Nicolas Thierry-Mieg

List of Publications by Year
in descending order

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Version: 2024-02-01

43 papers	3,994 citations	218592 26 h-index	254106 43 g-index
46 all docs	46 docs citations	46 times ranked	4904 citing authors

#	Article	IF	Citations
1	Whole-exome sequencing improves the diagnosis and care of men with non-obstructive azoospermia. American Journal of Human Genetics, 2022, 109, 508-517.	2.6	41
2	Combined Use of Whole Exome Sequencing and CRISPR/Cas9 to Study the Etiology of Non-Obstructive Azoospermia: Demonstration of the Dispensable Role of the Testis-Specific Genes C1orf185 and CCT6B. Cells, 2022, 11, 118.	1.8	1
3	A recurrent ZP1 variant is responsible for oocyte maturation defect with degenerated oocytes in infertile females. Clinical Genetics, 2022, 102, 22-29.	1.0	5
4	Defect in the nuclear pore membrane glycoprotein 210-like gene is associated with extreme uncondensed sperm nuclear chromatin and male infertility: a case report. Human Reproduction, 2021, 36, 693-701.	0.4	20
5	Genetic analyses of a large cohort of infertile patients with globozoospermia, DPY19L2 still the main actor, GGN confirmed as a guest player. Human Genetics, 2021, 140, 43-57.	1.8	24
6	The sodium/proton exchanger <scp>SLC9C1</scp> (<scp>sNHE</scp>) is essential for human sperm motility and fertility. Clinical Genetics, 2021, 99, 684-693.	1.0	26
7	Identification and Characterization of the Most Common Genetic Variant Responsible for Acephalic Spermatozoa Syndrome in Men Originating from North Africa. International Journal of Molecular Sciences, 2021, 22, 2187.	1.8	5
8	A missense mutation in IFT74, encoding for an essential component for intraflagellar transport of Tubulin, causes asthenozoospermia and male infertility without clinical signs of Bardetâ€“Biedl syndrome. Human Genetics, 2021, 140, 1031-1043.	1.8	20
9	Bi-allelic truncating variants in CFAP206 cause male infertility in human and mouse. Human Genetics, 2021, 140, 1367-1377.	1.8	23
10	Biallelic variants in MAATS1 encoding CFAP91, a calmodulin-associated and spoke-associated complex protein, cause severe astheno-teratozoospermia and male infertility. Journal of Medical Genetics, 2020, 57, 708-716.	1.5	43
11	Whole exome sequencing of men with multiple morphological abnormalities of the sperm flagella reveals novel homozygous QRICH2 mutations. Clinical Genetics, 2019, 96, 394-401.	1.0	30
12	CFAP70 mutations lead to male infertility due to severe astheno-teratozoospermia. A case report. Human Reproduction, 2019, 34, 2071-2079.	0.4	43
13	Bi-allelic Mutations in ARMC2 Lead to Severe Astheno-Teratozoospermia Due to Sperm Flagellum Malformations in Humans and Mice. American Journal of Human Genetics, 2019, 104, 331-340.	2.6	113
14	MatrixDB: integration of new data with a focus on glycosaminoglycan interactions. Nucleic Acids Research, 2019, 47, D376-D381.	6.5	93
15	<scp>PATL</scp> 2 is a key actor of oocyte maturation whose invalidation causes infertility in women and mice. EMBO Molecular Medicine, 2018, 10, .	3.3	53
16	Absence of CFAP69 Causes Male Infertility due to Multiple Morphological Abnormalities of the Flagella in Human and Mouse. American Journal of Human Genetics, 2018, 102, 636-648.	2.6	121
17	Mutations in CFAP43 and CFAP44 cause male infertility and flagellum defects in Trypanosoma and human. Nature Communications, 2018, 9, 686.	5.8	173
18	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. BMC Bioinformatics, 2018, 19, 134.	1.2	47

