

# Sandra Orchard

## List of Publications by Year in descending order

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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	UniProt: a worldwide hub of protein knowledge. <i>Nucleic Acids Research</i> , 2019, 47, D506-D515.	14.5	6,185
2	UniProt: the universal protein knowledgebase in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D480-D489.	14.5	4,709
3	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338.	14.5	3,474
4	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
5	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	14.5	1,838
6	The MIntAct project—IntAct as a common curation platform for 11 molecular interaction databases. <i>Nucleic Acids Research</i> , 2014, 42, D358-D363.	14.5	1,634
7	Reorganizing the protein space at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2012, 40, D71-D75.	14.5	1,196
8	Activities at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2014, 42, D191-D198.	14.5	1,162
9	The Universal Protein Resource (UniProt) in 2010. <i>Nucleic Acids Research</i> , 2010, 38, D142-D148.	14.5	1,131
10	The IntAct molecular interaction database in 2012. <i>Nucleic Acids Research</i> , 2012, 40, D841-D846.	14.5	962
11	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , 2004, 32, 452D-455.	14.5	864
12	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2007, 36, D190-D195.	14.5	852
13	IntAct—open source resource for molecular interaction data. <i>Nucleic Acids Research</i> , 2007, 35, D561-D565.	14.5	701
14	Ongoing and future developments at the Universal Protein Resource. <i>Nucleic Acids Research</i> , 2011, 39, D214-D219.	14.5	649
15	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	14.5	640
16	The HUPO PSI's Molecular Interaction format—a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	17.5	581
17	The IntAct molecular interaction database in 2010. <i>Nucleic Acids Research</i> , 2010, 38, D525-D531.	14.5	574
18	The Universal Protein Resource (UniProt) 2009. <i>Nucleic Acids Research</i> , 2009, 37, D169-D174.	14.5	548

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19	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	17.5	506
20	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , 2012, 9, 345-350.	19.0	500
21	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2007, 35, D193-D197.	14.5	488
22	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D201-D205.	14.5	478
23	Potent selective inhibitors of protein kinase C. <i>FEBS Letters</i> , 1989, 259, 61-63.	2.8	467
24	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	14.5	444
25	Phosphorylation of SLP-76 by the ZAP-70 Protein-tyrosine Kinase Is Required for T-cell Receptor Function. <i>Journal of Biological Chemistry</i> , 1996, 271, 19641-19644.	3.4	379
26	The SDR (short-chain dehydrogenase/reductase and related enzymes) nomenclature initiative. <i>Chemico-Biological Interactions</i> , 2009, 178, 94-98.	4.0	329
27	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	17.5	274
28	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	19.0	274
29	Non-coding RNA regulatory networks. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194417.	1.9	262
30	Broadening the horizon $\hat{\alpha}^c$ level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , 2007, 5, 44.	3.8	237
31	Inhibitors of protein kinase C. 2. Substituted bisindolylmaleimides with improved potency and selectivity. <i>Journal of Medicinal Chemistry</i> , 1992, 35, 994-1001.	6.4	210
32	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5495-5500.	7.1	206
33	The Proteomics Standards Initiative. <i>Proteomics</i> , 2003, 3, 1374-1376.	2.2	188
34	Inhibitors of protein kinase C. 1. 2,3-bisarylmaleimides. <i>Journal of Medicinal Chemistry</i> , 1992, 35, 177-184.	6.4	166
35	InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.	6.5	155
36	Therapeutic potential of protein kinase C inhibitors. <i>Agents and Actions</i> , 1993, 38, 135-147.	0.7	147

