

# Jaap Heringa

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1744852/publications.pdf>

Version: 2024-02-01

23  
papers

9,443  
citations

687363

13  
h-index

610901

24  
g-index

26  
all docs

26  
docs citations

26  
times ranked

21004  
citing authors

#	ARTICLE	IF	CITATIONS
1	The FAIR Guiding Principles for scientific data management and stewardship. <i>Scientific Data</i> , 2016, 3, 160018.	5.3	8,670
2	FAIR Principles: Interpretations and Implementation Considerations. <i>Data Intelligence</i> , 2020, 2, 10-29.	1.5	149
3	Multi-RELIEF: a method to recognize specificity determining residues from multiple sequence alignments using a Machine-Learning approach for feature weighting. <i>Bioinformatics</i> , 2008, 24, 18-25.	4.1	83
4	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019, 20, 693-701.	16.3	69
5	Seeing the trees through the forest: sequence-based homo- and heteromeric protein-protein interaction sites prediction using random forest. <i>Bioinformatics</i> , 2017, 33, 1479-1487.	4.1	66
6	Sequence comparison by sequence harmony identifies subtype-specific functional sites. <i>Nucleic Acids Research</i> , 2006, 34, 6540-6548.	14.5	64
7	Multi-Harmony: detecting functional specificity from sequence alignment. <i>Nucleic Acids Research</i> , 2010, 38, W35-W40.	14.5	51
8	Bridging the translational innovation gap through good biomarker practice. <i>Nature Reviews Drug Discovery</i> , 2017, 16, 587-588.	46.4	48
9	The potential use of big data in oncology. <i>Oral Oncology</i> , 2019, 98, 8-12.	1.5	40
10	Aurora kinase A (AURKA) interaction with Wnt and Ras-MAPK signalling pathways in colorectal cancer. <i>Scientific Reports</i> , 2018, 8, 7522.	3.3	38
11	Sequence harmony: detecting functional specificity from alignments. <i>Nucleic Acids Research</i> , 2007, 35, W495-W498.	14.5	34
12	SeRenDIP: SEquential REmasteriNg to Derive profiles for fast and accurate predictions of PPI interface positions. <i>Bioinformatics</i> , 2019, 35, 4794-4796.	4.1	21
13	Sequence specificity between interacting and non-interacting homologs identifies interface residues in a homodimer and monomer use case. <i>BMC Bioinformatics</i> , 2015, 16, 325.	2.6	18
14	Construction and Experimental Validation of a Petri Net Model of Wnt/ $\beta$ -Catenin Signaling. <i>PLoS ONE</i> , 2016, 11, e0155743.	2.5	16
15	Bioinformatics in the Netherlands: the value of a nationwide community. <i>Briefings in Bioinformatics</i> , 2019, 20, 375-383.	6.5	15
16	PIPENN: protein interface prediction from sequence with an ensemble of neural nets. <i>Bioinformatics</i> , 2022, 38, 2111-2118.	4.1	10
17	Both Intrinsic Substrate Preference and Network Context Contribute to Substrate Selection of Classical Tyrosine Phosphatases. <i>Journal of Biological Chemistry</i> , 2017, 292, 4942-4952.	3.4	8
18	Systematically linking transSMART, Galaxy and EGA for reusing human translational research data. <i>F1000Research</i> , 2017, 6, 1488.	1.6	8

#	ARTICLE	IF	CITATIONS
19	Motif-Aware PRALINE: Improving the alignment of motif regions. PLoS Computational Biology, 2018, 14, e1006547.	3.2	7
20	Integration of EGA secure data access into Galaxy. F1000Research, 2016, 5, 2841.	1.6	7
21	Training for translation between disciplines: a philosophy for life and data sciences curricula. Bioinformatics, 2018, 34, i4-i12.	4.1	5
22	Tailor-made multiple sequence alignments using the PRALINE 2 alignment toolkit. Bioinformatics, 2019, 35, 5315-5317.	4.1	4
23	A framework for exhaustive modelling of genetic interaction patterns using Petri nets. Bioinformatics, 2020, 36, 2142-2149.	4.1	3