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	Identification of histone deacetylase 10 (HDAC10) inhibitors that modulate autophagy in transformed cells. European Journal of Medicinal Chemistry, 2022, 234, 114272.	2.6	15
2	Synthesis, Molecular Docking and Biological Characterization of Pyrazine Linked 2-Aminobenzamides as New Class I Selective Histone Deacetylase (HDAC) Inhibitors with Anti-Leukemic Activity. International Journal of Molecular Sciences, 2022, 23, 369.	1.8	28
3	Efficient CRISPR-Cas9-mediated genome editing for characterization of essential genes in Trypanosoma cruzi. STAR Protocols, 2022, 3, 101324.	0.5	2
4	First Fluorescent Acetylspermidine Deacetylation Assay for HDAC10 Identifies Selective Inhibitors with Cellular Target Engagement**. ChemBioChem, 2022, 23, .	1.3	9
5	Design, Synthesis and Biological Characterization of Histone Deacetylase 8 (HDAC8) Proteolysis Targeting Chimeras (PROTACs) with Anti-Neuroblastoma Activity. International Journal of Molecular Sciences, 2022, 23, 7535.	1.8	15
6	Citrullination of pyruvate kinase M2 by PADI1 and PADI3 regulates glycolysis and cancer cell proliferation. Nature Communications, 2021, 12, 1718.	5.8	27
7	Binding Free Energy (BFE) Calculations and Quantitative Structureâ€“Activity Relationship (QSAR) Analysis of Schistosoma mansoni Histone Deacetylase 8 (smHDAC8) Inhibitors. Molecules, 2021, 26, 2584.	1.7	10
8	The structure of the mouse ADAT2/ADAT3 complex reveals the molecular basis for mammalian tRNA wobble adenosine-to-inosine deamination. Nucleic Acids Research, 2021, 49, 6529-6548.	6.5	18
9	Synthesis, structure-activity relationships, cocrystallization and cellular characterization of novel smHDAC8 inhibitors for the treatment of schistosomiasis. European Journal of Medicinal Chemistry, 2021, 225, 113745.	2.6	7
10	Species-selective targeting of pathogens revealed by the atypical structure and active site of Trypanosoma cruzi histone deacetylase DAC2. Cell Reports, 2021, 37, 110129.	2.9	10
11	Structureâ€Based Design, Synthesis, and Biological Evaluation of Triazoleâ€Based smHDAC8 Inhibitors. ChemMedChem, 2020, 15, 571-584.	1.6	18
12	Design, synthesis, and biological evaluation of dual targeting inhibitors of histone deacetylase 6/8 and bromodomain BRPF1. European Journal of Medicinal Chemistry, 2020, 200, 112338.	2.6	17
13	One-Atom Substitution Enables Direct and Continuous Monitoring of Histone Deacylase Activity. Biochemistry, 2019, 58, 4777-4789.	1.2	23
14	Structureâ€“Reactivity Relationships on Substrates and Inhibitors of the Lysine Deacylase Sirtuin 2 from Schistosoma mansoni (SmSirt2). Journal of Medicinal Chemistry, 2019, 62, 8733-8759.	2.9	18
15	Synthesis and Biological Investigation of Phenothiazine-Based Benzhydroxamic Acids as Selective Histone Deacetylase 6 Inhibitors. Journal of Medicinal Chemistry, 2019, 62, 1138-1166.	2.9	75
16	Isoform-selective HDAC1/6/8 inhibitors with an imidazo-ketopiperazine cap containing stereochemical diversity. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170364.	1.8	6
17	Characterization of Histone Deacetylase 8 (HDAC8) Selective Inhibition Reveals Specific Active Site Structural and Functional Determinants. Journal of Medicinal Chemistry, 2018, 61, 10000-10016.	2.9	81
18	Synthesis, Crystallization Studies, and in vitro Characterization of Cinnamic Acid Derivatives as SmHDAC8 Inhibitors for the Treatment of Schistosomiasis. ChemMedChem, 2018, 13, 1517-1529.	1.6	21

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19	Novel spiroindoline HDAC inhibitors: Synthesis, molecular modelling and biological studies. European Journal of Medicinal Chemistry, 2018, 157, 127-138.	2.6	39
