Kristian VlahoviÄek

List of Publications by Year
in descending order

58 papers	3,718 citations	218381 26 h-index	143772 57 g-index
66 all docs	66 docs citations	66 times ranked	6992 citing authors

#	Article	IF	Citations
1	Structure and function of cancer-related developmentally regulated GTP-binding protein 1 (DRG1) is conserved between sponges and humans. Scientific Reports, 2022, 12, .	1.6	2
2	Embryo-Like Features in Developing <i>Bacillus subtilis</i> Biofilms. Molecular Biology and Evolution, 2021, 38, 31-47.	3.5	25
3	Microbiota Alters Urinary Bladder Weight and Gene Expression. Microorganisms, 2020, 8, 421.	1.6	5
4	Evolutionary Analysis of the Bacillus subtilis Genome Reveals New Genes Involved in Sporulation. Molecular Biology and Evolution, 2020, 37, 1667-1678.	3.5	16
5	The most abundant maternal lncRNA Sirena1 acts post-transcriptionally and impacts mitochondrial distribution. Nucleic Acids Research, 2020, 48, 3211-3227.	6.5	25
6	Spatially clustered loci with multiple enhancers are frequent targets of HIV-1 integration. Nature Communications, 2019, 10, 4059.	5.8	84
7	Coupling AAV-mediated promoterless gene targeting to SaCas9 nuclease to efficiently correct liver metabolic diseases. JCI Insight, 2019, 4, .	2.3	28
8	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.	0.4	2
9	Heat-induced longevity in budding yeast requires respiratory metabolism and glutathione recycling. Aging, 2018, 10, 2407-2427.	1.4	11
10	Role of <i>Cnot6l</i> in maternal mRNA turnover. Life Science Alliance, 2018, 1, e201800084.	1.3	37
11	<scp>TORC</scp>1–mediated sensing of chaperone activity alters glucose metabolism and extends lifespan. Aging Cell, 2017, 16, 994-1005.	3.0	25
12	Long terminal repeats power evolution of genes and gene expression programs in mammalian oocytes and zygotes. Genome Research, 2017, 27, 1384-1394.	2.4	129
13	Long non-coding RNA exchange during the oocyte-to-embryo transition in mice. DNA Research, 2017, 24, dsw058.	1.5	37
14	Big Data, Evolution, and Metagenomes: Predicting Disease from Gut Microbiota Codon Usage Profiles. Methods in Molecular Biology, 2016, 1415, 509-531.	0.4	8
15	Cell-of-origin chromatin organization shapes the mutational landscape of cancer. Nature, 2015, 518, 360-364.	13.7	491
16	The first murine zygotic transcription is promiscuous and uncoupled from splicing and 3′ processing. EMBO Journal, 2015, 34, 1523-1537.	3.5	131
17	genomation: a toolkit to summarize, annotate and visualize genomic intervals. Bioinformatics, 2015, 31, 1127-1129.	1.8	263
18	Genome-Wide Analysis of the Chromatin Composition of Histone H2A and H3 Variants in Mouse Embryonic Stem Cells. PLoS ONE, 2014, 9, e92689.	1.1	18

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19	Environmental Shaping of Codon Usage and Functional Adaptation Across Microbial Communities. , 2014, , 1-8.		1
20	Exonic splicing signals impose constraints upon the evolution of enzymatic activity. Nucleic Acids Research, 2014, 42, 5790-5798.	6.5	8
21	A Retrotransposon-Driven Dicer Isoform Directs Endogenous Small Interfering RNA Production in Mouse Oocytes. Cell, 2013, 155, 807-816.	13.5	238
22	Environmental shaping of codon usage and functional adaptation across microbial communities. Nucleic Acids Research, 2013, 41, 8842-8852.	6.5	48
23	Molecular analysis of HEXA gene in Argentinean patients affected with Tayâ€"Sachs disease: Possible common origin of the prevalent c.459+5A>G mutation. Gene, 2012, 499, 262-265.	1.0	11
24	Prediction of Interacting Protein Residues Using Sequence and Structure Data. Methods in Molecular Biology, 2012, 819, 233-251.	0.4	3
25	PRO-MINE: A Bioinformatics Repository and Analytical Tool for TARDBP Mutations. Human Mutation, 2011, 32, E1948-E1958.	1.1	8
26	Translational Selection Is Ubiquitous in Prokaryotes. PLoS Genetics, 2010, 6, e1001004.	1.5	76
27	Demosponge EST Sequencing Reveals a Complex Genetic Toolkit of the Simplest Metazoans. Molecular Biology and Evolution, 2010, 27, 2747-2756.	3.5	45
28	Common aberrations from the normal human plasma N-glycan profile. Glycobiology, 2010, 20, 970-975.	1.3	44
29	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.	3.3	664
30	Prediction of Proteinâ€"Protein Interaction Sites in Sequences and 3D Structures by Random Forests. PLoS Computational Biology, 2009, 5, e1000278.	1.5	140
31	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.	0.7	22
32	PSAIA â€" Protein Structure and Interaction Analyzer. BMC Structural Biology, 2008, 8, 21.	2.3	152
33	MADNet: microarray database network web server. Nucleic Acids Research, 2008, 36, W332-W335.	6.5	8
34	Comparison of codon usage measures and their applicability in prediction of microbial gene expressivity. BMC Bioinformatics, 2005, 6, 182.	1.2	109
35	Identification and functional characterization of five novel mutant alleles in 58 Italian patients with Gaucher disease type 1. Human Mutation, 2005, 25, 100-100.	1.1	22
36	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.	1.1	37

