

# Francois Ehrenmann

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8486736/publications.pdf>

Version: 2024-02-01

24  
papers

2,356  
citations

361413

20  
h-index

642732

23  
g-index

24  
all docs

24  
docs citations

24  
times ranked

4288  
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-term and large-scale <i>Quercus petraea</i> population survey conducted in provenance tests installed in France. <i>Annals of Forest Science</i> , 2022, 79, .	2.0	2
2	Use of IMGT® Databases and Tools for Antibody Engineering and Humanization. <i>Methods in Molecular Biology</i> , 2018, 1827, 35-69.	0.9	15
3	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	9.3	303
4	Fine-scale species distribution changes in a mixed oak stand over two successive generations. <i>New Phytologist</i> , 2017, 215, 126-139.	7.3	33
5	Adaptive and plastic responses of <i>Quercus petraea</i> populations to climate across Europe. <i>Global Change Biology</i> , 2017, 23, 2831-2847.	9.5	92
6	High-density SNP assay development for genetic analysis in maritime pine ( <i>Pinus pinaster</i> ). <i>Molecular Ecology Resources</i> , 2016, 16, 574-587.	4.8	53
7	High-density linkage mapping and distribution of segregation distortion regions in the oak genome. <i>DNA Research</i> , 2016, 23, 115-124.	3.4	61
8	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016, 16, 254-265.	4.8	108
9	Evidence of intense chromosomal shuffling during conifer evolution. <i>Genome Biology and Evolution</i> , 2015, 7, evv185.	2.5	26
10	Single-nucleotide polymorphism discovery and validation in high-density SNP array for genetic analysis in European white oaks. <i>Molecular Ecology Resources</i> , 2015, 15, 1446-1459.	4.8	43
11	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. <i>BMC Genomics</i> , 2015, 16, 112.	2.8	49
12	De novo assembly of maritime pine transcriptome: implications for forest breeding and biotechnology. <i>Plant Biotechnology Journal</i> , 2014, 12, 286-299.	8.3	115
13	Genome-wide distribution of genetic diversity and linkage disequilibrium in a mass-selected population of maritime pine. <i>BMC Genomics</i> , 2014, 15, 171.	2.8	41
14	High-density linkage mapping in a pine tree reveals a genomic region associated with inbreeding depression and provides clues to the extent and distribution of meiotic recombination. <i>BMC Biology</i> , 2013, 11, 50.	3.8	63
15	IMGT/DomainGapAlign: The IMGT® Tool for the Analysis of IG, TR, MH, IgSF, and MhSF Domain Amino Acid Polymorphism. <i>Methods in Molecular Biology</i> , 2012, 882, 605-633.	0.9	28
16	Use of IMGT® Databases and Tools for Antibody Engineering and Humanization. <i>Methods in Molecular Biology</i> , 2012, 907, 3-37.	0.9	38
17	Mass Spectrometry Detection of G3m and IGHC3 Alleles and Follow-Up of Differential Mother and Neonate IgG3. <i>PLoS ONE</i> , 2012, 7, e46097.	2.5	26
18	IMGT/Collier de Perles: IMGT Standardized Representation of Domains (IG, TR, and IgSF Variable and) Tj ETQqO O O rgBT /Overlock 10 Tf . pdb.prot5635-pdb.prot5635.	0.3	61

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19	IMGT/DomainGapAlign: IMGT Standardized Analysis of Amino Acid Sequences of Variable, Constant, and Groove Domains (IG, TR, MH, IgSF, MhSF). Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5636.	0.3	62
20	IMGT/3Dstructure-DB: Querying the IMGT Database for 3D Structures in Immunology and Immunoinformatics (IG or Antibodies, TR, MH, RPI, and FPIA). Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5637.	0.3	62
21	IMGT/3Dstructure-DB and IMGT/DomainGapAlign: a database and a tool for immunoglobulins or antibodies, T cell receptors, MHC, IgSF and MhcSF. Nucleic Acids Research, 2010, 38, D301-D307.	14.5	232
22	Standardized Sequence and Structure Analysis of Antibody Using IMGT <sup>®</sup> . , 2010, , 11-31.		19
23	IMGT(R), the international ImMunoGeneTics information system(R). Nucleic Acids Research, 2009, 37, D1006-D1012.	14.5	753
24	IG, TR and IgSF, MHC and MhcSF: what do we learn from the IMGT Colliers de Perles?. Briefings in Functional Genomics & Proteomics, 2008, 6, 253-264.	3.8	71