Sandra Orchard

List of Publications by Year
in descending order

144 papers	39,681 citations	26630 56 h-index	5988 160 g-index
176 all docs	176 docs citations	176 times ranked	56082 citing authors

#	ARTICLE	IF	CITATIONS
1	Complex Portal 2022: new curation frontiers. Nucleic Acids Research, 2022, 50, D578-D586.	14.5	27
2	The IntAct database: efficient access to fine-grained molecular interaction data. Nucleic Acids Research, 2022, 50, D648-D653.	14.5	89
3	The gene regulation knowledge commons: the action area of GREEKC. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194768.	1.9	3
4	IMEx Databases: Displaying Molecular Interactions into a Single, Standards-Compliant Dataset. Methods in Molecular Biology, 2022, 2449, 27-42.	0.9	4
5	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). Bioinformatics, 2021, 36, 5712-5718.	4.1	14
6	UniProt: the universal protein knowledgebase in 2021. Nucleic Acids Research, 2021, 49, D480-D489.	14.5	4,709
7	Analysing the yeast complexome—the Complex Portal rising to the challenge. Nucleic Acids Research, 2021, 49, 3156-3167.	14.5	5
8	The Enzyme Portal: an integrative tool for enzyme information and analysis. FEBS Journal, 2021, , .	4.7	2
9	Integration of transcription coregulator complexes with sequence-specific DNA-binding factor interactomes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194749.	1.9	6
10	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
11	Gene Ontology curation of the blood–brain barrier to improve the analysis of Alzheimer's and other neurological diseases. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	6
12	Non-coding RNA regulatory networks. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194417.	1.9	262
13	Challenges in the annotation of pseudoenzymes in databases: the UniProtKB approach. FEBS Journal, 2020, 287, 4114-4127.	4.7	15
14	Towards a unified open access dataset of molecular interactions. Nature Communications, 2020, 11, 6144.	12.8	49
15	A Coordinated Approach by Public Domain Bioinformatics Resources to Aid the Fight Against Alzheimer's Disease Through Expert Curation of Key Protein Targets. Journal of Alzheimer's Disease, 2020, 77, 257-273.	2.6	7
16	Gene Ontology Curation of Neuroinflammation Biology Improves the Interpretation of Alzheimer's Disease Gene Expression Data. Journal of Alzheimer's Disease, 2020, 75, 1417-1435.	2.6	18
17	UniRule: a unified rule resource for automatic annotation in the UniProt Knowledgebase. Bioinformatics, 2020, 36, 4643-4648.	4.1	42
18	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. Bioinformatics, 2020, 36, 2636-2642.	4.1	47

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19	Caenorhabditis elegans phosphatase complexes in UniProtKB and Complex Portal. FEBS Journal, 2020, 287, 2664-2684.	4.7	3
20	Emerging concepts in pseudoenzyme classification, evolution, and signaling. Science Signaling, 2019, 12, .	3.6	80
21	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. Journal of Proteome Research, 2019, 18, 4108-4116.	3.7	82
22	UniProt: a worldwide hub of protein knowledge. Nucleic Acids Research, 2019, 47, D506-D515.	14.5	6,185
23	The Gene Ontology Resource: 20 years and still GOing strong. Nucleic Acids Research, 2019, 47, D330-D338.	14.5	3,474
24	Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes. Nucleic Acids Research, 2019, 47, D550-D558.	14.5	85
25	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
26	Searching and Extracting Data from the EMBL-EBI Complex Portal. Methods in Molecular Biology, 2018, 1764, 377-390.	0.9	7
27	Improving the Gene Ontology Resource to Facilitate More Informative Analysis and Interpretation of Alzheimer's Disease Data. Genes, 2018, 9, 593.	2.4	15
28	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. BMC Bioinformatics, 2018, 19, 134.	2.6	47
29	JAMI: a Java library for molecular interactions and data interoperability. BMC Bioinformatics, 2018, 19, 133.	2.6	6
30	Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338.	14.5	1,838
31	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. Journal of Proteome Research, 2017, 16, 4288-4298.	3.7	87
32	The yeast noncoding RNA interaction network. Rna, 2017, 23, 1479-1492.	3.5	25
33	ComplexViewer: visualization of curated macromolecular complexes. Bioinformatics, 2017, 33, 3673-3675.	4.1	10
34	Best practice data life cycle approaches for the life sciences. F1000Research, 2017, 6, 1618.	1.6	21
35	Best practice data life cycle approaches for the life sciences. F1000Research, 2017, 6, 1618.	1.6	23
36	The MIntAct Project and Molecular Interaction Databases. Methods in Molecular Biology, 2016, 1415, 55-69.	0.9	16

