

Andrey Rzhetsky

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

131
papers

10,115
citations

44
h-index

100
g-index

164
ext. papers

11,537
ext. citations

11
avg, IF

6.18
L-index

| # | Paper | IF | Citations |
|-----|---|------|-----------|
| 131 | Prevalence of Endocrine Disorders Among 6078 Individuals With Down Syndrome in the United States.. <i>Journal of Patient-centered Research and Reviews</i> , 2022 , 9, 70-74 | 1.5 | 1 |
| 130 | Prevalence of Mental Health Conditions Among 6078 Individuals With Down Syndrome in the United States.. <i>Journal of Patient-centered Research and Reviews</i> , 2022 , 9, 58-63 | 1.5 | 2 |
| 129 | Prevalence of Infectious Diseases Among 6078 Individuals With Down Syndrome in the United States.. <i>Journal of Patient-centered Research and Reviews</i> , 2022 , 9, 64-69 | 1.5 | |
| 128 | Testing the reproducibility and robustness of the cancer biology literature by robot.. <i>Journal of the Royal Society Interface</i> , 2022 , 19, 20210821 | 4.1 | 0 |
| 127 | Dissecting schizophrenia phenotypic variation: the contribution of genetic variation, environmental exposures, and gene-environment interactions. <i>NPJ Schizophrenia</i> , 2022 , 8, | 5.5 | 0 |
| 126 | HOME2 Study: Household Versus Personalized Decolonization in Households of Children With Methicillin-Resistant <i>Staphylococcus aureus</i> Skin and Soft Tissue Infection-A Randomized Clinical Trial. <i>Clinical Infectious Diseases</i> , 2021 , 73, e4568-e4577 | 11.6 | 4 |
| 125 | Targeting glioblastoma signaling and metabolism with a re-purposed brain-penetrant drug. <i>Cell Reports</i> , 2021 , 37, 109957 | 10.6 | 1 |
| 124 | Observable variations in human sex ratio at birth. <i>PLoS Computational Biology</i> , 2021 , 17, e1009586 | 5 | 2 |
| 123 | NERO: a biomedical named-entity (recognition) ontology with a large, annotated corpus reveals meaningful associations through text embedding. <i>Npj Systems Biology and Applications</i> , 2021 , 7, 38 | 5 | 0 |
| 122 | Prevalence of Common Disease Conditions in a Large Cohort of Individuals With Down Syndrome in the United States. <i>Journal of Patient-centered Research and Reviews</i> , 2021 , 8, 86-97 | 1.5 | 10 |
| 121 | Do psychiatric diseases follow annual cyclic seasonality?. <i>PLoS Biology</i> , 2021 , 19, e3001347 | 9.7 | 3 |
| 120 | Postnatal immune activation causes social deficits in a mouse model of tuberous sclerosis: Role of microglia and clinical implications. <i>Science Advances</i> , 2021 , 7, eabf2073 | 14.3 | 1 |
| 119 | Measurable health effects associated with the daylight saving time shift. <i>PLoS Computational Biology</i> , 2020 , 16, e1007927 | 5 | 8 |
| 118 | Environmental Methicillin-resistant <i>Staphylococcus aureus</i> Contamination, Persistent Colonization, and Subsequent Skin and Soft Tissue Infection. <i>JAMA Pediatrics</i> , 2020 , 174, 552-562 | 8.3 | 10 |
| 117 | Longitudinal, strain-specific <i>Staphylococcus aureus</i> introduction and transmission events in households of children with community-associated methicillin-resistant <i>S aureus</i> skin and soft tissue infection: a prospective cohort study. <i>Lancet Infectious Diseases</i> , 2020 , 20, 188-198 | 25.5 | 26 |
| 116 | Automated microfluidic platform for dynamic and combinatorial drug screening of tumor organoids. <i>Nature Communications</i> , 2020 , 11, 5271 | 17.4 | 64 |
| 115 | Electronic health record phenotypes associated with genetically regulated expression of CFTR and application to cystic fibrosis. <i>Genetics in Medicine</i> , 2020 , 22, 1191-1200 | 8.1 | 3 |

