# ENTRANCE EXAMINATION IN BIOTECHNOLOGY FOR APPLICANTS ENTERING MASTER'S PROGRAMS OF PHYSTECH SCHOOL OF BIOLOGICAL AND MEDICAL PHYSICS

**Structure of the program:** The program consists of two sections. Applicants in the "Applied Bioinformatics" competitive group pass an entrance test in accordance with section 1 of the program, those entering the "Medical Biotechnology" competitive group - in accordance with section 2.

## Section 1
## Regulations

The entrance test will be held in the form of an oral exam with preliminary preparation of the answer tothe questions from the sections below (1 question from each block).
During the oral interview with the examiner you have the opportunity to talk about your achievementsrelated to the subject in the fields of molecular biology, bioinformatics etc. It is better to prepare your portfolio in advance.
Additional questions are asked in accordance with the desired specialization to which the undergraduate isadmitted. These can be simple biochemistry tasks, you could find examples in the list of questions from block 2. Questions related to the subject of bioinformatics upon admission to this specialty may include simple tasks: writing a short program or finding errors in the code. You can use different programming languages, Python is preferred.
You can find more about this program as well as prepare for the exam using the online test by the link:https://bioinformatics.mipt.ru/

## Block 1: bioinformatics
1. Probability Theory: Conditional Probability. Definition of conditional probability, full probabilityformula, Bayes formula. Independence of events.
2. Probability theory: random variables, distribution function. Mathematical expectation, variance,correlation, covariance, their properties.
3. Probability theory: The main theorems of probability theory. Chebyshev inequality. The law of largenumbers. Central limit theorem.
4. Probability Theory: probability distributions. Standard discrete and continuous distributions, their mathematical expectations, variances and properties: binomial; uniform normal Poisson; exponential;geometric.
5. Probability theory: The concept of the Markov chain. Stationary state.
6. Programming, algorithms and data analysis. The simplest constructs of a programming language.Loops, branches, recursion.
7. Basic UNIX commands.
8. Programming and algorithms: binary search and search trees. Hash tables.
9. Programming and algorithms: Graphs, graph traversal in width and in depth.
10. Programming and algorithms: Sorts, the average and worst complexity of the algorithms.
11. Programming and algorithms: Regular expressions.
12. Statistics and data analysis: Sampling, likelihood.

13. Statistics and data analysis: Estimation of distribution parameters, maximum likelihood method.
14. Statistics and data analysis: Confidence intervals.
15. Statistics and data analysis: Basic concepts of machine learning. Delayed sampling, its shortcomings.Cross validation. Leave-one-out. Retraining.
16. Statistics and data analysis: Clustering. K-Means Algorithm. Assessment of the quality of clustering.

**Block 2: molecular biology and biochemistry**
1. Molecular biology: the central dogma of molecular biology.
2. The structure of DNA and the mechanism of heredity. Noncanonical DNA structures. Hyperchromiceffect. Supercoiling of ring genomes and plasmids. DNA, chromosomes and cell cycle. Chromatic fiber DNA packaging in eukaryotes. The device of the nucleosome. Histone code.
3. DNA replication. Polymerases involved in replication, their enzymatic activity. Replication fork and itscomponents. Topological problems of replication of circular and linear genomes.
4. Classification of DNA damage and mechanisms for their correction. Diseases caused by repair defects.The use of DNA damaging agents in medicine. The reaction of cells to double-stranded breaks in DNA. TUNEL Method
5. Homologous DNA recombination and its biological functions. Conservative site-specific recombination. The main classes of mobile genetic elements. Repetitions. Features of recombination inthe formation of immunoglobulin genes and T-cell receptors.
6. The use of DNA repair mechanisms for editing genomes. Restriction-modification systems, theirpurpose in bacteria and use in genetic engineering.
7. Genome editing technologies: zinc fingers, TALEN proteins, CRISPR. Purpose of the CRISPR / Cassystem in bacteria.
8. DNA transcription, supercoiled coils and nucleosomes. The structure of RNA polymerase. Stages of thetranscription cycle and principles of regulation. Attenuation of transcription. Common features and differences in transcription in bacteria and eukaryotes.
9. The main mechanisms of mRNA processing: capping, polyadenylation and splicing of introns. Modernideas about splicing mechanisms.
10. Modern ideas about the structure, functioning and evolutionary history of eukaryotic ribosomes.
11. The genetic code. Bounding frames. The structure and function of tRNA.
12. Translation initiation: general mechanisms and features in prokaryotes and eukaryotes. RNAstructures that control translation efficiency. Elongation cycle. Broadcast Termination.
13. The basic principles of broadcast regulation. Protein folding and processing. Post-translationalmodification of proteins. Peptide bond. Primary, secondary, tertiary structure of the protein.

14. Basic ideas about the structure of eukaryotic cells. Appointment of cellular organelles. Mitosis and itsphases. The cell cycle, stages of the cell cycle. Cell differentiation.
15. Regulatory sites in the genome: promoter, TATA box, enhancer, silencer, insulator.
16. Variety and function of short protein non-coding RNA. RNA interference. The biological role of RNAinterference. siRNA. Applied use of RNA interference
17. The principle of polymerase chain reaction. Real-time PCR. Reverse transcription PCR.
18. DNA sequencing methods. Sanger sequencing. Sequencing a new generation.
19. Molecular biology: genome, gene, GC composition, genetic code, its degeneracy and universality, ribosome, nucleotides, amino acids, tRNA, complementarity, ribosome binding site, reading frame, RNAsecondary structure.
20. Biochemistry: calculate the pH value of 6 nM hydrochloric acid solution
21. Biochemistry: indicate the possible amount of isomeric tripeptides that can be obtained bycondensation of three amino acids - leucine, arginine and glycine.
22. Biochemistry: starch and cellulose consist of the same monomer - glucose. Explain the possiblecauses of differences in the physicochemical properties of these polysaccharides.
23. Biochemistry: membrane phospholipids carry a significant charge. What is the sign of this charge?What ions can compensate for this charge?
24. Biochemistry: The concentration of the substrate of the enzymatic reaction is 4

