

Nicolas Le Novère

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5415431/publications.pdf>

Version: 2024-02-01

132
papers

14,959
citations

36691

53
h-index

21843

118
g-index

145
all docs

145
docs citations

145
times ranked

16988
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425. | 9.4 | 920 |
| 2 | The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741. | 9.4 | 828 |
| 3 | Nicotinic Receptors at the Amino Acid Level. <i>Annual Review of Pharmacology and Toxicology</i> , 2000, 40, 431-458. | 4.2 | 757 |
| 4 | BioModels Database: a free, centralized database of curated, published, quantitative kinetic models of biochemical and cellular systems. <i>Nucleic Acids Research</i> , 2006, 34, D689-D691. | 6.5 | 661 |
| 5 | The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942. | 9.4 | 613 |
| 6 | Minimum information requested in the annotation of biochemical models (MIRIAM). <i>Nature Biotechnology</i> , 2005, 23, 1509-1515. | 9.4 | 553 |
| 7 | A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160. | 9.4 | 530 |
| 8 | Reduced antinociception in mice lacking neuronal nicotinic receptor subunits. <i>Nature</i> , 1999, 398, 805-810. | 13.7 | 514 |
| 9 | Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896. | 9.4 | 506 |
| 10 | Subunit Composition of Functional Nicotinic Receptors in Dopaminergic Neurons Investigated with Knock-Out Mice. <i>Journal of Neuroscience</i> , 2003, 23, 7820-7829. | 1.7 | 473 |
| 11 | BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. <i>BMC Systems Biology</i> , 2010, 4, 92. | 3.0 | 467 |
| 12 | Quantitative and logic modelling of molecular and gene networks. <i>Nature Reviews Genetics</i> , 2015, 16, 146-158. | 7.7 | 406 |
| 13 | Molecular evolution of the nicotinic acetylcholine receptor: An example of multigene family in excitable cells. <i>Journal of Molecular Evolution</i> , 1995, 40, 155-172. | 0.8 | 378 |
| 14 | The diversity of subunit composition in nAChRs: Evolutionary origins, physiologic and pharmacologic consequences. <i>Journal of Neurobiology</i> , 2002, 53, 447-456. | 3.7 | 371 |
| 15 | Neuronal Nicotinic Receptor $\alpha 6$ Subunit mRNA is Selectively Concentrated in Catecholaminergic Nuclei of the Rat Brain. <i>European Journal of Neuroscience</i> , 1996, 8, 2428-2439. | 1.2 | 358 |
| 16 | BioModels: ten-year anniversary. <i>Nucleic Acids Research</i> , 2015, 43, D542-D548. | 6.5 | 334 |
| 17 | Brain nicotinic receptors: structure and regulation, role in learning and reinforcement ¹ Published on the World Wide Web on 24 October 1997.1. <i>Brain Research Reviews</i> , 1998, 26, 198-216. | 9.1 | 280 |
| 18 | Models of the extracellular domain of the nicotinic receptors and of agonist- and Ca ²⁺ -binding sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 3210-3215. | 3.3 | 263 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Novel pharmacological targets for the treatment of Parkinson's disease. <i>Nature Reviews Drug Discovery</i> , 2006, 5, 845-854. | 21.5 | 262 |
| 20 | Controlled vocabularies and semantics in systems biology. <i>Molecular Systems Biology</i> , 2011, 7, 543. | 3.2 | 246 |
| 21 | Reproducible computational biology experiments with SED-ML - The Simulation Experiment Description Markup Language. <i>BMC Systems Biology</i> , 2011, 5, 198. | 3.0 | 211 |
| 22 | Normal Mode Analysis Suggests a Quaternary Twist Model for the Nicotinic Receptor Gating Mechanism. <i>Biophysical Journal</i> , 2005, 88, 3954-3965. | 0.2 | 178 |
| 23 | Molecular model of a lattice of signalling proteins involved in bacterial chemotaxis. <i>Nature Cell Biology</i> , 2000, 2, 792-796. | 4.6 | 175 |
| 24 | The Identity of Plant Glutamate Receptors. <i>Science</i> , 2001, 292, 1486b-1487. | 6.0 | 175 |
