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**Federal State Autonomous Educational Institution of Higher Education**  
**«Patrice Lumumba Peoples' Friendship University of Russia»**  
**Institute of Biochemical Technology and Nanotechnology (IBHTN)**

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(name of the main educational unit (MEU) - the developer of the educational program of higher education (EP HE))

**WORKING PROGRAM OF THE DISCIPLINE**

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«Introduction to Bioinformatics»

(name of discipline/module)

**Recommended by the MCSD for the areas of training/specialty:**

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04.04.01 Chemistry

(code and name of the area of training / specialty)

**The study of the discipline is conducted within the framework of the main professional educational program of higher education (EP HE):**

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« Biochemical Technologies and Nanotechnology »

(name (profile/specialization) of the educational program)

**2023.**

## 1. PURPOSE OF THE DISCIPLINE

The purpose of the discipline "**Introduction to Bioinformatics**" is to provide students with an understanding of bioinformatics, relevant computational methods, the implementation of experimental work in molecular biology, biochemistry, genetics, as well as the development of algorithms for computer analysis of genomics and proteomics data, programs that allow to predict the spatial structure of biopolymers.

## 2. REQUIREMENTS FOR THE RESULTS OF THE DISCIPLINE

The study of the discipline "**Introduction to Bioinformatics**" is aimed at forming the following competencies (part of competencies):

*Table 2.1. The list of competencies formed in the development of the discipline (the results of the discipline)*

Code	Competence	Indicators of competence achievement (within this discipline)
<b>GPC -3.</b>	Able to use computational methods and adapt existing software products to solve tasks of professional activities	<b>GPC -3.2.</b> Uses standard and original software products, adapting them, if necessary, to solve problems of professional activity.
		<b>GPC -3.3.</b> Uses modern computational methods for processing data from chemical experiments, modeling the properties of substances (materials) and processes with their participation.
<b>GPC -5.</b>	Able to use the toolkit formalizations engineering, scientific technical tasks, application software for modeling and design of objects, systems, and processes	<b>GPC -5.2.</b> be able to apply methods of mathematical modeling in engineering and biological research, conduct data analysis.
		<b>GPC -5.3.</b> Uses modern computational methods for processing data from chemical experiments, modeling the properties of substances (materials) and processes with their participation.

## 3. THE PLACE OF THE DISCIPLINE IN THE STRUCTURE OF THE EP HE

The discipline "**Introduction to Bioinformatics**" is part of the formed by participants in the educational process and is the discipline of choice of block 1 of the curriculum profile "Biochemical technology and nanotechnology".

Within the framework of the EP HE students also master other disciplines and/or practices that contribute to the achievement of the planned results of mastering the discipline "**Introduction to Bioinformatics**".

*Table 3.1. List of components of the EP of Higher Education, contributing to the achievement of the planned results of mastering the discipline*

Code	Name of competence	Previous disciplines/modules, internships*	Subsequent disciplines/modules, internships*
GPC -3.	Able to use computational methods and adapt existing software products to solve tasks of professional activities	<ul style="list-style-type: none"> <li>Computer Technology in Scientific Research,</li> </ul>	
GPC -5.	Able to use formalization tools engineering, scientific and technical tasks, applied software for modeling and design of objects, systems, and processes	<ul style="list-style-type: none"> <li>Computer Technology in Scientific Research,</li> </ul>	

\* - to be filled in accordance with the competence matrix and the curriculum of the EP HE

#### 4. SCOPE OF THE DISCIPLINE AND TYPES OF WORK

The total labor capacity of the discipline "**Introduction to Bioinformatics**" is 3 credit units.

*Table 4.1. Types of educational work by periods of study of the program of higher education for FULL-TIME forms of learning*

Type of study work	TOTAL, ac.h.	Semester(s)			
		1	2	3	4
<i>Contact work, ac.h.</i>	40		40		
Including:					
Lectures (LC)	16		16		
Laboratory work (LW)	16		16		
Practical/seminar classes (SP)	8		8		
<i>Independent work of students, ac.h.</i>	41		41		
<i>Control (exam / pass with grade), ac.h.</i>	27		27		
<b>Total labor input of the discipline</b>	ac.h	<b>108</b>		<b>108</b>	
	Credit	<b>3</b>		<b>3</b>	

*Таблица 4.2. Types of educational work by periods of study of the program of higher education for exact-correspondenc forms of learning*

