

Marc Ruff

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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	Crystal structure of the ligand-binding domain of the human nuclear receptor RXR-alpha. <i>Nature</i> , 1995 , 375, 377-82	50.4	1062
56	Crystal structure of the RAR-gamma ligand-binding domain bound to all-trans retinoic acid. <i>Nature</i> , 1995 , 378, 681-9	50.4	1032
55	Class II aminoacyl transfer RNA synthetases: crystal structure of yeast aspartyl-tRNA synthetase complexed with tRNA(Asp). <i>Science</i> , 1991 , 252, 1682-9	33.3	669
54	Yeast tRNA(Asp) recognition by its cognate class II aminoacyl-tRNA synthetase. <i>Nature</i> , 1993 , 362, 181-4	50.4	290
53	Crystal structure of the human RXRalpha ligand-binding domain bound to its natural ligand: 9-cis retinoic acid. <i>EMBO Journal</i> , 2000 , 19, 2592-601	13	265
52	HSPA8/HSC70 chaperone protein: structure, function, and chemical targeting. <i>Autophagy</i> , 2013 , 9, 1937-54	54.2	193
51	The active site of yeast aspartyl-tRNA synthetase: structural and functional aspects of the aminoacylation reaction.. <i>EMBO Journal</i> , 1994 , 13, 327-337	13	179
50	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> , 1998 , 94, 239-49	56.2	136
49	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> , 2001 , 276, 15059-65	5.4	106
48	Estrogen receptor transcription and transactivation: Structure-function relationship in DNA- and ligand-binding domains of estrogen receptors. <i>Breast Cancer Research</i> , 2000 , 2, 353-9	8.3	91
47	Dual inhibition of HIV-1 replication by integrase-LEDGF allosteric inhibitors is predominant at the post-integration stage. <i>Retrovirology</i> , 2013 , 10, 144	3.6	88
46	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> , 2001 , 307, 577-86	6.5	88
45	Binding of estrogenic compounds to recombinant estrogen receptor-alpha: application to environmental analysis. <i>Environmental Health Perspectives</i> , 2005 , 113, 278-84	8.4	84
44	Structural basis for HIV-1 DNA integration in the human genome, role of the LEDGF/P75 cofactor. <i>EMBO Journal</i> , 2009 , 28, 980-91	13	83
43	Overexpression, purification, and crystal structure of native ER alpha LBD. <i>Protein Expression and Purification</i> , 2001 , 22, 165-73	2	73
42	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> , 2012 , 109, E588-94	11.5	62
41	The impact of protein characterization in structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1125-36		51

40	A high resolution diffracting crystal form of the complex between yeast tRNA ^{Asp} and aspartyl-tRNA synthetase. <i>Journal of Molecular Biology</i> , 1988 , 201, 235-6	6.5	51
39	Preliminary X-ray investigation of 70 S ribosome crystals from <i>Thermus thermophilus</i> . <i>Journal of Molecular Biology</i> , 1989 , 209, 327-8	6.5	41
38	Estrogen receptor-ligand complexes measured by chip-based nanoelectrospray mass spectrometry: an approach for the screening of endocrine disruptors. <i>Protein Science</i> , 2007 , 16, 938-46	6.3	37
37	HSPA8/HSC70 in Immune Disorders: A Molecular Rheostat that Adjusts Chaperone-Mediated Autophagy Substrates. <i>Cells</i> , 2019 , 8,	7.9	31
36	Different ligands-different receptor conformations: modeling of the hER alpha LBD in complex with agonists and antagonists. <i>Medicinal Research Reviews</i> , 2001 , 21, 523-39	14.4	31
35	Intasome architecture and chromatin density modulate retroviral integration into nucleosome. <i>Retrovirology</i> , 2015 , 12, 13	3.6	29
34	Purification of active matrix metalloproteinase catalytic domains and its use for screening of specific stromelysin-3 inhibitors. <i>Protein Expression and Purification</i> , 1999 , 16, 76-83	2	29
33	Mutations affecting interaction of integrase with TNPO3 do not prevent HIV-1 cDNA nuclear import. <i>Retrovirology</i> , 2011 , 8, 104	3.6	28
32	Purification, functional characterization, and crystallization of the ligand binding domain of the retinoid X receptor. <i>Protein Expression and Purification</i> , 1995 , 6, 604-8	2	28
31	Dynamics of Methylated Cytosine Flipping by UHRF1. <i>Journal of the American Chemical Society</i> , 2017 , 139, 2520-2528	16.4	27
30	Structure-function analyses unravel distinct effects of allosteric inhibitors of HIV-1 integrase on viral maturation and integration. <i>Journal of Biological Chemistry</i> , 2018 , 293, 6172-6186	5.4	23
29	Structural Basis for <i>E. coli</i> Penicillin Binding Protein (PBP) 2 Inhibition, a Platform for Drug Design. <i>Journal of Medicinal Chemistry</i> , 2019 , 62, 4742-4754	8.3	19
28	Monitoring ligand modulation of protein-protein interactions by mass spectrometry: estrogen receptor alpha-SRC1. <i>Analytical Chemistry</i> , 2008 , 80, 7833-9	7.8	19
27	Structural and functional role of IN1 and LEDGF in the HIV-1 preintegration complex. <i>PLoS ONE</i> , 2013 , 8, e60734	3.7	18
26	Modulation of chromatin structure by the FACT histone chaperone complex regulates HIV-1 integration. <i>Retrovirology</i> , 2017 , 14, 39	3.6	16
25	Functional relationship between matrix metalloproteinase-11 and matrix metalloproteinase-14. <i>Cancer Medicine</i> , 2014 , 3, 1197-210	4.8	16
24	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> , 1997 , 230, 293-6	3.4	16
23	DNA Physical Properties and Nucleosome Positions Are Major Determinants of HIV-1 Integrase Selectivity. <i>PLoS ONE</i> , 2015 , 10, e0129427	3.7	15

