

Baris E Suzek

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.

28

papers

12,061

citations

19

h-index

33

g-index

33

ext. papers

13,779

ext. citations

11.1

avg, IF

7.91

L-index

#	Paper	IF	Citations
28	ML-AdVInfect: A Machine-Learning Based Adenoviral Infection Predictor. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 647424	5.6	1
27	Preclinical Molecular Signatures of Spinal Cord Functional Restoration: Optimizing the Metamorphic Axolotl () Model in Regenerative Medicine. <i>OMICS A Journal of Integrative Biology</i> , 2020 , 24, 370-378	3.8	2
26	In Silico Analysis of a Highly Mutated Gene in Cancer Provides Insight into Abnormal mRNA Splicing: Splicing Factor 3B Subunit 1 Mutant. <i>Biomolecules</i> , 2020 , 10,	5.9	4
25	Comparison of protein expression profile of limb regeneration between neotenic and metamorphic axolotl. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 522, 428-434	3.4	11
24	UniProt: a hub for protein information. <i>Nucleic Acids Research</i> , 2015 , 43, D204-12	20.1	3425
23	UniRef clusters: a comprehensive and scalable alternative for improving sequence similarity searches. <i>Bioinformatics</i> , 2015 , 31, 926-32	7.2	614
22	Activities at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2014 , 42, D191-8	20.1	1007
21	In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. <i>BMC Immunology</i> , 2014 , 15, 61	3.7	17
20	A novel knowledge representation framework for the statistical validation of quantitative imaging biomarkers. <i>Journal of Digital Imaging</i> , 2013 , 26, 614-29	5.3	6
19	Quantitative imaging biomarker ontology (QIBO) for knowledge representation of biomedical imaging biomarkers. <i>Journal of Digital Imaging</i> , 2013 , 26, 630-41	5.3	12
18	A fast Peptide Match service for UniProt Knowledgebase. <i>Bioinformatics</i> , 2013 , 29, 2808-9	7.2	73
17	Update on activities at the Universal Protein Resource (UniProt) in 2013. <i>Nucleic Acids Research</i> , 2013 , 41, D43-7	20.1	589
16	Reorganizing the protein space at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2012 , 40, D71-5	20.1	1096
15	Life sciences domain analysis model. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2012 , 19, 1095-102	8.6	5
14	Informatics and data quality at collaborative multicenter Breast and Colon Cancer Family Registries. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2012 , 19, e125-8	8.6	9
13	Ongoing and future developments at the Universal Protein Resource. <i>Nucleic Acids Research</i> , 2011 , 39, D214-9	20.1	592
12	A comprehensive protein-centric ID mapping service for molecular data integration. <i>Bioinformatics</i> , 2011 , 27, 1190-1	7.2	51

11	The Universal Protein Resource (UniProt) 2009. <i>Nucleic Acids Research</i> , 2009 , 37, D169-74	20.1	509
10	Infrastructure for the life sciences: design and implementation of the UniProt website. <i>BMC Bioinformatics</i> , 2009 , 10, 136	3.6	366
9	Orchestrating caGrid Services in Taverna 2008 ,		3
8	The universal protein resource (UniProt). <i>Nucleic Acids Research</i> , 2008 , 36, D190-5	20.1	746
7	UniRef: comprehensive and non-redundant UniProt reference clusters. <i>Bioinformatics</i> , 2007 , 23, 1282-8	7.2	788
6	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2007 , 35, D193-7	20.1	437
5	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , 2006 , 34, D187-91	20.1	839
4	PIRSF: family classification system at the Protein Information Resource. <i>Nucleic Acids Research</i> , 2004 , 32, D112-4	20.1	165
3	The Protein Information Resource. <i>Nucleic Acids Research</i> , 2003 , 31, 345-7	20.1	304
2	The Protein Information Resource: an integrated public resource of functional annotation of proteins. <i>Nucleic Acids Research</i> , 2002 , 30, 35-7	20.1	150
1	A probabilistic method for identifying start codons in bacterial genomes. <i>Bioinformatics</i> , 2001 , 17, 1123-30		162