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| 114 | Measurable health effects associated with the daylight saving time shift 2020 , 16, e1007927 | | |
| 113 | Measurable health effects associated with the daylight saving time shift 2020 , 16, e1007927 | | |
| 112 | Measurable health effects associated with the daylight saving time shift 2020 , 16, e1007927 | | |
| 111 | Measurable health effects associated with the daylight saving time shift 2020 , 16, e1007927 | | |
| 110 | Measurable health effects associated with the daylight saving time shift 2020 , 16, e1007927 | | |
| 109 | Measurable health effects associated with the daylight saving time shift 2020 , 16, e1007927 | | |
| 108 | Ultra-multiplexed analysis of single-cell dynamics reveals logic rules in differentiation. <i>Science Advances</i> , 2019 , 5, eaav7959 | 14.3 | 28 |
| 107 | Environmental pollution is associated with increased risk of psychiatric disorders in the US and Denmark. <i>PLoS Biology</i> , 2019 , 17, e3000353 | 9.7 | 68 |
| 106 | Centralized scientific communities are less likely to generate replicable results. <i>ELife</i> , 2019 , 8, | 8.9 | 8 |
| 105 | GRIK5 Genetically Regulated Expression Associated with Eye and Vascular Phenomes: Discovery through Iteration among Biobanks, Electronic Health Records, and Zebrafish. <i>American Journal of Human Genetics</i> , 2019 , 104, 503-519 | 11 | 10 |
| 104 | Estimating heritability and genetic correlations from large health datasets in the absence of genetic data. <i>Nature Communications</i> , 2019 , 10, 5508 | 17.4 | 9 |
| 103 | Human Organoids Share Structural and Genetic Features with Primary Pancreatic Adenocarcinoma Tumors. <i>Molecular Cancer Research</i> , 2019 , 17, 70-83 | 6.6 | 45 |
| 102 | Interplay of personal, pet, and environmental colonization in households affected by community-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>Journal of Infection</i> , 2019 , 78, 200-207 | 18.9 | 17 |
| 101 | Associations between environmental quality and adult asthma prevalence in medical claims data. <i>Environmental Research</i> , 2018 , 166, 529-536 | 7.9 | 11 |
| 100 | Comprehensive modeling reveals proximity, seasonality, and hygiene practices as key determinants of MRSA colonization in exposed households. <i>Pediatric Research</i> , 2018 , 84, 668-676 | 3.2 | 13 |
| 99 | Conjunction of factors triggering waves of seasonal influenza. <i>ELife</i> , 2018 , 7, | 8.9 | 30 |
| 98 | Geographically Resolved Rhythms in Twitter Use Reveal Social Pressures on Daily Activity Patterns. <i>Current Biology</i> , 2018 , 28, 3763-3775.e5 | 6.3 | 17 |
| 97 | Patchwork of contrasting medication cultures across the USA. <i>Nature Communications</i> , 2018 , 9, 4022 | 17.4 | 2 |

