

# Christophe Romier

## List of Publications by Year in descending order

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80  
papers

4,175  
citations

101384

36  
h-index

123241

61  
g-index

83  
all docs

83  
docs citations

83  
times ranked

5092  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence-Specific Transcription Factor NF-Y Displays Histone-like DNA Binding and H2B-like Ubiquitination. <i>Cell</i> , 2013, 152, 132-143.	13.5	249
2	The NF-YB/NF-YC Structure Gives Insight into DNA Binding and Transcription Regulation by CCAAT Factor NF-Y. <i>Journal of Biological Chemistry</i> , 2003, 278, 1336-1345.	1.6	239
3	ANP32E is a histone chaperone that removes H2A.Z from chromatin. <i>Nature</i> , 2014, 505, 648-653.	13.7	217
4	HDAC8: a multifaceted target for therapeutic interventions. <i>Trends in Pharmacological Sciences</i> , 2015, 36, 481-492.	4.0	210
5	Human TAFII28 and TAFII18 Interact through a Histone Fold Encoded by Atypical Evolutionary Conserved Motifs Also Found in the SPT3 Family. <i>Cell</i> , 1998, 94, 239-249.	13.5	149
6	Structural Basis for the Inhibition of Histone Deacetylase 8 (HDAC8), a Key Epigenetic Player in the Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003645.	2.1	136
7	The histone fold is a key structural motif of transcription factor TFIID. <i>Trends in Biochemical Sciences</i> , 2001, 26, 250-257.	3.7	127
8	Deciphering correct strategies for multiprotein complex assembly by co-expression: Application to complexes as large as the histone octamer. <i>Journal of Structural Biology</i> , 2011, 175, 178-188.	1.3	116
9	Co-expression of protein complexes in prokaryotic and eukaryotic hosts: experimental procedures, database tracking and case studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1232-1242.	2.5	113
10	Structure-Based Design and Synthesis of Novel Inhibitors Targeting HDAC8 from <i>Schistosoma mansoni</i> for the Treatment of Schistosomiasis. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 2423-2435.	2.9	107
11	Recognition of single-stranded DNA by nuclease P1: High resolution crystal structures of complexes with substrate analogs. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 32, 414-424.	1.5	101
12	Automated unrestricted multigene recombineering for multiprotein complex production. <i>Nature Methods</i> , 2009, 6, 447-450.	9.0	98
13	Robots, pipelines, polyproteins: Enabling multiprotein expression in prokaryotic and eukaryotic cells. <i>Journal of Structural Biology</i> , 2011, 175, 198-208.	1.3	92
14	Synthesis and Biological Investigation of Oxazole Hydroxamates as Highly Selective Histone Deacetylase 6 (HDAC6) Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 1545-1555.	2.9	90
15	The Human TFIID Components TAF <sub>II</sub> 135 and TAF <sub>II</sub> 20 and the Yeast SAGA Components ADA1 and TAF <sub>II</sub> 68 Heterodimerize to Form Histone-Like Pairs. <i>Molecular and Cellular Biology</i> , 2000, 20, 340-351.	1.1	86
16	Characterization of Histone Deacetylase 8 (HDAC8) Selective Inhibition Reveals Specific Active Site Structural and Functional Determinants. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 10000-10016.	2.9	81
17	Synthesis and Biological Investigation of Phenothiazine-Based Benzhydroxamic Acids as Selective Histone Deacetylase 6 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 1138-1166.	2.9	75
18	Zinc-finger UBPs: regulators of deubiquitylation. <i>Trends in Biochemical Sciences</i> , 2008, 33, 369-375.	3.7	71