22	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> , 2017 , 14, 50	3.6	14
21	Post-translational modifications in DNA topoisomerase 2 highlight the role of a eukaryote-specific residue in the ATPase domain. <i>Scientific Reports</i> , 2018 , 8, 9272	4.9	12
20	DNA minicircles clarify the specific role of DNA structure on retroviral integration. <i>Nucleic Acids Research</i> , 2016 , 44, 7830-47	20.1	12
19	Towards high-throughput identification of endocrine disrupting compounds with mass spectrometry. <i>Toxicology in Vitro</i> , 2009 , 23, 704-9	3.6	11
18	Site-Selective Monitoring of the Interaction of the SRA Domain of UHRF1 with Target DNA Sequences Labeled with 2-Aminopurine. <i>Biochemistry</i> , 2015 , 54, 6012-20	3.2	10
17	Vectors for recombinational cloning and gene expression in mammalian cells using modified vaccinia virus Ankara. <i>Analytical Biochemistry</i> , 2010 , 404, 103-5	3.1	10
16	Modulation of the functional association between the HIV-1 intasome and the nucleosome by histone amino-terminal tails. <i>Retrovirology</i> , 2017 , 14, 54	3.6	9
15	Crystallization and preliminary X-ray analysis of Escherichia coli methionyl-tRNA(fMet) formyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 139-41	4.2	8
14	Human H4 tail stimulates HIV-1 integration through binding to the carboxy-terminal domain of integrase. <i>Nucleic Acids Research</i> , 2019 , 47, 3607-3618	20.1	6
13	Using Vaccinia's innate ability to introduce DNA into mammalian cells for production of recombinant proteins. <i>Journal of Biotechnology</i> , 2011 , 156, 211-3	3.7	6
12	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> , 2008 , 64, 54-7		6
11	Crystallization and preliminary crystallographic analysis of human glycosylated haemoglobin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 106-9		6
10	The dual role of CHAPS in the crystallization of stromelysin-3 catalytic domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 603-6		6
9	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> , 1996 , 52, 211-4		6
8	Production of unstable proteins through the formation of stable core complexes. <i>Nature Communications</i> , 2016 , 7, 10932	17.4	4
7	A Molecular Tool Targeting the Base-Flipping Activity of Human UHRF1. <i>Chemistry - A European Journal</i> , 2019 , 25, 13363-13375	4.8	2
6	Identification of Endocrine-Disrupting Compounds Using Nanoelectrospray Ionization Mass Spectrometry. <i>Chimia</i> , 2008 , 62, 329-334	1.3	2
5	NKNK: a New Essential Motif in the C-Terminal Domain of HIV-1 Group M Integrases. <i>Journal of Virology</i> , 2020 , 94,	6.6	2

4	Structural basis for HIV-1 DNA integration in the human genome. <i>Retrovirology</i> , 2009 , 6, P79	3.6	1
3	Modulation of the intrinsic chromatin binding property of HIV-1 integrase by LEDGF/p75. <i>Nucleic Acids Research</i> , 2021 , 49, 11241-11256	20.1	1
2	Expression of functional full-length hSRC-1 in eukaryotic cells using modified vaccinia virus Ankara and baculovirus. <i>Analytical Biochemistry</i> , 2012 , 426, 106-8	3.1	0
1	Unstable Protein Purification Through the Formation of Stable Complexes. <i>Methods in Molecular Biology</i> , 2018 , 1764, 315-328	1.4	