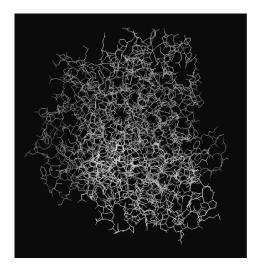
Channel Proteins in Protein Data Bank (PDB)

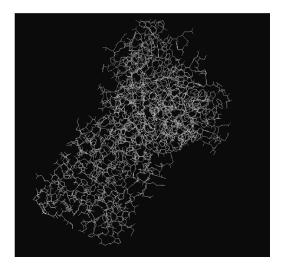
Yoshinori Nagai, Hiroshi Wako, and Stephen Hyde

We can find a lot of partly structure data in Protein Data Bank (PDB). Almost entirely atom sequence of channel proteins can be found. We looked at 3RUB, 6EBL, and 6BYO (These are PBP identification labels). These proteins are Crystallized structure of following PDB data. The PDB data of those three proteins show the details.

3RUB is "THE UNACTIVATED FORM OF RIBULOSE-1,5-BISPHOSPHATE CARBOXY-LASE (SLASH) OXYGENASE FROM TOBACCO REFINED AT 2.0-ANGSTROMS RESOLUTION".

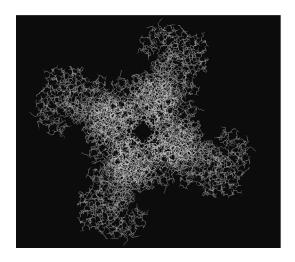
Crystallized structure

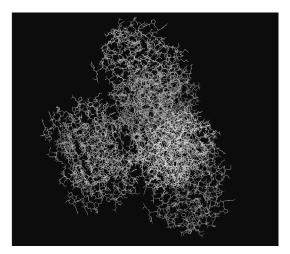




6BEL is "THE VOLTAGE-ACTIVATED KV1.2–2.1 PADDLE CHIMERA CHANNEL IN LIPID ANODISCS, CYTOSOLIC DOMAIN".

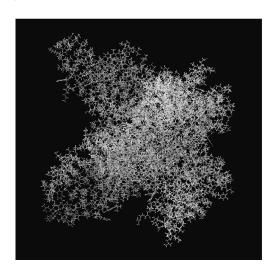
Crystallized structure

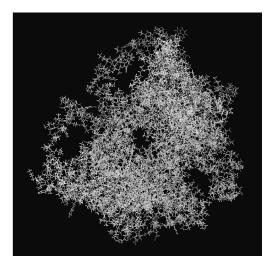




6BYO is "RESIDUE ASSIGNMENT CORRECTION TO THE VOLTAGE GATED CALCIUM CAV1.1 RABBIT ALPHA 1 SUBUNIT PDB ENTRIES 3JBR & 5GJV".

Crystallized structure





Above figures are depicted using software (RasMol) to look the form of channel proteins together with entire atoms. Each channel protein have many atoms. So we can consider analyzing manner for channel proteins. We started to analyze PDB data 6EBL, since the structure of 6EBL has good feature as the channel protein. We want to know the pore size of channel. So we consider how to obtain pore size of channel for no use of viewing image that is the first step of our thoughts.