Nicolas Le NovÃ¨re

List of Publications by Year
in descending order

132 papers	14,959 citations	31976 53 h-index	19190 118 g-index
145 all docs	145 docs citations	145 times ranked	15168 citing authors

#	Article	IF	Citations
1	A community-driven global reconstruction of human metabolism. Nature Biotechnology, 2013, 31, 419-425.	17.5	920
2	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	17.5	828
3	Nicotinic Receptors at the Amino Acid Level. Annual Review of Pharmacology and Toxicology, 2000, 40, 431-458.	9.4	757
4	BioModels Database: a free, centralized database of curated, published, quantitative kinetic models of biochemical and cellular systems. Nucleic Acids Research, 2006, 34, D689-D691.	14.5	661
5	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	17.5	613
6	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	17.5	553
7	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	17.5	530
8	Reduced antinociception in mice lacking neuronal nicotinic receptor subunits. Nature, 1999, 398, 805-810.	27.8	514
9	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	17.5	506
10	Subunit Composition of Functional Nicotinic Receptors in Dopaminergic Neurons Investigated with Knock-Out Mice. Journal of Neuroscience, 2003, 23, 7820-7829.	3.6	473
11	BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. BMC Systems Biology, 2010, 4, 92.	3.0	467
12	Quantitative and logic modelling of molecular and gene networks. Nature Reviews Genetics, 2015, 16, 146-158.	16.3	406
13	Molecular evolution of the nicotinic acetylcholine receptor: An example of multigene family in excitable cells. Journal of Molecular Evolution, 1995, 40, 155-172.	1.8	378
14	The diversity of subunit composition in nAChRs: Evolutionary origins, physiologic and pharmacologic consequences. Journal of Neurobiology, 2002, 53, 447-456.	3.6	371
15	Neuronal Nicotinic Receptor a6 Subunit mRNA is Selectively Concentrated in Catecholaminergic Nuclei of the Rat Brain. European Journal of Neuroscience, 1996, 8, 2428-2439.	2.6	358
16	BioModels: ten-year anniversary. Nucleic Acids Research, 2015, 43, D542-D548.	14.5	334
17	Brain nicotinic receptors: structure and regulation, role in learning and reinforcement1Published on the World Wide Web on 24 October 1997.1. Brain Research Reviews, 1998, 26, 198-216.	9.0	280
18	Models of the extracellular domain of the nicotinic receptors and of agonist- and Ca2+-binding sites. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3210-3215.	7.1	263

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19	Novel pharmacological targets for the treatment of Parkinson's disease. Nature Reviews Drug Discovery, 2006, 5, 845-854.	46.4	262
20	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	7.2	246
21	Reproducible computational biology experiments with SED-ML - The Simulation Experiment Description Markup Language. BMC Systems Biology, 2011, 5, 198.	3.0	211
22	Normal Mode Analysis Suggests a Quaternary Twist Model for the Nicotinic Receptor Gating Mechanism. Biophysical Journal, 2005, 88, 3954-3965.	0.5	178
23	Molecular model of a lattice of signalling proteins involved in bacterial chemotaxis. Nature Cell Biology, 2000, 2, 792-796.	10.3	175
24	The Identity of Plant Glutamate Receptors. Science, 2001, 292, 1486b-1487.	12.6	175
25	Identifiers.org and MIRIAM Registry: community resources to provide persistent identification. Nucleic Acids Research, 2012, 40, D580-D586.	14.5	162
26	PTEN Regulates PI(3,4)P2 Signaling Downstream of Class I PI3K. Molecular Cell, 2017, 68, 566-580.e10.	9.7	149
27	SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. BMC Systems Biology, 2013, 7, 135.	3.0	145
28	Path2Models: large-scale generation of computational models from biochemical pathway maps. BMC Systems Biology, 2013, 7, 116.	3.0	145
29	Localization of nAChR subunit mRNAs in the brain of Macaca mulatta. European Journal of Neuroscience, 2000, 12, 3664-3674.	2.6	139
30	DARPP-32 Is a Robust Integrator of Dopamine and Glutamate Signals. PLoS Computational Biology, 2006, 2, e176.	3.2	139
31	Epicardial cells derived from human embryonic stem cells augment cardiomyocyte-driven heart regeneration. Nature Biotechnology, 2019, 37, 895-906.	17.5	139
32	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	3.2	133
33	Experimentally based model of a complex between a snake toxin and the Â7 nicotinic receptor. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3216-3221.	7.1	121
34	COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. BMC Bioinformatics, 2014, 15, 369.	2.6	114
35	BioModels Database: A Repository of Mathematical Models of Biological Processes. Methods in Molecular Biology, 2013, 1021, 189-199.	0.9	102
36	Improved Secondary Structure Predictions for a Nicotinic Receptor Subunit: Incorporation of Solvent Accessibility and Experimental Data into a Two-Dimensional Representation. Biophysical Journal, 1999, 76, 2329-2345.	0.5	98