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19	Whole-exome sequencing identifies mutations in FSIP2 as a recurrent cause of multiple morphological abnormalities of the sperm flagella. Human Reproduction, 2018, 33, 1973-1984.	0.4	93
20	A Homozygous Ancestral SVA-Insertion-Mediated Deletion in WDR66 Induces Multiple Morphological Abnormalities of the Sperm Flagellum and Male Infertility. American Journal of Human Genetics, 2018, 103, 400-412.	2.6	81
21	<scp>SPINK</scp>2 deficiency causes infertility by inducing sperm defects in heterozygotes and azoospermia inÂhomozygotes. EMBO Molecular Medicine, 2017, 9, 1132-1149.	3.3	95
22	Selective termination of lnc <scp>RNA</scp> transcription promotes heterochromatin silencing and cell differentiation. EMBO Journal, 2017, 36, 2626-2641.	3.5	45
23	Homozygous mutation of PLCZ1 leads to defective human oocyte activation and infertility that is not rescued by the WW-binding protein PAWP. Human Molecular Genetics, 2016, 25, 878-891.	1.4	112
24	MatrixDB, the extracellular matrix interaction database: updated content, a new navigator and expanded functionalities. Nucleic Acids Research, 2015, 43, D321-D327.	6.5	118
25	Mutations in DNAH1, which Encodes an Inner Arm Heavy Chain Dynein, Lead to Male Infertility from Multiple Morphological Abnormalities of the Sperm Flagella. American Journal of Human Genetics, 2014, 94, 95-104.	2.6	328
26	Fine Characterisation of a Recombination Hotspot at the DPY19L2 Locus and Resolution of the Paradoxical Excess of Duplications over Deletions in the General Population. PLoS Genetics, 2013, 9, e1003363.	1.5	25
27	Proto-genes and de novo gene birth. Nature, 2012, 487, 370-374.	13.7	555
28	Mapping Interactomes with High Coverage and Efficiency Using the Shifted Transversal Design. Methods in Molecular Biology, 2012, 812, 147-159.	0.4	0
29	MatrixDB, the extracellular matrix interaction database. Nucleic Acids Research, 2011, 39, D235-D240.	6.5	117
30	Interaction networks as a tool to investigate the mechanisms of aging. Biogerontology, 2010, 11, 463-473.	2.0	14
31	New insights into protein-protein interaction data lead to increased estimates of the S. cerevisiae interactome size. BMC Bioinformatics, 2010, 11, 605.	1.2	39
32	Shifted Transversal Design smart-pooling for high coverage interactome mapping. Genome Research, 2009, 19, 1262-1269.	2.4	36
33	MatrixDB, a database focused on extracellular proteinâ€“protein and proteinâ€“carbohydrate interactions. Bioinformatics, 2009, 25, 690-691.	1.8	88
34	T Cellâ€“Mediated Inflammation in Adipose Tissue Does Not Cause Insulin Resistance in Hyperlipidemic Mice. Circulation Research, 2009, 104, 961-968.	2.0	41
35	Interaction networks: From protein functions to drug discovery. A review. Pathologie Et Biologie, 2009, 57, 324-333.	2.2	101
36	Interpool: interpreting smart-pooling results. Bioinformatics, 2008, 24, 696-703.	1.8	16

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37	Pooling in systems biology becomes smart. Nature Methods, 2006, 3, 161-162.	9.0	11
38	A new pooling strategy for high-throughput screening: the Shifted Transversal Design. BMC Bioinformatics, 2006, 7, 28.	1.2	72
39	A proteinâ€“protein interaction map of the Caenorhabditis elegans 26S proteasome. EMBO Reports, 2001, 2, 821-828.	2.0	173
40	Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans. Nature Genetics, 2001, 27, 332-336.	9.4	159
41	InterDB, a Prediction-Oriented Protein Interaction Database for C. elegans. Lecture Notes in Computer Science, 2001, , 135-146.	1.0	0
42	Protein Interaction Mapping in C. elegans Using Proteins Involved in Vulval Development. Science, 2000, 287, 116-122.	6.0	766
43	A Model of Elegance. American Journal of Human Genetics, 1998, 63, 955-961.	2.6	22