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| 96 | RIDDLE: Race and ethnicity Imputation from Disease history with Deep LEarning. <i>PLoS Computational Biology</i> , 2018 , 14, e1006106 | 5 | 9 |
| 95 | Classification of common human diseases derived from shared genetic and environmental determinants. <i>Nature Genetics</i> , 2017 , 49, 1319-1325 | 36.3 | 110 |
| 94 | Preexisting Type 2 Immune Activation Protects against the Development of Sepsis. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017 , 57, 628-630 | 5.7 | 9 |
| 93 | Understanding Toxoplasmosis in the United States Through "Large Data" Analyses. <i>Clinical Infectious Diseases</i> , 2016 , 63, 468-75 | 11.6 | 30 |
| 92 | Health ROI as a measure of misalignment of biomedical needs and resources. <i>Nature Biotechnology</i> , 2015 , 33, 807-11 | 44.5 | 15 |
| 91 | Genetic similarity between cancers and comorbid Mendelian diseases identifies candidate driver genes. <i>Nature Communications</i> , 2015 , 6, 7033 | 17.4 | 22 |
| 90 | Tradition and Innovation in Scientists Research Strategies. <i>American Sociological Review</i> , 2015 , 80, 875-908 | 108.1 | 244 |
| 89 | Towards a Computable Data Corpus of Temporal Correlations between Drug Administration and Lab Value Changes. <i>PLoS ONE</i> , 2015 , 10, e0136131 | 3.7 | 4 |
| 88 | Choosing experiments to accelerate collective discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 14569-74 | 11.5 | 84 |
| 87 | Systems analysis of human multigene disorders. Preface. <i>Advances in Experimental Medicine and Biology</i> , 2014 , 799, v - viii | 3.6 | 3 |
| 86 | Environmental and state-level regulatory factors affect the incidence of autism and intellectual disability. <i>PLoS Computational Biology</i> , 2014 , 10, e1003518 | 5 | 40 |
| 85 | Quantifying the impact and extent of undocumented biomedical synonymy. <i>PLoS Computational Biology</i> , 2014 , 10, e1003799 | 5 | 7 |
| 84 | DiseaseConnect: a comprehensive web server for mechanism-based disease-disease connections. <i>Nucleic Acids Research</i> , 2014 , 42, W137-46 | 20.1 | 75 |
| 83 | Representation of probabilistic scientific knowledge. <i>Journal of Biomedical Semantics</i> , 2013 , 4 Suppl 1, S7 | 2.2 | 10 |
| 82 | A nondegenerate code of deleterious variants in Mendelian loci contributes to complex disease risk. <i>Cell</i> , 2013 , 155, 70-80 | 56.2 | 160 |
| 81 | Representation of research hypotheses. <i>Journal of Biomedical Semantics</i> , 2011 , 2 Suppl 2, S9 | 2.2 | 10 |
| 80 | A distributed look-up architecture for text mining applications using MapReduce 2011 , | | 3 |
| 79 | A Distributed Look-up Architecture for Text Mining Applications using MapReduce 2011 , 2011, | | 3 |

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| 78 | Advancing science through mining libraries, ontologies, and communities. <i>Journal of Biological Chemistry</i> , 2011 , 286, 23659-66 | 5.4 | 12 |
| 77 | Conflicting biomedical assumptions for mathematical modeling: the case of cancer metastasis. <i>PLoS Computational Biology</i> , 2011 , 7, e1002132 | 5 | 11 |
| 76 | War of ontology worlds: mathematics, computer code, or Esperanto?. <i>PLoS Computational Biology</i> , 2011 , 7, e1002191 | 5 | 4 |
| 75 | Benchmarking ontologies: bigger or better?. <i>PLoS Computational Biology</i> , 2011 , 7, e1001055 | 5 | 14 |
| 74 | The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010 , 28, 935-42 | 44.5 | 499 |
| 73 | Discovering and Counting Biomedical Verbs 2010 , | | 1 |
| 72 | Philosophy of science. Machine science. <i>Science</i> , 2010 , 329, 399-400 | 33.3 | 51 |
| 71 | Novel opportunities for computational biology and sociology in drug discovery. <i>Trends in Biotechnology</i> , 2010 , 28, 161-70 | 15.1 | 17 |
| 70 | Looking at cerebellar malformations through text-mined interactomes of mice and humans. <i>PLoS Computational Biology</i> , 2009 , 5, e1000559 | 5 | 15 |
| 69 | How to get the most out of your curation effort. <i>PLoS Computational Biology</i> , 2009 , 5, e1000391 | 5 | 18 |
| 68 | Analysis of Drosophila segmentation network identifies a JNK pathway factor overexpressed in kidney cancer. <i>Science</i> , 2009 , 323, 1218-22 | 33.3 | 99 |
| 67 | Novel opportunities for computational biology and sociology in drug discovery. <i>Trends in Biotechnology</i> , 2009 , 27, 531-40 | 15.1 | 9 |
| 66 | Getting started in text mining: part two. <i>PLoS Computational Biology</i> , 2009 , 5, e1000411 | 5 | 26 |
| 65 | Six senses in the literature. The bleak sensory landscape of biomedical texts. <i>EMBO Reports</i> , 2008 , 9, 212-5 | 6.5 | 4 |
| 64 | Seeking a new biology through text mining. <i>Cell</i> , 2008 , 134, 9-13 | 56.2 | 66 |
| 63 | Quantitative systems-level determinants of human genes targeted by successful drugs. <i>Genome Research</i> , 2008 , 18, 206-13 | 9.7 | 58 |
| 62 | Network properties of genes harboring inherited disease mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 4323-8 | 11.5 | 235 |
| 61 | Multi-dimensional classification of biomedical text: toward automated, practical provision of high-utility text to diverse users. <i>Bioinformatics</i> , 2008 , 24, 2086-93 | 7.2 | 71 |

