# Grading of Problem Set #4: Chromatin and Epigenetics

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 #4

**General principles used for Problem Set #4**

* Clear explanation of molecular mechanisms
* Correct interpretation of experimental data
* Understanding of epigenetic principles and models
* Proper analysis of simulation results
* Integration and reference of lecture material and literature
* Please indicate in a comment if unreferenced use of AI tools is suspected

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### Question 1: HP1 Binding to Nucleosome Substrates (12 points total)

**1a) 4 points - Dissociation constant estimation**

* 2 points: Correct identification of KD values for all three substrates
* 1 point: Proper methodology for determining KD from binding curves
* 1 point: Recognition of relative binding affinity pattern

**1b) 4 points - HP1 binding modes**

* 1 point: Description of monovalent vs. bivalent binding
* 1 point: Explanation of nucleosome conformation effects
* 1 point: Discussion of HP1 dimerization/oligomerization
* 1 point: Analysis of linker DNA contributions

**1c) 4 points - Theoretical model selection**

* 1.5 points: Identification of appropriate binding model(s)
* 1.5 points: Explanation of model parameters and applicability
* 1 point: Discussion of limitations and considerations for model selection

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### Question 2: Dynamics of Epigenetic Modifications (12 points total)

**2a) 4 points - Comparison of modification lifetimes**

* 1.5 points: Correct characterization of DNA methylation stability
* 1.5 points: Correct characterization of histone methylation and acetylation stability
* 1 point: Quantitative comparison with appropriate time scales

**2b) 4 points - Factors affecting modification stability**

* 1 point: Discussion of molecular/chemical properties
* 1 point: Analysis of enzymatic regulation mechanisms
* 1 point: Explanation of replication and inheritance effects
* 1 point: Consideration of protein complex/reader contributions

**2c) 4 points - Maintenance of stable epigenetic patterns**

* 1 point: Description of feedback loops and self-reinforcement
* 1 point: Discussion of cooperative interactions between modifications
* 1 point: Explanation of maintenance mechanisms during DNA replication
* 1 point: Analysis of additional stabilizing factors (e.g., spatial organization, lncRNAs)

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### Question 3: Simulations of Epigenetic Chromatin States (12 points total)

**3a) 4 points - Simulation plots**

* 2 points: Generation of appropriate plots for at least three F values
* 1 point: Clear presentation of results with proper labeling
* 1 point: Selection of meaningful comparison for analysis

**3b) 4 points - Analysis of simulation results**

* 1 point: Identification of key features in the plots
* 1 point: Comparison between different parameter settings
* 1 point: Discussion of effects on bistability
* 1 point: Explanation of selection rationale

**3c) 4 points - Prediction and experimental design**

* 2 points: Clear, testable prediction based on simulation results
* 2 points: Appropriate experimental design to test the prediction

## 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