDBTitle:** solution structure of the n-terminal sam-domain of e74-like2 factor 3
68	d1sv0a_	Alignment	not modelled	9.6	40	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
69	c4tvrA_	Alignment	not modelled	9.6	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf2; **PDBTitle:** tandem tudor and phd domains of uhrf2
70	d1kf6a1	Alignment	not modelled	8.9	30	**Fold:**Spectrin repeat-like **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
71	c6b9tH_	Alignment	not modelled	8.6	27	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**methylphosphonate synthase; **PDBTitle:** crystal structure of mpns with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
72	c5n4dA_	Alignment	not modelled	8.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl oligopeptidase; **PDBTitle:** prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
73	c5uzwD_	Alignment	not modelled	8.3	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**peptide cyclase 1; **PDBTitle:** pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
74	d1ji7a_	Alignment	not modelled	8.2	20	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
75	c3hftA_	Alignment	not modelled	8.1	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wbms, polysaccharide deacetylase involved in o-antigen **PDBTitle:** crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution
76	d1sxea_	Alignment	not modelled	7.8	50	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
77	c5fjqB_	Alignment	not modelled	7.8	18	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**carbohydrate binding protein, putative, cpb33a; **PDBTitle:** structural and functional analysis of a lytic2 polysaccharide monooxygenase important for efficient3 utilization of chitin in cellvibrio japonicus
78	c6if7A_	Alignment	not modelled	7.7	27	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**chitin binding protein; **PDBTitle:** crystal structure of aa10 lytic polysaccharide monooxygenase from2 tectaria macrodonta
						Fold:mu transposase, C-terminal domain

79	d1bcoa1	Alignment	not modelled	7.6	10	**Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
80	c6h3cC_	Alignment	not modelled	7.5	20	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**brisc and brca1-a complex member 2; **PDBTitle:** cryo-em structure of the brisc complex bound to shmt2
81	d1jz8a1	Alignment	not modelled	7.5	50	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
82	c4k1cB_	Alignment	not modelled	7.4	10	**PDB header:**membrane protein/metal transport **Chain:** B: **PDB Molecule:**vacuolar calcium ion transporter; **PDBTitle:** vcx1 calcium/proton exchanger
83	c4gy5A_	Alignment	not modelled	7.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the tandem tudor domain and plant homeodomain of2 uhrf1 with histone h3k9me3
84	c3mkuB_	Alignment	not modelled	7.3	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
85	d1sm3h2	Alignment	not modelled	7.2	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
86	c2yowB_	Alignment	not modelled	7.2	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rbam17540; **PDBTitle:** bacillus amyloliquefaciens cbm33
87	d1wmib1	Alignment	not modelled	7.2	31	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**RelB-like **Family:**RelB-like
88	c4k1cA_	Alignment	not modelled	7.1	10	**PDB header:**membrane protein/metal transport **Chain:** A: **PDB Molecule:**vacuolar calcium ion transporter; **PDBTitle:** vcx1 calcium/proton exchanger
89	c4luqB_	Alignment	not modelled	7.1	15	**PDB header:**protein binding/toxin inhibitor **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of virulence effector tse3 in complex with2 neutralizer tsi3
90	d1ji8a_	Alignment	not modelled	7.1	11	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
91	c5lw4A_	Alignment	not modelled	7.1	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative chitin binding protein; **PDBTitle:** crystal structure of the chitin-active lytic polysaccharide2 monooxygenase bllpmo10a
92	d1lk3h2	Alignment	not modelled	7.1	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
93	c3hfxA_	Alignment	not modelled	7.0	3	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
94	c3uamD_	Alignment	not modelled	7.0	9	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**chitin binding domain; **PDBTitle:** crystal structure of a chitin binding domain from burkholderia2 pseudomallei
95	c4bbaA_	Alignment	not modelled	7.0	12	**PDB header:**protein-binding protein **Chain:** A: **PDB Molecule:**glucokinase regulatory protein; **PDBTitle:** crystal structure of glucokinase regulatory protein complexed to2 phosphate
96	d2bema_	Alignment	not modelled	6.9	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
97	c2bklB_	Alignment	not modelled	6.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
98	c2dkxA_	Alignment	not modelled	6.8	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam pointed domain-containing ets transcription **PDBTitle:** solution structure of the sam_pnt-domain of ets2 transcription factor pdef (prostate ets)
99	c2gleA_	Alignment	not modelled	6.8	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**neurabin-1; **PDBTitle:** solution structure of neurabin sam domain