Kristian VlahoviÄek

List of Publications by Year
in descending order

58	3,718	218677	144013
papers	citations	26	57
		h-index	g-index

66	66	66	6992
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Histone modification levels are predictive for gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2926-2931.	7.1	664
2	Cell-of-origin chromatin organization shapes the mutational landscape of cancer. Nature, 2015, 518, 360-364.	27.8	491
3	genomation: a toolkit to summarize, annotate and visualize genomic intervals. Bioinformatics, 2015, 31, 1127-1129.	4.1	263
4	A Retrotransposon-Driven Dicer Isoform Directs Endogenous Small Interfering RNA Production in Mouse Oocytes. Cell, 2013, 155, 807-816.	28.9	238
5	PSAIA â€" Protein Structure and Interaction Analyzer. BMC Structural Biology, 2008, 8, 21.	2.3	152
6	Prediction of Proteinâ€"Protein Interaction Sites in Sequences and 3D Structures by Random Forests. PLoS Computational Biology, 2009, 5, e1000278.	3.2	140
7	The first murine zygotic transcription is promiscuous and uncoupled from splicing and 3â€² processing. EMBO Journal, 2015, 34, 1523-1537.	7.8	131
8	Long terminal repeats power evolution of genes and gene expression programs in mammalian oocytes and zygotes. Genome Research, 2017, 27, 1384-1394.	5.5	129
9	Rod models of DNA: sequence-dependent anisotropic elastic modelling of local bending phenomena. Trends in Biochemical Sciences, 1998, 23, 341-347.	7.5	122
10	DNA analysis servers: plot.it, bend.it, model.it and IS. Nucleic Acids Research, 2003, 31, 3686-3687.	14.5	117
11	Comparison of codon usage measures and their applicability in prediction of microbial gene expressivity. BMC Bioinformatics, 2005, 6, 182.	2.6	109
12	INCA: synonymous codon usage analysis and clustering by means of self-organizing map. Bioinformatics, 2004, 20, 2329-2330.	4.1	103
13	Spatially clustered loci with multiple enhancers are frequent targets of HIV-1 integration. Nature Communications, 2019, 10, 4059.	12.8	84
14	Translational Selection Is Ubiquitous in Prokaryotes. PLoS Genetics, 2010, 6, e1001004.	3.5	76
15	Environmental shaping of codon usage and functional adaptation across microbial communities. Nucleic Acids Research, 2013, 41, 8842-8852.	14.5	48
16	Demosponge EST Sequencing Reveals a Complex Genetic Toolkit of the Simplest Metazoans. Molecular Biology and Evolution, 2010, 27, 2747-2756.	8.9	45
17	Common aberrations from the normal human plasma N-glycan profile. Glycobiology, 2010, 20, 970-975.	2.5	44
18	Molecular analysis of theHEXAgene in Italian patients with infantile and late Onset Tay-Sachs disease: detection of fourteen novel alleles. Human Mutation, 2005, 26, 282-282.	2.5	37

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19	Long non-coding RNA exchange during the oocyte-to-embryo transition in mice. DNA Research, 2017, 24, dsw058.	3.4	37
20	Role of *Cnot6l* in maternal mRNA turnover. Life Science Alliance, 2018, 1, e201800084.	2.8	37
21	Highly reactive cysteine residues are part of the substrate binding site of mammalian dipeptidyl peptidases III. International Journal of Biochemistry and Cell Biology, 2004, 36, 434-446.	2.8	36
22	Distribution of sequence‐dependent curvature in genomic DNA sequences. FEBS Letters, 1997, 406, 69-74.	2.8	33
23	Prediction of Protein Functional Domains from Sequences Using Artificial Neural Networks. Genome Research, 2001, 11, 1410-1417.	5.5	33
24	Efficient recognition of folds in protein 3D structures by the improved PRIDE algorithm. Bioinformatics, 2005, 21, 3322-3323.	4.1	30
25	Coupling AAV-mediated promoterless gene targeting to SaCas9 nuclease to efficiently correct liver metabolic diseases. JCI Insight, 2019, 4, .	5.0	28
26	The SBASE protein domain library, release 5.0: a collection of annotated protein sequence segments. Nucleic Acids Research, 1997, 25, 240-243.	14.5	25
27	The SBASE domain sequence resource, release 12: prediction of protein domain-architecture using support vector machines. Nucleic Acids Research, 2004, 33, D223-D225.	14.5	25
28	TORC1‐mediated sensing of chaperone activity alters glucose metabolism and extends lifespan. Aging Cell, 2017, 16, 994-1005.	6.7	25
29	The most abundant maternal lncRNA Sirena1 acts post-transcriptionally and impacts mitochondrial distribution. Nucleic Acids Research, 2020, 48, 3211-3227.	14.5	25
30	Embryo-Like Features in Developing *Bacillus subtilis* Biofilms. Molecular Biology and Evolution, 2021, 38, 31-47.	8.9	25
31	Identification and functional characterization of five novel mutant alleles in 58 Italian patients with Gaucher disease type 1. Human Mutation, 2005, 25, 100-100.	2.5	22
32	Molecular and functional analysis of the HEXB gene in Italian patients affected with Sandhoff disease: identification of six novel alleles. Neurogenetics, 2009, 10, 49-58.	1.4	22
33	The SBASE protein domain library, release 8.0: a collection of annotated protein sequence segments. Nucleic Acids Research, 2001, 29, 58-60.	14.5	21
34	The SBASE protein domain library, release 6.0: a collection of annotated protein sequence segments. Nucleic Acids Research, 1999, 27, 257-259.	14.5	20
35	CX, DPX and PRIDE: WWW servers for the analysis and comparison of protein 3D structures. Nucleic Acids Research, 2005, 33, W252-W254.	14.5	18
36	Genome-Wide Analysis of the Chromatin Composition of Histone H2A and H3 Variants in Mouse Embryonic Stem Cells. PLoS ONE, 2014, 9, e92689.	2.5	18

