

Arsen Arakelyan

CURRICULUM VITAE

Personal Information

Full name: Arsen Arakelyan
Address: 2, G. Njdeh Str., apt 31, 0006,
Yerevan
Phone: +37410 440566
Cell: +37492 792301
Year of Birth: 10 Feb 1979
Place of Birth: Yerevan, Armenia
Citizenship: Republic of Armenia
E-mail: arakelyanaa@zoho.com

Current Work Details

Position: Senior Researcher, Head of Group
Degree: PhD
Organization: Institute of Molecular Biology (IMB)
NAS RA
Work address: 7 Hasratyan Str., 0014, Yerevan
Work phone: +37410 282622
Fax: +37410 282622
E-mail: aarakelyan@sci.am

Education

2001-2004 **PhD in Biology**
Specialization: Molecular and Cellular Biology
IMB NAS RA
1999-2001 **Master's degree in Biochemistry**
Specialization: Biochemistry
Faculty of Biology, Yerevan State University
1995-1999 **Bachelor's degree in Biochemistry**
Specialization: Biochemistry
Faculty of Biology, Yerevan State University

Professional Experience (*Permanent and part time positions*)

2015-to date **Director**, IMB NAS RA
2011-to date **Group Leader**, Research Group of Bioinformatics, IMB NAS RA
2008-2014 **Deputy Director**, IMB NAS RA
1998-2011 **Researcher**, Laboratory of Macromolecular Complexes, IMB NAS RA
2014-to date **Adjunct Lecturer**, American University of Armenia
2015-to date **Head of Bioinformatics Department**, Russian-Armenian (Slavonic) University

Scientific interests

Bioinformatics, high-throughput data analysis, -omics data analysis, pathway discovery and signal flow analysis, systems biology, functional genomics, telomere biology, data classification, marker discovery

Research grants

2015-2017 Assessment of the impact of genomic and epigenetic alterations on gene expression and biological pathway activation in cancers (PI) SCS MES RA (15T-1F150)

2013-2015	Analysis of biomolecular pathways involved in complex human diseases (PI) SCS MES RA (13YR-1F0022)
2014	Multiclass growing support set algorithm for analysis of high-throughput gene expression data (PI), ANSEF, USA (molbio-3507)
2011-2013	In silico structure-function characterization of Familial Mediterranean fever gene product (pyrin): insights into disease pathogenesis (PI) SCS MES RA (11B-1f014)
2012	Express test-system for diagnostics of overtraining syndrome (PI), ME RA & CRDF, USA (CRDF-9070)
2011	Growing support sets for pathway specific microarray gene expression analysis (PI), ANSEF, USA (NS-molbio-2319)

Publications (10 selected)

1. **Arakelyan A**, Nersisyan L, Hakobyan A. Application of MATLAB in -Omics and Systems Biology. Applications from Engineering with MATLAB Concepts, Associate Prof. Jan Valdman (Ed.), ISBN: 978-953-51-2459-7. InTech, Croatia, 2016. DOI: 10.5772/62847.
1. **Arakelyan A**, Nersisyan L, Petrek M, Löffler-Wirth H, Binder H. Cartography of Pathway Signal Perturbations Identifies Distinct Molecular Pathomechanisms in Malignant and Chronic Lung Diseases. *Front. Genet.* 2016.
2. Nersisyan L, Löffler-Wirth H, **Arakelyan A**, Binder H. Gene Set- and Pathway- Centered Knowledge Discovery Assigns Transcriptional Activation Patterns in Brain, Blood, and Colon Cancer: A Bioinformatics Perspective. *International Journal of Knowledge Discovery in Bioinformatics (IJKDB)* 2016, 4(2):46-49.
3. Hakobyan A, Nersisyan L, **Arakelyan A**. Quantitative trait association study for mean telomere length in the South Asian Genomes. *Bioinformatics* 2016. doi: 10.1093/bioinformatics/btw027
4. Hopp L., Nersisyan L., Löffler-Wirth H, **Arakelyan A**, Binder H. Epigenetic heterogeneity of B-cell lymphoma: Chromatin modifiers. *Genes* 2015, 6(4):1076-1112.
5. Nersisyan L, Johnson G, Riel-Mehan M, Pico A, **Arakelyan A**. PSFC: a Pathway Signal Flow Calculator App for Cytoscape [version 1; referees: 1 approved] *F1000Research* 2015, 4:480.
6. Nersisyan L, Arakelyan A. Computel: computation of mean telomere length from whole-genome next-generation sequencing data. *PLoS One.* 2015;10(4):e0125201.
7. Binder H, Wirth H, **Arakelyan A**, Lembcke K, Tiys ES, Ivanisenko VA, Kolchanov NA, Kononikhin A, Popov I, Nikolaev EN, Pastushkova L, Larina IM. Time-course human urine proteomics in space-flight simulation experiments. *BMC Genomics.* 2014; 15 Suppl 12:S2.
8. Nersisyan L, Samsonyan R, **Arakelyan A**. CyKEGGParser: tailoring KEGG pathways to fit into systems biology analysis workflows. Version 2. *F1000Res.* 2014 Jul 1 [revised 2014 Aug 14];3:145. doi: 10.12688/f1000research.4410.2. eCollection 2014.
9. **Arakelyan A**, Nersisyan L. KEGGParser: parsing and editing KEGG pathway maps in Matlab. *Bioinformatics.* 2013 Feb 15;29(4):518-9. doi: 10.1093/bioinformatics/bts730. Epub 2013 Jan 3.
10. **Arakelyan A**, Aslanyan L, Boyajyan A. High-throughput Gene Expression Analysis Concepts and Applications. *Sequence and Genome Analysis II – Bacteria, Viruses and Metabolic Pathways.* ISBN: 978-1-480254-14-5. iConcept Press Ltd, USA , 2013, 71-95