

# Pascale Gaudet

## List of Publications by Year in descending order

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84  
papers

10,767  
citations

159585

30  
h-index

66911

78  
g-index

91  
all docs

91  
docs citations

91  
times ranked

21071  
citing authors

#	ARTICLE	IF	CITATIONS
1	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	14.5	117
2	The gene regulation knowledge commons: the action area of GREEKC. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194768.	1.9	3
3	Missing Links Between Gene Function and Physiology in Genomics. <i>Frontiers in Physiology</i> , 2022, 13, 815874.	2.8	1
4	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). <i>Bioinformatics</i> , 2021, 36, 5712-5718.	4.1	14
5	Gene Ontology representation for transcription factor functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194752.	1.9	17
6	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
7	Formalization of gene regulation knowledge using ontologies and gene ontology causal activity models. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194766.	1.9	6
8	A GO catalogue of human DNA-binding transcription factors. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194765.	1.9	15
9	The neXtProt knowledgebase in 2020: data, tools and usability improvements. <i>Nucleic Acids Research</i> , 2020, 48, D328-D334.	14.5	121
10	Term Matrix: a novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns. <i>Open Biology</i> , 2020, 10, 200149.	3.6	7
11	The Feature-Viewer: a visualization tool for positional annotations on a sequence. <i>Bioinformatics</i> , 2020, 36, 3244-3245.	4.1	18
12	The Gene Ontology. , 2019, , 1-7.		3
13	Gene Ontology Causal Activity Modeling (GO-CAM) moves beyond GO annotations to structured descriptions of biological functions and systems. <i>Nature Genetics</i> , 2019, 51, 1429-1433.	21.4	76
14	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. <i>Neuron</i> , 2019, 103, 217-234.e4.	8.1	518
15	Annotation of gene product function from high-throughput studies using the Gene Ontology. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	21
16	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338.	14.5	3,474
17	ECO, the Evidence & Conclusion Ontology: community standard for evidence information. <i>Nucleic Acids Research</i> , 2019, 47, D1186-D1194.	14.5	67
18	Accelerating annotation of articles via automated approaches: evaluation of the neXtA5 curation-support tool by neXtProt. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	6

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19	Overview of the BioCreative VI text-mining services for Kinome Curation Track. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	3
20	A new bioinformatics tool to help assess the significance of BRCA1 variants. Human Genomics, 2018, 12, 36.	2.9	10
21	Kinases and Cancer. Cancers, 2018, 10, 63.	3.7	93
22	Integrative annotation and knowledge discovery of kinase post-translational modifications and cancer-associated mutations through federated protein ontologies and resources. Scientific Reports, 2018, 8, 6518.	3.3	31
23	Annotation of functional impact of voltage-gated sodium channel mutations. Human Mutation, 2017, 38, 485-493.	2.5	12
24	Gene Ontology: Pitfalls, Biases, and Remedies. Methods in Molecular Biology, 2017, 1446, 189-205.	0.9	109
25	Triage by ranking to support the curation of protein interactions. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	10
26	Best Practices in Manual Annotation with the Gene Ontology. Methods in Molecular Biology, 2017, 1446, 41-54.	0.9	21
27	Primer on the Gene Ontology. Methods in Molecular Biology, 2017, 1446, 25-37.	0.9	63
28	The neXtProt knowledgebase on human proteins: 2017 update. Nucleic Acids Research, 2017, 45, D177-D182.	14.5	145
29	ICEPO: the ion channel electrophysiology ontology. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw017.	3.0	9
30	neXtA5: accelerating annotation of articles via automated approaches in neXtProt. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw098.	3.0	10
31	Large-scale inference of gene function through phylogenetic annotation of Gene Ontology terms: case study of the apoptosis and autophagy cellular processes. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw155.	3.0	12
32	The health care and life sciences community profile for dataset descriptions. PeerJ, 2016, 4, e2331.	2.0	18
33	Converting neXtProt into Linked Data and nanopublications. Semantic Web, 2015, 6, 147-153.	1.9	13
34	The Confidence Information Ontology: a step towards a standard for asserting confidence in annotations. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav043-bav043.	3.0	37
35	Deep Question Answering for protein annotation. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav081.	3.0	17
36	The neXtProt knowledgebase on human proteins: current status. Nucleic Acids Research, 2015, 43, D764-D770.	14.5	94

