attached title

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Abstract

Metalloproteins compose approximately 40 percent (look up how to do percents in latex) of all known proteins, and use some metallic group to accomplish their chemistry. One such metallic group is heme. Heme is a member of the porphyrin family, which are able to catalyze a broad range of reactions. Heme in particular catalyzes many different reactions and is present in many proteins. However, the underlying structural requirements to host heme in a protein are not well studied.

In this study, all heme or heme-c containing proteins as of xx were downloaded and processed in order to determine underlying structural characteristics these proteins may have in common. Parameters that were examined include: xx. Overall, we found: xx. These results may have implications for protein engineering; or if I fucked up this illustrates the difficulty of the field and demonstrate the wide range of acceptable environments of heme; it may therefore be more appropriate to take a more hands-on approach until perhaps other computational methods evolve to better examine structure-function relationships.

See? Not so bad of a worst-case scenario. Just, an unusual sentiment to see in modern science.

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Chapter 1

Introduction

*insert the abstract's first paragraph basically here later

In previous work, only 125 hemoproteins were studied. Although pdbs were thoroughly examined and the datasets were culled, the sample size of this study is very small compared to the amount of hemoproteins available in the pdb a decade later (10,000 HEM-containing proteins and xx). While not possible to cull as in this study, the additional sample size is of interest to examine for other structural motifs or underlying characteristics.

These characteristics include: xx. They are achieved by either scanning the pdb for them or calculation as detailed below.

All of these characteristics have implications in the field of protein engineering or basic research into hemoproteins. Examples of the uses of these results include [SUPER BLOOD STUDY] and [OTHER PROTEIN ENGINEERING STUFF]. Not sure how much we can reference those other papers besides doing that besides in the conclusion.

Notable results from some of the prior studies include: xx and xx. These characteristics are also examined in this dataset, while some are not due to different study approaches.

Chapter 2

Methods

Perhaps I need something right here first?

- Download from PDB using the script they've provided at RCSB for many, many files
- Use UCSF Chimera to determine:
  - Volume
  - SA
  - Nearby AA
- R to process raw data and produce tables
- Whatever other software we use to achieve the other results. E.g. E, or availability to solvent etc. likely will stick w Chimera I suspect. Or somehow implement the Python script to open both chimera for the first part of what we've done or for something else later. The script we've written is a python script, not a chimera script. We're initializing it with chimera and excluding the necessary code... to initialize chimera and specify chimera to receive the commands

Chapter 3

Equipment

Chapter 4

Results

Chapter 5

Dicussion

Chapter 6

Conclusion

this is just as master's and in basic research don't feel the need to replicate what took some god forsaken, sad, overworked, impoverished PhD students years + with help of their PIs and with generous word fluff to hide fuck ups. 0 -¿ thesis in approx. 3-4 months during global catastrophe is nifty