| 25 | Identifiers.org and MIRIAM Registry: community resources to provide persistent identification. <i>Nucleic Acids Research</i> , 2012, 40, D580-D586. | 6.5 | 162 |
| 26 | PTEN Regulates PI(3,4)P2 Signaling Downstream of Class I PI3K. <i>Molecular Cell</i> , 2017, 68, 566-580.e10. | 4.5 | 149 |
| 27 | SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. <i>BMC Systems Biology</i> , 2013, 7, 135. | 3.0 | 145 |
| 28 | Path2Models: large-scale generation of computational models from biochemical pathway maps. <i>BMC Systems Biology</i> , 2013, 7, 116. | 3.0 | 145 |
| 29 | Localization of nAChR subunit mRNAs in the brain of <i>Macaca mulatta</i> . <i>European Journal of Neuroscience</i> , 2000, 12, 3664-3674. | 1.2 | 139 |
| 30 | DARPP-32 Is a Robust Integrator of Dopamine and Glutamate Signals. <i>PLoS Computational Biology</i> , 2006, 2, e176. | 1.5 | 139 |
| 31 | Epicardial cells derived from human embryonic stem cells augment cardiomyocyte-driven heart regeneration. <i>Nature Biotechnology</i> , 2019, 37, 895-906. | 9.4 | 139 |
| 32 | Minimum Information About a Simulation Experiment (MIASE). <i>PLoS Computational Biology</i> , 2011, 7, e1001122. | 1.5 | 133 |
| 33 | Experimentally based model of a complex between a snake toxin and the $\alpha 7$ nicotinic receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 3216-3221. | 3.3 | 121 |
| 34 | COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. <i>BMC Bioinformatics</i> , 2014, 15, 369. | 1.2 | 114 |
| 35 | BioModels Database: A Repository of Mathematical Models of Biological Processes. <i>Methods in Molecular Biology</i> , 2013, 1021, 189-199. | 0.4 | 102 |
| 36 | Improved Secondary Structure Predictions for a Nicotinic Receptor Subunit: Incorporation of Solvent Accessibility and Experimental Data into a Two-Dimensional Representation. <i>Biophysical Journal</i> , 1999, 76, 2329-2345. | 0.2 | 98 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | The ligand gated ion channel database. <i>Nucleic Acids Research</i> , 1999, 27, 340-342. | 6.5 | 93 |
| 38 | Localization of [3H]nicotine, [3H]cytisine, [3H]epibatidine, and [125I]α-bungarotoxin binding sites in the brain of <i>Macaca mulatta</i> . <i>Journal of Comparative Neurology</i> , 2003, 461, 49-60. | 0.9 | 91 |
| 39 | Calcium Input Frequency, Duration and Amplitude Differentially Modulate the Relative Activation of Calcineurin and CaMKII. <i>PLoS ONE</i> , 2012, 7, e43810. | 1.1 | 86 |
| 40 | Systems medicine disease maps: community-driven comprehensive representation of disease mechanisms. <i>Npj Systems Biology and Applications</i> , 2018, 4, 21. | 1.4 | 84 |
| 41 | MIRIAM Resources: tools to generate and resolve robust cross-references in Systems Biology. <i>BMC Systems Biology</i> , 2007, 1, 58. | 3.0 | 82 |
| 42 | An allosteric model of calmodulin explains differential activation of PP2B and CaMKII. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10768-10773. | 3.3 | 81 |
| 43 | JSBML: a flexible Java library for working with SBML. <i>Bioinformatics</i> , 2011, 27, 2167-2168. | 1.8 | 81 |
| 44 | Involvement of α6 nicotinic receptor subunit in nicotine-elicited locomotion, demonstrated by in vivo antisense oligonucleotide infusion. <i>NeuroReport</i> , 1999, 10, 2497-2501. | 0.6 | 78 |
| 45 | Control of neurulation by the nucleosome assembly protein-1-like 2. <i>Nature Genetics</i> , 2000, 25, 431-435. | 9.4 | 78 |
| 46 | The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, . | 1.0 | 78 |
| 47 | Software support for SBCN maps: SBCN-ML and LibSBCN. <i>Bioinformatics</i> , 2012, 28, 2016-2021. | 1.8 | 74 |
| 48 | An Extracellular Protein Microdomain Controls Up-regulation of Neuronal Nicotinic Acetylcholine Receptors by Nicotine. <i>Journal of Biological Chemistry</i> , 2004, 279, 18767-18775. | 1.6 | 73 |