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19	The Human SPT20-Containing SAGA Complex Plays a Direct Role in the Regulation of Endoplasmic Reticulum Stress-Induced Genes. <i>Molecular and Cellular Biology</i> , 2009, 29, 1649-1660.	1.1	71
20	Molecular basis and specificity of H2A.Z-H2B recognition and deposition by the histone chaperone YL1. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 309-316.	3.6	67
21	Histone Folds Mediate Selective Heterodimerization of Yeast TAF II 25 with TFIID Components yTAF II 47 and yTAF II 65 and with SAGA Component ySPT7. <i>Molecular and Cellular Biology</i> , 2001, 21, 1841-1853.	1.1	66
22	Dissecting the interaction network of multiprotein complexes by pairwise coexpression of subunits in <i>E. coli</i> Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 2001, 306, 363-373.	2.0	64
23	The TFIID Components Human TAF II 140 and Drosophila BIP2 (TAF II 155) Are Novel Metazoan Homologues of Yeast TAF II 47 Containing a Histone Fold and a PHD Finger. <i>Molecular and Cellular Biology</i> , 2001, 21, 5109-5121.	1.1	62
24	NF-Y Recruitment of TFIID, Multiple Interactions with Histone Fold TAFIIs. <i>Journal of Biological Chemistry</i> , 2002, 277, 5841-5848.	1.6	62
25	Molecular Basis for the Antiparasitic Activity of a Mercaptoacetamide Derivative That Inhibits Histone Deacetylase 8 (HDAC8) from the Human Pathogen <i>Schistosoma mansoni</i> . <i>Journal of Molecular Biology</i> , 2014, 426, 3442-3453.	2.0	60
26	The structure of an Iws1/Spt6 complex reveals an interaction domain conserved in TFIIS, Elongin A and Med26. <i>EMBO Journal</i> , 2010, 29, 3979-3991.	3.5	58
27	Discovery of Inhibitors of <i>Schistosoma mansoni</i> HDAC8 by Combining Homology Modeling, Virtual Screening, and in Vitro Validation. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 3005-3019.	2.5	58
28	Crystal Structure of a Subcomplex of Human Transcription Factor TFIID Formed by TATA Binding Protein-associated Factors hTAF4 (hTAFII135) and hTAF12 (hTAFII20). <i>Journal of Biological Chemistry</i> , 2002, 277, 45502-45509.	1.6	56
29	Structure-Based Design and Biological Characterization of Selective Histone Deacetylase 8 (HDAC8) Inhibitors with Anti-Neuroblastoma Activity. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 10188-10204.	2.9	56
30	Mutagenesis and Crystallographic Studies of <i>Zymomonas mobilis</i> RNA-Guanine Transglycosylase Reveal Aspartate 102 as the Active Site Nucleophile. <i>Biochemistry</i> , 1996, 35, 15734-15739.	1.2	52
31	Noncanonical Tandem SH2 Enables Interaction of Elongation Factor Spt6 with RNA Polymerase II. <i>Journal of Biological Chemistry</i> , 2010, 285, 38389-38398.	1.6	52
32	Solution structure of human corticotropin releasing factor by 1H NMR and distance geometry with restrained molecular dynamics. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 149-156.	1.0	43
33	Slight sequence variations of a common fold explain the substrate specificities of tRNA-guanine transglycosylases from the three kingdoms. <i>FEBS Letters</i> , 1997, 416, 93-98.	1.3	42
34	Expression of protein complexes using multiple <i>Escherichia coli</i> protein co-expression systems: A benchmarking study. <i>Journal of Structural Biology</i> , 2011, 175, 159-170.	1.3	39
35	Homology modeling of parasite histone deacetylases to guide the structure-based design of selective inhibitors. <i>Journal of Molecular Graphics and Modelling</i> , 2015, 62, 342-361.	1.3	39
36	Novel spiroindoline HDAC inhibitors: Synthesis, molecular modelling and biological studies. <i>European Journal of Medicinal Chemistry</i> , 2018, 157, 127-138.	2.6	39