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|----|--|------|-----|
| 60 | Genetic-linkage mapping of complex hereditary disorders to a whole-genome molecular-interaction network. <i>Genome Research</i> , 2008 , 18, 1150-62 | 9.7 | 57 |
| 59 | How many scientific papers should be retracted?. <i>EMBO Reports</i> , 2007 , 8, 422-3 | 6.5 | 46 |
| 58 | Response by Cokol et al. <i>EMBO Reports</i> , 2007 , 8, 793-793 | 6.5 | 78 |
| 57 | Probing genetic overlap among complex human phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11694-9 | 11.5 | 278 |
| 56 | A recipe for high impact. <i>Genome Biology</i> , 2007 , 8, 406 | 18.3 | 8 |
| 55 | New directions in biomedical text annotation: definitions, guidelines and corpus construction. <i>BMC Bioinformatics</i> , 2006 , 7, 356 | 3.6 | 81 |
| 54 | Imitating manual curation of text-mined facts in biomedicine. <i>PLoS Computational Biology</i> , 2006 , 2, e1185 | | 22 |
| 53 | Microparadigms: chains of collective reasoning in publications about molecular interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 4940-5 | 11.5 | 37 |
| 52 | Self-correcting maps of molecular pathways. <i>PLoS ONE</i> , 2006 , 1, e61 | 3.7 | 10 |
| 51 | Emergent behavior of growing knowledge about molecular interactions. <i>Nature Biotechnology</i> , 2005 , 23, 1243-7 | 44.5 | 44 |
| 50 | Listening to viral tongues: comparing viral trees using a stochastic context-free grammar. <i>Molecular Biology and Evolution</i> , 2005 , 22, 905-13 | 8.3 | 1 |
| 49 | Probabilistic inference of molecular networks from noisy data sources. <i>Bioinformatics</i> , 2004 , 20, 1205-13 | 7.2 | 27 |
| 48 | Molecular triangulation: bridging linkage and molecular-network information for identifying candidate genes in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 15148-53 | 11.5 | 134 |
| 47 | GeneWays: a system for extracting, analyzing, visualizing, and integrating molecular pathway data. <i>Journal of Biomedical Informatics</i> , 2004 , 37, 43-53 | 10.2 | 196 |
| 46 | The genomic sequence of the accidental pathogen <i>Legionella pneumophila</i> . <i>Science</i> , 2004 , 305, 1966-8 | 33.3 | 391 |
| 45 | HUMAN AND DROSOPHILA ABC PROTEINS | | 5 |
| 44 | Learning to predict protein-protein interactions from protein sequences. <i>Bioinformatics</i> , 2003 , 19, 1875-81 | | 128 |
| 43 | Identification of the <i>Anopheles gambiae</i> ATP-binding cassette transporter superfamily genes. <i>Molecules and Cells</i> , 2003 , 15, 150-8 | 3.5 | 46 |

