Francois Ehrenmann

List of Publications by Year
in descending order

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	IMGT(R), the international ImMunoGeneTics information system(R). Nucleic Acids Research, 2009, 37, D1006-D1012.	14.5	753
2	Oak genome reveals facets of long lifespan. Nature Plants, 2018, 4, 440-452.	9.3	303
3	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
4	*De novo* assembly of maritime pine transcriptome: implications for forest breeding and biotechnology. Plant Biotechnology Journal, 2014, 12, 286-299.	8.3	115
5	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. Molecular Ecology Resources, 2016, 16, 254-265.	4.8	108
6	Adaptive and plastic responses of *Quercus petraea* populations to climate across Europe. Global Change Biology, 2017, 23, 2831-2847.	9.5	92
7	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
8	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. BMC Biology, 2013, 11, 50.	3.8	63
9	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
10	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
11	IMGT/Collier de Perles: IMGT Standardized Representation of Domains (IG, TR, and IgSF Variable and) Tj ETQq1 1 0.784314 rgBT /Over pdb.prot5635-pdb.prot5635.	0.3	61
12	High-density linkage mapping and distribution of segregation distortion regions in the oak genome. DNA Research, 2016, 23, 115-124.	3.4	61
13	High‐density <scp>SNP</scp> assay development for genetic analysis in maritime pine (*<scp>P</scp>inus pinaster*). Molecular Ecology Resources, 2016, 16, 574-587.	4.8	53
14	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. BMC Genomics, 2015, 16, 112.	2.8	49
15	Single‐nucleotide polymorphism discovery and validation in high‐density <scp>SNP</scp> array for genetic analysis in European white oaks. Molecular Ecology Resources, 2015, 15, 1446-1459.	4.8	43
16	Genome-wide distribution of genetic diversity and linkage disequilibrium in a mass-selected population of maritime pine. BMC Genomics, 2014, 15, 171.	2.8	41
17	Use of IMGTÂ® Databases and Tools for Antibody Engineering and Humanization. Methods in Molecular Biology, 2012, 907, 3-37.	0.9	38
18	Fine‐scale species distribution changes in a mixed oak stand over two successive generations. New Phytologist, 2017, 215, 126-139.	7.3	33

#	Article	IF	Citations
19	IMGT/DomainGapAlign: The IMGTÂ® Tool for the Analysis of IG, TR, MH, IgSF, and MhSF Domain Amino Acid Polymorphism. Methods in Molecular Biology, 2012, 882, 605-633.	0.9	28
20	Evidence of intense chromosomal shuffling during conifer evolution. Genome Biology and Evolution, 2015, 7, evv185.	2.5	26
21	Mass Spectrometry Detection of G3m and IGHG3 Alleles and Follow-Up of Differential Mother and Neonate IgG3. PLoS ONE, 2012, 7, e46097.	2.5	26
22	Standardized Sequence and Structure Analysis of Antibody Using IMGTÂ®. , 2010, , 11-31.		19
23	Use of IMGTÂ® Databases and Tools for Antibody Engineering and Humanization. Methods in Molecular Biology, 2018, 1827, 35-69.	0.9	15
24	Long-term and large-scale Quercus petraea population survey conducted in provenance tests installed in France. Annals of Forest Science, 2022, 79, .	2.0	2