| 49 | SBOL Visual: A Graphical Language for Genetic Designs. <i>PLoS Biology</i> , 2015, 13, e1002310. | 2.6 | 73 |
| 50 | Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 19. | 2.0 | 72 |
| 51 | Model storage, exchange and integration. <i>BMC Neuroscience</i> , 2006, 7, S11. | 0.8 | 66 |
| 52 | LGICdb: the ligand-gated ion channel database. <i>Nucleic Acids Research</i> , 2001, 29, 294-295. | 6.5 | 61 |
| 53 | The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, . | 1.0 | 57 |
| 54 | An H-bond between two residues from different loops of the acetylcholine binding site contributes to the activation mechanism of nicotinic receptors. <i>EMBO Journal</i> , 2003, 22, 1990-2003. | 3.5 | 54 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 55 | Designing and encoding models for synthetic biology. <i>Journal of the Royal Society Interface</i> , 2009, 6, S405-17. | 1.5 | 51 |
| 56 | BioModels.net Web Services, a free and integrated toolkit for computational modelling software. <i>Briefings in Bioinformatics</i> , 2010, 11, 270-277. | 3.2 | 50 |
| 57 | Tia1 dependent regulation of mRNA subcellular location and translation controls p53 expression in B cells. <i>Nature Communications</i> , 2017, 8, 530. | 5.8 | 48 |
| 58 | Community-driven roadmap for integrated disease maps. <i>Briefings in Bioinformatics</i> , 2019, 20, 659-670. | 3.2 | 48 |
| 59 | Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 271. | 1.0 | 42 |
| 60 | Modeling Meets Metabolomicsâ€”The WormJam Consensus Model as Basis for Metabolic Studies in the Model Organism <i>Caenorhabditis elegans</i> . <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 96. | 1.6 | 40 |
| 61 | Host lipidome analysis during rhinovirus replication in HBECs identifies potential therapeutic targets. <i>Journal of Lipid Research</i> , 2018, 59, 1671-1684. | 2.0 | 37 |
| 62 | SED-ML â€” An XML Format for the Implementation of the MIASE Guidelines. <i>Lecture Notes in Computer Science</i> , 2008, , 176-190. | 1.0 | 37 |
| 63 | Particle-Based Stochastic Simulation in Systems Biology. <i>Current Bioinformatics</i> , 2006, 1, 315-320. | 0.7 | 36 |
| 64 | New Otx2 mRNA isoforms expressed in the mouse brain. <i>Journal of Neurochemistry</i> , 2003, 84, 840-853. | 2.1 | 35 |
| 65 | The evolution of standards and data management practices in systems biology. <i>Molecular Systems Biology</i> , 2015, 11, 851. | 3.2 | 35 |
| 66 | Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 340-381. | 1.0 | 35 |
| 67 | The Ligand Gated Ion Channel database: an example of a sequence database in neuroscience. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2001, 356, 1121-1130. | 1.8 | 33 |
| 68 | Meredys, a multi-compartment reaction-diffusion simulator using multistate realistic molecular complexes. <i>BMC Systems Biology</i> , 2010, 4, 24. | 3.0 | 33 |
| 69 | CellML2SBML: conversion of CellML into SBML. <i>Bioinformatics</i> , 2006, 22, 1018-1020. | 1.8 | 32 |
| 70 | Retrieval, alignment, and clustering of computational models based on semantic annotations. <i>Molecular Systems Biology</i> , 2011, 7, 512. | 3.2 | 32 |
| 71 | The systems biology format converter. <i>BMC Bioinformatics</i> , 2016, 17, 154. | 1.2 | 30 |
| 72 | Communicating Structure and Function in Synthetic Biology Diagrams. <i>ACS Synthetic Biology</i> , 2019, 8, 1818-1825. | 1.9 | 30 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 73 | SBMLeditor: effective creation of models in the Systems Biology Markup Language (SBML). BMC Bioinformatics, 2007, 8, 79. | 1.2 | 29 |
| 74 | Rational Understanding of Nicotinic Receptors Drug Binding. Current Topics in Medicinal Chemistry, 2004, 4, 645-651. | 1.0 | 28 |