Michaelis constants.What will be the ratio of the speed of this reaction?
25. Biochemistry: Fats are divided into saturated (solid) and unsaturated (liquid) in the composition oftheir higher fatty acids. What fats will have a higher energy content per gram of matter? Explain the answer.
26. Biochemistry: Some types of RNA (tRNA, rRNA, etc.) form stable secondary structures (hairpins).How their boundaries can be determined by the primary sequence of RNA?
27. Biochemistry: What parameters of amino acids should be considered when predicting transmembraneregions of proteins?

**Recommended literature**
1. Alberts B. et al. Molecular Biology of the Cell in Cell 4th. – 2002.
2. Murray R. K. et al. Harper's illustrated biochemistry. – Mcgraw-hill, 2014.
3. "Introduction to bioinformatics algorithms" Jones, Pevzner
4. "Bioinformatics - From Genome to Therapies" - Lengauer et al (2007)

**Section 2**
**Regulations**

The entrance test will take the form of an oral examination with preliminary preparation of answersto the questions from the following sections.

During the oral interview with the examiner, you have the opportunity to talk about your achievements in the subject in the fields of molecular biology, bioinformatics, etc. It is better to prepare your portfolio in advance.

**Molecular biology and biochemistry**
1. Molecular biology: the central dogma of molecular biology.
2. The structure of DNA and the mechanism of heredity. Noncanonical DNA structures. Hyperchromic effect. Supercoiling of ring genomes and plasmids. DNA, chromosomes and cellcycle. Chromatic fiber DNA packaging in eukaryotes. The device of the nucleosome. Histone code.
3. DNA replication. Polymerases involved in replication, their enzymatic activity. Replicationfork and its components. Topological problems of replication of circular and linear genomes.
4. Classification of DNA damage and mechanisms for their correction. Diseases caused by repairdefects. The use of DNA damaging agents in medicine. The reaction of cells to double-stranded breaks in DNA. TUNEL Method
5. Homologous DNA recombination and its biological functions. Conservative site-specificrecombination. The main classes of mobile genetic elements. Repetitions. Features of recombination in the formation of immunoglobulin genes and T-cell receptors.
6. The use of DNA repair mechanisms for editing genomes. Restriction-modification systems,their purpose in bacteria and use in genetic engineering.
7. Genome editing technologies: zinc fingers, TALEN proteins, CRISPR. Purpose of theCRISPR / Cas system in bacteria.
8. DNA transcription, supercoiled coils and nucleosomes. The structure of RNA polymerase.Stages of the transcription cycle and principles of regulation. Attenuation of transcription. Common features and differences in transcription in bacteria and eukaryotes.
9. The main mechanisms of mRNA processing: capping, polyadenylation and splicing of introns.Modern ideas about splicing mechanisms.
10. Modern ideas about the structure, functioning and evolutionary history of eukaryoticribosomes.
11. The genetic code. Bounding frames. The structure and function of tRNA.
12. Translation initiation: general mechanisms and features in prokaryotes and eukaryotes.

RNAstructures that control translation efficiency. Elongation cycle. Broadcast Termination.
13. The basic principles of broadcast regulation. Protein folding and processing. Post-translational modification of proteins. Peptide bond. Primary, secondary, tertiary structure of theprotein.
14. Basic ideas about the structure of eukaryotic cells. Appointment of cellular organelles.Mitosis and its phases. The cell cycle, stages of the cell cycle. Cell differentiation.
15. Regulatory sites in the genome: promoter, TATA box, enhancer, silencer, insulator.
16. Variety and function of short protein non-coding RNA. RNA interference. The biological role ofRNA interference. siRNA. Applied use of RNA interference
17. The principle of polymerase chain reaction. Real-time PCR. Reverse transcription PCR.
18. DNA sequencing methods. Sanger sequencing. Sequencing a new generation.
19. Molecular biology: genome, gene, GC composition, genetic code, its degeneracy and universality, ribosome, nucleotides, amino acids, tRNA, complementarity, ribosome binding site,reading frame, RNA secondary structure.
20. Biochemistry: calculate the pH value of 6 nM hydrochloric acid solution
21. Biochemistry: indicate the possible amount of isomeric tripeptides that can be obtained bycondensation of three amino acids - leucine, arginine and glycine.
22. Biochemistry: starch and cellulose consist of the same monomer - glucose. Explain thepossible causes of differences in the physicochemical properties of these polysaccharides.
23. Biochemistry: membrane phospholipids carry a significant charge. What is the sign of thischarge? What ions can compensate for this charge?
24. Biochemistry: The concentration of the substrate of the enzymatic reaction is 4 Michaelisconstants. What will be the ratio of the speed of this reaction?
25. Biochemistry: Fats are divided into saturated (solid) and unsaturated (liquid) in the composition of their higher fatty acids. What fats will have a higher energy content per gram ofmatter? Explain the answer.
26. Biochemistry: Some types of RNA (tRNA, rRNA, etc.) form stable secondary structures(hairpins). How their boundaries can be determined by the primary sequence of RNA?
27. Biochemistry: What parameters of amino acids should be considered when predictingtransmembrane regions of proteins?

**Recommended literature**
1. Alberts B. et al. Molecular Biology of the Cell in Cell 4th. – 2002.
2. Murray R. K. et al. Harper's illustrated biochemistry. – Mcgraw-hill, 2014.