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37	The ligand gated ion channel database. Nucleic Acids Research, 1999, 27, 340-342.	14.5	93
38	Localization of [3H]nicotine, [3H]cytisine, [3H]epibatidine, and [125I]Î±-bungarotoxin binding sites in the brain ofMacaca mulatta. Journal of Comparative Neurology, 2003, 461, 49-60.	1.6	91
39	Calcium Input Frequency, Duration and Amplitude Differentially Modulate the Relative Activation of Calcineurin and CaMKII. PLoS ONE, 2012, 7, e43810.	2.5	86
40	Systems medicine disease maps: community-driven comprehensive representation of disease mechanisms. Npj Systems Biology and Applications, 2018, 4, 21.	3.0	84
41	MIRIAM Resources: tools to generate and resolve robust cross-references in Systems Biology. BMC Systems Biology, 2007, 1, 58.	3.0	82
42	An allosteric model of calmodulin explains differential activation of PP2B and CaMKII. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10768-10773.	7.1	81
43	JSBML: a flexible Java library for working with SBML. Bioinformatics, 2011, 27, 2167-2168.	4.1	81
44	Involvement of Î±6 nicotinic receptor subunit in nicotine-elicited locomotion, demonstrated by in vivo antisense oligonucleotide infusion. NeuroReport, 1999, 10, 2497-2501.	1.2	78
45	Control of neurulation by the nucleosome assembly protein-1â€"like 2. Nature Genetics, 2000, 25, 431-435.	21.4	78
46	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	78
47	Software support for SBGN maps: SBGN-ML and LibSBGN. Bioinformatics, 2012, 28, 2016-2021.	4.1	74
48	An Extracellular Protein Microdomain Controls Up-regulation of Neuronal Nicotinic Acetylcholine Receptors by Nicotine. Journal of Biological Chemistry, 2004, 279, 18767-18775.	3.4	73
49	SBOL Visual: A Graphical Language for Genetic Designs. PLoS Biology, 2015, 13, e1002310.	5.6	73
50	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. Frontiers in Bioengineering and Biotechnology, 2015, 3, 19.	4.1	72
51	Model storage, exchange and integration. BMC Neuroscience, 2006, 7, S11.	1.9	66
52	LGICdb: the ligand-gated ion channel database. Nucleic Acids Research, 2001, 29, 294-295.	14.5	61
53	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	57
54	An H-bond between two residues from different loops of the acetylcholine binding site contributes to the activation mechanism of nicotinic receptors. EMBO Journal, 2003, 22, 1990-2003.	7.8	54

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55	Designing and encoding models for synthetic biology. Journal of the Royal Society Interface, 2009, 6, S405-17.	3.4	51
56	BioModels.net Web Services, a free and integrated toolkit for computational modelling software. Briefings in Bioinformatics, 2010, 11, 270-277.	6.5	50
57	Tia1 dependent regulation of mRNA subcellular location and translation controls p53 expression in B cells. Nature Communications, 2017, 8, 530.	12.8	48
58	Community-driven roadmap for integrated disease maps. Briefings in Bioinformatics, 2019, 20, 659-670.	6.5	48
59	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. Journal of Integrative Bioinformatics, 2015, 12, 271.	1.5	42
60	Modeling Meets Metabolomicsâ€"The WormJam Consensus Model as Basis for Metabolic Studies in the Model Organism Caenorhabditis elegans. Frontiers in Molecular Biosciences, 2018, 5, 96.	3.5	40
61	Host lipidome analysis during rhinovirus replication in HBECs identifies potential therapeutic targets. Journal of Lipid Research, 2018, 59, 1671-1684.	4.2	37
62	SED-ML â€" An XML Format for the Implementation of the MIASE Guidelines. Lecture Notes in Computer Science, 2008, , 176-190.	1.3	37
63	Particle-Based Stochastic Simulation in Systems Biology. Current Bioinformatics, 2006, 1, 315-320.	1.5	36
64	New <i>Otx2</i> mRNA isoforms expressed in the mouse brain. Journal of Neurochemistry, 2003, 84, 840-853.	3.9	35
65	The evolution of standards and data management practices in systems biology. Molecular Systems Biology, 2015, 11, 851.	7.2	35
66	Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. Journal of Integrative Bioinformatics, 2015, 12, 340-381.	1.5	35
67	The Ligand Gated Ion Channel database: an example of a sequence database in neuroscience. Philosophical Transactions of the Royal Society B: Biological Sciences, 2001, 356, 1121-1130.	4.0	33
68	Meredys, a multi-compartment reaction-diffusion simulator using multistate realistic molecular complexes. BMC Systems Biology, 2010, 4, 24.	3.0	33
69	CellML2SBML: conversion of CellML into SBML. Bioinformatics, 2006, 22, 1018-1020.	4.1	32
70	Retrieval, alignment, and clustering of computational models based on semantic annotations. Molecular Systems Biology, 2011, 7, 512.	7.2	32
71	The systems biology format converter. BMC Bioinformatics, 2016, 17, 154.	2.6	30
72	Communicating Structure and Function in Synthetic Biology Diagrams. ACS Synthetic Biology, 2019, 8, 1818-1825.	3.8	30

