

Erik Verschueren

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

3,221
citations

236925

25
h-index

377865

34
g-index

37
all docs

37
docs citations

37
times ranked

7651
citing authors

#	ARTICLE	IF	CITATIONS
1	The E3 ligase TRIM1 ubiquitinates LRRK2 and controls its localization, degradation, and toxicity. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	8
2	Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling. <i>Cell Reports</i> , 2022, 39, 110690.	6.4	12
3	Serum Lysophosphatidic Acid Measurement by Liquid Chromatography–Mass Spectrometry in COPD Patients. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1987-1997.	2.8	4
4	The neutrophil protein CD177 is a novel PDPN receptor that regulates human cancer-associated fibroblast physiology. <i>PLoS ONE</i> , 2021, 16, e0260800.	2.5	9
5	Structure of the essential inner membrane lipopolysaccharide–PbgA complex. <i>Nature</i> , 2020, 584, 479-483.	27.8	58
6	MassIVE.quant: a community resource of quantitative mass spectrometry–based proteomics datasets. <i>Nature Methods</i> , 2020, 17, 981-984.	19.0	66
7	The Immunoglobulin Superfamily Receptome Defines Cancer-Relevant Networks Associated with Clinical Outcome. <i>Cell</i> , 2020, 182, 329-344.e19.	28.9	66
8	A Quantitative Genetic Interaction Map of HIV Infection. <i>Molecular Cell</i> , 2020, 78, 197-209.e7.	9.7	17
9	Global site-specific neddylation profiling reveals that NEDDylated cofilin regulates actin dynamics. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 210-220.	8.2	61
10	Synthetic Essentiality of Metabolic Regulator PDHK1 in PTEN-Deficient Cells and Cancers. <i>Cell Reports</i> , 2019, 28, 2317-2330.e8.	6.4	12
11	PPAR γ 3 Interaction with UBR5/ATMIN Promotes DNA Repair to Maintain Endothelial Homeostasis. <i>Cell Reports</i> , 2019, 26, 1333-1343.e7.	6.4	54
12	The Gag protein PEG10 binds to RNA and regulates trophoblast stem cell lineage specification. <i>PLoS ONE</i> , 2019, 14, e0214110.	2.5	48
13	PTCD1 Is Required for Mitochondrial Oxidative-Phosphorylation: Possible Genetic Association with Alzheimer's Disease. <i>Journal of Neuroscience</i> , 2019, 39, 4636-4656.	3.6	26
14	Enterovirus pathogenesis requires the host methyltransferase SETD3. <i>Nature Microbiology</i> , 2019, 4, 2523-2537.	13.3	51
15	Selective autophagy of the adaptor TRIF regulates innate inflammatory signaling. <i>Nature Immunology</i> , 2018, 19, 246-254.	14.5	99
16	OTULIN limits cell death and inflammation by deubiquitinating LUBAC. <i>Nature</i> , 2018, 559, 120-124.	27.8	151
17	The mTOR Complex Controls HIV Latency. <i>Cell Host and Microbe</i> , 2016, 20, 785-797.	11.0	179
18	Non-degradative Ubiquitination of Protein Kinases. <i>PLoS Computational Biology</i> , 2016, 12, e1004898.	3.2	31

#	ARTICLE	IF	CITATIONS
19	Scoring Large-scale Affinity Purification Mass Spectrometry Datasets with MiST. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 8.19.1-8.19.16.	25.8	58
20	Meta- and Orthogonal Integration of Influenza α -OMICs Data Defines a Role for UBR4 in Virus Budding. <i>Cell Host and Microbe</i> , 2015, 18, 723-735.	11.0	868
21	Global Mapping of Herpesvirus-Host Protein Complexes Reveals a Transcription Strategy for Late Genes. <i>Molecular Cell</i> , 2015, 57, 349-360.	9.7	165
22	A Combined Proteomics/Genomics Approach Links Hepatitis C Virus Infection with Nonsense-Mediated mRNA Decay. <i>Molecular Cell</i> , 2015, 57, 329-340.	9.7	124
23	Global Mapping of the Inc-Human Interactome Reveals that Retromer Restricts Chlamydia Infection. <i>Cell Host and Microbe</i> , 2015, 18, 109-121.	11.0	174
24	Evolution of the SH3 Domain Specificity Landscape in Yeasts. <i>PLoS ONE</i> , 2015, 10, e0129229.	2.5	8
25	Pharmacological dimerization and activation of the exchange factor eIF2B antagonizes the integrated stress response. <i>ELife</i> , 2015, 4, e07314.	6.0	212
26	Affinity purification mass spectrometry and network analysis to understand protein-protein interactions. <i>Nature Protocols</i> , 2014, 9, 2539-2554.	12.0	169
27	Integration of Protein Abundance and Structure Data Reveals Competition in the ErbB Signaling Network. <i>Science Signaling</i> , 2013, 6, ra109.	3.6	48
28	Protein-Peptide Complex Prediction through Fragment Interaction Patterns. <i>Structure</i> , 2013, 21, 789-797.	3.3	59
29	The multiple specificity landscape of modular peptide recognition domains. <i>Molecular Systems Biology</i> , 2011, 7, 484.	7.2	78
30	Computational design of peptide ligands. <i>Trends in Biotechnology</i> , 2011, 29, 231-239.	9.3	146
31	Protein design with fragment databases. <i>Current Opinion in Structural Biology</i> , 2011, 21, 452-459.	5.7	32
32	BriX: a database of protein building blocks for structural analysis, modeling and design. <i>Nucleic Acids Research</i> , 2011, 39, D435-D442.	14.5	48
33	Modeling protein-peptide interactions using protein fragments: fitting the pieces?. <i>BMC Bioinformatics</i> , 2010, 11, .	2.6	1
34	Enhanced SnapShot: Macromolecular Machines. <i>Cell</i> , 2010, 143, 652-652.e1.	28.9	0
35	Protein-Peptide Interactions Adopt the Same Structural Motifs as Monomeric Protein Folds. <i>Structure</i> , 2009, 17, 1128-1136.	3.3	79