

# Marc Ruff

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/215937/marc-ruff-publications-by-year.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

57  
papers

5,161  
citations

27  
h-index

69  
g-index

69  
ext. papers

5,564  
ext. citations

9.1  
avg, IF

4.68  
L-index

#	Paper	IF	Citations
57	Modulation of the intrinsic chromatin binding property of HIV-1 integrase by LEDGF/p75. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 11241-11256	20.1	1
56	NKKNK: a New Essential Motif in the C-Terminal Domain of HIV-1 Group M Integrases. <i>Journal of Virology</i> , <b>2020</b> , 94,	6.6	2
55	Structural Basis for E. coli Penicillin Binding Protein (PBP) 2 Inhibition, a Platform for Drug Design. <i>Journal of Medicinal Chemistry</i> , <b>2019</b> , 62, 4742-4754	8.3	19
54	Human H4 tail stimulates HIV-1 integration through binding to the carboxy-terminal domain of integrase. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 3607-3618	20.1	6
53	HSPA8/HSC70 in Immune Disorders: A Molecular Rheostat that Adjusts Chaperone-Mediated Autophagy Substrates. <i>Cells</i> , <b>2019</b> , 8,	7.9	31
52	A Molecular Tool Targeting the Base-Flipping Activity of Human UHRF1. <i>Chemistry - A European Journal</i> , <b>2019</b> , 25, 13363-13375	4.8	2
51	Structure-function analyses unravel distinct effects of allosteric inhibitors of HIV-1 integrase on viral maturation and integration. <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 6172-6186	5.4	23
50	Unstable Protein Purification Through the Formation of Stable Complexes. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1764, 315-328	1.4	
49	Post-translational modifications in DNA topoisomerase 2 highlight the role of a eukaryote-specific residue in the ATPase domain. <i>Scientific Reports</i> , <b>2018</b> , 8, 9272	4.9	12
48	Dynamics of Methylated Cytosine Flipping by UHRF1. <i>Journal of the American Chemical Society</i> , <b>2017</b> , 139, 2520-2528	16.4	27
47	Modulation of chromatin structure by the FACT histone chaperone complex regulates HIV-1 integration. <i>Retrovirology</i> , <b>2017</b> , 14, 39	3.6	16
46	The HIV-1 integrase-LEDGF allosteric inhibitor MUT-A: resistance profile, impairment of virus maturation and infectivity but without influence on RNA packaging or virus immunoreactivity. <i>Retrovirology</i> , <b>2017</b> , 14, 50	3.6	14
45	Modulation of the functional association between the HIV-1 intasome and the nucleosome by histone amino-terminal tails. <i>Retrovirology</i> , <b>2017</b> , 14, 54	3.6	9
44	Production of unstable proteins through the formation of stable core complexes. <i>Nature Communications</i> , <b>2016</b> , 7, 10932	17.4	4
43	DNA minicircles clarify the specific role of DNA structure on retroviral integration. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 7830-47	20.1	12
42	Intasome architecture and chromatin density modulate retroviral integration into nucleosome. <i>Retrovirology</i> , <b>2015</b> , 12, 13	3.6	29
41	Site-Selective Monitoring of the Interaction of the SRA Domain of UHRF1 with Target DNA Sequences Labeled with 2-Aminopurine. <i>Biochemistry</i> , <b>2015</b> , 54, 6012-20	3.2	10

40	DNA Physical Properties and Nucleosome Positions Are Major Determinants of HIV-1 Integrase Selectivity. <i>PLoS ONE</i> , <b>2015</b> , 10, e0129427	3.7	15
39	Functional relationship between matrix metalloproteinase-11 and matrix metalloproteinase-14. <i>Cancer Medicine</i> , <b>2014</b> , 3, 1197-210	4.8	16
38	Structural and functional role of INI1 and LEDGF in the HIV-1 preintegration complex. <i>PLoS ONE</i> , <b>2013</b> , 8, e60734	3.7	18
37	Dual inhibition of HIV-1 replication by integrase-LEDGF allosteric inhibitors is predominant at the post-integration stage. <i>Retrovirology</i> , <b>2013</b> , 10, 144	3.6	88
36	HSPA8/HSC70 chaperone protein: structure, function, and chemical targeting. <i>Autophagy</i> , <b>2013</b> , 9, 1937-54.2	5.2	193
35	Expression of functional full-length hSRC-1 in eukaryotic cells using modified vaccinia virus Ankara and baculovirus. <i>Analytical Biochemistry</i> , <b>2012</b> , 426, 106-8	3.1	0
34	Structural basis for a molecular allosteric control mechanism of cofactor binding to nuclear receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, E588-94	11.5	62
33	Using Vaccinia's innate ability to introduce DNA into mammalian cells for production of recombinant proteins. <i>Journal of Biotechnology</i> , <b>2011</b> , 156, 211-3	3.7	6
32	Mutations affecting interaction of integrase with TNPO3 do not prevent HIV-1 cDNA nuclear import. <i>Retrovirology</i> , <b>2011</b> , 8, 104	3.6	28
31	Vectors for recombinational cloning and gene expression in mammalian cells using modified vaccinia virus Ankara. <i>Analytical Biochemistry</i> , <b>2010</b> , 404, 103-5	3.1	10
30	Structural basis for HIV-1 DNA integration in the human genome, role of the LEDGF/P75 cofactor. <i>EMBO Journal</i> , <b>2009</b> , 28, 980-91	13	83
29	Towards high-throughput identification of endocrine disrupting compounds with mass spectrometry. <i>Toxicology in Vitro</i> , <b>2009</b> , 23, 704-9	3.6	11
28	Structural basis for HIV-1 DNA integration in the human genome. <i>Retrovirology</i> , <b>2009</b> , 6, P79	3.6	1
27	Monitoring ligand modulation of protein-protein interactions by mass spectrometry: estrogen receptor alpha-SRC1. <i>Analytical Chemistry</i> , <b>2008</b> , 80, 7833-9	7.8	19
26	Identification of Endocrine-Disrupting Compounds Using Nano electrospray Ionization Mass Spectrometry. <i>Chimia</i> , <b>2008</b> , 62, 329-334	1.3	2
25	Cleaved thioredoxin fusion protein enables the crystallization of poorly soluble ERalpha in complex with synthetic ligands. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2008</b> , 64, 54-7		6
24	Estrogen receptor-ligand complexes measured by chip-based nano electrospray mass spectrometry: an approach for the screening of endocrine disruptors. <i>Protein Science</i> , <b>2007</b> , 16, 938-46	6.3	37
23	The impact of protein characterization in structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2006</b> , 62, 1125-36		51