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37	Efficient recognition of folds in protein 3D structures by the improved PRIDE algorithm. Bioinformatics, 2005, 21, 3322-3323.	1.8	30
38	CX, DPX and PRIDE: WWW servers for the analysis and comparison of protein 3D structures. Nucleic Acids Research, 2005, 33, W252-W254.	6.5	18
39	The SBASE domain sequence resource, release 12: prediction of protein domain-architecture using support vector machines. Nucleic Acids Research, 2004, 33, D223-D225.	6.5	25
40	INCA: synonymous codon usage analysis and clustering by means of self-organizing map. Bioinformatics, 2004, 20, 2329-2330.	1.8	103
41	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.	1.2	36
42	Design of peptide mimetics of HIV-1 gp120 for prevention and therapy of HIV disease. Chemical Biology and Drug Design, 2003, 62, 158-166.	1.2	12
43	The DNA secondary structure of theBacillus subtilisgenome. FEMS Microbiology Letters, 2003, 218, 23-30.	0.7	5
44	DNA analysis servers: plot.it, bend.it, model.it and IS. Nucleic Acids Research, 2003, 31, 3686-3687.	6.5	117
45	The SBASE domain sequence library, release 10: domain architecture prediction. Nucleic Acids Research, 2003, 31, 403-405.	6.5	11
46	The SBASE protein domain library, release 9.0: an online resource for protein domain identification. Nucleic Acids Research, 2002, 30, 273-275.	6.5	17
47	The PRIDE server for protein three-dimensional similarity. Journal of Applied Crystallography, 2002, 35, 648-649.	1.9	5
48	Prediction of Protein Functional Domains from Sequences Using Artificial Neural Networks. Genome Research, 2001, 11, 1410-1417.	2.4	33
49	The SBASE protein domain library, release 8.0: a collection of annotated protein sequence segments. Nucleic Acids Research, 2001, 29, 58-60.	6.5	21
50	model.it : building three dimensional DNA models from sequence data. Bioinformatics, 2000, 16, 1044-1045.	1.8	15
51	The SBASE protein domain library, release 7.0: a collection of annotated protein sequence segments. Nucleic Acids Research, 2000, 28, 260-262.	6.5	9
52	A simple probabilistic scoring method for protein domain identification. Bioinformatics, 2000, 16, 1155-1156.	1.8	14
53	The domain-server: direct prediction of protein domain-homologies from BLAST search. Bioinformatics, 1999, 15, 343-344.	1.8	8
54	The SBASE protein domain library, release 6.0: a collection of annotated protein sequence segments. Nucleic Acids Research, 1999, 27, 257-259.	6.5	20

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55	Sequence-dependent modelling of local DNA bending phenomena: curvature prediction and vibrational analysis. Genetica, 1999, 106, 63-73.	0.5	7
56	Rod models of DNA: sequence-dependent anisotropic elastic modelling of local bending phenomena. Trends in Biochemical Sciences, 1998, 23, 341-347.	3.7	122
57	The SBASE protein domain library, release 5.0: a collection of annotated protein sequence segments. Nucleic Acids Research, 1997, 25, 240-243.	6.5	25
58	Distribution of sequence-dependent curvature in genomic DNA sequences. FEBS Letters, 1997, 406, 69-74.	1.3	33