| 75 | Modulation of Calmodulin Lobes by Different Targets: An Allosteric Model with Hemiconcerted Conformational Transitions. PLoS Computational Biology, 2015, 11, e1004063. | 1.5 | 28 |
| 76 | LGICdb: a manually curated sequence database after the genomes. Nucleic Acids Research, 2006, 34, D267-D269. | 6.5 | 27 |
| 77 | The systems biology simulation core algorithm. BMC Systems Biology, 2013, 7, 55. | 3.0 | 27 |
| 78 | Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 3 (L1V3). Journal of Integrative Bioinformatics, 2018, 15, . | 1.0 | 27 |
| 79 | Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions. Nature Precedings, 2007, , . | 0.1 | 26 |
| 80 | The long journey to a Systems Biology of neuronal function. BMC Systems Biology, 2007, 1, 28. | 3.0 | 26 |
| 81 | Ranked retrieval of Computational Biology models. BMC Bioinformatics, 2010, 11, 423. | 1.2 | 24 |
| 82 | Significance of stroma in biology of oral squamous cell carcinoma. Tumori, 2018, 104, 9-14. | 0.6 | 24 |
| 83 | BNC1 regulates cell heterogeneity in human pluripotent stem cell derived-epicardium. Development (Cambridge), 2019, 146, . | 1.2 | 24 |
| 84 | Reciprocal regulation of ARPP-16 by PKA and MAST3 kinases provides a cAMP-regulated switch in protein phosphatase 2A inhibition. ELife, 2017, 6, . | 2.8 | 24 |
| 85 | Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions. Nature Precedings, 2008, , . | 0.1 | 23 |
| 86 | Integration of Biochemical and Electrical Signaling-Multiscale Model of the Medium Spiny Neuron of the Striatum. PLoS ONE, 2013, 8, e66811. | 1.1 | 22 |
| 87 | ATG13 dynamics in nonselective autophagy and mitophagy: insights from live imaging studies and mathematical modeling. Autophagy, 2021, 17, 1131-1141. | 4.3 | 22 |
| 88 | Meeting report from the fourth meeting of the Computational Modeling in Biology Network (COMBINE). Standards in Genomic Sciences, 2014, 9, 1285-1301. | 1.5 | 21 |
| 89 | Systems Biology Graphical Notation: Entity Relationship language Level 1 Version 2. Journal of Integrative Bioinformatics, 2015, 12, 281-339. | 1.0 | 21 |
| 90 | Synthetic Biology Open Language Visual (SBOL Visual) Version 2.0. Journal of Integrative Bioinformatics, 2018, 15, . | 1.0 | 21 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 91 | Systems Biology Graphical Notation: Entity Relationship language Level 1 Version 2. Journal of Integrative Bioinformatics, 2015, 12, 264. | 1.0 | 21 |
| 92 | Qualitative translation of relations from BioPAX to SBML qual. Bioinformatics, 2012, 28, 2648-2653. | 1.8 | 20 |
| 93 | Structural Analysis and Stochastic Modelling Suggest a Mechanism for Calmodulin Trapping by CaMKII. PLoS ONE, 2012, 7, e29406. | 1.1 | 20 |
| 94 | Systems Biology Graphical Notation: Process Description language Level 1 Version 1.3. Journal of Integrative Bioinformatics, 2015, 12, 263. | 1.0 | 20 |
| 95 | Computing phenomenologic Adair-Klotz constants from microscopic MWC parameters. BMC Systems Biology, 2009, 3, 68. | 3.0 | 19 |
| 96 | Ligand Depletion in vivo Modulates the Dynamic Range and Cooperativity of Signal Transduction. PLoS ONE, 2010, 5, e8449. | 1.1 | 18 |
| 97 | Neurogranin stimulates Ca ²⁺ /calmodulin-dependent kinase II by suppressing calcineurin activity at specific calcium spike frequencies. PLoS Computational Biology, 2020, 16, e1006991. | 1.5 | 18 |
| 98 | Systems Biology Graphical Notation: Process Description language Level 1 Version 1.3. Journal of Integrative Bioinformatics, 2015, 12, 213-280. | 1.0 | 15 |
| 99 | SPARQL-enabled identifier conversion with Identifiers.org. Bioinformatics, 2015, 31, 1875-1877. | 1.8 | 14 |
| 100 | Mathematical Models of Pluripotent Stem Cells: At the Dawn of Predictive Regenerative Medicine. Methods in Molecular Biology, 2016, 1386, 331-350. | 0.4 | 14 |
| 101 | Specifications of Standards in Systems and Synthetic Biology. Journal of Integrative Bioinformatics, 2015, 12, 258. | 1.0 | 14 |
