

Hedi Hegyi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11812355/publications.pdf>

Version: 2024-02-01

16
papers

1,775
citations

516710

16
h-index

940533

16
g-index

16
all docs

16
docs citations

16
times ranked

2453
citing authors

#	ARTICLE	IF	CITATIONS
1	The relationship between protein structure and function: a comprehensive survey with application to the yeast genome. <i>Journal of Molecular Biology</i> , 1999, 288, 147-164.	4.2	384
2	Panmicrobial Oligonucleotide Array for Diagnosis of Infectious Diseases. <i>Emerging Infectious Diseases</i> , 2007, 13, 73-81.	4.3	298
3	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5495-5500.	7.1	206
4	Molecular Fossils in the Human Genome: Identification and Analysis of the Pseudogenes in Chromosomes 21 and 22. <i>Genome Research</i> , 2002, 12, 272-280.	5.5	167
5	The relationship between proteome size, structural disorder and organism complexity. <i>Genome Biology</i> , 2011, 12, R120.	9.6	161
6	Structural disorder promotes assembly of protein complexes. <i>BMC Structural Biology</i> , 2007, 7, 65.	2.3	96
7	Comparing genomes in terms of protein structure: surveys of a finite parts list. <i>FEMS Microbiology Reviews</i> , 1998, 22, 277-304.	8.6	79
8	Intrinsic Structural Disorder Confers Cellular Viability on Oncogenic Fusion Proteins. <i>PLoS Computational Biology</i> , 2009, 5, e1000552.	3.2	74
9	Annotation Transfer for Genomics: Measuring Functional Divergence in Multi-Domain Proteins. <i>Genome Research</i> , 2001, 11, 1632-1640.	5.5	69
10	Identification and correction of abnormal, incomplete and mispredicted proteins in public databases. <i>BMC Bioinformatics</i> , 2008, 9, 353.	2.6	55
11	Intrinsically Disordered Proteins Display No Preference for Chaperone Binding In Vivo. <i>PLoS Computational Biology</i> , 2008, 4, e1000017.	3.2	48
12	Verification of alternative splicing variants based on domain integrity, truncation length and intrinsic protein disorder. <i>Nucleic Acids Research</i> , 2011, 39, 1208-1219.	14.5	46
13	Structural genomics analysis: Characteristics of atypical, common, and horizontally transferred folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 126-141.	2.6	33
14	Increased structural disorder of proteins encoded on human sex chromosomes. <i>Molecular BioSystems</i> , 2012, 8, 229-236.	2.9	22
15	Comprehensive viral oligonucleotide probe design using conserved protein regions. <i>Nucleic Acids Research</i> , 2008, 36, e3-e3.	14.5	21
16	SNPs on human chromosomes 21 and 22 – analysis in terms of protein features and pseudogenes. <i>Pharmacogenomics</i> , 2002, 3, 393-402.	1.3	16