#flo #ref

1 | Integrative modeling of membrane-associated protein assemblies

- membrane proteins are really hard to study with experimental tech
- but we can get around this through deposited structures of membrane proteins?
  - and use a method called ”docking”
- MP = membrane protein
- two major classifications, peripheral and integral
  - peripheral is located on the sides and attached through non coavelent ’interactions’
  - IMPs are inserted into the membrane and only exposed on one side or span the entire lipid bilayer?

transmembrane are the ones that span the whole lipid bilayer, and are important for protein - protein interactions

these TMs are valuable targets for drug discorvery

we use crystals to make really good microscopes to study well, but the crystals are hard to get?

docking is about creating a bunch of possible conformations and then evaluating them called sampling and scoring scoring can be done with ml?

they are proposing a new method for modeling membrane-associated protein assemblies - which are compexes with membrane embeded protein and something soluable?

lightdoc is attracted towards the energetically favorable docking poses?