#	Article	IF	Citations
37	The SBASE protein domain library, release 9.0: an online resource for protein domain identification. Nucleic Acids Research, 2002, 30, 273-275.	14.5	17
38	Evolutionary Analysis of the Bacillus subtilis Genome Reveals New Genes Involved in Sporulation. Molecular Biology and Evolution, 2020, 37, 1667-1678.	8.9	16
39	model.it : building three dimensional DNA models from sequence data. Bioinformatics, 2000, 16, 1044-1045.	4.1	15
40	A simple probabilistic scoring method for protein domain identification. Bioinformatics, 2000, 16, 1155-1156.	4.1	14
41	Design of peptide mimetics of HIV-1 gp120 for prevention and therapy of HIV disease. Chemical Biology and Drug Design, 2003, 62, 158-166.	1.1	12
42	The SBASE domain sequence library, release 10: domain architecture prediction. Nucleic Acids Research, 2003, 31, 403-405.	14.5	11
43	Molecular analysis of HEXA gene in Argentinean patients affected with Tay–Sachs disease: Possible common origin of the prevalent c.459+5A>G mutation. Gene, 2012, 499, 262-265.	2.2	11
44	Heat-induced longevity in budding yeast requires respiratory metabolism and glutathione recycling. Aging, 2018, 10, 2407-2427.	3.1	11
45	The SBASE protein domain library, release 7.0: a collection of annotated protein sequence segments. Nucleic Acids Research, 2000, 28, 260-262.	14.5	9
46	The domain-server: direct prediction of protein domain-homologies from BLAST search. Bioinformatics, 1999, 15, 343-344.	4.1	8
47	MADNet: microarray database network web server. Nucleic Acids Research, 2008, 36, W332-W335.	14.5	8
48	PRO-MINE: A Bioinformatics Repository and Analytical Tool for TARDBP Mutations. Human Mutation, 2011, 32, E1948-E1958.	2.5	8
49	Exonic splicing signals impose constraints upon the evolution of enzymatic activity. Nucleic Acids Research, 2014, 42, 5790-5798.	14.5	8
50	Big Data, Evolution, and Metagenomes: Predicting Disease from Gut Microbiota Codon Usage Profiles. Methods in Molecular Biology, 2016, 1415, 509-531.	0.9	8
51	Sequence-dependent modelling of local DNA bending phenomena: curvature prediction and vibrational analysis. Genetica, 1999, 106, 63-73.	1.1	7
52	The PRIDE server for protein three-dimensional similarity. Journal of Applied Crystallography, 2002, 35, 648-649.	4.5	5
53	The DNA secondary structure of theBacillus subtilisgenome. FEMS Microbiology Letters, 2003, 218, 23-30.	1.8	5
54	Microbiota Alters Urinary Bladder Weight and Gene Expression. Microorganisms, 2020, 8, 421.	3.6	5

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55	Prediction of Interacting Protein Residues Using Sequence and Structure Data. Methods in Molecular Biology, 2012, 819, 233-251.	0.9	3
56	Dynamics of exhaled breath temperature after smoking a cigarette and its association with lung function changes predictive of COPD risk in smokers: a cross-sectional study. Arhiv Za Higijenu Rada I Toksikologiju, 2019, 70, 123-129.	0.7	2
57	Structure and function of cancer-related developmentally regulated GTP-binding protein 1 (DRG1) is conserved between sponges and humans. Scientific Reports, 2022, 12, .	3.3	2
58	Environmental Shaping of Codon Usage and Functional Adaptation Across Microbial Communities. , 2014, , 1-8.		1