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37	Diabetogenic milieus induce specific changes in mitochondrial transcriptome and differentiation of human pancreatic islets. <i>Human Molecular Genetics</i> , 2015, 24, 5270-5284.	2.9	31
38	Target discovery from protein databases: challenges for curation. <i>Drug Discovery Today: Technologies</i> , 2015, 14, 11-16.	4.0	1
39	GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. <i>PLoS Computational Biology</i> , 2015, 11, e1004143.	3.2	52
40	Metrics for the Human Proteome Project 2013â€“2014 and Strategies for Finding Missing Proteins. <i>Journal of Proteome Research</i> , 2014, 13, 15-20.	3.7	124
41	Querying neXtProt nanopublications and their value for insights on sequence variants and tissue expression. <i>Web Semantics</i> , 2014, 29, 3-11.	2.9	12
42	A Chromosome-centric Human Proteome Project (C-HPP) to Characterize the Sets of Proteins Encoded in Chromosome 17. <i>Journal of Proteome Research</i> , 2013, 12, 45-57.	3.7	35
43	neXtProt: Organizing Protein Knowledge in the Context of Human Proteome Projects. <i>Journal of Proteome Research</i> , 2013, 12, 293-298.	3.7	116
44	The Human Diabetes Proteome Project (HDPP): From network biology to targets for therapies and prevention. <i>Translational Proteomics</i> , 2013, 1, 3-11.	1.2	18
45	DATABASE, The Journal of Biological Databases and Curation, is now the official journal of the International Society for Biocuration. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat077-bat077.	3.0	1
46	Changes in Mitochondrial Carriers Exhibit Stress-Specific Signatures in INS-1E <sup>2</sup> -Cells Exposed to Glucose Versus Fatty Acids. <i>PLoS ONE</i> , 2013, 8, e82364.	2.5	21
47	Biocurators and Biocuration: surveying the 21st century challenges. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar059-bar059.	3.0	59
48	neXtProt: a knowledge platform for human proteins. <i>Nucleic Acids Research</i> , 2012, 40, D76-D83.	14.5	167
49	Toward interoperable bioscience data. <i>Nature Genetics</i> , 2012, 44, 121-126.	21.4	362
50	Agenda of the "BioSharing workshop - Unifying Bio-Resources Descriptors". <i>Nature Precedings</i> , 2011, , .	0.1	0
51	Towards BioDBcore: a community-defined information specification for biological databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, baq027-baq027.	3.0	30
52	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	14.5	32
53	Phylogenetic-based propagation of functional annotations within the Gene Ontology consortium. <i>Briefings in Bioinformatics</i> , 2011, 12, 449-462.	6.5	723
54	dictyBase update 2011: web 2.0 functionality and the initial steps towards a genome portal for the Amoebozoa. <i>Nucleic Acids Research</i> , 2011, 39, D620-D624.	14.5	39

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55	Meeting Report: BioSharing at ISMB 2010. Standards in Genomic Sciences, 2010, 3, 254-258.	1.5	19
56	Meeting Report from the Second "Minimum Information for Biological and Biomedical Investigations" (MIBBI) workshop. Standards in Genomic Sciences, 2010, 3, 259-266.	1.5	32
57	A community of biocurators. Nature Precedings, 2010, , .	0.1	0
58	PANTHER version 7: improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium. Nucleic Acids Research, 2010, 38, D204-D210.	14.5	553
59	The Gene Ontology's Reference Genome Project: *A Unified Framework for Functional Annotation across Species. Nature Precedings, 2009, , .	0.1	1
60	dictyBase" a Dictyostelium bioinformatics resource update. Nucleic Acids Research, 2009, 37, D515-D519.	14.5	71
61	An anatomy ontology to represent biological knowledge in Dictyostelium discoideum. BMC Genomics, 2008, 9, 130.	2.8	39
62	Making Permanent Stocks of Dictyostelium. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5101-pdb.prot5101.	0.3	5
63	Growth and Maintenance of <i>Dictyostelium</i> Cells. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5099.	0.3	7
64	Extraction of DNA from <i>Dictyostelium</i> . Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5105.	0.3	2
65	Extraction of RNA from Dictyostelium. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5106-pdb.prot5106.	0.3	2
66	Multicellular Development of Dictyostelium. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5100-pdb.prot5100.	0.3	6
67	Selection of Dictyostelium Transformants. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5104-pdb.prot5104.	0.3	3
68	Transformation of Dictyostelium with Plasmid DNA by Calcium Phosphate Precipitation. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5102-pdb.prot5102.	0.3	3
69	Transformation of Dictyostelium with Plasmid DNA by Electroporation. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5103-pdb.prot5103.	0.3	6
70	<i>Dictyostelium discoideum</i> : The Social Ameba. Cold Spring Harbor Protocols, 2008, 2008, pdb.emo109.	0.3	14
71	Mitochondrial carrier family: Repertoire and peculiarities of the cellular slime mould Dictyostelium discoideum. Biochimie, 2007, 89, 1058-1069.	2.6	23
72	Protocols for growth and development of Dictyostelium discoideum. Nature Protocols, 2007, 2, 1307-1316.	12.0	197

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73	Transformation of Dictyostelium discoideum with plasmid DNA. Nature Protocols, 2007, 2, 1317-1324.	12.0	102
74	A reliable general purpose method for extracting genomic DNA from Dictyostelium cells. Nature Protocols, 2007, 2, 1325-1328.	12.0	18
75	A general purpose method for extracting RNA from Dictyostelium cells. Nature Protocols, 2007, 2, 1329-1332.	12.0	11
76	Generation, annotation, and analysis of an extensive Aspergillus niger EST collection. BMC Microbiology, 2006, 6, 7.	3.3	34
77	DNA Damage Signalling and Repair in <i>Dictyostelium discoideum</i> . Cell Cycle, 2006, 5, 702-708.	2.6	21
78	dictyBase, the model organism database for Dictyostelium discoideum. Nucleic Acids Research, 2006, 34, D423-D427.	14.5	101
79	dictyBase and the Dicty Stock Center. , 2006, 346, 51-74.		17
80	Regulation of the ribonucleotide reductase small subunit gene by DNA-damaging agents in Dictyostelium discoideum. Nucleic Acids Research, 1999, 27, 3042-3048.	14.5	9
81	Identification of cis-Regulating Elements and trans-Acting Factors Regulating the Expression of the Gene Encoding the Small Subunit of Ribonucleotide Reductase in Dictyostelium discoideum. Journal of Biological Chemistry, 1999, 274, 20384-20390.	3.4	9
82	BioDBcore: a community-defined information specification for biological databases. Nature Precedings, 0, , .	0.1	1
83	Querying NeXtProt Nanopublications and Their Value for Insights on Sequence Variants and Tissue Expression. SSRN Electronic Journal, 0, , .	0.4	2
84	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677.	1.6	0