Kotlov Nikita

Male, 15 February 1995

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Place of residence: Moscow
Nationality: Russian Federation

Education

High school

2010 – 2012

Advanced Educational Scientific Center of M.V.Lomonosov Moscow State University — A.N.Kolmogorov School, Moscow

10-11 grade

Higher education

2012 – now (2018)

Lomonosov Moscow State University, Moscow

119234, Moscow, GSP-1, Leninskiye Gory, MSU, 1-73, office 433.
TEL/FAX: +7 (495) 939-41-95
4th-year student, Faculty of Bioengineering and Bioinformatics

Work in scientific labs

September 2012 – now
3 years 2 months

Enzyme kinetics laboratory, International Centre for Research in Biotechnology, MSU

119234, Moscow, GSP-1, Leninskiye Gory, MSU, 1-73, office 612.
TEL/FAX: +7 (495) 938-23-23

Student

1-2 term work	Program complex for automatic protein-target preparation for docking *in silico* development, 2014
3 term work	Docking quality of AutoDock 4.2, AutoDock VINA and SOL programs comparison on the example of membrane HEM-containing protein COX *in silico*, 2015
4 term work	Program complex for docking results scoring in big scales on the example of COX enzyme *in silico*, 2016

June 2015 – August 2015
1 month

Leiden Genome Technology Center, LUMC

The Netherlands, Leiden, http://www.lgtc.nl/

Student

Project	CYP2D6 genotyping using the single-molecule real-time PacBio RSII» Curator: Seyed Yahya Anvar, Systems Biology, Bioinformatics at Leiden University Medical Center, Leiden.

Conferences & posters

XI FBB MSU student's conference, 2014

Poster “Program complex for automatic protein-target preparation *in silico* development” (1-st prize in bioinformatic section) (english)

XIV INTERNATIONAL CONFERENCE FOR YOUNG SCIENTISTS “BIOCHEMICAL PHYSICS” AND SCHOLL “MODERN PROBLEMS OF BIOCHEMICAL PHYSICS”, 2014

Poster “Program complex for automatic protein-target preparation for docking in silico” (russian)

International scientific conference "Lomonosov", bioinformatic section, 2015

Report “Docking quality of AutoDock 4.2, AutoDock VINA and SOL programs comparison on the example of membrane HEM-containing protein COX *in silico*” (english)

Publications

Polar biology, 2015

Glafira D. Kolbasova, Arthur O. Zalevsky, Azamat R. Gafurov, Philipp O. Gusev, Margarita A. Ezhova, Anna A. Zheludkevich, Olga P. Konovalova, Ksenia N. Kosobokova, Nikita U. Kotlov, Natalia O. Lanina, Anna S. Lapashina, Dmitry O. Medvedev, Katerina S. Nosikova, Ekaterina O. Nuzhdina, Georgii A. Bazykin, and Neretina Tatyana. **A new species of cyanea jellyfish sympatric to c. capillata in the white sea**. *Polar Biology*, pages 1–13, 2015. [DOI]

Bioinformatics projects

2012 – now, Moscow

Bioinformatic programm PDBParser development (C++) (Github).

Pdbparser is a multi-functional tool for files in pdb format. It helps with preparing files for docking and with also with results analysis. Main functions:

- Correcting PDB format errors in .pdb files
- Atoms and residues sorting
- Atoms in residue resorting
- Cutting structures into monomers
- Ligands' extraction and deletion
- Ligands' additions
- ROC diagrams creation and AUC values calculations
- AutoDock 4.2 and AutoDock Vina results analysis
- MOPAC post-processing
- NAMD post-processing
- Open Babel post-processing and pdb-format errors fixing
- Structure moving and turning

2012 – now, Moscow

Automatic preparing for docking system (C++, MPI, bash).

2015, The Netherlands, Leiden

«CYP2D6 genotyping using the single-molecule real-time PacBio RSII», Summer bioinformatics school 2015, Leiden University Medical Center. Curator: Seyed Yahya Anvar, *Systems Biology, Bioinformatics at Leiden*

University Medical Center, Leiden.

A complex of programs in python, bash, R, php/html/css/js for automatic sequences haplotypes resolving. Graphical output helps doctors to easier understand results and to treat patients more efficient.

Additional courses

Bioinformatics institute, http://bioinformaticsinstitute.ru/	2015	**Genomic bioinformatics intensive**
Stepic.org	2015	**Introduction to Linux**
Kaspersky Lab	2013	**Kaspersky anti-virus school**
Summer programming school, lksh.ru	2012	**Algorithmic programming, parallel B**
	2011	**Algorithmic programming, parallel C+**
	2011	**Algorithmic programming, parallel C**
Specialist, specialist.ru	2011	**HTML/CSS**
	2007	**PC repairing and administrating course**

Working experience (5 years)

September 2015 – now

«BostonGene»

Moscow, http://bostongene.com/

Software developer, bioinformatician

February 2015 – September 2015

CJSC «NORSI-TRANS»

Moscow, http://www.norsi-trans.ru/

Software developer

August 2012 - now

International Centre for Research in Biotechnology MSU

Moscow, http://biocentr.msu.ru/

Student

August 2011 – December 2014
3 years 5 month

NCO "IRLEM"

Moscow

System administrator, web programmer

Certificates

2015	Introduction to Linux
	Genomic bioinformatic intensive
	1st bioinformatics hackaton
2011	HTML & CSS. Level 1. W3C standards of sites development. HTML 5 and CSS 3
	HTML & CSS. Level 2. Cross-browser development and bases of a usability
	Office and home PC administration and setup level 1
2008	Office and home PC administration and setup level 2

Primary skills

Languages	Russian – native English – Speaking: Advanced. Reading: I read professional literature
Professional skills	PC administration and repairing, web programming and design, OOP, DDD, Unix, Microsoft Office, BigData, programming parallel programs, Cloud computing, Docker, OpenStack, Genome assembly, Quality control, Gene annotation, SNP identification, Fusions identification
Programming languages	C/C++ (>5 years), Python (>3 years), BASH (>3 years), Java (~1 year), Visual Basic, R, HTML4-5/CSS3/JavaScript (>5 years), AngularJs (~1 year), PHP (~1 year)
OS	Windows – administrator, advanced user Unix (Linux) – administrator, advanced user, command line
Bioinformatics soft	AutoDock 4.2, AutoDock Vina, SOL, Aplite, VMD, NAMD, Open Babel, PyMOL, Jmol, JalView, Mopac, Mega, MGLTools, PTools, Emboss, BLASR, ChemSketch, Origin, Bowtie, BWA, FastQC, SOAPFuse, Chimerascan, FuMa, Ericscan, SAMtools, Trimmomatic, Galaxy
Bioinformatics databases	Pubmed, PDB, PDBe, PDBBind, ChemSpider, SwissParam, Swissprot, Ensembl, Uniprot, Brenda, UCSC, Cath
Bioinformatics online services	Blast, Muscle, T-coffee, VEP, Chemmine-tools, Mutalyzer, KEGG, SwissParam.ch, Galaxy

Personal achievements

2015, Moscow	Captain of the team at The first bioinformatics hackathon (genehack.ru), winner of the In Silico Medicine & PONKC companies prize.

Other information

Area of interest	Docking, molecular modeling, genome variation data analysis, genome assembly, new bioinformatics tools development, database development, processes automation, big data, programs projecting, cloud computing, contanerisation.
About me	I am capable to cope with almost any new software I have excellent learning ability I am full of ideas and energy I have leadership skills I like playing volleyball and other active games