

# Maria A Krestyaninova

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6561488/publications.pdf>

Version: 2024-02-01

19  
papers

4,631  
citations

516710

16  
h-index

839539

18  
g-index

19  
all docs

19  
docs citations

19  
times ranked

11171  
citing authors

#	ARTICLE	IF	CITATIONS
1	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. <i>European Journal of Human Genetics</i> , 2016, 24, 521-528.	2.8	27
2	PPISURV: a novel bioinformatics tool for uncovering the hidden role of specific genes in cancer survival outcome. <i>Oncogene</i> , 2014, 33, 1621-1628.	5.9	54
3	Data Integration between Swedish National Clinical Health Registries and Biobanks Using an Availability System. <i>Lecture Notes in Computer Science</i> , 2014, , 32-40.	1.3	0
4	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. <i>American Journal of Human Genetics</i> , 2013, 93, 876-890.	6.2	330
5	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012, 44, 1084-1089.	21.4	701
6	Services Design in a Collaborative Network for Multidisciplinary Research Projects. <i>International Federation for Information Processing</i> , 2012, , 273-279.	0.4	1
7	SAIL—a software system for sample and phenotype availability across biobanks and cohorts. <i>Bioinformatics</i> , 2011, 27, 589-591.	4.1	14
8	Human metabolic profiles are stably controlled by genetic and environmental variation. <i>Molecular Systems Biology</i> , 2011, 7, 525.	7.2	158
9	A Genome-Wide Metabolic QTL Analysis in Europeans Implicates Two Loci Shaped by Recent Positive Selection. <i>PLoS Genetics</i> , 2011, 7, e1002270.	3.5	132
10	Sequence variants at CHRN3 affect smoking behavior. <i>Nature Genetics</i> , 2010, 42, 448-453.	21.4	649
11	R spider: a network-based analysis of gene lists by combining signaling and metabolic pathways from Reactome and KEGG databases. <i>Nucleic Acids Research</i> , 2010, 38, W78-W83.	14.5	62
12	A System for Information Management in BioMedical Studies—SIMBioMS. <i>Bioinformatics</i> , 2009, 25, 2768-2769.	4.1	27
13	ArrayExpress update—from an archive of functional genomics experiments to the atlas of gene expression. <i>Nucleic Acids Research</i> , 2009, 37, D868-D872.	14.5	380
14	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009, 41, 77-81.	21.4	662
15	PASSIM—an open source software system for managing information in biomedical studies. <i>BMC Bioinformatics</i> , 2007, 8, 52.	2.6	24
16	Standards for systems biology. <i>Nature Reviews Genetics</i> , 2006, 7, 593-605.	16.3	137
17	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D201-D205.	14.5	478
18	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	14.5	640

#	ARTICLE	IF	CITATIONS
19	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	6.5	155