# 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

**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