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37	Analyzing Protein-Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2012, 11, 2014-2031.	3.7	145
38	Protein kinase C: is its pivotal role in cellular activation over-stated?. <i>Trends in Pharmacological Sciences</i> , 1994, 15, 53-57.	8.7	141
39	BioJS: an open source JavaScript framework for biological data visualization. <i>Bioinformatics</i> , 2013, 29, 1103-1104.	4.1	110
40	Common interchange standards for proteomics data: Public availability of tools and schemaReport on the Proteomic Standards Initiative Workshop, 2nd Annual HUPO Congress, Montreal, Canada, 8-11th October 2003. <i>Proteomics</i> , 2004, 4, 490-491.	2.2	100
41	The complex portal - an encyclopaedia of macromolecular complexes. <i>Nucleic Acids Research</i> , 2015, 43, D479-D484.	14.5	100
42	Charting plant interactomes: possibilities and challenges. <i>Trends in Plant Science</i> , 2008, 13, 183-191.	8.8	93
43	Omics Technologies, Data and Bioinformatics Principles. <i>Methods in Molecular Biology</i> , 2011, 719, 3-30.	0.9	92
44	A new reference implementation of the PSICQUIC web service. <i>Nucleic Acids Research</i> , 2013, 41, W601-W606.	14.5	91
45	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2022, 50, D648-D653.	14.5	89
46	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017, 16, 4288-4298.	3.7	87
47	Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes. <i>Nucleic Acids Research</i> , 2019, 47, D550-D558.	14.5	85
48	The effect of new potent selective inhibitors of protein kinase C on the neutrophil respiratory burst. <i>Biochemical and Biophysical Research Communications</i> , 1990, 171, 1087-1092.	2.1	82
49	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. <i>Journal of Proteome Research</i> , 2019, 18, 4108-4116.	3.7	82
50	Minimum information about a bioactive entity (MIABE). <i>Nature Reviews Drug Discovery</i> , 2011, 10, 661-669.	46.4	80
51	Emerging concepts in pseudoenzyme classification, evolution, and signaling. <i>Science Signaling</i> , 2019, 12, .	3.6	80
52	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the <i>Journal of Biological Databases and Curation</i> , 2013, 2013, bat009-bat009.	3.0	76
53	Molecular interaction databases. <i>Proteomics</i> , 2012, 12, 1656-1662.	2.2	72
54	K252a is a potent and selective inhibitor of phosphorylase kinase. <i>Biochemical and Biophysical Research Communications</i> , 1990, 171, 148-154.	2.1	68

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55	Submit Your Interaction Data the IMEx Way. <i>Proteomics</i> , 2007, 7, 28-34.	2.2	65
56	Ro 09-2210 Exhibits Potent Anti-proliferative Effects on Activated T Cells by Selectively Blocking MKK Activity. <i>Biochemistry</i> , 1998, 37, 9579-9585.	2.5	60
57	A Protein Interaction Network for the Large Conductance Ca <sup>2+</sup> -activated K <sup>+</sup> Channel in the Mouse Cochlea. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1972-1987.	3.8	56
58	Expert curation in UniProtKB: a case study on dealing with conflicting and erroneous data. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau016-bau016.	3.0	56
59	Development of data representation standards by the human proteome organization proteomics standards initiative. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 495-506.	4.4	54
60	A novel conformationally restricted protein kinase C inhibitor, Ro 31-8425, inhibits human neutrophil superoxide generation by soluble, particulate and post-receptor stimuli. <i>FEBS Letters</i> , 1991, 293, 169-172.	2.8	51
61	Proteomic Temporal Profile of Human Brain Endothelium After Oxidative Stress. <i>Stroke</i> , 2011, 42, 37-43.	2.0	51
62	Minimum information about a protein affinity reagent (MIAPAR). <i>Nature Biotechnology</i> , 2010, 28, 650-653.	17.5	50
63	Towards a unified open access dataset of molecular interactions. <i>Nature Communications</i> , 2020, 11, 6144.	12.8	49
64	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. <i>BMC Bioinformatics</i> , 2018, 19, 134.	2.6	47
65	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020, 36, 2636-2642.	4.1	47
66	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 Supérieure (ENS), Lyon, France. <i>Proteomics</i> , 2007, 7, 3436-3440.	2.2	46
67	UniRule: a unified rule resource for automatic annotation in the UniProt Knowledgebase. <i>Bioinformatics</i> , 2020, 36, 4643-4648.	4.1	42
68	A domain level interaction network of amyloid precursor protein and A $\beta$ of Alzheimer's disease. <i>Proteomics</i> , 2010, 10, 2377-2395.	2.2	41
69	The Annotation of Both Human and Mouse Kinomes in UniProtKB/Swiss-Prot. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1409-1419.	3.8	39
70	Conserved BK Channel-Protein Interactions Reveal Signals Relevant to Cell Death and Survival. <i>PLoS ONE</i> , 2011, 6, e28532.	2.5	39
71	The HUPO proteomics standards initiative--easing communication and minimizing data loss in a changing world. <i>Briefings in Bioinformatics</i> , 2007, 9, 166-173.	6.5	38
72	A visual review of the interactome of LRRK2: Using deep-curated molecular interaction data to represent biology. <i>Proteomics</i> , 2015, 15, 1390-1404.	2.2	38

