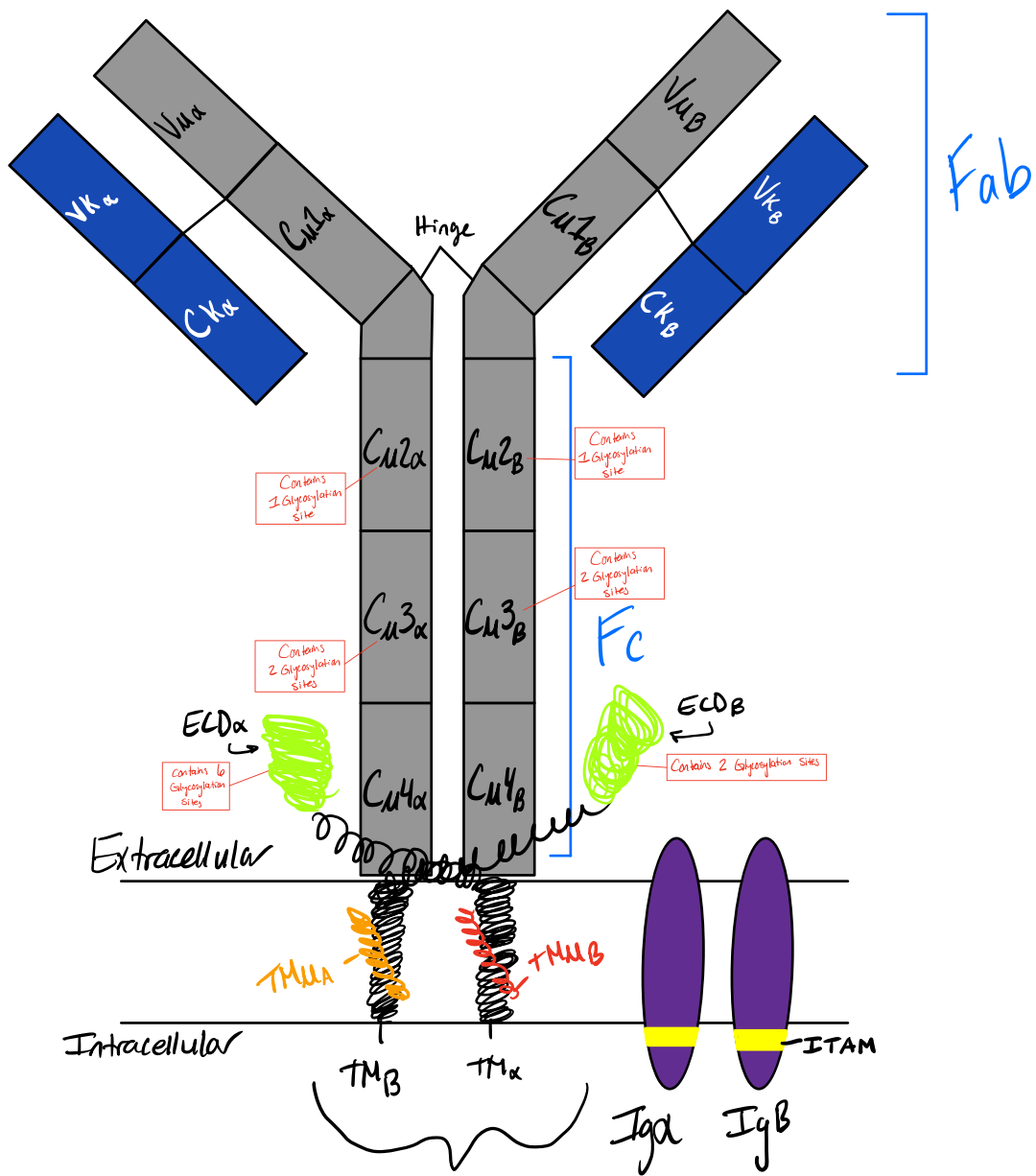


V = Variable
 C = Constant

● = Heavy Chain
 ● = Light Chain



TM_α, TM_β, TM_γ, & TM_δ
 form a four-helix bundle

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BIOL 302

Draw IgM

My drawing showcases the structure of the human Immunoglobulin-B cell receptor (IgM-BCR). The chains that are colored in grey are the heavy chains and the chains colored in dark blue are the light chains. One of the fragment antibodies, or Fab, consists of $V_{\mu\alpha}$, $V_{\kappa\alpha}$, $C_{\mu 1\alpha}$, and $C_{\kappa\alpha}$. The other Fab consists of $V_{\mu\beta}$, $V_{\kappa\beta}$, $C_{\mu 1\beta}$, and $C_{\kappa\beta}$. Everything labeled with a "V" is a variable region and everything labeled with a "C" is a constant region. The first fragment crystallizable (or Fc) portion is made up of $C_{\mu 2\alpha}$, $C_{\mu 3\alpha}$, and $C_{\mu 4\alpha}$. The second Fc is made up of $C_{\mu 2\beta}$, $C_{\mu 3\beta}$, and $C_{\mu 4\beta}$. $C_{\mu 2\alpha}$ and $C_{\mu 2\beta}$ both have one glycosylation site, while $C_{\mu 3\alpha}$ and $C_{\mu 3\beta}$ both have two glycosylation sites. There are two extracellular domains (ECD) attached to the IgM-BCR; they are ECD_{α} and ECD_{β} . ECD_{α} contains six glycosylation sites and ECD_{β} contains two glycosylation sites. The total number of glycosylation sites is 14. There are six components that are membrane spanning domains. They are $TM_{\mu A}$, $TM_{\mu B}$, TM_{α} , TM_{β} , Ig_{α} , and Ig_{β} . $TM_{\mu A}$, $TM_{\mu B}$, TM_{α} , TM_{β} form a four-helix bundle in the transmembrane domain. This molecule of IgM (mIgM) differs from soluble IgM (sIgM) in that it is not a pentamer or a hexamer. sIgM has two C-terminal β strands that result in oligomerization. On the other hand, mIgM has two C-terminal α helices ($TM_{\mu A}$ and $TM_{\mu B}$) that secure it into the cell membrane. When IgM is attached to the cell membrane (mIgM), it is known as a BCR. When IgM is no longer attached to the cell membrane (sIgM), it is known as an antibody.