Type of study work		ВСЕГО, ак.ч.	Семестр(-ы)			
			1	2	3	4
<i>Contact work, ac.h.</i>		32		32		
Including:						
Lectures (LC)		16		16		
Laboratory work (LW)		8		8		
Practical/seminar classes (SP)		8		8		
<i>Independent work of students, ac.h.</i>		58		58		
<i>Control (exam / pass with grade), ac.h.</i>		18		18		
<b>Total labor input of the discipline</b>		ac.h	<b>108</b>		<b>108</b>	
		Credit	<b>3</b>		<b>3</b>	

## 5. DISCIPLINE CONTENT

*Table 5.1. Content of the discipline (module) by type of study work*

<b>Name of discipline section</b>	<b>Section (topic) content</b>	<b>Type of study*</b>
Section 1: Introduction	Topic 1.1. Goals, objectives and methods, main applications. Basic concepts. Amino acids, structure, and properties. DNA, RNA, nucleotides. Sequence analysis.	LC, LW, SP
Section 2: Databases	Internet for bioinformatics. Ways of presenting of information . About sequences. Basics of database structures: records, fields, objects. FASTA, BLAST, GenBank, PDB record formats. Classification of databases (automatic, archival, curated). Main databases: GenBank, EMBL, SwissProt, TrEMBL, PIR, PDB, protein family banks (ProDom, PFAM, InterPro, SCOP), metabolic databases, gene banks (physical maps, OMIM), specialized data banks. Search of homologous sequences in databases.	LC, LW, SP
Section 3: Levels of structural organization of proteins	Analysis of nucleotide sequences. DNA molecule structure, packaging, complementarity. Genes, regulatory sequences. Mathematical foundations of symbol sequence alignment. Amino acid substitution matrices, pairwise alignment and its evaluation, multiple alignment, computational resources. Global alignment: the Niedelman-Wunsch algorithm. Local alignment: Smith-Waterman algorithm. Other alignment options. Statistical significance of alignments. The dependence of alignment on parameters. Multiple alignment. Application of alignment in bioinformatics.	LC, LW, SP
Section 4: Sequence Comparison	Analysis of nucleotide sequences. DNA molecule structure, packaging, complementarity. Genes, regulatory sequences. Mathematical foundations of symbol sequence alignment. Amino acid substitution matrices, pairwise alignment and its evaluation, multiple alignment, computational resources. Global alignment: the Niedelman-Wunsch algorithm. Local alignment: the Smith Waterman algorithm. Other variants of alignments. Statistical significance of alignments. The dependence of alignment on parameters. Multiple alignment. Application of Alignment in Bioinformatics	LC, LW, SP
Section 5. Methods for determining the spatial structure biopolymers	Structure of the PDB record. Analysis of structural features. Prediction of secondary structure. Prediction of tertiary structure of proteins by homology. Homology modeling. Folding and its recognition.	LC, LW, SP

Section 6: Predicting Biopolymer Function by Sequence	Homolog analysis and functional signals. Leader peptides and transmembrane segments. Protein modification sites (glycosylation, phosphorylation, etc.). Functional sites of DNA. Prokaryote and eukaryote genes. Comparative methods of gene prediction. Search for RNA with given structure (tRNA, etc., mRNA regulatory sites).	LC, LW, SP
Section 7: Evolution at the molecular level	Evolution of molecules and organisms (horizontal transfer, orthologues, paralogues, gene trees). Phylogenetic tree. Models of evolution. Evolution at genome level. Population data analysis	LC, LW, SP
Section 8. Actual problems in bioinformatics	Genome annotation, gene search, search for replication sites in the human genome. Predicting the structure, function, and cellular localization proteins. Medical and Chemoinformatics.	LC, LW, SP

\* - - to be filled in only for **FULL-TIME** education: *LC* - lectures; *LW* - laboratory work; *SP* – seminar/practical classes.

## 6. MATERIAL AND TECHNICAL SUPPORT OF THE DISCIPLINE

Table 6.1. Material and technical support of the discipline

Type of auditory	Classroom equipment	Specialized training/laboratory equipment, software and materials for mastering the discipline (if necessary)
Computer class	Study room for lectures, Laboratory work, Practical/seminar classes Computer class No. 622.	Set of specialized furniture, technical means: 20 Computer workstations: Lenovo IdeaCentre 19.5" HD+Cel J1800/4Gb/500Gb/DVDRW/DOS/kb/m/black 1600x900 (19 pcs.), Lenovo IdeaCentre 23" C560 (57331093) i3-4160T (3.1GHz)/4G/1Tb/DVD- (19 pcs.) SMulti/23FHD91920x1080)/NV 800M 2G/Wi-Fi/cam/White (1pc.). Internet access is provided
Auditorium for independent work	Auditorium № 636 for students' independent work, equipped with a computer with access to the electronic information and entertainment system.	Multimedia projector Everycom Laptop Lenovo Thinkpad L530 Intel Core i3-2370M_2.4GHz/DDR3 4 GB, 1pc Internet access provided. Presentation Kit. Windows XP, Microsoft Office 2007, Microsoft Security Essentials

\* - the classroom for students' independent work **MUST** be specified!