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37	Gene regulation knowledge commons: community action takes care of DNA binding transcription factors. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw088.	3.0	12
38	Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119.	3.0	36
39	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
40	Shared resources, shared costs—leveraging biocuration resources. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	13
41	The complex portal - an encyclopaedia of macromolecular complexes. Nucleic Acids Research, 2015, 43, D479-D484.	14.5	100
42	A visual review of the interactome of LRRK2: Using deep-curated molecular interaction data to represent biology. Proteomics, 2015, 15, 1390-1404.	2.2	38
43	Development of data representation standards by the human proteome organization proteomics standards initiative. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 495-506.	4.4	54
44	Expert curation in UniProtKB: a case study on dealing with conflicting and erroneous data. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau016-bau016.	3.0	56
45	The MIntAct project—IntAct as a common curation platform for 11 molecular interaction databases. Nucleic Acids Research, 2014, 42, D358-D363.	14.5	1,634
46	Activities at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2014, 42, D191-D198.	14.5	1,162
47	Data Standardization and Sharing—The work of the HUPO-PSI. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 82-87.	2.3	22
48	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 98-107.	2.3	36
49	BioJS: an open source JavaScript framework for biological data visualization. Bioinformatics, 2013, 29, 1103-1104.	4.1	110
50	Capturing cooperative interactions with the PSI-MI format. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat066.	3.0	10
51	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat009-bat009.	3.0	76
52	A new reference implementation of the PSICQUIC web service. Nucleic Acids Research, 2013, 41, W601-W606.	14.5	91
53	Minimum Information about a Molecular Interaction Experiment (MIMIx). , 2013, , 1361-1363.		0
54	PSICQUIC. , 2013, , 1801-1801.		0

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55	Proteomics Standards Initiative. , 2013, , 1797-1798.		0
56	Reorganizing the protein space at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2012, 40, D71-D75.	14.5	1,196
57	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	19.0	500
58	The IntAct molecular interaction database in 2012. Nucleic Acids Research, 2012, 40, D841-D846.	14.5	962
59	Shouldn't enantiomeric purity be included in the 'minimum information about a bioactive entity? Response from the MIABE group. Nature Reviews Drug Discovery, 2012, 11, 730-730.	46.4	0
60	Ten Years of Standardizing Proteomic Data: A Report on the HUPO–PSI Spring Workshop. Proteomics, 2012, 12, 2767-2772.	2.2	16
61	Molecular interaction databases. Proteomics, 2012, 12, 1656-1662.	2.2	72
62	Analyzing Protein–Protein Interaction Networks. Journal of Proteome Research, 2012, 11, 2014-2031.	3.7	145
63	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	19.0	274
64	Minimum information about a bioactive entity (MIABE). Nature Reviews Drug Discovery, 2011, 10, 661-669.	46.4	80
65	Omics Technologies, Data and Bioinformatics Principles. Methods in Molecular Biology, 2011, 719, 3-30.	0.9	92
66	Proteomic Temporal Profile of Human Brain Endothelium After Oxidative Stress. Stroke, 2011, 42, 37-43.	2.0	51
67	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	3.0	30
68	Ongoing and future developments at the Universal Protein Resource. Nucleic Acids Research, 2011, 39, D214-D219.	14.5	649
69	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	14.5	32
70	Preparing Molecular Interaction Data for Publication. Methods in Molecular Biology, 2011, 694, 229-236.	0.9	1
71	Data Standardization by the HUPO-PSI: How has the Community Benefitted?. Methods in Molecular Biology, 2011, 696, 149-160.	0.9	9
72	Conserved BK Channel-Protein Interactions Reveal Signals Relevant to Cell Death and Survival. PLoS ONE, 2011, 6, e28532.	2.5	39

