1. Predicting a list of crystallography conditions present from amino acid structures: <https://mlcb.github.io/mlcb2019_proceedings/papers/paper_3.pdf>
   1. They note (and this is 2019) that “To the best of our knowledge, direct prediction of crystallization conditions from raw sequence has not been explored,” which seems about consistent with what I’m seeing
   2. They also have a nice list in section 2 of related attempts that also seems pretty consistent with my research: lots of attempts to predict crystallization propensity, a few papers on pH from pI, and one paper saying it’s not possible
2. Amino acid sequence similarity as determined by BLAST is independent of <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6404862/>
   1. My two big complaints with this paper are (1) they show these graphs arguing there’s no correlation between conditions and amino acid sequence identity but they never quantify any of that information and (2) they make a big deal about there not being a trend in the 99-100% identity range, but it seems that that regions should be about constant anyways
3. Predicting crystallization pH from pI: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4410668/>
   1. Conclusion is that pH should be within 1 unit of pI (potentially within 2), so if we have a model giving predictions within 0.8 pH on average that seems about reasonble