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|----|---|------|------|
| 42 | Birth and death of protein domains: a simple model of evolution explains power law behavior. <i>BMC Evolutionary Biology</i> , 2002 , 2, 18 | 3 | 134 |
| 41 | Two biomedical sublanguages: a description based on the theories of Zellig Harris. <i>Journal of Biomedical Informatics</i> , 2002 , 35, 222-35 | 10.2 | 128 |
| 40 | Automatically identifying gene/protein terms in MEDLINE abstracts. <i>Journal of Biomedical Informatics</i> , 2002 , 35, 322-30 | 10.2 | 27 |
| 39 | Of truth and pathways: chasing bits of information through myriads of articles. <i>Bioinformatics</i> , 2002 , 18 Suppl 1, S249-57 | 7.2 | 23 |
| 38 | Immunity-related genes and gene families in <i>Anopheles gambiae</i> . <i>Science</i> , 2002 , 298, 159-65 | 33.3 | 743 |
| 37 | The Human ATP-Binding Cassette (ABC) Transporter Superfamily. <i>Genome Research</i> , 2001 , 11, 1156-1166 | 9.7 | 1167 |
| 36 | Human and mouse orthologs of a new ATP-binding cassette gene, ABCG4. <i>Cytogenetic and Genome Research</i> , 2001 , 94, 196-201 | 1.9 | 38 |
| 35 | Disambiguating proteins, genes, and RNA in text: a machine learning approach. <i>Bioinformatics</i> , 2001 , 17 Suppl 1, S97-106 | 7.2 | 107 |
| 34 | Birth of scale-free molecular networks and the number of distinct DNA and protein domains per genome. <i>Bioinformatics</i> , 2001 , 17, 988-96 | 7.2 | 123 |
| 33 | GENIES: a natural-language processing system for the extraction of molecular pathways from journal articles. <i>Bioinformatics</i> , 2001 , 17 Suppl 1, S74-82 | 7.2 | 300 |
| 32 | Two new genes from the human ATP-binding cassette transporter superfamily, ABCC11 and ABCC12, tandemly duplicated on chromosome 16q12. <i>Gene</i> , 2001 , 273, 89-96 | 3.8 | 135 |
| 31 | A chemosensory gene family encoding candidate gustatory and olfactory receptors in <i>Drosophila</i> . <i>Cell</i> , 2001 , 104, 661-73 | 56.2 | 522 |
| 30 | Markov chain Monte Carlo computation of confidence intervals for substitution-rate variation in proteins. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2001 , 203-14 | 1.3 | 1 |
| 29 | TOWARDS THE PREDICTION OF COMPLETE PROTEIN-PROTEIN INTERACTION NETWORKS 2001 , | | 2 |
| 28 | Probabilistic prediction of unknown metabolic and signal-transduction networks. <i>Genetics</i> , 2001 , 159, 1291-8 | 4 | 32 |
| 27 | A knowledge model for analysis and simulation of regulatory networks. <i>Bioinformatics</i> , 2000 , 16, 1120-8 | 7.2 | 57 |
| 26 | A Novel Hypothesis Regarding the Evolutionary Origins of the Immunoglobulin Fold. <i>Current Medical Research and Opinion</i> , 2000 , 16, 88-93 | 2.5 | 8 |
| 25 | Using BLAST for identifying gene and protein names in journal articles. <i>Gene</i> , 2000 , 259, 245-52 | 3.8 | 133 |