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73	Modulation of cellular processes by H7, a non-selective inhibitor of protein kinases. Agents and Actions, 1991, 32, 188-193.	0.7	37
74	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
75	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 98-107.	2.3	36
76	Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119.	3.0	36
77	A Community Standard Format for the Representation of Protein Affinity Reagents. Molecular and Cellular Proteomics, 2010, 9, 1-10.	3.8	35
78	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
79	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
80	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	14.5	32
81	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
82	Current status of proteomic standards development. Expert Review of Proteomics, 2004, 1, 179-183.	3.0	29
83	Advances in the development of common interchange standards for proteomic data. Proteomics, 2004, 4, 2363-2365.	2.2	29
84	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
85	Complex Portal 2022: new curation frontiers. Nucleic Acids Research, 2022, 50, D578-D586.	14.5	27
86	Potent collagenase inhibitors prevent interleukin-1-induced cartilage degradation in vitro. International Journal of Tissue Reactions, 1991, 13, 237-41.	0.2	27
87	T-cell signal transduction and the role of protein kinase C. Cellular and Molecular Life Sciences, 1998, 54, 1122-1144.	5.4	26
88	The HUPO Proteomics Standards Initiative Meeting: Towards Common Standards for Exchanging Proteomics Data. Comparative and Functional Genomics, 2003, 4, 16-19.	2.0	26
89	The yeast noncoding RNA interaction network. Rna, 2017, 23, 1479-1492.	3.5	25
90	Annotating the Human Proteome. Molecular and Cellular Proteomics, 2005, 4, 435-440.	3.8	24

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91	MINT and IntAct contribute to the Second BioCreative challenge: serving the text-mining community with high quality molecular interaction data. <i>Genome Biology</i> , 2008, 9, S5.	9.6	24
92	Best practice data life cycle approaches for the life sciences. <i>F1000Research</i> , 2017, 6, 1618.	1.6	23
93	Data Standardization and Sharing – The work of the HUPO-PSI. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 82-87.	2.3	22
94	Best practice data life cycle approaches for the life sciences. <i>F1000Research</i> , 2017, 6, 1618.	1.6	21
95	Human Proteome Organization Proteomics Standards Initiative. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1666-1667.	3.8	20
96	The Protein Feature Ontology: a tool for the unification of protein feature annotations. <i>Bioinformatics</i> , 2008, 24, 2767-2772.	4.1	19
97	Meeting Report: BioSharing at ISMB 2010. <i>Standards in Genomic Sciences</i> , 2010, 3, 254-258.	1.5	19
98	Gene Ontology Curation of Neuroinflammation Biology Improves the Interpretation of Alzheimer’s Disease Gene Expression Data. <i>Journal of Alzheimer’s Disease</i> , 2020, 75, 1417-1435.	2.6	18
99	Molecular Interactions and Data Standardisation. <i>Methods in Molecular Biology</i> , 2010, 604, 309-318.	0.9	17
100	Progress in Establishing Common Standards for Exchanging Proteomics Data: The Second Meeting of the HUPO Proteomics Standards Initiative. <i>Comparative and Functional Genomics</i> , 2003, 4, 203-206.	2.0	16
101	Ten Years of Standardizing Proteomic Data: A Report on the HUPO-PSI Spring Workshop. <i>Proteomics</i> , 2012, 12, 2767-2772.	2.2	16
102	The MIntAct Project and Molecular Interaction Databases. <i>Methods in Molecular Biology</i> , 2016, 1415, 55-69.	0.9	16
103	Improving the Gene Ontology Resource to Facilitate More Informative Analysis and Interpretation of Alzheimer’s Disease Data. <i>Genes</i> , 2018, 9, 593.	2.4	15
104	Challenges in the annotation of pseudoenzymes in databases: the UniProtKB approach. <i>FEBS Journal</i> , 2020, 287, 4114-4127.	4.7	15
105	The Minimum Information about a Molecular Interaction CAusal STATEment (MI2CAST). <i>Bioinformatics</i> , 2021, 36, 5712-5718.	4.1	14
106	THE USE OF COMMON ONTOLOGIES AND CONTROLLED VOCABULARIES TO ENABLE DATA EXCHANGE AND DEPOSITION FOR COMPLEX PROTEOMIC EXPERIMENTS. , 2004, , .		14
107	The use of common ontologies and controlled vocabularies to enable data exchange and deposition for complex proteomic experiments. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005, , 186-96.	0.7	14
108	Proteomics and Beyond A report on the 3rd Annual Spring Workshop of the HUPO-PSI 21st April 2006, San Francisco, CA, USA. <i>Proteomics</i> , 2006, 6, 4439-4443.	2.2	13