## 7. EDUCATIONAL-METHODICAL AND INFORMATION SUPPORT OF THE DISCIPLINE

*Basic Literature:*

1. Chasovskikh, N. Y. Bioinformatics: Textbook / N. Y. Chasovskikh. - Moscow : GEOTAR-Media, 2020. - 352 c. - ISBN 978-5-9704-5542-5.

*Additional literature:*

2. Tore Samuelsson Genomics and Bioinformatics An Introduction to Programming Tools for Life Scientists From Bioinformatics Basics to Working Code - eBook on the Mylibrary publishing platform.

*Resources of information and telecommunication network "Internet":*

1. RUDN Libraries and third-party Libraries, to which university students have access to, based on contracts:
  - RUDN-ELS (electronic library system) RUDN <http://lib.rudn.ru/MegaPro/Web>
  - University Library Online ELS <http://www.biblioclub.ru>
  - ELS Yurite <http://www.biblio-online.ru>
  - Student's Consultant ELS [www.studentlibrary.ru](http://www.studentlibrary.ru)
  - ELS "Lan" <http://e.lanbook.com/>
  - Trinity Bridge ELS
2. Databases and search engines:
  - electronic collection of legal and regulatory and technical documentation <http://docs.cntd.ru/>
  - Yandex search engine <https://www.yandex.ru/>
  - Google search engine <https://www.google.ru/>
  - referral base SCOPUS <http://www.elsevierscience.ru/products/scopus/>
  - Federal Institute for Industrial Property (FIPS) <https://new.fips.ru>

*Teaching materials for students' independent work while mastering the discipline/module\*:*

1. Course of lectures on the discipline "**Introduction to Bioinformatics**".
2. Laboratory and practical work on the discipline "**Introduction to Bioinformatics**" (in the presence of laboratory works).

\* All didactic-methodical materials for students' independent work are placed according to the current order on the page of the discipline in **E-system**!

## **8. ASSESSMENT MATERIALS AND POINT-RATING SYSTEM FOR EVALUATING THE LEVEL OF COMPETENCE IN THE DISCIPLINE**

Assessment materials and score-rating system for evaluating the level of competence (part of competence) for the discipline "**Introduction to Bioinformatics**" are presented in the Appendix to this Working Program of the discipline.

\* - Grading materials and the scoring system are formed on the basis of the requirements of the corresponding RUDN local normative act.

**DEVELOPERS:**

Assistant Professor IBHTN

Job title, MEU



Signature

Kezimana Parfait

Full name

**HEAD OF THE MEU:**

Director of IBHTN

Наименование БУП



Signature

Y.M. Stanishevskiy

Full name

**HEAD OF THE EP HE:**

Director of IBHTN

Должность, БУП



Signature

Y.M. Stanishevskiy

Full name



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HE))

## **ASSESSMENT TOOLKIT FOR THE DISCIPLINE**

**«Introduction to Bioinformatics»**

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(name of discipline/module)

**04.04.01 - "Chemistry"**

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(code and name of the area of training / specialty)

**"Biochemical Technologies and Nanotechnology"**

---

(name (profile/specialization) of the educational program)

**Master**

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Graduate qualification (degree)

**2023.**



**Questions to prepare for the credit  
In the discipline "Introduction to Bioinformatics"**

1. The first question from:

- Bioinformatics: definition, basic concepts, goals and objectives.
- Relationships of Bioinformatics with Other Disciplines of Biology
- Basics of Molecular Biology
- Sequencing methods
- Biopolymers - proteins, nucleic acids.
- Amino acid and nucleotide sequences as the main information component of bioinformatics.
- File formats used in bioinformatics.
- Recording amino acid sequences.
- Recording nucleotide sequences.
- NCBI - GenBank database.
- Sources of biological information and databases
- Classification and types of databases.
- Comprehensive, universal and combined databases.
- Organism-specific databases.
- Databases on types of molecules.
- Database problems
- EMBL nucleotide sequence database.
- SwissProt Protein Database.
- PDB - Protein Data Bank.
- Small molecule and drug databases.
- Databases on metabolomics and its applications.
- Toxicological databases
- Built-in tools for working with databases on the Internet.
- Internet tools for working with information from biological
- BLAST
- Alignment, local, global.
- Multiple Alignment.
- Phylogenetic analysis and visualizations