20	A Novel Class of Schistosoma mansoni Histone Deacetylase 8 (HDAC8) Inhibitors Identified by Structure-Based Virtual Screening and In Vitro Testing. Molecules, 2018, 23, 566.	1.7	37
21	Design, Multicomponent Synthesis, and Anticancer Activity of a Focused Histone Deacetylase (HDAC) Inhibitor Library with Peptoid-Based Cap Groups. Journal of Medicinal Chemistry, 2017, 60, 5493-5506.	2.9	32
22	Structure-Based Design and Biological Characterization of Selective Histone Deacetylase 8 (HDAC8) Inhibitors with Anti-Neuroblastoma Activity. Journal of Medicinal Chemistry, 2017, 60, 10188-10204.	2.9	56
23	Isophthalic Acidâ€Based HDAC Inhibitors as Potent Inhibitors of HDAC8 from Schistosoma mansoni. Archiv Der Pharmazie, 2017, 350, 1700096.	2.1	16
24	Alkoxyurea-Based Histone Deacetylase Inhibitors Increase Cisplatin Potency in Chemoresistant Cancer Cell Lines. Journal of Medicinal Chemistry, 2017, 60, 5334-5348.	2.9	37
25	Histone deacetylase inhibition modulates histone acetylation at gene promoter regions and affects genome-wide gene transcription in Schistosoma mansoni. PLoS Neglected Tropical Diseases, 2017, 11, e0005539.	1.3	22
26	Complex Reconstitution and Characterization by Combining Co-expression Techniques in Escherichia coli with High-Throughput. Advances in Experimental Medicine and Biology, 2016, 896, 43-58.	0.8	5
27	Large-Scale Overproduction and Purification of Recombinant Histone Deacetylase 8 (HDAC8) from the Human-Pathogenic Flatworm Schistosoma mansoni. Methods in Molecular Biology, 2016, 1436, 109-118.	0.4	3
28	Synthesis and Biological Investigation of Oxazole Hydroxamates as Highly Selective Histone Deacetylase 6 (HDAC6) Inhibitors. Journal of Medicinal Chemistry, 2016, 59, 1545-1555.	2.9	90
29	Structure-Based Design and Synthesis of Novel Inhibitors Targeting HDAC8 from Schistosoma mansoni for the Treatment of Schistosomiasis. Journal of Medicinal Chemistry, 2016, 59, 2423-2435.	2.9	107
30	Molecular basis and specificity of H2A.Zâ€“H2B recognition and deposition by the histone chaperone YL1. Nature Structural and Molecular Biology, 2016, 23, 309-316.	3.6	67
31	HDAC8: a multifaceted target for therapeutic interventions. Trends in Pharmacological Sciences, 2015, 36, 481-492.	4.0	210
32	Fluorescence-Based Screening Assays for the NAD+-Dependent Histone Deacetylase smSirt2 from Schistosoma mansoni. Journal of Biomolecular Screening, 2015, 20, 112-121.	2.6	18
33	Homology modeling of parasite histone deacetylases to guide the structure-based design of selective inhibitors. Journal of Molecular Graphics and Modelling, 2015, 62, 342-361.	1.3	39
34	Schistosome sirtuins as drug targets. Future Medicinal Chemistry, 2015, 7, 765-782.	1.1	19
35	Drugging the schistosome zinc-dependent HDACs: current progress and future perspectives. Future Medicinal Chemistry, 2015, 7, 783-800.	1.1	22
36	Characterization and Production of Protein Complexes by Co-expression in Escherichia coli. Methods in Molecular Biology, 2015, 1261, 63-89.	0.4	14

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37	Structural Basis of Base Exchange by tRNA-Guanine Transglycosylases. , 2014, , 169-182.		1
38	Characterization of the interaction between protein Snu13p/15.5K and the Rsa1p/NUFIP factor and demonstration of its functional importance for snoRNP assembly. Nucleic Acids Research, 2014, 42, 2015-2036.	6.5	34
39	Molecular Basis for the Antiparasitic Activity of a Mercaptoacetamide Derivative That Inhibits Histone Deacetylase 8 (HDAC8) from the Human Pathogen Schistosoma mansoni. Journal of Molecular Biology, 2014, 426, 3442-3453.	2.0	60