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37	Expression in <i>Escherichia coli</i> : becoming faster and more complex. <i>Current Opinion in Structural Biology</i> , 2013, 23, 326-334.	2.6	37
38	Alkoxyurea-Based Histone Deacetylase Inhibitors Increase Cisplatin Potency in Chemoresistant Cancer Cell Lines. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 5334-5348.	2.9	37
39	A Novel Class of <i>Schistosoma mansoni</i> Histone Deacetylase 8 (HDAC8) Inhibitors Identified by Structure-Based Virtual Screening and In Vitro Testing. <i>Molecules</i> , 2018, 23, 566.	1.7	37
40	TAF4, a subunit of transcription factor II D, directs promoter occupancy of nuclear receptor HNF4A during post-natal hepatocyte differentiation. <i>ELife</i> , 2014, 3, e03613.	2.8	35
41	Characterization of the interaction between protein Snu13p/15.5K and the Rsa1p/NUFIP factor and demonstration of its functional importance for snoRNP assembly. <i>Nucleic Acids Research</i> , 2014, 42, 2015-2036.	6.5	34
42	Purification, crystallization, and preliminary X-ray diffraction studies of tRNA-guanine transglycosylase from <i>Zymomonas mobilis</i> . , 1996, 24, 516-519.		33
43	Assembly of Protein Complexes by Coexpression in Prokaryotic and Eukaryotic Hosts: an Overview. <i>Methods in Molecular Biology</i> , 2008, 426, 247-256.	0.4	33
44	Design, Multicomponent Synthesis, and Anticancer Activity of a Focused Histone Deacetylase (HDAC) Inhibitor Library with Peptoid-Based Cap Groups. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 5493-5506.	2.9	32
45	The structural plasticity of SCA7 domains defines their differential nucleosome binding properties. <i>EMBO Reports</i> , 2010, 11, 612-618.	2.0	28
46	Synthesis, Molecular Docking and Biological Characterization of Pyrazine Linked 2-Aminobenzamides as New Class I Selective Histone Deacetylase (HDAC) Inhibitors with Anti-Leukemic Activity. <i>International Journal of Molecular Sciences</i> , 2022, 23, 369.	1.8	28
47	Citrullination of pyruvate kinase M2 by PADI1 and PADI3 regulates glycolysis and cancer cell proliferation. <i>Nature Communications</i> , 2021, 12, 1718.	5.8	27
48	TFIID TAF6-TAF9 Complex Formation Involves the HEAT Repeat-containing C-terminal Domain of TAF6 and Is Modulated by TAF5 Protein. <i>Journal of Biological Chemistry</i> , 2012, 287, 27580-27592.	1.6	26
49	Functional Analysis of the TFIID-specific Yeast TAF4 (yTAFII48) Reveals an Unexpected Organization of Its Histone-fold Domain. <i>Journal of Biological Chemistry</i> , 2002, 277, 45510-45517.	1.6	25
50	Synergistic Transcriptional Activation by TATA-Binding Protein and hTAF <sub>II</sub> 28 Requires Specific Amino Acids of the hTAF <sub>II</sub> 28 Histone Fold. <i>Molecular and Cellular Biology</i> , 1999, 19, 5050-5060.	1.1	23
51	One-Atom Substitution Enables Direct and Continuous Monitoring of Histone Deacetylase Activity. <i>Biochemistry</i> , 2019, 58, 4777-4789.	1.2	23
52	Drugging the schistosome zinc-dependent HDACs: current progress and future perspectives. <i>Future Medicinal Chemistry</i> , 2015, 7, 783-800.	1.1	22
53	Histone deacetylase inhibition modulates histone acetylation at gene promoter regions and affects genome-wide gene transcription in <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005539.	1.3	22
54	Crystal Structure, Biochemical and Genetic Characterization of Yeast and <i>E. cuniculi</i> TAFII5 N-terminal Domain: Implications for TFIID Assembly. <i>Journal of Molecular Biology</i> , 2007, 368, 1292-1306.	2.0	21

