

# Hans W Hombauer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3401324/publications.pdf>

Version: 2024-02-01

19  
papers

1,291  
citations

566801

15  
h-index

794141

19  
g-index

19  
all docs

19  
docs citations

19  
times ranked

1898  
citing authors

#	ARTICLE	IF	CITATIONS
1	SRD5A3 Is Required for Converting Polyprenol to Dolichol and Is Mutated in a Congenital Glycosylation Disorder. <i>Cell</i> , 2010, 142, 203-217.	13.5	253
2	Visualization of Eukaryotic DNA Mismatch Repair Reveals Distinct Recognition and Repair Intermediates. <i>Cell</i> , 2011, 147, 1040-1053.	13.5	183
3	Mismatch Repair, But Not Heteroduplex Rejection, Is Temporally Coupled to DNA Replication. <i>Science</i> , 2011, 334, 1713-1716.	6.0	109
4	New insights into the mechanism of DNA mismatch repair. <i>Chromosoma</i> , 2015, 124, 443-462.	1.0	103
5	A novel and essential mechanism determining specificity and activity of protein phosphatase 2A (PP2A) in vivo. <i>Genes and Development</i> , 2003, 17, 2138-2150.	2.7	89
6	PCNA and Msh2-Msh6 Activate an Mlh1-Pms1 Endonuclease Pathway Required for Exo1-Independent Mismatch Repair. <i>Molecular Cell</i> , 2014, 55, 291-304.	4.5	89
7	Identification of a Subunit of a Novel Kleisin- $\hat{\nu}$ 2/SMC Complex as a Potential Substrate of Protein Phosphatase 2A. <i>Current Biology</i> , 2003, 13, 2058-2064.	1.8	84
8	Generation of Active Protein Phosphatase 2A Is Coupled to Holoenzyme Assembly. <i>PLoS Biology</i> , 2007, 5, e155.	2.6	74
9	Checkpoint Kinases Regulate a Global Network of Transcription Factors in Response to DNA Damage. <i>Cell Reports</i> , 2013, 4, 174-188.	2.9	61
10	Dominant Mutations in <i>S. cerevisiae</i> PMS1 Identify the Mlh1-Pms1 Endonuclease Active Site and an Exonuclease 1-Independent Mismatch Repair Pathway. <i>PLoS Genetics</i> , 2013, 9, e1003869.	1.5	52
11	Cdc28/Cdk1 positively and negatively affects genome stability in <i>S. cerevisiae</i> . <i>Journal of Cell Biology</i> , 2009, 185, 423-437.	2.3	37
12	Mlh2 Is an Accessory Factor for DNA Mismatch Repair in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2014, 10, e1004327.	1.5	36
13	Alterations in cellular metabolism triggered by <i>URA7</i> or <i>GLN3</i> inactivation cause imbalanced dNTP pools and increased mutagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4442-E4451.	3.3	30
14	Extensive 5' surveillance guards against non-canonical NAD-caps of nuclear mRNAs in yeast. <i>Nature Communications</i> , 2020, 11, 5508.	5.8	28
15	Ligation of newly replicated DNA controls the timing of DNA mismatch repair. <i>Current Biology</i> , 2021, 31, 1268-1276.e6.	1.8	19
16	Visualization of mismatch repair complexes using fluorescence microscopy. <i>DNA Repair</i> , 2016, 38, 58-67.	1.3	16
17	A genetic screen pinpoints ribonucleotide reductase residues that sustain dNTP homeostasis and specifies a highly mutagenic type of dNTP imbalance. <i>Nucleic Acids Research</i> , 2019, 47, 237-252.	6.5	16
18	Inactivation of folic/polyglutamate synthetase Met7 results in genome instability driven by an increased dUTP/dTTP ratio. <i>Nucleic Acids Research</i> , 2020, 48, 264-277.	6.5	7

#	ARTICLE	IF	CITATIONS
19	Identification of MLH2/hPMS1 dominant mutations that prevent DNA mismatch repair function. Communications Biology, 2020, 3, 751.	2.0	5