Baris E Suzek

List of Publications by Citations

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	UniProt: a hub for protein information. *Nucleic Acids Research*, **2015**, 43, D204-12	20.1	3425
27	Reorganizing the protein space at the Universal Protein Resource (UniProt). *Nucleic Acids Research*, **2012**, 40, D71-5	20.1	1096
26	Activities at the Universal Protein Resource (UniProt). *Nucleic Acids Research*, **2014**, 42, D191-8	20.1	1007
25	The Universal Protein Resource (UniProt): an expanding universe of protein information. *Nucleic Acids Research*, **2006**, 34, D187-91	20.1	839
24	UniRef: comprehensive and non-redundant UniProt reference clusters. *Bioinformatics*, **2007**, 23, 1282-8	7.2	788
23	The universal protein resource (UniProt). *Nucleic Acids Research*, **2008**, 36, D190-5	20.1	746
22	UniRef clusters: a comprehensive and scalable alternative for improving sequence similarity searches. *Bioinformatics*, **2015**, 31, 926-32	7.2	614
21	Ongoing and future developments at the Universal Protein Resource. *Nucleic Acids Research*, **2011**, 39, D214-9	20.1	592
20	Update on activities at the Universal Protein Resource (UniProt) in 2013. *Nucleic Acids Research*, **2013**, 41, D43-7	20.1	589
19	The Universal Protein Resource (UniProt) 2009. *Nucleic Acids Research*, **2009**, 37, D169-74	20.1	509
18	The Universal Protein Resource (UniProt). *Nucleic Acids Research*, **2007**, 35, D193-7	20.1	437
17	Infrastructure for the life sciences: design and implementation of the UniProt website. *BMC Bioinformatics*, **2009**, 10, 136	3.6	366
16	The Protein Information Resource. *Nucleic Acids Research*, **2003**, 31, 345-7	20.1	304
15	PIRSF: family classification system at the Protein Information Resource. *Nucleic Acids Research*, **2004**, 32, D112-4	20.1	165
14	A probabilistic method for identifying start codons in bacterial genomes. *Bioinformatics*, **2001**, 17, 1123-30	7.2	162
13	The Protein Information Resource: an integrated public resource of functional annotation of proteins. *Nucleic Acids Research*, **2002**, 30, 35-7	20.1	150
12	A fast Peptide Match service for UniProt Knowledgebase. *Bioinformatics*, **2013**, 29, 2808-9	7.2	73

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11	A comprehensive protein-centric ID mapping service for molecular data integration. *Bioinformatics*, **2011**, 27, 1190-1	7.2	51
10	In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. *BMC Immunology*, **2014**, 15, 61	3.7	17
9	Quantitative imaging biomarker ontology (QIBO) for knowledge representation of biomedical imaging biomarkers. *Journal of Digital Imaging*, **2013**, 26, 630-41	5.3	12
8	Comparison of protein expression profile of limb regeneration between neotenic and metamorphic axolotl. *Biochemical and Biophysical Research Communications*, **2020**, 522, 428-434	3.4	11
7	Informatics and data quality at collaborative multicenter Breast and Colon Cancer Family Registries. *Journal of the American Medical Informatics Association: JAMIA*, **2012**, 19, e125-8	8.6	9
6	A novel knowledge representation framework for the statistical validation of quantitative imaging biomarkers. *Journal of Digital Imaging*, **2013**, 26, 614-29	5.3	6
5	Life sciences domain analysis model. *Journal of the American Medical Informatics Association: JAMIA*, **2012**, 19, 1095-102	8.6	5
4	In Silico Analysis of a Highly Mutated Gene in Cancer Provides Insight into Abnormal mRNA Splicing: Splicing Factor 3B Subunit 1 Mutant. *Biomolecules*, **2020**, 10,	5.9	4
3	Orchestrating caGrid Services in Taverna **2008**,		3
2	Preclinical Molecular Signatures of Spinal Cord Functional Restoration: Optimizing the Metamorphic Axolotl () Model in Regenerative Medicine. *OMICS A Journal of Integrative Biology*, **2020**, 24, 370-378	3.8	2
1	ML-AdVInfect: A Machine-Learning Based Adenoviral Infection Predictor. *Frontiers in Molecular Biosciences*, **2021**, 8, 647424	5.6	1