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| 24 | A graphic editor for analyzing signal-transduction pathways. <i>Gene</i> , 2000 , 259, 235-44 | 3.8 | 14 |
| 23 | Molecular pathogenesis of B-cell chronic lymphocytic leukemia: analysis of 13q14 chromosomal deletions. <i>Current Topics in Microbiology and Immunology</i> , 2000 , 252, 275-84 | 3.3 | 8 |
| 22 | A new method for characterizing replacement rate variation in molecular sequences. Application of the Fourier and wavelet models to <i>Drosophila</i> and mammalian proteins. <i>Genetics</i> , 2000 , 154, 381-95 | 4 | 21 |
| 21 | The enigma of intron origins. <i>Cellular and Molecular Life Sciences</i> , 1999 , 55, 3-6 | 10.3 | 9 |
| 20 | A spatial map of olfactory receptor expression in the <i>Drosophila</i> antenna. <i>Cell</i> , 1999 , 96, 725-36 | 56.2 | 902 |
| 19 | Molecular Clocks and the Origin of Animals 1999 , 151-169 | | |
| 18 | Human aldehyde dehydrogenase gene family. <i>FEBS Journal</i> , 1998 , 251, 549-57 | | 356 |
| 17 | Tools for visualization and integration of intermediate sequencing results in large disease gene discovery projects. <i>Gene</i> , 1998 , 208, 31-5 | 3.8 | 1 |
| 16 | Analysis of a 69-kb contiguous genomic sequence at a putative tumor suppressor gene locus on human chromosome 6q27. <i>DNA Sequence</i> , 1998 , 9, 189-204 | | 6 |
| 15 | Origin of the metazoan phyla: molecular clocks confirm paleontological estimates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 606-11 | 11.5 | 275 |
| 14 | Exon/intron structure of aldehyde dehydrogenase genes supports the "introns-late" theory. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 6820-5 | 11.5 | 69 |
| 13 | When is it safe to use an oversimplified substitution model in tree-making?. <i>Molecular Biology and Evolution</i> , 1996 , 13, 1255-65 | 8.3 | 28 |
| 12 | Evolutionary relationships of eukaryotic kingdoms. <i>Journal of Molecular Evolution</i> , 1996 , 42, 183-93 | 3.1 | 135 |
| 11 | Assessing dissimilarity of genes by comparing their RNase A mismatch cleavage patterns. <i>Genetics</i> , 1996 , 144, 1975-83 | 4 | 3 |
| 10 | Four-cluster analysis: a simple method to test phylogenetic hypotheses. <i>Molecular Biology and Evolution</i> , 1995 , 12, 163-7 | 8.3 | 40 |
| 9 | Tests of applicability of several substitution models for DNA sequence data. <i>Molecular Biology and Evolution</i> , 1995 , 12, 131-51 | 8.3 | 128 |
| 8 | METREE: a program package for inferring and testing minimum-evolution trees. <i>Bioinformatics</i> , 1994 , 10, 409-12 | 7.2 | 19 |
| 7 | Unbiased estimates of the number of nucleotide substitutions when substitution rate varies among different sites. <i>Journal of Molecular Evolution</i> , 1994 , 38, 295-9 | 3.1 | 36 |

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| 6 | Quick assessment of similarity of two sequences by comparison of their L-tuple frequencies. <i>BioSystems</i> , 1993 , 30, 93-111 | 1.9 | 9 |
| 5 | Statistical properties of the ordinary least-squares, generalized least-squares, and minimum-evolution methods of phylogenetic inference. <i>Journal of Molecular Evolution</i> , 1992 , 35, 367-75 ^{3.1} | | 269 |
| 4 | VOSTORG: a package of microcomputer programs for sequence analysis and construction of phylogenetic trees. <i>Gene</i> , 1991 , 101, 251-4 | 3.8 | 53 |
| 3 | Reconstruction of Phylogenetic Trees and Evolution of Major Histocompatibility Complex Genes 1991 , 13-27 | | 3 |
| 2 | The Legionella pneumophila Sequencing Project 97-104 | | 2 |
| 1 | A Novel Hypothesis Regarding the Evolutionary Origins of the Immunoglobulin Fold | | 4 |