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73	SBMLeditor: effective creation of models in the Systems Biology Markup Language (SBML). BMC Bioinformatics, 2007, 8, 79.	2.6	29
74	Rational Understanding of Nicotinic Receptors Drug Binding. Current Topics in Medicinal Chemistry, 2004, 4, 645-651.	2.1	28
75	Modulation of Calmodulin Lobes by Different Targets: An Allosteric Model with Hemiconcerted Conformational Transitions. PLoS Computational Biology, 2015, 11, e1004063.	3.2	28
76	LGICdb: a manually curated sequence database after the genomes. Nucleic Acids Research, 2006, 34, D267-D269.	14.5	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, .	1.5	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.	2.6	24
82	Significance of stroma in biology of oral squamous cell carcinoma. Tumori, 2018, 104, 9-14.	1.1	24
83	BNC1 regulates cell heterogeneity in human pluripotent stem cell derived-epicardium. Development (Cambridge), 2019, 146, .	2.5	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, .	6.0	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.	2.5	22
87	ATG13 dynamics in nonselective autophagy and mitophagy: insights from live imaging studies and mathematical modeling. Autophagy, 2021, 17, 1131-1141.	9.1	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.	1.5	21
90	Synthetic Biology Open Language Visual (SBOL Visual) Version 2.0. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	21

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91	Systems Biology Graphical Notation: Entity Relationship language Level 1 Version 2. Journal of Integrative Bioinformatics, 2015, 12, 264.	1.5	21
92	Qualitative translation of relations from BioPAX to SBML qual. Bioinformatics, 2012, 28, 2648-2653.	4.1	20
93	Structural Analysis and Stochastic Modelling Suggest a Mechanism for Calmodulin Trapping by CaMKII. PLoS ONE, 2012, 7, e29406.	2.5	20
94	Systems Biology Graphical Notation: Process Description language Level 1 Version 1.3. Journal of Integrative Bioinformatics, 2015, 12, 263.	1.5	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.	2.5	18
97	Neurogranin stimulates Ca2+/calmodulin-dependent kinase II by suppressing calcineurin activity at specific calcium spike frequencies. PLoS Computational Biology, 2020, 16, e1006991.	3.2	18
98	Systems Biology Graphical Notation: Process Description language Level 1 Version 1.3. Journal of Integrative Bioinformatics, 2015, 12, 213-280.	1.5	15
99	SPARQL-enabled identifier conversion with Identifiers.org. Bioinformatics, 2015, 31, 1875-1877.	4.1	14
100	Mathematical Models of Pluripotent Stem Cells: At the Dawn of Predictive Regenerative Medicine. Methods in Molecular Biology, 2016, 1386, 331-350.	0.9	14
101	Specifications of Standards in Systems and Synthetic Biology. Journal of Integrative Bioinformatics, 2015, 12, 258.	1.5	14
102	Towards the Collaborative Curation of the Registry underlying identifiers.org. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat017.	3.0	13
103	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	13
104	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. Journal of Integrative Bioinformatics, 2016, 13, 1-7.	1.5	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.	1.5	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

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109	Comparative models of P2X2 receptor support inter-subunit ATP-binding sites. Biochemical and Biophysical Research Communications, 2008, 375, 405-409.	2.1	8
110	Looking inside the box: bacterial transistor arrays. Molecular Microbiology, 2008, 69, 5-9.	2.5	7
111	Meeting report from the first meetings of the Computational Modeling in Biology Network (COMBINE). Standards in Genomic Sciences, 2011, 5, 230-242.	1.5	7
112	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. Journal of Integrative Bioinformatics, 2015, 12, 731-901.	1.5	7
113	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2017. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	7
114	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. Journal of Integrative Bioinformatics, 2016, 13, 289.	1.5	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. PLoS Computational Biology, 2018, 14, e1005740.	3.2	6
117	Software that goes with the flow in systems biology. BMC Biology, 2010, 8, 140.	3.8	5
118	The Molecular Pages of the mesotelencephalic dopamine consortium (DopaNet). BMC Bioinformatics, 2004, 5, 174.	2.6	4
119	Controlled Annotations for Systems Biology. Methods in Molecular Biology, 2013, 1021, 227-245.	0.9	4
120	SBML Models and MathSBML. , 2007, , 395-421.		3
121	Using Chemical Kinetics to Model Biochemical Pathways. Methods in Molecular Biology, 2013, 1021, 147-167.	0.9	3
122	Schizophrenic: forever young?. Genome Medicine, 2010, 2, 32.	8.2	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. Nature Precedings, 0, , .	0.1	1
125	Data Integration and Semantic Enrichment of Systems Biology Models and Simulations. Lecture Notes in Computer Science, 2009, , 5-15.	1.3	1
126	SBGN. , 2013, , 1893-1895.		1

#	ARTICLE	IF	CITATIONS
127	Approches thÃ©oriques et pratiques en hybridation in situ et autoradiographie rÃ©ceptorielle. Annales De L'Institut Pasteur / ActualitÃ©s, 1998, 9, 259-270.	0.1	0
128	LibSBGN: Electronic Processing of SBGN 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