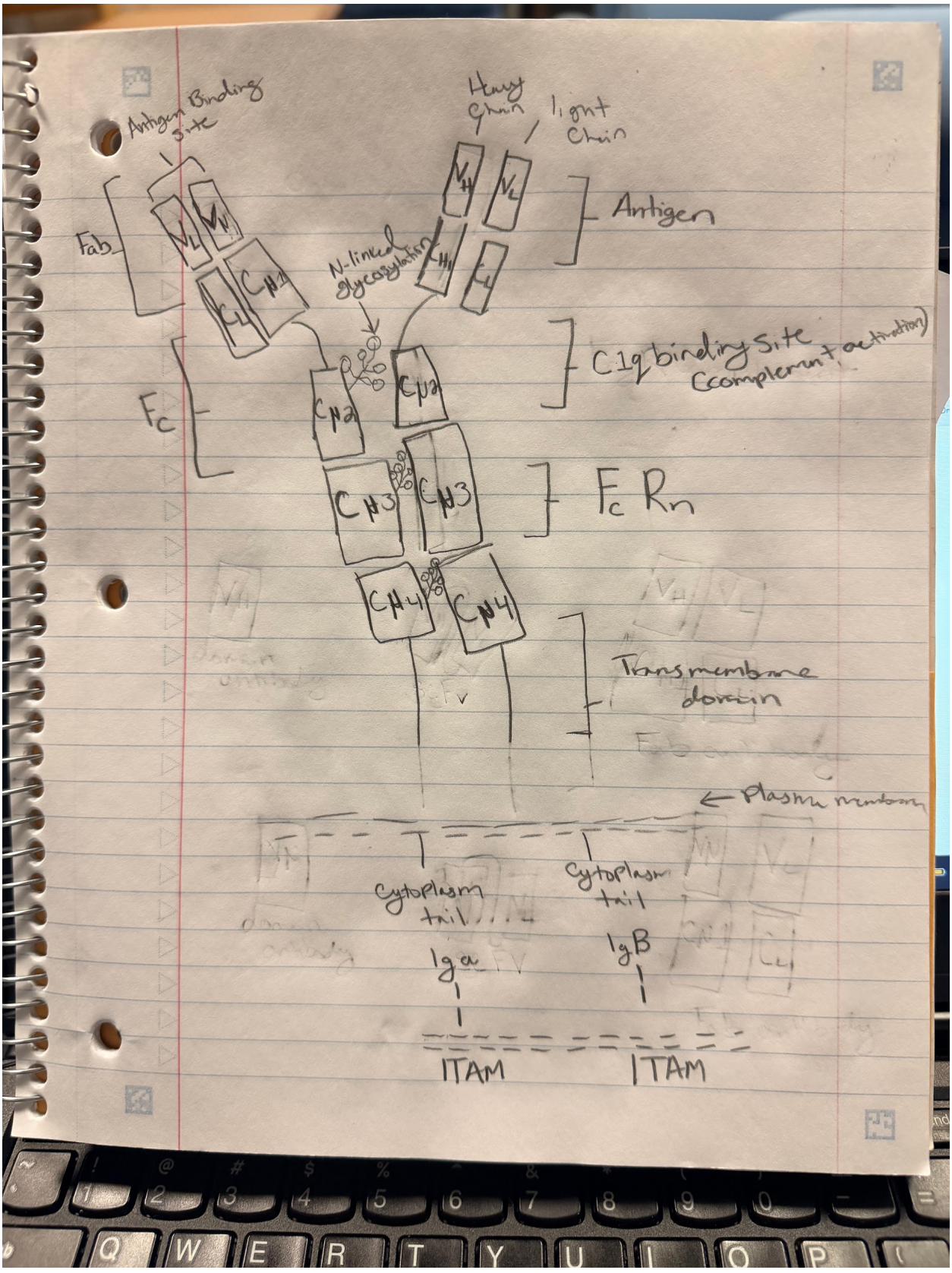
Antigen Binding site
Heavy Chain
Light Chain
Fab
Antigen
N-linked glycosylation
C1q binding site (complement activation)
Fc
FcRn
Transmembrane domain
Plasma membrane
Cytoplasm tail
Cytoplasm tail
Iga
IgB
ITAM
ITAM

Membrane-bound IgM B-cell receptor(BCR) is structured as a monomeric immunoglobulin structure composed of two heavy chains and two light chains. Additionally, membrane-bound IgM forms two Fab regions that are responsible for regulating antigen recognition and four constant domains within each heavy chain. Moreover, the fragmented, crystallizable portion includes the N-linked glycosylation, which helps to stabilize the IgM structure as displayed in the recent cyro-Em structural analyses. Unlike its soluble counterpart, the membrane-bound IgM has a hydrophobic transmembrane domain that anchors to the plasma membrane and associates with IgA and IgB heterodimer through van der Waals forces. Additionally, its cytoplasmic immunoreceptor tyrosine-based activation motifs play a crucial role in regulating the intracellular signaling pathway following antigen binding. While on the other hand, soluble IgM lacks these transmembrane regions and arranges into a pentamer stabilized by a J chain, and primarily functions in complement activation rather than antigen receptor signaling.