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109	Shared resources, shared costsâ€”leveraging biocuration resources. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	13
110	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
111	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
112	Proteomic Data Exchange and Storage: The Need for Common Standards and Public Repositories. , 2007, 367, 261-270.		10
113	Capturing cooperative interactions with the PSI-MI format. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat066.	3.0	10
114	ComplexViewer: visualization of curated macromolecular complexes. Bioinformatics, 2017, 33, 3673-3675.	4.1	10
115	Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. Bioinformatics, 2008, 24, 1100-1101.	4.1	9
116	Annual Spring Meeting of the Proteomics Standards Initiative. Proteomics, 2009, 9, 4429-4432.	2.2	9
117	Data Standardization by the HUPO-PSI: How has the Community Benefitted?. Methods in Molecular Biology, 2011, 696, 149-160.	0.9	9
118	Minimum Reporting Guidelines for Proteomics Released by the Proteomics Standards Initiative. Molecular and Cellular Proteomics, 2008, 7, 2067-2068.	3.8	7
119	Searching and Extracting Data from the EMBL-EBI Complex Portal. Methods in Molecular Biology, 2018, 1764, 377-390.	0.9	7
120	A Coordinated Approach by Public Domain Bioinformatics Resources to Aid the Fight Against Alzheimerâ€™s Disease Through Expert Curation of Key Protein Targets. Journal of Alzheimer's Disease, 2020, 77, 257-273.	2.6	7
121	Second Joint HUPO Publication and Proteomics Standards Initiative Workshop. Proteomics, 2009, 9, 4426-4428.	2.2	6
122	JAMI: a Java library for molecular interactions and data interoperability. BMC Bioinformatics, 2018, 19, 133.	2.6	6
123	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
124	Gene Ontology curation of the bloodâ€”brain barrier to improve the analysis of Alzheimerâ€™s and other neurological diseases. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	6
125	Debunking minimum information myths: one hat need not fit all. New Biotechnology, 2009, 25, 171-172.	4.4	5
126	The Publication and Database Deposition of Molecular Interaction Data. Current Protocols in Protein Science, 2010, 60, Unit 25.3.	2.8	5



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127	Analysing the yeast complexome – the Complex Portal rising to the challenge. <i>Nucleic Acids Research</i> , 2021, 49, 3156-3167.	14.5	5
128	Standardising Proteomics Data – the Work of the HUPO Proteomics Standards Initiative. <i>Journal of Proteomics and Bioinformatics</i> , 2008, 01, 003-005.	0.4	5
129	Substrate specificity and inhibitor profile of human recombinant p56lck from a baculovirus expression vector. <i>Inflammation Research</i> , 1996, 45, 412-415.	4.0	4
130	IMEx Databases: Displaying Molecular Interactions into a Single, Standards-Compliant Dataset. <i>Methods in Molecular Biology</i> , 2022, 2449, 27-42.	0.9	4
131	The inhibitory profiles of hog pancreatic and human rheumatoid synovial cell phospholipases A2. <i>Agents and Actions</i> , 1986, 17, 299-301.	0.7	3
132	Caenorhabditis elegans phosphatase complexes in UniProtKB and Complex Portal. <i>FEBS Journal</i> , 2020, 287, 2664-2684.	4.7	3
133	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
134	Human Proteome Organization Proteomics Standards Initiative: data standardization, a view on developments and policy. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1666-7.	3.8	3
135	Proteomics and data standardisation. <i>Drug Discovery Today Biosilico</i> , 2004, 2, 91-93.	0.7	2
136	The Enzyme Portal: an integrative tool for enzyme information and analysis. <i>FEBS Journal</i> , 2021, , .	4.7	2
137	Ending the ‘Publish and Vanish’ Culture: How the Data Standardization Process Will Assist in Data Harvesting. <i>Journal of Proteome Research</i> , 2009, 8, 3219-3219.	3.7	1
138	Preparing Molecular Interaction Data for Publication. <i>Methods in Molecular Biology</i> , 2011, 694, 229-236.	0.9	1
139	Kinases as targets: prospects for chronic therapy. <i>Current Opinion in Drug Discovery &amp; Development</i> , 2002, 5, 713-7.	1.9	1
140	Data standardization and the HUPO proteomics standards initiative. , 2005, , .		0
141	Shouldn't enantiomeric purity be included in the 'minimum information about a bioactive entity? Response from the MIABE group. <i>Nature Reviews Drug Discovery</i> , 2012, 11, 730-730.	46.4	0
142	Minimum Information about a Molecular Interaction Experiment (MIMIx). , 2013, , 1361-1363.		0
143	PSICQUIC. , 2013, , 1801-1801.		0
144	Proteomics Standards Initiative. , 2013, , 1797-1798.		0