

# Ronald J Hause

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4899329/publications.pdf>

Version: 2024-02-01

24  
papers

2,574  
citations

516710

16  
h-index

552781

26  
g-index

28  
all docs

28  
docs citations

28  
times ranked

4896  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identifying Optimal Loci for the Molecular Diagnosis of Microsatellite Instability. <i>Clinical Chemistry</i> , 2020, 66, 1310-1318.	3.2	15
2	Anti- $\alpha$ B-cell Maturation Antigen Chimeric Antigen Receptor T cell Function against Multiple Myeloma Is Enhanced in the Presence of Lenalidomide. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 2246-2257.	4.1	61
3	Markers of Initial and Long-Term Responses to Idecabtagene Vicleucel (Ide-Cel; bb2121) in the CRB-401 Study in Relapsed/Refractory Multiple Myeloma. <i>Blood</i> , 2019, 134, 4328-4328.	1.4	3
4	Statistical Learning Approaches for Predicting Lisocabtagene Maraleucel (liso-cel) Drug Product Composition from Donor-Selected Material Composition. <i>Blood</i> , 2019, 134, 591-591.	1.4	4
5	Lisocabtagene Maraleucel (liso-cel) Manufacturing Process Control and Robustness across CD19+ Hematological Malignancies. <i>Blood</i> , 2019, 134, 593-593.	1.4	12
6	Accurate Pan-Cancer Molecular Diagnosis of Microsatellite Instability by Single-Molecule Molecular Inversion Probe Capture and High-Throughput Sequencing. <i>Clinical Chemistry</i> , 2018, 64, 950-958.	3.2	57
7	Quantitative Missense Variant Effect Prediction Using Large-Scale Mutagenesis Data. <i>Cell Systems</i> , 2018, 6, 116-124.e3.	6.2	176
8	Multiplex assessment of protein variant abundance by massively parallel sequencing. <i>Nature Genetics</i> , 2018, 50, 874-882.	21.4	323
9	Identification of Novel Protein Expression Changes Following Cisplatin Treatment and Application to Combination Therapy. <i>Journal of Proteome Research</i> , 2017, 16, 4227-4236.	3.7	3
10	Analysis of Large-Scale Mutagenesis Data To Assess the Impact of Single Amino Acid Substitutions. <i>Genetics</i> , 2017, 207, 53-61.	2.9	101
11	Genetic Variants Contributing to Colistin Cytotoxicity: Identification of TGIF1 and HOXD10 Using a Population Genomics Approach. <i>International Journal of Molecular Sciences</i> , 2017, 18, 661.	4.1	2
12	Mapping 3D genome architecture through in situ DNase Hi-C. <i>Nature Protocols</i> , 2016, 11, 2104-2121.	12.0	106
13	Classification and characterization of microsatellite instability across 18 cancer types. <i>Nature Medicine</i> , 2016, 22, 1342-1350.	30.7	726
14	Massively Parallel Functional Analysis of BRCA1 RING Domain Variants. <i>Genetics</i> , 2015, 200, 413-422.	2.9	272
15	Enhanced Prediction of Src Homology 2 (SH2) Domain Binding Potentials Using a Fluorescence Polarization-derived c-Met, c-Kit, ErbB, and Androgen Receptor Interactome. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1705-1723.	3.8	16
16	Protein Quantitative Trait Loci Identify Novel Candidates Modulating Cellular Response to Chemotherapy. <i>PLoS Genetics</i> , 2014, 10, e1004192.	3.5	29
17	Genetic Variation Meets Replication Origins. <i>Cell</i> , 2014, 159, 973-974.	28.9	2
18	Identification and Validation of Genetic Variants that Influence Transcription Factor and Cell Signaling Protein Levels. <i>American Journal of Human Genetics</i> , 2014, 95, 194-208.	6.2	54

#	ARTICLE	IF	CITATIONS
19	Saturation editing of genomic regions by multiplex homology-directed repair. <i>Nature</i> , 2014, 513, 120-123.	27.8	301
20	Investigating Models of Protein Function and Allostery With a Widespread Mutational Analysis of a Light-Activated Protein. <i>Biophysical Journal</i> , 2013, 105, 1027-1036.	0.5	48
21	Natural Genetic Variation for Growth and Development Revealed by High-Throughput Phenotyping in <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 29-34.	1.8	56
22	Caffeic Acid Phenethyl Ester Suppresses the Proliferation of Human Prostate Cancer Cells through Inhibition of p70S6K and Akt Signaling Networks. <i>Cancer Prevention Research</i> , 2012, 5, 788-797.	1.5	96
23	Comprehensive Binary Interaction Mapping of SH2 Domains via Fluorescence Polarization Reveals Novel Functional Diversification of ErbB Receptors. <i>PLoS ONE</i> , 2012, 7, e44471.	2.5	60
24	Targeted protein-omic methods are bridging the gap between proteomic and hypothesis-driven protein analysis approaches. <i>Expert Review of Proteomics</i> , 2011, 8, 565-575.	3.0	22