# Baris E Suzek

List of Publications by Year
in descending order

| 31 papers | 14,834 citations | 394286 19 h-index | 526166 27 g-index |
|-----------|------------------|-----------------|------------------|
| 33 all docs | 33 docs citations | 33 times ranked | 27303 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | UniProt: a hub for protein information. Nucleic Acids Research, 2015, 43, D204-D212. | 6.5 | 4,370 |
| 2 | UniRef clusters: a comprehensive and scalable alternative for improving sequence similarity searches. Bioinformatics, 2015, 31, 926-932. | 1.8 | 1,223 |
| 3 | Reorganizing the protein space at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2012, 40, D71-D75. | 6.5 | 1,196 |
| 4 | Activities at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2014, 42, D191-D198. | 6.5 | 1,162 |
| 5 | UniRef: comprehensive and non-redundant UniProt reference clusters. Bioinformatics, 2007, 23, 1282-1288. | 1.8 | 1,144 |
| 6 | The Universal Protein Resource (UniProt): an expanding universe of protein information. Nucleic Acids Research, 2006, 34, D187-D191. | 6.5 | 961 |
| 7 | The Universal Protein Resource (UniProt). Nucleic Acids Research, 2007, 36, D190-D195. | 6.5 | 852 |
| 8 | Ongoing and future developments at the Universal Protein Resource. Nucleic Acids Research, 2011, 39, D214-D219. | 6.5 | 649 |
| 9 | Update on activities at the Universal Protein Resource (UniProt) in 2013. Nucleic Acids Research, 2012, 41, D43-D47. | 6.5 | 620 |
| 10 | The Universal Protein Resource (UniProt) 2009. Nucleic Acids Research, 2009, 37, D169-D174. | 6.5 | 548 |
| 11 | The Universal Protein Resource (UniProt). Nucleic Acids Research, 2007, 35, D193-D197. | 6.5 | 488 |
| 12 | Infrastructure for the life sciences: design and implementation of the UniProt website. BMC Bioinformatics, 2009, 10, 136. | 1.2 | 405 |
| 13 | The Protein Information Resource. Nucleic Acids Research, 2003, 31, 345-347. | 6.5 | 385 |
| 14 | PIRSF: family classification system at the Protein Information Resource. Nucleic Acids Research, 2004, 32, 112D-114. | 6.5 | 193 |
| 15 | The Protein Information Resource: an integrated public resource of functional annotation of proteins. Nucleic Acids Research, 2002, 30, 35-37. | 6.5 | 186 |
| 16 | A probabilistic method for identifying start codons in bacterial genomes. Bioinformatics, 2001, 17, 1123-1130. | 1.8 | 180 |
| 17 | A fast Peptide Match service for UniProt Knowledgebase. Bioinformatics, 2013, 29, 2808-2809. | 1.8 | 101 |
| 18 | A comprehensive protein-centric ID mapping service for molecular data integration. Bioinformatics, 2011, 27, 1190-1191. | 1.8 | 70 |

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|---|---------|-----|-----------|
| 19 | In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. BMC Immunology, 2014, 15, 61. | 0.9 | 21 |
| 20 | Comparison of protein expression profile of limb regeneration between neotenic and metamorphic axolotl. Biochemical and Biophysical Research Communications, 2020, 522, 428-434. | 1.0 | 19 |
| 21 | Quantitative Imaging Biomarker Ontology (QIBO) for Knowledge Representation of Biomedical Imaging Biomarkers. Journal of Digital Imaging, 2013, 26, 630-641. | 1.6 | 12 |
| 22 | Informatics and data quality at collaborative multicenter Breast and Colon Cancer Family Registries. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, e125-e128. | 2.2 | 10 |
| 23 | ML-AdVInfect: A Machine-Learning Based Adenoviral Infection Predictor. Frontiers in Molecular Biosciences, 2021, 8, 647424. | 1.6 | 10 |
| 24 | Preclinical Molecular Signatures of Spinal Cord Functional Restoration: Optimizing the Metamorphic Axolotl (*Ambystoma mexicanum*) Model in Regenerative Medicine. OMICS A Journal of Integrative Biology, 2020, 24, 370-378. | 1.0 | 8 |
| 25 | Life sciences domain analysis model. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 1095-1102. | 2.2 | 6 |
| 26 | A Novel Knowledge Representation Framework for the Statistical Validation of Quantitative Imaging Biomarkers. Journal of Digital Imaging, 2013, 26, 614-629. | 1.6 | 6 |
| 27 | In Silico Analysis of a Highly Mutated Gene in Cancer Provides Insight into Abnormal mRNA Splicing: Splicing Factor 3B Subunit 1K700E Mutant. Biomolecules, 2020, 10, 680. | 1.8 | 6 |
| 28 | Orchestrating caGrid Services in Taverna. , 2008, , . | | 3 |
| 29 | In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. , 2013, , . | | 0 |
| 30 | In silico Analysis of Vaccination Adverse Events. Journal of Allergy and Clinical Immunology, 2015, 135, AB104. | 1.5 | 0 |
| 31 | Taxonomic diversity-based domain interaction prediction. Pamukkale University Journal of Engineering Sciences, 2019, 25, 215-222. | 0.2 | 0 |