Grading of problem set #2

Lecture “Interactions of Proteins and Nucleic Acids: Biophysical Concepts and Theoretical Descriptions (BPC2024)”

Winter Term 2024/2025 | Prof. Dr. Karsten Rippe

Web page: https://malone.bioquant.uni-heidelberg.de/teaching/BPC\_lectures/BPC\_1+2.html

Grading rubric (per question)

**Note**: The distribution of the maximum point value per question part is given below. Full points can be awarded despite solutions not being perfect.

**11.0-12.0: Excellent**

* Complete, correct methodology
* Clear reasoning
* Independent analysis demonstrated
* Proper units
* **Note 1 to the grader**: Be lenient on minor calculation errors
* **Note 2 to the grader**: Give full points for correct calculations even if explanations are brief

**8.0-10.75: Very Good**

* Minor gaps or errors
* Good reasoning shown
* Some improvements possible
* Mostly independent work

**5.5-7.75: Good**

* Significant gaps present
* Basic understanding shown
* Major improvements needed
* Partial independence

**3.0-5.25: Fair**

* Major conceptual errors
* Some correct elements
* Substantial revision needed
* Limited independent thought

**0-2.75: Insufficient**

* Missing or minimal correct content
* Major misunderstandings
* No demonstrated understanding
* No independent analysis

**Common Point Deductions**

* Missing units: -0.5 per instance
* Unexplained assumptions: -0.5 per instance
* Calculation errors: -0.25 to -1 depending on impact
* Missing references: -0.5 per required citation
* Unclear reasoning: -1 to -2 per section

Distribution of points between question parts for problem set #2

**General principles used for problem set #2**

- Clear explanation of molecular mechanisms

- Correct use of structural biology concepts

- Understanding of thermodynamic principles

- Proper reference to experimental evidence

- Integration and reference of lecture material and literature

- Please indicate in a comment if unreferenced use of AI tools is suspected

**Question 1 (12 points total)**

1a) 5 points - Specific interactions and structure

- 2 points: Correct example of guanine interaction with molecular detail

- 2 points: Correct example of adenine interaction with molecular detail

- 1 point: Correct explanation of α-helix role and major groove geometry (1.2 nm match)

1b) 3 points - Unspecific binding

- 1.5 points: Complete list of relevant amino acids (Lys, Arg, His, Ser, Thr, Asn, Gln)

- 1.5 points: Correct identification of forces (electrostatic, H-bonds, van der Waals)

1c) 4 points - Function and distortion

- 1 point: Clear examples of distorting proteins (TBP, CAP)

- 1 point: Clear examples of non-distorting proteins (histones)

- 1 point: Mechanistic explanation of distortion (e.g., transcription initiation)

- 1 point: Biological function implications (e.g., regulation, accessibility)

**Question 2 (12 points total)**

2a) 5 points - Histone-DNA interactions

- 2 points: Correct analysis of backbone vs base interactions (with ~57% quantification)

- 2 points: Correct periodicity determination (5 bp) with explanation

- 1 point: Methodology description/evidence

2b) 4 points - DNA fragment analysis

- 2 points: Correct length determination (147 bp)

- 2 points: Accurate sequence identification at both ends

2c) 3 points - Unfolded regions

- 1.5 points: Identification of N-terminal tails

- 1.5 points: Description of modification roles and function

**Question 3 (12 points total)**

3a) 4 points - Entropy contributions

- 1.5 points: Hydrophobic effect explanation

- 1.5 points: Conformational entropy explanation

- 1 point: Additional contribution (e.g., rigid body, ions)

3b) 4 points - Binding/dissociation factors

- 2 points: Clear identification of binding-driving factors

- 2 points: Clear identification of dissociation-favoring factors

3c) 4 points - Specific vs unspecific binding

- 2 points: Identification of relevant entropy term

- 2 points: Explanation of differences between specific/unspecific binding

**Point Deductions**

- -0.25 points: Minor omissions or unclear explanations

- -0.5 points: Missing references where needed

- -0.75 points: Significant gaps in explanation

- -1 point: Major conceptual errors

Format of student problem set #2 grading

**[Student Name] ([File Reference])**

Total: XX/36

**1. Specific and Unspecific Interactions: XX/12**

* a) X/5 - Full points or (-Y) with specific reason why points were deducted
* b) X/3 - Full points or (-Y) with specific reason why points were deducted
* c) X/4 - Full points or (-Y) with specific reason why points were deducted

**2. Nucleosome Analysis: XX/12**

* a) X/5 - Full points or (-Y) with specific reason why points were deducted
* b) X/4 - Full points or (-Y) with specific reason why points were deducted
* c) X/3 - Full points or (-Y) with specific reason why points were deducted

**3. Binding Thermodynamics: XX/12**

* a) X/4 - Full points or (-Y) with specific reason why points were deducted
* b) X/4 - Full points or (-Y) with specific reason why points were deducted
* c) X/4 - Full points or (-Y) with specific reason why points were deducted

**Specific feedback:**

* Strength: [Main strength of the submission]
* Area for improvement: [Key area needing improvement]
* Notable aspect: [Something particularly noteworthy]
* Presentation: [Comment on organization/clarity]
* References: [Comment on use of sources]

**Key features of this format:**

1. Points are only deducted when specific required elements are missing
2. Each deduction includes specific reason
3. Full points are given when all required elements are present
4. Individual feedback for each student
5. Follows point distribution from grading criteria document