Writing up your results

BIOL3004 electives

In General
- every paper has a very distinct and clear aim
- precise the focus of the paper in the title
- every paper is different
- different proteins have different stories
- for some the structure is the main focus
- for some the evolution is more important
- others concentrate on the function
- good papers focus in on one topic but also cover all the other areas
- personal style of author
  - However, rules of scientific writing apply

Step 1
- Discuss in your group
  - what information can you present
    - methods, results & discussion
    - how do you put your data into order
    - what background information is needed
    - introduction
  - Often it helps to draw a conceptional map
  - Look at papers of related structures: how are they written?

Step 2
- Start a draft of your paper
  - Structured outline (title page, abstract, introduction, methods, results & discussion, conclusion)
  - Order of writing is different between people, that’s how I do it:
    - Start with introduction (background) and give a short summary (road map) of what is in the paper
    - prepare figures and tables in publication quality and include them into the draft
    - add methods, results and discussion section
    - methods = how did you do it
    - results = what data/information do you present
    - discussion = what does it mean and how do your results fit into the larger picture of knowledge
    - when the body of the paper is finished add
      - abstract = precise outline of key points in your paper
      - and conclusion = summary of key points and potential future work

Step 3
- proof reading
  - give the paper to anyone you can think of
    - your peers, your spouse, your grandmother
  - reader may not understand the topic but s/he can give you valuable feedback on grammar and logic
  - if it’s a good paper your grandma will know it

What you have to discuss

Only a tentative pointer. You may have much more material to include.
Background
- if function is known describe context
- often a figure is better than many words
- copyright!!!!!!

Describe your structure
- In methods, give experimental data
  - compare with other papers
- Describe fold, class, structural elements, ligand binding sites, conserved residues, surface properties, etc
- figures of structure (= details, surface, ...)
- Add labels, arrows into figures to highlight features

Compare your structure
- to structures with similar folds
  - how similar are they
    - by structure
    - by sequence
    - by function (relative to each other)
  - use figure to illustrate differences/similarities

Describe sequence features
- conserved residues (or properties)
- non-conserved sequences with similar structures
- quality of alignment
- if complete alignment is necessary if your protein is very long
  - But prepare a figure of the complete alignment as supplementary information
  - Use clear sequence labels (GenBank:895291384)

Function in context of structure
- describe (likely) function
- Functional important features in structure
  - catalytic residues, binding sites, flexible sites, conserved regions
  - how well is molecular function supported by cellular function?
  - expression data (= very noisy data!!)
  - is the organismal distribution of the gene in agreement with its function, or has function possibly changed over time?
show best tree possible (exclude sequences if necessary)
- clear labels
- indicate in text the reliability (bootstrapping)
- beautify tree
- in discussion: point out missing phyla/organisms

### X-ray Structure Determination of Human Profilins II: A Comparative Structural Analysis of Human Profilins

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Human profilins are multifaceted, single-chain proteins which define a new superfamily. They are a major component of the nucleoid in eukaryotic cells and are involved in a variety of cellular processes such as DNA replication, transcription, and repair. They are also found in the cytoskeleton and are involved in actin polymerization. The crystal structure of profilin II from rabbit sperm is presented, and its predicted structure is compared with that of profilin I from human sperm. The two structures are similar, but the profilin II structure is more extended and has a different orientation of the actin-bound domain. The filamentous actin binding site is highly conserved, and the profilin II structure is consistent with the observed actin filament binding properties of profilin II.

### Layout

- **Title, Authors, Abstract, Introduction, Results, Discussion, Materials and Methods, References**
- use sub-headings to structure text
- references and citations in JMB style
- no word or figure limit, but write succinct and concise and only include figures clearly help your argument

### Reference


### Results

- Actin filament binding studies
- Chemical modification experiments
- In vitro kinase assays
- Polymerization assays
- Functional implications

### Conclusion

The crystal structure of profilin II provides insights into the mechanisms by which profilins regulate actin filament dynamics and the interactions between profilins and other proteins involved in actin cytoskeleton organization.

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*Publication* Information:
- Article available online at [tcnaria]{#tcnaria} on July 1, 1993 (JMB 230, 1113-1123).

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*Journal Information*:
- *Journal of Molecular Biology* (J Mol Biol)
- Volume 230, Issue 3, 1113-1123
- Published online: 1 July 1993

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*Funding*:
- National Institutes of Health (NIH) Grant GM-35385
- American Heart Association (AHA) Grants 9150065N and 9310073N

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*Keywords*:
- Profilin
- Actin filament binding
- Crystal structure
- Chemical modification
- In vitro assays

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*Published*:
- 1993
- Volume: 230
- Issue: 3
- Pages: 1113-1123
Materials and Methods

Table 1. Data collection and statistics

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Structure determination

Results from NMR analysis were employed to a molecular replacement approach followed by an automated search of available databases and when none were found, a structure determination was performed using thetilium dialis. The coordinates were determined using the program CNS (Brünger et al., 1998). The space group was determined to be P2_12_1. The initial model was built using O (Dobler et al., 1993). The first models of refinement all NMR structures were based on additional restraints were obtained using the program CNS (Brünger et al., 1998). The space groups were determined to be P2_12_1. The final models of refinement all NMR structures were based on additional restraints were obtained using the program CNS (Brünger et al., 1998). The space groups were determined to be P2_12_1. The final models of refinement all NMR structures were based on additional restraints were obtained using the program CNS (Brünger et al., 1998). The space groups were determined to be P2_12_1. The final models of refinement all NMR structures were based on additional restraints were obtained using the program CNS (Brünger et al., 1998).

References


Rewards

- Please indicate on Wiki if you’d like to be considered for scholarship
- completion of work for publication
- scholarship includes registration to East Coast Protein Meeting to present your work
- Scholarships have no influence on marks