Sandra Orchard

List of Publications by Year in Descending Order

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137 papers	25,993 citations	53 h-index	161 g-index
176 ext. papers	34,640 ext. citations	10.7 avg, IF	8.88 L-index

#	Paper	IF	Citations
137	IMEx Databases: Displaying Molecular Interactions into a Single, Standards-Compliant Dataset.. *Methods in Molecular Biology*, **2022**, 2449, 27-42	1.4	1
136	Complex Portal 2022: new curation frontiers. *Nucleic Acids Research*, **2021**,	20.1	4
135	The IntAct database: efficient access to fine-grained molecular interaction data. *Nucleic Acids Research*, **2021**,	20.1	15
134	The gene regulation knowledge commons: the action area of GREEKC. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1865, 194768	6	1
133	The Gene Ontology resource: enriching a GOld mine. *Nucleic Acids Research*, **2021**, 49, D325-D334	20.1	494
132	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). *Bioinformatics*, **2021**, 36, 5712-5718	7.2	5
131	UniProt: the universal protein knowledgebase in 2021. *Nucleic Acids Research*, **2021**, 49, D480-D489	20.1	1073
130	Analysing the yeast complexome-the Complex Portal rising to the challenge. *Nucleic Acids Research*, **2021**, 49, 3156-3167	20.1	1
129	Integration of transcription coregulator complexes with sequence-specific DNA-binding factor interactomes. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1864, 194749	6	2
128	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	4.3	6
127	UniRule: a unified rule resource for automatic annotation in the UniProt Knowledgebase. *Bioinformatics*, **2020**, 36, 4643-4648	7.2	19
126	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. *Bioinformatics*, **2020**, 36, 2636-2642	7.2	29
125	Caenorhabditis elegans phosphatase complexes in UniProtKB and Complex Portal. *FEBS Journal*, **2020**, 287, 2664-2684	5.7	1
124	Challenges in the annotation of pseudoenzymes in databases: the UniProtKB approach. *FEBS Journal*, **2020**, 287, 4114-4127	5.7	7
123	Towards a unified open access dataset of molecular interactions. *Nature Communications*, **2020**, 11, 6144	17.4	26
122	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	4.3	2
121	Non-coding RNA regulatory networks. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2020**, 1863, 194417	6	93

120	Emerging concepts in pseudoenzyme classification, evolution, and signaling. *Science Signaling*, **2019** , 12,	8.8	51
119	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. *Journal of Proteome Research*, **2019**, 18, 4108-4116	5.6	37
118	An intrinsically disordered proteins community for ELIXIR. *F1000Research*, **2019**, 8,	3.6	7
117	UniProt: a worldwide hub of protein knowledge. *Nucleic Acids Research*, **2019**, 47, D506-D515	20.1	3656
116	The Gene Ontology Resource: 20 years and still GOing strong. *Nucleic Acids Research*, **2019**, 47, D330-D338	20.1	1962
115	Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes. *Nucleic Acids Research*, **2019**, 47, D550-D558	20.1	44
114	Searching and Extracting Data from the EMBL-EBI Complex Portal. *Methods in Molecular Biology*, **2018**, 1764, 377-390	1.4	3
113	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. *BMC Bioinformatics*, **2018**, 19, 134	3.6	31
112	JAMI: a Java library for molecular interactions and data interoperability. *BMC Bioinformatics*, **2018**, 19, 133	3.6	5
111	Improving the Gene Ontology Resource to Facilitate More Informative Analysis and Interpretation of Alzheimer's Disease Data. *Genes*, **2018**, 9,	4.2	6
110	Expansion of the Gene Ontology knowledgebase and resources. *Nucleic Acids Research*, **2017**, 45, D331-D338	20.1	1258
109	ComplexViewer: visualization of curated macromolecular complexes. *Bioinformatics*, **2017**, 33, 3673-3675	7.2	8
108	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. *Journal of Proteome Research*, **2017**, 16, 4288-4298	5.6	61
107	The yeast noncoding RNA interaction network. *Rna*, **2017**, 23, 1479-1492	5.8	19
106	Best practice data life cycle approaches for the life sciences. *F1000Research*, **2017**, 6, 1618	3.6	14
105	Best practice data life cycle approaches for the life sciences. *F1000Research*, **2017**, 6, 1618	3.6	14
104	Gene regulation knowledge commons: community action takes care of DNA binding transcription factors. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	10
103	Overview of the interactive task in BioCreative V. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	31