| 102 | Towards the Collaborative Curation of the Registry underlying identifiers.org. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat017. | 1.4 | 13 |
| 103 | The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. Journal of Integrative Bioinformatics, 2018, 15, . | 1.0 | 13 |
| 104 | Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. Journal of Integrative Bioinformatics, 2016, 13, 1-7. | 1.0 | 12 |
| 105 | BioModels linked dataset. BMC Systems Biology, 2014, 8, 91. | 3.0 | 11 |
| 106 | Specifications of Standards in Systems and Synthetic Biology. Journal of Integrative Bioinformatics, 2015, 12, 1-3. | 1.0 | 11 |
| 107 | Brownian diffusion of AMPA receptors is sufficient to explain fast onset of LTP. BMC Systems Biology, 2010, 4, 25. | 3.0 | 10 |
| 108 | SBpipe: a collection of pipelines for automating repetitive simulation and analysis tasks. BMC Systems Biology, 2017, 11, 46. | 3.0 | 10 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 109 | Comparative models of P2X2 receptor support inter-subunit ATP-binding sites. <i>Biochemical and Biophysical Research Communications</i> , 2008, 375, 405-409. | 1.0 | 8 |
| 110 | Looking inside the box: bacterial transistor arrays. <i>Molecular Microbiology</i> , 2008, 69, 5-9. | 1.2 | 7 |
| 111 | Meeting report from the first meetings of the Computational Modeling in Biology Network (COMBINE). <i>Standards in Genomic Sciences</i> , 2011, 5, 230-242. | 1.5 | 7 |
| 112 | Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 731-901. | 1.0 | 7 |
| 113 | Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2017. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, . | 1.0 | 7 |
| 114 | Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 289. | 1.0 | 7 |
| 115 | A brief history of COMBINE. , 2017, , . | | 6 |
| 116 | Quick tips for creating effective and impactful biological pathways using the Systems Biology Graphical Notation. <i>PLoS Computational Biology</i> , 2018, 14, e1005740. | 1.5 | 6 |
| 117 | Software that goes with the flow in systems biology. <i>BMC Biology</i> , 2010, 8, 140. | 1.7 | 5 |
| 118 | The Molecular Pages of the mesotelencephalic dopamine consortium (DopaNet). <i>BMC Bioinformatics</i> , 2004, 5, 174. | 1.2 | 4 |
| 119 | Controlled Annotations for Systems Biology. <i>Methods in Molecular Biology</i> , 2013, 1021, 227-245. | 0.4 | 4 |
| 120 | SBML Models and MathSBML. , 2007, , 395-421. | | 3 |
| 121 | Using Chemical Kinetics to Model Biochemical Pathways. <i>Methods in Molecular Biology</i> , 2013, 1021, 147-167. | 0.4 | 3 |
| 122 | Schizophrenic: forever young?. <i>Genome Medicine</i> , 2010, 2, 32. | 3.6 | 2 |
| 123 | BioModels Database: A Repository of Mathematical Models of Biological Processes. , 2013, , 134-138. | | 2 |
| 124 | Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions. <i>Nature Precedings</i> , 0, , . | 0.1 | 1 |
| 125 | Data Integration and Semantic Enrichment of Systems Biology Models and Simulations. <i>Lecture Notes in Computer Science</i> , 2009, , 5-15. | 1.0 | 1 |
| 126 | SBGN. , 2013, , 1893-1895. | | 1 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 127 | Approches théoriques et pratiques en hybridation in situ et autoradiographie réceptorielle. Annales De L'Institut Pasteur / Actualités, 1998, 9, 259-270. | 0.1 | 0 |
| 128 | LibSBN: Electronic Processing of SBN maps. Nature Precedings, 2010, , . | 0.1 | 0 |
| 129 | MIRIAM Guidelines. , 2013, , 1367-1367. | | 0 |
| 130 | MIRIAM URI. , 2013, , 1367-1368. | | 0 |
| 131 | BioModels Database: a public repository for sharing models of biological processes. , 2013, , 1-5. | | 0 |
| 132 | BioModels Database: A Public Repository for Sharing Models of Biological Processes. , 2022, , 463-467. | | 0 |