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55	DNA Binding by Sgf11 Protein Affects Histone H2B Deubiquitination by Spt-Ada-Gcn5-Acetyltransferase (SAGA). <i>Journal of Biological Chemistry</i> , 2014, 289, 8989-8999.	1.6	21
56	Synthesis, Crystallization Studies, and in vitro Characterization of Cinnamic Acid Derivatives as HDAC8 Inhibitors for the Treatment of Schistosomiasis. <i>ChemMedChem</i> , 2018, 13, 1517-1529.	1.6	21
57	Schistosome sirtuins as drug targets. <i>Future Medicinal Chemistry</i> , 2015, 7, 765-782.	1.1	19
58	Fluorescence-Based Screening Assays for the NAD <sup>+</sup> -Dependent Histone Deacetylase smSirt2 from <i>Schistosoma mansoni</i> . <i>Journal of Biomolecular Screening</i> , 2015, 20, 112-121.	2.6	18
59	Structure-Activity Relationships on Substrates and Inhibitors of the Lysine Deacylase Sirtuin 2 from <i>Schistosoma mansoni</i> (smSirt2). <i>Journal of Medicinal Chemistry</i> , 2019, 62, 8733-8759.	2.9	18
60	Structure-Based Design, Synthesis, and Biological Evaluation of Triazole-Based smHDAC8 Inhibitors. <i>ChemMedChem</i> , 2020, 15, 571-584.	1.6	18
61	The structure of the mouse ADAT2/ADAT3 complex reveals the molecular basis for mammalian tRNA wobble adenosine-to-inosine deamination. <i>Nucleic Acids Research</i> , 2021, 49, 6529-6548.	6.5	18
62	Design, synthesis, and biological evaluation of dual targeting inhibitors of histone deacetylase 6/8 and bromodomain BRPF1. <i>European Journal of Medicinal Chemistry</i> , 2020, 200, 112338.	2.6	17
63	Baculovirus VP1054 Is an Acquired Cellular Protein, a Nucleic Acid-Binding Protein Specific for GGN Repeats. <i>Journal of Virology</i> , 2013, 87, 8465-8480.	1.5	16
64	Isophthalic Acid-Based HDAC Inhibitors as Potent Inhibitors of HDAC8 from <i>Schistosoma mansoni</i> . <i>Archiv Der Pharmazie</i> , 2017, 350, 1700096.	2.1	16
65	Identification of histone deacetylase 10 (HDAC10) inhibitors that modulate autophagy in transformed cells. <i>European Journal of Medicinal Chemistry</i> , 2022, 234, 114272.	2.6	15
66	Design, Synthesis and Biological Characterization of Histone Deacetylase 8 (HDAC8) Proteolysis Targeting Chimeras (PROTACs) with Anti-Neuroblastoma Activity. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7535.	1.8	15
67	Characterization and Production of Protein Complexes by Co-expression in <i>Escherichia coli</i> . <i>Methods in Molecular Biology</i> , 2015, 1261, 63-89.	0.4	14
68	Strategies for bacterial expression of protein-peptide complexes: Application to solubilization of papillomavirus E6. <i>Protein Expression and Purification</i> , 2011, 80, 8-16.	0.6	11
69	Binding Free Energy (BFE) Calculations and Quantitative Structure-Activity Relationship (QSAR) Analysis of <i>Schistosoma mansoni</i> Histone Deacetylase 8 (smHDAC8) Inhibitors. <i>Molecules</i> , 2021, 26, 2584.	1.7	10
70	Species-selective targeting of pathogens revealed by the atypical structure and active site of <i>Trypanosoma cruzi</i> histone deacetylase DAC2. <i>Cell Reports</i> , 2021, 37, 110129.	2.9	10
71	First Fluorescent Acetylspermidine Deacetylation Assay for HDAC10 Identifies Selective Inhibitors with Cellular Target Engagement**. <i>ChemBioChem</i> , 2022, 23, .	1.3	9
72	Hydroxamates of para-aminobenzoic acid as selective inhibitors of HDAC8. <i>Bioorganic Chemistry</i> , 2014, 57, 116-120.	2.0	8

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73	Synthesis, structure-activity relationships, cocrystallization and cellular characterization of novel smHDAC8 inhibitors for the treatment of schistosomiasis. <i>European Journal of Medicinal Chemistry</i> , 2021, 225, 113745.	2.6	7
74	Isoform-selective HDAC1/6/8 inhibitors with an imidazo-ketopiperazine cap containing stereochemical diversity. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170364.	1.8	6
75	Sequence and structure requirements for specific recognition of HIV-1 TAR and DIS RNA by the HIV-1 Vif protein. <i>RNA Biology</i> , 2012, 9, 966-977.	1.5	5
76	Complex Reconstitution and Characterization by Combining Co-expression Techniques in <i>Escherichia coli</i> with High-Throughput. <i>Advances in Experimental Medicine and Biology</i> , 2016, 896, 43-58.	0.8	5
77	Large-Scale Overproduction and Purification of Recombinant Histone Deacetylase 8 (HDAC8) from the Human-Pathogenic Flatworm <i>Schistosoma mansoni</i> . <i>Methods in Molecular Biology</i> , 2016, 1436, 109-118.	0.4	3
78	Crystallization and preliminary crystallographic analysis of eukaryotic transcription and mRNA export factor <i>lws1</i> from <i>Encephalitozoon cuniculi</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 207-210.	0.7	2
79	Efficient CRISPR-Cas9-mediated genome editing for characterization of essential genes in <i>Trypanosoma cruzi</i> . <i>STAR Protocols</i> , 2022, 3, 101324.	0.5	2
80	Structural Basis of Base Exchange by tRNA-Guanine Transglycosylases. , 2014, , 169-182.		1