2. The second and third question: solving specific problems using methods:

- Alignment
- Phylogenetic analysis

### **Module test No. 1**

#### **"Introduction to Bioinformatics"**

1. Bioinformatics: definition, basic concepts, goals and objectives.
2. Relationships of Bioinformatics with Other Disciplines of Biology
3. Basics of Molecular Biology
4. Sequencing methods
5. Biopolymers - proteins, nucleic acids.
6. Amino acid and nucleotide sequences as the main information component of bioinformatics.
7. File formats used in bioinformatics.
8. Recording amino acid sequences.
9. Recording nucleotide sequences.

### **Module test No. 2**

#### **"Introduction to Bioinformatics"**

1. NCBI - GenBank database.
2. Sources of biological information and databases
3. Classification and types of databases.
4. Comprehensive, universal and combined databases.
5. Organism-specific databases.
6. Databases on types of molecules.
7. Database problems
8. EMBL nucleotide sequence database.
9. SwissProt Protein Database.
10. PDB - Protein Data Bank.
11. Small molecule and drug databases.
12. Databases on metabolomics and its applications. Toxicological databases

### **Module test No 3**

#### **"Introduction to Bioinformatics"**

1. Built-in tools for working with databases on the Internet.
2. Internet tools for working with information from biological
3. BLAST
4. Alignment, local, global.
5. Multiple Alignment.
6. Phylogenetic analysis and visualizations

**Laboratory (seminar) works**  
**"Introduction to Bioinformatics"**

1. Familiarization with popular databases - GeneBank, EMBL, Swiss-Prot, UniProt and others
2. BLAST search engine, MUSCLE, CLUSTAL and others
3. We have a sequence of a gene. Its nucleotide sequence is given. Determine what this gene is and select primers so that we can determine the presence of this gene in the transformed organism.
4. What is the normal function of the protein encoded by this gene? Is there a homologue of this gene in the genome of some organism? If so, what is the function of this gene? Which chromosome contains a region homologous to this gene?
5. Algorithms for assembling genomic sequences from fragments
6. Alignment construction of two short artificial sequences
7. Alignment construction of two real sequences
8. Alignment editing
9. Alignment of sequences with similar function (possible homologs)
10. Alignment of sequences containing homology sites
11. Find the sequence from the fragment
12. Use BLAST to search the database for a specific gene/protein
13. Compare the multiple alignment constructed by Clustal
14. Make a pattern by multiple alignment
15. Find a document in the database that contains information about a protein
16. Phylogenetic analyses of PhyML

**DEVELOPERS:**

Assistant Professor IBHTN

Job title, MEU



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**INDEPENDENT STUDY OF THE STUDENT  
FOR THE DISCIPLINE**

«Introduction to Bioinformatics»

---

(name of discipline/module)

04.04.01 - "Chemistry"

---

(code and name of the area of training / specialty)

"Biochemical Technologies and Nanotechnology"

---

(name (profile/specialization) of the educational program)

Master

---

Graduate qualification (degree)

**2023.**

## Essay topics

1. Structure and functions of genes and proteins.
2. Are discoveries and advances in molecular biology and genetics related to the emergence of bioinformatics?
3. Characteristics of the genome of an organism.
4. The main tasks of bioinformatics
5. Methods for Recognizing Functional Segments in Nucleotide Sequences
6. Methods for comparing the primary structures of biopolymer molecules
7. Problems of phylogeny of genomic sequences.
8. Predicting gene functions.
9. Genome comparison
10. Pharmacogenomics and pharmacogenetics
11. Genetic basis of individual drug sensitivity.
12. Genetic differences in drug receptors.
13. Clinical significance of pharmacodynamic gene polymorphisms

### DEVELOPERS:

Assistant Professor IBHTN

Job title, MEU



Signature

Kezimana Parfait

Full name

The program is compiled in accordance with the requirements to the Educational standard of higher education of RUDN University.

### HEAD OF THE MEU:

Director of IBHTN

Наименование БУП



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Должность, БУП



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