102	The MIntAct Project and Molecular Interaction Databases. *Methods in Molecular Biology*, **2016**, 1415, 55-69	1.4	14
101	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	8.6	42
100	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	5	27
99	Shared resources, shared costs--leveraging biocuration resources. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015,	5	10
98	The complex portal--an encyclopaedia of macromolecular complexes. *Nucleic Acids Research*, **2015**, 43, D479-84	20.1	68
97	A visual review of the interactome of LRRK2: Using deep-curated molecular interaction data to represent biology. *Proteomics*, **2015**, 15, 1390-404	4.8	33
96	Activities at the Universal Protein Resource (UniProt). *Nucleic Acids Research*, **2014**, 42, D191-8	20.1	1007
95	Data standardization and sharing-the work of the HUPO-PSI. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2014**, 1844, 82-7	4	17
94	Controlled vocabularies and ontologies in proteomics: overview, principles and practice. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2014**, 1844, 98-107	4	26
93	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	5	49
92	The MIntAct project--IntAct as a common curation platform for 11 molecular interaction databases. *Nucleic Acids Research*, **2014**, 42, D358-63	20.1	1111
91	BioJS: an open source JavaScript framework for biological data visualization. *Bioinformatics*, **2013**, 29, 1103-4	7.2	88
90	Capturing cooperative interactions with the PSI-MI format. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat066	5	9
89	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat009	5	56
88	A new reference implementation of the PSICQUIC web service. *Nucleic Acids Research*, **2013**, 41, W601-6	20.1	70
87	ShouldnPt enantiomeric purity be included in the Pminimum information about a bioactive entity? Response from the MIABE group. *Nature Reviews Drug Discovery*, **2012**, 11, 730-730	64.1	
86	Ten years of standardizing proteomic data: a report on the HUPO-PSI Spring Workshop: April 12-14th, 2012, San Diego, USA. *Proteomics*, **2012**, 12, 2767-72	4.8	15
85	Molecular interaction databases. *Proteomics*, **2012**, 12, 1656-62	4.8	55

84	Analyzing protein-protein interaction networks. *Journal of Proteome Research*, **2012**, 11, 2014-31	5.6	103
83	Reorganizing the protein space at the Universal Protein Resource (UniProt). *Nucleic Acids Research*, **2012**, 40, D71-5	20.1	1096
82	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. *Nature Methods*, **2012**, 9, 345-50	21.6	375
81	The IntAct molecular interaction database in 2012. *Nucleic Acids Research*, **2012**, 40, D841-6	20.1	779
80	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. *Nature Methods*, **2011**, 8, 528-9	21.6	227
79	Minimum information about a bioactive entity (MIABE). *Nature Reviews Drug Discovery*, **2011**, 10, 661-9	64.1	69
78	Omics technologies, data and bioinformatics principles. *Methods in Molecular Biology*, **2011**, 719, 3-30	1.4	64
77	Proteomic temporal profile of human brain endothelium after oxidative stress. *Stroke*, **2011**, 42, 37-43	6.7	50
76	Ongoing and future developments at the Universal Protein Resource. *Nucleic Acids Research*, **2011**, 39, D214-9	20.1	592
75	Conserved BK channel-protein interactions reveal signals relevant to cell death and survival. *PLoS ONE*, **2011**, 6, e28532	3.7	38
74	Preparing molecular interaction data for publication. *Methods in Molecular Biology*, **2011**, 694, 229-36	1.4	1
73	Data standardization by the HUPO-PSI: how has the community benefitted?. *Methods in Molecular Biology*, **2011**, 696, 149-60	1.4	7
72	Minimum information about a protein affinity reagent (MIAPAR). *Nature Biotechnology*, **2010**, 28, 650-3	44.5	37
71	A community standard format for the representation of protein affinity reagents. *Molecular and Cellular Proteomics*, **2010**, 9, 1-10	7.6	33
70	The Universal Protein Resource (UniProt) in 2010. *Nucleic Acids Research*, **2010**, 38, D142-8	20.1	1035
69	The IntAct molecular interaction database in 2010. *Nucleic Acids Research*, **2010**, 38, D525-31	20.1	522
68	The publication and database deposition of molecular interaction data. *Current Protocols in Protein Science*, **2010**, Chapter 25, Unit 25.3	3.1	5
67	Meeting Report: BioSharing at ISMB 2010. *Standards in Genomic Sciences*, **2010**, 3, 254-8		18