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73	Meeting Report: BioSharing at ISMB 2010. Standards in Genomic Sciences, 2010, 3, 254-258.	1.5	19
74	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
75	From protein sequences to 3D-structures and beyond: the example of the UniProt Knowledgebase. Cellular and Molecular Life Sciences, 2010, 67, 1049-1064.	5.4	33
76	A domain level interaction network of amyloid precursor protein and AÎ² of Alzheimer's disease. Proteomics, 2010, 10, 2377-2395.	2.2	41
77	Minimum information about a protein affinity reagent (MIAPAR). Nature Biotechnology, 2010, 28, 650-653.	17.5	50
78	A Community Standard Format for the Representation of Protein Affinity Reagents. Molecular and Cellular Proteomics, 2010, 9, 1-10.	3.8	35
79	The Universal Protein Resource (UniProt) in 2010. Nucleic Acids Research, 2010, 38, D142-D148.	14.5	1,131
80	The IntAct molecular interaction database in 2010. Nucleic Acids Research, 2010, 38, D525-D531.	14.5	574
81	The Publication and Database Deposition of Molecular Interaction Data. Current Protocols in Protein Science, 2010, 60, Unit 25.3.	2.8	5
82	Molecular Interactions and Data Standardisation. Methods in Molecular Biology, 2010, 604, 309-318.	0.9	17
83	The Universal Protein Resource (UniProt) 2009. Nucleic Acids Research, 2009, 37, D169-D174.	14.5	548
84	The SDR (short-chain dehydrogenase/reductase and related enzymes) nomenclature initiative. Chemico-Biological Interactions, 2009, 178, 94-98.	4.0	329
85	Debunking minimum information myths: one hat need not fit all. New Biotechnology, 2009, 25, 171-172.	4.4	5
86	Nucleoside diphosphate kinase (NDPK, NM23, AWD): recent regulatory advances in endocytosis, metastasis, psoriasis, insulin release, fetal erythroid lineage and heart failure; translational medicine exemplified. Molecular and Cellular Biochemistry, 2009, 329, 3-15.	3.1	27
87	Second Joint HUPO Publication and Proteomics Standards Initiative Workshop. Proteomics, 2009, 9, 4426-4428.	2.2	6
88	Annual Spring Meeting of the Proteomics Standards Initiative. Proteomics, 2009, 9, 4429-4432.	2.2	9
89	Ending the "Publish and Vanish" Culture: How the Data Standardization Process Will Assist in Data Harvesting. Journal of Proteome Research, 2009, 8, 3219-3219.	3.7	1
90	A Protein Interaction Network for the Large Conductance Ca2+-activated K+ Channel in the Mouse Cochlea. Molecular and Cellular Proteomics, 2009, 8, 1972-1987.	3.8	56

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91	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	17.5	506
92	MINT and IntAct contribute to the Second BioCreative challenge: serving the text-mining community with high quality molecular interaction data. Genome Biology, 2008, 9, S5.	9.6	24
93	Charting plant interactomes: possibilities and challenges. Trends in Plant Science, 2008, 13, 183-191.	8.8	93
94	Minimum Reporting Guidelines for Proteomics Released by the Proteomics Standards Initiative. Molecular and Cellular Proteomics, 2008, 7, 2067-2068.	3.8	7
95	The Protein Feature Ontology: a tool for the unification of protein feature annotations. Bioinformatics, 2008, 24, 2767-2772.	4.1	19
96	The Annotation of Both Human and Mouse Kinomes in UniProtKB/Swiss-Prot. Molecular and Cellular Proteomics, 2008, 7, 1409-1419.	3.8	39
97	Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. Bioinformatics, 2008, 24, 1100-1101.	4.1	9
98	Standardising Proteomics Data â€" the W ork of the HUPO Proteomics Standards Initiative. Journal of Proteomics and Bioinformatics, 2008, 01, 003-005.	0.4	5
99	Proteomic Data Exchange and Storage: The Need for Common Standards and Public Repositories. , 2007, 367, 261-270.		10
100	IntAct--open source resource for molecular interaction data. Nucleic Acids Research, 2007, 35, D561-D565.	14.5	701
101	New developments in the InterPro database. Nucleic Acids Research, 2007, 35, D224-D228.	14.5	444
102	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2007, 35, D193-D197.	14.5	488
103	The implications of alternative splicing in the ENCODE protein complement. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5495-5500.	7.1	206
104	The HUPO proteomics standards initiative--easing communication and minimizing data loss in a changing world. Briefings in Bioinformatics, 2007, 9, 166-173.	6.5	38
105	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2007, 36, D190-D195.	14.5	852
106	Broadening the horizon â€" level 2.5 of the HUPO-PSI format for molecular interactions. BMC Biology, 2007, 5, 44.	3.8	237
107	Submit Your Interaction Data the IMEx Way. Proteomics, 2007, 7, 28-34.	2.2	65
108	Five years of progress in the Standardization of Proteomics Data 4th Annual Spring Workshop of the HUPO-Proteomics Standards Initiative April 23â€"25, 2007 Ecole Nationale SupÃ©rieure (ENS), Lyon, France. Proteomics, 2007, 7, 3436-3440.	2.2	46