40	ANP32E is a histone chaperone that removes H2A.Z from chromatin. Nature, 2014, 505, 648-653.	13.7	217
41	Discovery of Inhibitors of Schistosoma mansoni HDAC8 by Combining Homology Modeling, Virtual Screening, and in Vitro Validation. Journal of Chemical Information and Modeling, 2014, 54, 3005-3019.	2.5	58
42	Hydroxamates of para-aminobenzoic acid as selective inhibitors of HDAC8. Bioorganic Chemistry, 2014, 57, 116-120.	2.0	8
43	DNA Binding by Sgf11 Protein Affects Histone H2B Deubiquitination by Spt-Ada-Gcn5-Acetyltransferase (SAGA). Journal of Biological Chemistry, 2014, 289, 8989-8999.	1.6	21
44	TAF4, a subunit of transcription factor II D, directs promoter occupancy of nuclear receptor HNF4A during post-natal hepatocyte differentiation. ELife, 2014, 3, e03613.	2.8	35
45	Expression in Escherichia coli: becoming faster and more complex. Current Opinion in Structural Biology, 2013, 23, 326-334.	2.6	37
46	Sequence-Specific Transcription Factor NF-Y Displays Histone-like DNA Binding and H2B-like Ubiquitination. Cell, 2013, 152, 132-143.	13.5	249
47	Structural Basis for the Inhibition of Histone Deacetylase 8 (HDAC8), a Key Epigenetic Player in the Blood Fluke Schistosoma mansoni. PLoS Pathogens, 2013, 9, e1003645.	2.1	136
48	Baculovirus VP1054 Is an Acquired Cellular PURÎ±, a Nucleic Acid-Binding Protein Specific for GGN Repeats. Journal of Virology, 2013, 87, 8465-8480.	1.5	16
49	Sequence and structure requirements for specific recognition of HIV-1 TAR and DIS RNA by the HIV-1 Vif protein. RNA Biology, 2012, 9, 966-977.	1.5	5
50	TFIID TAF6-TAF9 Complex Formation Involves the HEAT Repeat-containing C-terminal Domain of TAF6 and Is Modulated by TAF5 Protein. Journal of Biological Chemistry, 2012, 287, 27580-27592.	1.6	26
51	Deciphering correct strategies for multiprotein complex assembly by co-expression: Application to complexes as large as the histone octamer. Journal of Structural Biology, 2011, 175, 178-188.	1.3	116
52	Expression of protein complexes using multiple Escherichia coli protein co-expression systems: A benchmarking study. Journal of Structural Biology, 2011, 175, 159-170.	1.3	39
53	Robots, pipelines, polyproteins: Enabling multiprotein expression in prokaryotic and eukaryotic cells. Journal of Structural Biology, 2011, 175, 198-208.	1.3	92
54	Strategies for bacterial expression of proteinâ€“peptide complexes: Application to solubilization of papillomavirus E6. Protein Expression and Purification, 2011, 80, 8-16.	0.6	11

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55	Crystallization and preliminary crystallographic analysis of eukaryotic transcription and mRNA export factor Iws1 fromEncephalitozoon cuniculi. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 207-210.	0.7	2
56	The structure of an Iws1/Spt6 complex reveals an interaction domain conserved in TFIIS, Elongin A and Med26. EMBO Journal, 2010, 29, 3979-3991.	3.5	58
57	The structural plasticity of SCA7 domains defines their differential nucleosomeâ€binding properties. EMBO Reports, 2010, 11, 612-618.	2.0	28
58	Noncanonical Tandem SH2 Enables Interaction of Elongation Factor Spt6 with RNA Polymerase II. Journal of Biological Chemistry, 2010, 285, 38389-38398.	1.6	52
59	The Human SPT20-Containing SAGA Complex Plays a Direct Role in the Regulation of Endoplasmic Reticulum Stress-Induced Genes. Molecular and Cellular Biology, 2009, 29, 1649-1660.	1.1	71
60	Automated unrestricted multigene recombineering for multiprotein complex production. Nature Methods, 2009, 6, 447-450.	9.0	98