66	Meeting Report from the Second "Minimum Information for Biological and Biomedical Investigations" (MIBBI) workshop. *Standards in Genomic Sciences*, **2010**, 3, 259-66		26
65	From protein sequences to 3D-structures and beyond: the example of the UniProt knowledgebase. *Cellular and Molecular Life Sciences*, **2010**, 67, 1049-64	10.3	25
64	A domain level interaction network of amyloid precursor protein and Abeta of Alzheimer's disease. *Proteomics*, **2010**, 10, 2377-95	4.8	38
63	Molecular interactions and data standardisation. *Methods in Molecular Biology*, **2010**, 604, 309-18	1.4	17
62	The Universal Protein Resource (UniProt) 2009. *Nucleic Acids Research*, **2009**, 37, D169-74	20.1	509
61	The SDR (short-chain dehydrogenase/reductase and related enzymes) nomenclature initiative. *Chemico-Biological Interactions*, **2009**, 178, 94-8	5	273
60	Debunking minimum information myths: one hat need not fit all. *New Biotechnology*, **2009**, 25, 171-2	6.4	5
59	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	4.2	25
58	Second Joint HUPO publication and Proteomics Standards Initiative workshop. *Proteomics*, **2009**, 9, 4426-8	4.8	6
57	Annual spring meeting of the Proteomics Standards Initiative. *Proteomics*, **2009**, 9, 4429-32	4.8	8
56	A protein interaction network for the large conductance Ca(2+)-activated K(+) channel in the mouse cochlea. *Molecular and Cellular Proteomics*, **2009**, 8, 1972-87	7.6	46
55	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. *Nature Biotechnology*, **2008**, 26, 889-96	44.5	417
54	MINT and IntAct contribute to the Second BioCreative challenge: serving the text-mining community with high quality molecular interaction data. *Genome Biology*, **2008**, 9 Suppl 2, S5	18.3	21
53	Charting plant interactomes: possibilities and challenges. *Trends in Plant Science*, **2008**, 13, 183-91	13.1	64
52	Minimum reporting guidelines for proteomics released by the Proteomics Standards Initiative. *Molecular and Cellular Proteomics*, **2008**, 7, 2067-8	7.6	7
51	The Protein Feature Ontology: a tool for the unification of protein feature annotations. *Bioinformatics*, **2008**, 24, 2767-72	7.2	16
50	The annotation of both human and mouse kinomes in UniProtKB/Swiss-Prot: one small step in manual annotation, one giant leap for full comprehension of genomes. *Molecular and Cellular Proteomics*, **2008**, 7, 1409-19	7.6	37
49	Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. *Bioinformatics*, **2008**, 24, 1100-1	7.2	9

48	The universal protein resource (UniProt). *Nucleic Acids Research*, **2008**, 36, D190-5	20.1	746
47	The HUPO proteomics standards initiative--easing communication and minimizing data loss in a changing world. *Briefings in Bioinformatics*, **2008**, 9, 166-73	13.4	33
46	Standardising Proteomics Data the Work of the HUPO Proteomics Standards Initiative. *Journal of Proteomics and Bioinformatics*, **2008**, 01, 003-005	2.1	4
45	Broadening the horizon--level 2.5 of the HUPO-PSI format for molecular interactions. *BMC Biology*, **2007**, 5, 44	7.3	204
44	Submit your interaction data the IMEx way: a step by step guide to trouble-free deposition. *Proteomics*, **2007**, 7 Suppl 1, 28-34	4.8	56
43	Five years of progress in the Standardization of Proteomics Data 4th Annual Spring Workshop of the HUPO-Proteomics Standards Initiative April 23-25, 2007 Ecole Nationale Supérieure (ENS), Lyon, France. *Proteomics*, **2007**, 7, 3436-40	4.8	42
42	The minimum information required for reporting a molecular interaction experiment (MIMIx). *Nature Biotechnology*, **2007**, 25, 894-8	44.5	229
41	Proteomic data exchange and storage: the need for common standards and public repositories. *Methods in Molecular Biology*, **2007**, 367, 261-70	1.4	9
40	IntAct--open source resource for molecular interaction data. *Nucleic Acids Research*, **2007**, 35, D561-5	20.1	626
39	New developments in the InterPro database. *Nucleic Acids Research*, **2007**, 35, D224-8	20.1	397
38	The Universal Protein Resource (UniProt). *Nucleic Acids Research*, **2007**, 35, D193-7	20.1	437
37	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, 5495-500	11.5	177
36	Human Proteome Organization Proteomics Standards Initiative. *Molecular and Cellular Proteomics*, **2007**, 6, 1666-1667	7.6	13
35	Human Proteome Organization Proteomics Standards Initiative: data standardization, a view on developments and policy. *Molecular and Cellular Proteomics*, **2007**, 6, 1666-7	7.6	3
34	Proteomic Data Standardization, Deposition and Exchange. *Methods and Principles in Medicinal Chemistry*, **2006**, 19-30	0.4	
33	Proteomics and Beyond: a report on the 3rd Annual Spring Workshop of the HUPO-PSI 21-23 April 2006, San Francisco, CA, USA. *Proteomics*, **2006**, 6, 4439-43	4.8	12
32	InterPro, progress and status in 2005. *Nucleic Acids Research*, **2005**, 33, D201-5	20.1	426
31	Annotating the human proteome. *Molecular and Cellular Proteomics*, **2005**, 4, 435-40	7.6	22