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109	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	17.5	274
110	Human Proteome Organization Proteomics Standards Initiative. Molecular and Cellular Proteomics, 2007, 6, 1666-1667.	3.8	20
111	Human Proteome Organization Proteomics Standards Initiative: data standardization, a view on developments and policy. Molecular and Cellular Proteomics, 2007, 6, 1666-7.	3.8	3
112	Proteomics and Beyond A report on the 3rd Annual Spring Workshop of the HUPO-PSI 21â€"23 April 2006, San Francisco, CA, USA. Proteomics, 2006, 6, 4439-4443.	2.2	13
113	Data standardization and the HUPO proteomics standards initiative. , 2005, , .		0
114	Annotating the Human Proteome. Molecular and Cellular Proteomics, 2005, 4, 435-440.	3.8	24
115	The use of common ontologies and controlled vocabularies to enable data exchange and deposition for complex proteomic experiments. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 186-96.	0.7	14
116	InterPro, progress and status in 2005. Nucleic Acids Research, 2004, 33, D201-D205.	14.5	478
117	IntAct: an open source molecular interaction database. Nucleic Acids Research, 2004, 32, 452D-455.	14.5	864
118	Current status of proteomic standards development. Expert Review of Proteomics, 2004, 1, 179-183.	3.0	29
119	The HUPO PSI's Molecular Interaction formatâ€"a community standard for the representation of protein interaction data. Nature Biotechnology, 2004, 22, 177-183.	17.5	581
120	Common interchange standards for proteomics data: Public availability of tools and schemaReport on the Proteomic Standards Initiative Workshop, 2nd Annual HUPO Congress, Montreal, Canada, 8â€"11th October 2003. Proteomics, 2004, 4, 490-491.	2.2	100
121	Advances in the development of common interchange standards for proteomic data. Proteomics, 2004, 4, 2363-2365.	2.2	29
122	Proteomics and data standardisation. Drug Discovery Today Biosilico, 2004, 2, 91-93.	0.7	2
123	THE USE OF COMMON ONTOLOGIES AND CONTROLLED VOCABULARIES TO ENABLE DATA EXCHANGE AND DEPOSITION FOR COMPLEX PROTEOMIC EXPERIMENTS. , 2004, , .		14
124	The HUPO Proteomics Standards Initiative Meeting: Towards Common Standards for Exchanging Proteomics Data. Comparative and Functional Genomics, 2003, 4, 16-19.	2.0	26
125	Progress in Establishing Common Standards for Exchanging Proteomics Data: The Second Meeting of the HUPO Proteomics Standards Initiative. Comparative and Functional Genomics, 2003, 4, 203-206.	2.0	16
126	The Proteomics Standards Initiative. Proteomics, 2003, 3, 1374-1376.	2.2	188

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127	The InterPro Database, 2003 brings increased coverage and new features. Nucleic Acids Research, 2003, 31, 315-318.	14.5	640
128	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	6.5	155
129	Kinases as targets: prospects for chronic therapy. Current Opinion in Drug Discovery & Development, 2002, 5, 713-7.	1.9	1
130	T-cell signal transduction and the role of protein kinase C. Cellular and Molecular Life Sciences, 1998, 54, 1122-1144.	5.4	26
131	Ro 09-2210 Exhibits Potent Anti-proliferative Effects on Activated T Cells by Selectively Blocking MKK Activity. Biochemistry, 1998, 37, 9579-9585.	2.5	60
132	Substrate specificity and inhibitor profile of human recombinant p56lck from a baculovirus expression vector. Inflammation Research, 1996, 45, 412-415.	4.0	4
133	Phosphorylation of SLP-76 by the ZAP-70 Protein-tyrosine Kinase Is Required for T-cell Receptor Function. Journal of Biological Chemistry, 1996, 271, 19641-19644.	3.4	379
134	Protein kinase C: is its pivotal role in cellular activation over-stated?. Trends in Pharmacological Sciences, 1994, 15, 53-57.	8.7	141
135	Therapeutic potential of protein kinase C inhibitors. Agents and Actions, 1993, 38, 135-147.	0.7	147
136	Inhibitors of protein kinase C. 1. 2,3-bisarylmaleimides. Journal of Medicinal Chemistry, 1992, 35, 177-184.	6.4	166
137	Inhibitors of protein kinase C. 2. Substituted bisindolylmaleimides with improved potency and selectivity. Journal of Medicinal Chemistry, 1992, 35, 994-1001.	6.4	210
138	A novel conformationally restricted protein kinase C inhibitor, Ro 31-8425, inhibits human neutrophil superoxide generation by soluble, particulate and post-receptor stimuli. FEBS Letters, 1991, 293, 169-172.	2.8	51
139	Modulation of cellular processes by H7, a non-selective inhibitor of protein kinases. Agents and Actions, 1991, 32, 188-193.	0.7	37
140	Potent collagenase inhibitors prevent interleukin-1-induced cartilage degradation in vitro. International Journal of Tissue Reactions, 1991, 13, 237-41.	0.2	27
141	The effect of new potent selective inhibitors of protein kinase C on the neutrophil respiratory burst. Biochemical and Biophysical Research Communications, 1990, 171, 1087-1092.	2.1	82
142	K252a is a potent and selective inhibitor of phosphorylase kinase. Biochemical and Biophysical Research Communications, 1990, 171, 148-154.	2.1	68
143	Potent selective inhibitors of protein kinase C. FEBS Letters, 1989, 259, 61-63.	2.8	467
144	The inhibitory profiles of hog pancreatic and human rheumatoid synovial cell phospholipases A2. Agents and Actions, 1986, 17, 299-301.	0.7	3