61	Zinc-finger UBPs: regulators of deubiquitylation. Trends in Biochemical Sciences, 2008, 33, 369-375.	3.7	71
62	Assembly of Protein Complexes by Coexpression in Prokaryotic and Eukaryotic Hosts: an Overview. Methods in Molecular Biology, 2008, 426, 247-256.	0.4	33
63	Crystal Structure, Biochemical and Genetic Characterization of Yeast and E. cuniculi TAFII5 N-terminal Domain: Implications for TFIID Assembly. Journal of Molecular Biology, 2007, 368, 1292-1306.	2.0	21
64	Co-expression of protein complexes in prokaryotic and eukaryotic hosts: experimental procedures, database tracking and case studies. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1232-1242.	2.5	113
65	The NF-YB/NF-YC Structure Gives Insight into DNA Binding and Transcription Regulation by CCAAT Factor NF-Y. Journal of Biological Chemistry, 2003, 278, 1336-1345.	1.6	239
66	Crystal Structure of a Subcomplex of Human Transcription Factor TFIID Formed by TATA Binding Protein-associated Factors hTAF4 (hTAFII135) and hTAF12 (hTAFII20). Journal of Biological Chemistry, 2002, 277, 45502-45509.	1.6	56
67	NF-Y Recruitment of TFIID, Multiple Interactions with Histone Fold TAFIIs. Journal of Biological Chemistry, 2002, 277, 5841-5848.	1.6	62
68	Functional Analysis of the TFIID-specific Yeast TAF4 (yTAFII48) Reveals an Unexpected Organization of Its Histone-fold Domain. Journal of Biological Chemistry, 2002, 277, 45510-45517.	1.6	25
69	Dissecting the interaction network of multiprotein complexes by pairwise coexpression of subunits in E. coli11Edited by K. Nagai. Journal of Molecular Biology, 2001, 306, 363-373.	2.0	64
70	The histone fold is a key structural motif of transcription factor TFIID. Trends in Biochemical Sciences, 2001, 26, 250-257.	3.7	127
71	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. Molecular and Cellular Biology, 2001, 21, 1841-1853.	1.1	66
72	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. Molecular and Cellular Biology, 2001, 21, 5109-5121.	1.1	62

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73	The Human TFIID Components TAF_{II}135 and TAF_{II}20 and the Yeast SAGA Components ADA1 and TAF_{II}68 Heterodimerize to Form Histone-Like Pairs. Molecular and Cellular Biology, 2000, 20, 340-351.	1.1	86
74	Synergistic Transcriptional Activation by TATA-Binding Protein and hTAF_{II}28 Requires Specific Amino Acids of the hTAF_{II}28 Histone Fold. Molecular and Cellular Biology, 1999, 19, 5050-5060.	1.1	23
75	Recognition of single-stranded DNA by nuclease P1: High resolution crystal structures of complexes with substrate analogs. Proteins: Structure, Function and Bioinformatics, 1998, 32, 414-424.	1.5	101
76	Human TAFII28 and TAFII18 Interact through a Histone Fold Encoded by Atypical Evolutionary Conserved Motifs Also Found in the SPT3 Family. Cell, 1998, 94, 239-249.	13.5	149
77	Slight sequence variations of a common fold explain the substrate specificities of tRNA-guanine transglycosylases from the three kingdoms. FEBS Letters, 1997, 416, 93-98.	1.3	42
78	Mutagenesis and Crystallographic Studies ofZymomonas mobilistRNA-Guanine Transglycosylase Reveal Aspartate 102 as the Active Site Nucleophileâ€,â€¡. Biochemistry, 1996, 35, 15734-15739.	1.2	52
79	Purification, crystallization, and preliminary X-ray diffraction studies of tRNA-guanine transglycosylase fromZymomonas mobilis. , 1996, 24, 516-519.		33
80	Solution structure of human corticotropin releasing factor by 1H NMR and distance geometry with restrained molecular dynamics. Protein Engineering, Design and Selection, 1993, 6, 149-156.	1.0	43