BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Eugene V Koonin

eRA COMMONS USER NAME (credential, e.g., agency login): NIH/NLM/DIR ekoonin

POSITION TITLE: Senior Investigator, NCBI/NLM; Adjunct Professor, Boston University

EDUCATION/TRAINING

| INSTITUTION AND LOCATION | DEGREE(if applicable) | Completion DateMM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- |
| Moscow State University  | MSc | 06/1978 | Biochemistry |
| Moscow State University | Ph.D. | 12/1983 | Virology |
|  |  |  |  |
|  |  |  |  |

1. **Personal statement**

I am interested in origin and evolution of life. My technical expertise and experience are primarily in the field of evolutionary genomics. I also have training in virology. My major research directions are:

* Comparative analysis of sequenced genomes and automatic methods for genome-scale annotation of gene functions.
* Evolutionary systems biology: emergence and evolution of genomic and organizational complexity in biological systems.
* Application of comparative genomics for phylogenetic analysis, reconstruction of ancestral life forms and building large-scale evolutionary scenarios.
* Mathematical modeling of genome evolution.
* Comparative-genomic study of the major transitions in the evolution of life, such as the origin of eukaryotes.
* Origin of cells and viruses.
* Comprehensive study of the evolution and taxonomy of viruses.
* Coevolution of mobile genetic elements and host defense systems.
* Testing fundamental predictions of evolutionary theory, in particular, the relationship between neutral evolution and various modes of selection, using genome-wide sequence comparison.
* Developing a general theory of evolution using principles and models of statistical physics.

**B. Positions and Honors**

**Current Positions**

2019-present: ***NIH Distinguished*** ***Investigator,*** National Center for Biotechnology Information, National Library of Medicine, N.I.H., Bethesda, MD

1996-2019: ***Senior Investigator,*** National Center for Biotechnology Information, National Library of Medicine, N.I.H., Bethesda, MD

2002-present: Adjunct Professor of Bioinformatics, Program in Bioinformatics, Boston University, Boston, MA

**Honors**

2019 – Benjamin Franklin Award

2019 – Foreign Member, Russian Academy of Sciences

2018 - Doctor *Honoris Causa*, Wageningen University (the Netherlands)

2016 – NIH Director’s Award

2016 – Member, National Academy of Sciences of the USA

2014 – Batsheva de Rotschild Lectureship Award, Israel

2013 – Fellow, American Academy of Arts and Sciences

2013 – Associate Member, European Molecular Biology Organization

2012 – Fellow, American Academy of Microbiology

2012 – Doctor *Honoris Causa*, Université Aix-Marseille, France

2011 - Israel Pollak Distinguished Lecture Award from The Technion (Haifa, Israel)

2009 - Fellow, Institute of Biology, UK

2008 - Co-Organizer, Aspen Workshop in Physics “From Atoms to Organisms”

2007 - Chair, Gordon Research Conference on

 “Structural, Functional and Evolutionary Genomics” (Hinxton, Cambridge, UK)

2005 - Vice-Chair, Gordon Research Conference on

 “Structural, Functional and Evolutionary Genomics” (Bates College, Maine)

2005 - Co-organizer, International Workshop on Complex biomolecular networks:
 structure, evolution, and function (Montauk, NJ)

2001- Fellow, American College of Medical Informatics

1999- National Library of Medicine Board of Regents’ Award

**C. Contributions to science.**

My complete citation list is available at Google Scholar: <https://scholar.google.com/citations?user=F4P3ghEAAAAJ&hl=ru&oi=ao>

Total number of citations: 191,939 (68,992 since 2015); h-index: 209.

Number of publication in PubMed: 906.

My key contributions to science are in the field of evolutionary genomics. I proposed the concept of

Clusters of Orthologous Genes (COGs) that is central to functional and evolutionary analysis of

genomes. With my colleagues, we developed methods for COG identification and applied these

methods for evolutionary reconstruction and functional annotation of numerous genomes of

prokaryotes and eukaryotes, and a minimal cell genome that has become foundational for synthetic

biology. We discovered the extensive non-orthologous gene displacement and massive horizontal

gene transfer between domains of life, and reappraised the Tree of Life concept on the basis of these

discoveries. Using comparative genomic methods, we predicted the existence and mechanism of

action of an adaptive immunity system in Archaea and Bacteria (known as CRISPR), contributed to

the experimental validation of this prediction, and thoroughly investigated CRISPR evolution. Using

dedicated computational methods that we developed, we also discovered several numerous other defense systems of bacteria and archaea. We discovered many new groups of RNA and DNA viruses by searching the extensive metagenomic sequence databases. We performed comprehensive studies on virus evolution, successfully

predicting functions of numerous viral genes, and developing a general scenario for the evolution of the virosphere. We then developed a comprehensive taxonomy of viruses that has been formally adopted by the International Committee of Taxonomy of Viruses. Among several major theoretical developments, we used a theoretical framework from condensed matter physics to propose a general concept of the evolution of biological complexity driven by competing interactions and frustrated states