22	Crystallization and preliminary crystallographic analysis of human glycosylated haemoglobin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2006</b> , 62, 106-9		6
21	Binding of estrogenic compounds to recombinant estrogen receptor-alpha: application to environmental analysis. <i>Environmental Health Perspectives</i> , <b>2005</b> , 113, 278-84	8.4	84
20	The dual role of CHAPS in the crystallization of stromelysin-3 catalytic domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 603-6		6
19	Different ligands-different receptor conformations: modeling of the hER alpha LBD in complex with agonists and antagonists. <i>Medicinal Research Reviews</i> , <b>2001</b> , 21, 523-39	14.4	31
18	Crystal structure of a mutant hERalpha ligand-binding domain reveals key structural features for the mechanism of partial agonism. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 15059-65	5.4	106
17	Overexpression, purification, and crystal structure of native ER alpha LBD. <i>Protein Expression and Purification</i> , <b>2001</b> , 22, 165-73	2	73
16	Crystal structure of the stromelysin-3 (MMP-11) catalytic domain complexed with a phosphinic inhibitor mimicking the transition-state. <i>Journal of Molecular Biology</i> , <b>2001</b> , 307, 577-86	6.5	88
15	Crystal structure of the human RXRalpha ligand-binding domain bound to its natural ligand: 9-cis retinoic acid. <i>EMBO Journal</i> , <b>2000</b> , 19, 2592-601	13	265
14	Estrogen receptor transcription and transactivation: Structure-function relationship in DNA- and ligand-binding domains of estrogen receptors. <i>Breast Cancer Research</i> , <b>2000</b> , 2, 353-9	8.3	91
13	Purification of active matrix metalloproteinase catalytic domains and its use for screening of specific stromelysin-3 inhibitors. <i>Protein Expression and Purification</i> , <b>1999</b> , 16, 76-83	2	29
12	Human TAF(II)28 and TAF(II)18 interact through a histone fold encoded by atypical evolutionary conserved motifs also found in the SPT3 family. <i>Cell</i> , <b>1998</b> , 94, 239-49	56.2	136
11	Purification of the human RARgamma ligand-binding domain and crystallization of its complex with all-trans retinoic acid. <i>Biochemical and Biophysical Research Communications</i> , <b>1997</b> , 230, 293-6	3.4	16
10	Crystallization of Escherichia coli aspartyl-tRNA synthetase in its free state and in a complex with yeast tRNA(Asp). <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1996</b> , 52, 211-4		6
9	Crystallization and preliminary X-ray analysis of Escherichia coli methionyl-tRNA(fMet) formyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1996</b> , 25, 139-41	4.2	8
8	Crystal structure of the ligand-binding domain of the human nuclear receptor RXR-alpha. <i>Nature</i> , <b>1995</b> , 375, 377-82	50.4	1062
7	Crystal structure of the RAR-gamma ligand-binding domain bound to all-trans retinoic acid. <i>Nature</i> , <b>1995</b> , 378, 681-9	50.4	1032
6	Purification, functional characterization, and crystallization of the ligand binding domain of the retinoid X receptor. <i>Protein Expression and Purification</i> , <b>1995</b> , 6, 604-8	2	28
5	The active site of yeast aspartyl-tRNA synthetase: structural and functional aspects of the aminoacylation reaction.. <i>EMBO Journal</i> , <b>1994</b> , 13, 327-337	13	179

- 4 Yeast tRNA(Asp) recognition by its cognate class II aminoacyl-tRNA synthetase. *Nature*, **1993**, 362, 181-450.4 290
- 3 Class II aminoacyl transfer RNA synthetases: crystal structure of yeast aspartyl-tRNA synthetase complexed with tRNA(Asp). *Science*, **1991**, 252, 1682-9 333 669
- 2 Preliminary X-ray investigation of 70 S ribosome crystals from *Thermus thermophilus*. *Journal of Molecular Biology*, **1989**, 209, 327-8 6.5 41
- 1 A high resolution diffracting crystal form of the complex between yeast tRNA<sup>Asp</sup> and aspartyl-tRNA synthetase. *Journal of Molecular Biology*, **1988**, 201, 235-6 6.5 51