30	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	1.3	14
29	IntAct: an open source molecular interaction database. *Nucleic Acids Research*, **2004**, 32, D452-5	20.1	670
28	Current status of proteomic standards development. *Expert Review of Proteomics*, **2004**, 1, 179-83	4.2	25
27	The HUPO PSI's molecular interaction format--a community standard for the representation of protein interaction data. *Nature Biotechnology*, **2004**, 22, 177-83	44.5	504
26	Common interchange standards for proteomics data: Public availability of tools and schema. *Proteomics*, **2004**, 4, 490-1	4.8	88
25	Advances in the development of common interchange standards for proteomic data. *Proteomics*, **2004**, 4, 2363-5	4.8	24
24	Proteomics and data standardisation. *Drug Discovery Today Biosilico*, **2004**, 2, 91-93		2
23	THE USE OF COMMON ONTOLOGIES AND CONTROLLED VOCABULARIES TO ENABLE DATA EXCHANGE AND DEPOSITION FOR COMPLEX PROTEOMIC EXPERIMENTS **2004**,		4
22	The HUPO Proteomics Standards Initiative Meeting: Towards Common Standards for Exchanging Proteomics Data. *Comparative and Functional Genomics*, **2003**, 4, 16-9		22
21	Progress in Establishing Common Standards for Exchanging Proteomics Data: The Second Meeting of the HUPO Proteomics Standards Initiative. *Comparative and Functional Genomics*, **2003**, 4, 203-6		14
20	The proteomics standards initiative. *Proteomics*, **2003**, 3, 1374-6	4.8	159
19	The InterPro Database, 2003 brings increased coverage and new features. *Nucleic Acids Research*, **2003**, 31, 315-8	20.1	556
18	InterPro: an integrated documentation resource for protein families, domains and functional sites. *Briefings in Bioinformatics*, **2002**, 3, 225-35	13.4	137
17	Kinases as targets: prospects for chronic therapy. *Current Opinion in Drug Discovery & Development*, **2002**, 5, 713-7		1
16	T-cell signal transduction and the role of protein kinase C. *Cellular and Molecular Life Sciences*, **1998**, 54, 1122-44	10.3	21
15	Ro 09-2210 exhibits potent anti-proliferative effects on activated T cells by selectively blocking MKK activity. *Biochemistry*, **1998**, 37, 9579-85	3.2	58
14	Substrate specificity and inhibitor profile of human recombinant p56lck from a baculovirus expression vector. *Inflammation Research*, **1996**, 45, 412-5	7.2	3
13	Phosphorylation of SLP-76 by the ZAP-70 protein-tyrosine kinase is required for T-cell receptor function. *Journal of Biological Chemistry*, **1996**, 271, 19641-4	5.4	335

12	Protein kinase C: is its pivotal role in cellular activation over-stated?. *Trends in Pharmacological Sciences*, **1994**, 15, 53-7	13.2	126
11	Therapeutic potential of protein kinase C inhibitors. *Agents and Actions*, **1993**, 38, 135-47		139
10	Inhibitors of protein kinase C. 1. 2,3-Bisarylmaleimides. *Journal of Medicinal Chemistry*, **1992**, 35, 177-84	8.3	152
9	Inhibitors of protein kinase C. 2. Substituted bisindolylmaleimides with improved potency and selectivity. *Journal of Medicinal Chemistry*, **1992**, 35, 994-1001	8.3	200
8	Modulation of cellular processes by H7, a non-selective inhibitor of protein kinases. *Agents and Actions*, **1991**, 32, 188-93		35
7	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, 169-72	3.8	42
6	Potent collagenase inhibitors prevent interleukin-1-induced cartilage degradation in vitro. *International Journal of Tissue Reactions*, **1991**, 13, 237-41		26
5	The effect of new potent selective inhibitors of protein kinase C on the neutrophil respiratory burst. *Biochemical and Biophysical Research Communications*, **1990**, 171, 1087-92	3.4	75
4	K252a is a potent and selective inhibitor of phosphorylase kinase. *Biochemical and Biophysical Research Communications*, **1990**, 171, 148-54	3.4	61
3	Potent selective inhibitors of protein kinase C. *FEBS Letters*, **1989**, 259, 61-3	3.8	410
2	The inhibitory profiles of hog pancreatic and human rheumatoid synovial cell phospholipases A2. *Agents and Actions*, **1986**, 17, 299-301		3
1	Capturing variation impact on molecular interactions: the IMEx Consortium mutations data set		1