**Key publications:**

|  |  |
| --- | --- |
| Year | Details of Publication |
| 1992 | Koonin EV, Gorbalenya AE, Purdy MA, Rozanov MN, Reyes GR, Bradley DW.Computer-assisted assignment of functional domains in the nonstructural polyprotein of hepatitis E virus: delineation of an additional group of positive-strand RNA plant and animal viruses. Proc Natl Acad Sci U S A.; 89: 8259-63. |
| 1995 | Koonin EV, Tatusov RL, Rudd KE. Sequence similarity analysis of Escherichia coli proteins: functional and evolutionary implications. Proc Natl Acad Sci USA; 92: 11921-5 |
| 1996 | Mushegian AR, Koonin EV. A minimal gene set for cellular life derived by comparison of complete bacterial genomes. Proc Natl Acad Sci USA 93:10268-73 |
| 1997 | Tatusov RL, Koonin EV, Lipman DJ. A genomic perspective on protein families. Science 278: 631-637 |
| 2001 | [Aravind L](http://www.ncbi.nlm.nih.gov/pubmed?term=%22Aravind%20L%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstract), [Dixit VM](http://www.ncbi.nlm.nih.gov/pubmed?term=%22Dixit%20VM%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstract), [Koonin EV](http://www.ncbi.nlm.nih.gov/pubmed?term=%22Koonin%20EV%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstract). Apoptotic molecular machinery: vastly increased complexity in vertebrates revealed by genome comparisons. Science 291: 1279-84 |
| 2002 | [Koonin EV](http://www.ncbi.nlm.nih.gov/pubmed?term=%22Koonin%20EV%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstract), [Wolf YI](http://www.ncbi.nlm.nih.gov/pubmed?term=%22Wolf%20YI%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstract), [Karev GP](http://www.ncbi.nlm.nih.gov/pubmed?term=%22Karev%20GP%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstract). The structure of the protein universe and genome evolution. Nature 420: 218-223 |
| 2006 | Martin W, Koonin EV. Introns and the origin of nucleus-cytosol compartmentalization. Nature 440:41-45 |
| 2006 | Makarova KS, Grishin NV, Shabalina SA, Wolf, YI, Koonin EV. A putative RNA-interference-based immune system in prokaryotes: computational analysis of the predicted enzymatic machinery, functional analogies with eukaryotic RNAi, and hypothetical mechanisms of action. Biol Direct 1:7 |
| 2008 | Brouns SJ, Jore MM, Lundgren M, Westra ER, Slijkhuis RJ, Snijders AP, Dickman MJ, Makarova KS, Koonin EV, van der Oost J. Small CRISPR RNAs guide antiviral defense in prokaryotes. Science 321: 960-964 |
| 2011 | Makarova KS, Haft DH, Barrangou R, Brouns SJ, Charpentier E, Horvath P,Moineau S, Mojica FJ, Wolf YI, Yakunin AF, van der Oost J, Koonin EV. Evolution and classification of the CRISPR-Cas systems. Nat Rev Microbiol 9:467-477 |
| 2012 | Weinberger AD, Wolf YI, Lobkovsky AE, Gilmore MS, Koonin EV. Viral diversity threshold for adaptive immunity in prokaryotes. MBio 3:e00456-12. |
| 2014201520172018 2018 2019 2020   | Ran W, Kristensen DM, Koonin EV. Coupling between protein level selection and codon usage optimization in the evolution of bacteria and archaea. MBio. 5:e00956-14Shmakov S, Abudayyeh OO, Makarova KS, Wolf YI, Gootenberg JS, Semenova E, Minakhin L, Joung J, Konermann S, Severinov K, Zhang F, Koonin EV. Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. Mol Cell. 2015 Nov 5;60(3):385-97Shmakov S, Smargon A, Scott D, Cox D, Pyzocha N, Yan W, Abudayyeh OO,Gootenberg JS, Makarova KS, Wolf YI, Severinov K, Zhang F, Koonin EV. Diversityand evolution of class 2 CRISPR-Cas systems. Nat Rev Microbiol. 2017Mar;15(3):169-182Wolf YI, Kazlauskas D, Iranzo J, Lucía-Sanz A, Kuhn JH, Krupovic M, Dolja VV, Koonin EV. Origins and Evolution of the Global RNA Virome. mBio. 2018 Nov 27;9(6)Yutin N, Makarova KS, Gussow AB, Krupovic M, Segall A, Edwards RA, Koonin EV. Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. Nat Microbiol. 2018 Jan;3(1):38-46Katsnelson MI, Wolf YI, Koonin EV. On the feasibility of saltationalevolution. Proc Natl Acad Sci U S A. 2019 Oct 15;116(42):21068-21075Koonin EV, Dolja VV, Krupovic M, Varsani A, Wolf YI, Yutin N, Zerbini FM, Kuhn JH. Global Organization and Proposed Megataxonomy of the Virus World. Microbiol Mol Biol Rev. 2020 Mar 4;84(2). pii: e00061-19 |

D. Research Support

NCBI/NLM, Division of Intramural Research, Core Support, ca $2.0 M/yr

US-Israel Binational Science Foundation, 2010-2012 “Analytical framework for a comprehensive analysis of the prokaryotic mobilome”, $100,000