- Thesis Intro
  - 1 What are pLGICs
    - 1.1 What is an ion channel
      - ~~1.1.1 Conducts ions across membrane~~
      - ~~1.1.2 Transmembrane proteins~~
      - 1.1.3 Essential for various cellular functions (EXPLAIN)
    - ~~1.2 What are the general structural features of pLGICs~~
      - ~~1.2.1 Ion channels made of 5 subunits~~
      - ~~1.2.2 ECD beta sheets with binding pockets-Gated by various ligands~~
      - ~~1.2.3 TMD 5 bundles of 4 alpha helices - interacts with membrane~~
    - 1.3 What is the physiological significance of pLGICs, ie: what do they do
      - 1.3.1 Eucariot: Mediate neuronal function
        - ~~1.3.1.1 nAChR and 5-HT3R - cationic receptors activate action potential~~
        - ~~1.3.1.2 GABAaR glycine receptors - anionic receptors inhibit action potential~~
      - ~~1.3.2 Procariotic ELIC GLIC - We don't know~~
    - 1.4 Where are pLGICS found in Mammals
      - ~~1.4.1 Centural and periferal nervous system~~
      - ~~1.4.2 Post-synaptic junction in brain and muscle~~
    - ~~1.5 Health related issues of pLGICs~~
      - ~~1.5.1 See most recent paper~~
  - 2 Lipids and membranes
    - 2.1 Model Membranes
      - 2.1.1 What is a lipid
      - 2.1.2 What is a membrane
      - ~~2.1.3 What causes domain formation~~
      - ~~2.1.4 What effect does Chol have on a membrane~~
        - ~~Merge Lipids and Membranes, sub group native and model~~
      - 2.1.5 What effect do PUFAs have on a membrane
    - 2.2 Native Membranes
      - ~~2.2.1 How does membrane compositions vary across cell types~~
      - 2.2.2 What are medical issues of too few n-3 PUFAs
  - 3 Protein modulation by lipids
    - ~~3.1 Which lipids have been most studied~~
      - ~~3.1.1 Cholesterol, saturated, mono-unsaturated, sphingo - Anionic, Neutral~~
    - 3.2 How do Lipids affect function
      - 3.2.1 Modulate function
    - ~~3.3 What are known functional effects of chol~~
      - ~~3.3.1 Required for function, ~ 20-30% of membrane composition~~
    - 3.4 What conditions have anionic lipids promoted function
      - 3.4.1 I do not know...
  - 4 Sequence/Structure and lipid binding
    - 4.1 What role might structure of the protein play in lipid occ
      - 4.1.1 M4 as a lipid sensor
      - ~~4.1.2 M4 cone/star resulting shape effect minimized by PUFAs, and stabilized by CHOL~~
      - ~~4.1.3 Inter-subunit "cone" stabilized by chol, occupied by saturated~~
    - 4.2 How might sequence play a role in lipid- protein binding
      - ~~4.2.1 Charge repells anionic lipids~~
    - 4.3 How/why can proteins deform membranes
      - ~~4.3.1 M4 provides cone/star shape, unfavorable to membrane~~
      - 4.3.2 Size of TMD my cause hydrophobic mismatch
  - 5 pLGIC boundary lipids
    - 5.1 Are boundary lipids conserved across pLGICS sequences
      - ~~5.1.1 No, anionic lipid occupation changes based on location of cationic amiono acids~~
    - 5.2 What are possible mechanisms by which lipids could affect protein function
      - ~~5.2.1 Prevent protein from "colapsing"~~
      - ~~5.2.2 Minimize deformation energetics~~
    - 5.3 How would the membrane composition affect boundary lipids
      - ~~5.3.1 Different membranes, different lipids. How much of lipid x can you get and does lipid y act as a reasonable replacement?~~
    - 5.4 Why might the distribution of lipids matter
      - ~~5.4.1 function~~
      - ~~5.4.2 Deformation energy minimization~~
      - ~~5.4.3 Some lipids may exacerbate poor function if bound to specific locations~~
  - 6 Methods
    - 6.1 Where are pLGICs experimented in
      - 6.1.1 Model membranes : boundary lipid studies
      - 6.1.2 Oocytes : functional studies
      - 6.1.3 Model "rings" structural studies
    - ~~6.2 What are the experimental approaches that have been used to identify boundary lipids for membrane proteins~~
      - 6.2.1 Florences quenching
      - 6.2.2 Mass Spec
      - 6.2.3 Spin Label
      - 6.2.4 Cryo-EM or x-ray Chrystalography (lesser extent)
    - ~~6.3 How can we determine whether a lipid affects function via domain formation vs direct ligand-like interactions~~
      - 6.3.1 Electrophysiology
      - 6.3.2 Florences quenching
      - 6.3.3 NMR?
    - ~~6.4 Why do MD simulations~~
      - 6.4.1 Computational Microscope
      - 6.4.2 Rooted in physics
      - 6.4.3 Acts as predictor, or supporter for experimental studies
    - 6.5 What computational tech have been used to predict pLGIC-boundary lipids?
      - 6.5.1 Atomistic simulations
      - 6.5.2 Docking
      - 6.5.3 Coarse-Grained SImulations
    - 6.6 Why is docking not ideal
      - 6.6.1 I DO NOT REMEMBER
  - 7 Point of this thesis
    - 7.1 What is the knowledge gap- ie What general question does this particular thesis hope to answer
    - 7.2 What was the trajectory of the thesis? Ie how do the different chapters fit together and build on eachother?