

Laurence A Florens

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6850522/publications.pdf>

Version: 2024-02-01

256
papers

28,158
citations

7251

80
h-index

7836

155
g-index

290
all docs

290
docs citations

290
times ranked

35724
citing authors

#	ARTICLE	IF	CITATIONS
1	Cytidine acetylation yields a hypoinflammatory synthetic messenger RNA. <i>Cell Chemical Biology</i> , 2022, 29, 312-320.e7.	2.5	14
2	A putative cap binding protein and the methyl phosphate capping enzyme Bin3/MePCE function in telomerase biogenesis. <i>Nature Communications</i> , 2022, 13, 1067.	5.8	10
3	Functional genomics of RAP proteins and their role in mitoribosome regulation in <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , 2022, 13, 1275.	5.8	12
4	Mediator recruits the cohesin loader Scc2 to RNA Pol II-transcribed genes and promotes sister chromatid cohesion. <i>Current Biology</i> , 2022, 32, 2884-2896.e6.	1.8	11
5	The <i>Caenorhabditis elegans</i> ASPP homolog APE-1 is a junctional protein phosphatase 1 modulator. <i>Genetics</i> , 2022, 222, .	1.2	2
6	Genome-Wide Binding Analyses of HOXB1 Revealed a Novel DNA Binding Motif Associated with Gene Repression. <i>Journal of Developmental Biology</i> , 2021, 9, 6.	0.9	9
7	The methyltransferase SETD2 couples transcription and splicing by engaging mRNA processing factors through its SHI domain. <i>Nature Communications</i> , 2021, 12, 1443.	5.8	42
8	K63-linked ubiquitination of DYRK1A by TRAF2 alleviates Sprouty 2-mediated degradation of EGFR. <i>Cell Death and Disease</i> , 2021, 12, 608.	2.7	13
9	Decellularization Enables Characterization and Functional Analysis of Extracellular Matrix in Planarian Regeneration. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100137.	2.5	11
10	Multiple roles for PARP1 in ALC1-dependent nucleosome remodeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	3
11	Proteome plasticity in response to persistent environmental change. <i>Molecular Cell</i> , 2021, 81, 3294-3309.e12.	4.5	12
12	The disordered regions of the methyltransferase SETD2 govern its function by regulating its proteolysis and phase separation. <i>Journal of Biological Chemistry</i> , 2021, 297, 101075.	1.6	8
13	MOCS2 links nucleotide metabolism to nucleoli function. <i>Journal of Molecular Cell Biology</i> , 2021, , .	1.5	3
14	Harnessing Ionic Selectivity in Acetyltransferase Chemoproteomic Probes. <i>ACS Chemical Biology</i> , 2021, 16, 27-34.	1.6	5
15	Structural basis of the interaction between SETD2 methyltransferase and hnRNP L paralogs for governing co-transcriptional splicing. <i>Nature Communications</i> , 2021, 12, 6452.	5.8	12
16	Generating topological protein interaction scores and data visualization with TopS. <i>Methods</i> , 2020, 184, 13-18.	1.9	5
17	A Systems Chemoproteomic Analysis of Acyl-CoA/Protein Interaction Networks. <i>Cell Chemical Biology</i> , 2020, 27, 322-333.e5.	2.5	20
18	β-Catenin and Associated Proteins Regulate Lineage Differentiation in Ground State Mouse Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2020, 15, 662-676.	2.3	11

#	ARTICLE	IF	CITATIONS
19	A six-amino-acid motif is a major determinant in functional evolution of HOX1 proteins. <i>Genes and Development</i> , 2020, 34, 1680-1696.	2.7	16
20	Driving integrative structural modeling with serial capture affinity purification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31861-31870.	3.3	8
21	Differential Complex Formation via Paralogs in the Human Sin3 Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1468-1484.	2.5	26
22	Dynamic RNA acetylation revealed by quantitative cross-evolutionary mapping. <i>Nature</i> , 2020, 583, 638-643.	13.7	175
23	NRBP1-Containing CRL2/CRL4A Regulates Amyloid β Production by Targeting BRI2 and BRI3 for Degradation. <i>Cell Reports</i> , 2020, 30, 3478-3491.e6.	2.9	20
24	New and Improved Tools for the Omics Crew. <i>Journal of Proteome Research</i> , 2020, 19, 2525-2528.	1.8	1
25	The role of Mediator and Little Elongation Complex in transcription termination. <i>Nature Communications</i> , 2020, 11, 1063.	5.8	21
26	Integrative Modeling of a Sin3/HDAC Complex Sub-structure. <i>Cell Reports</i> , 2020, 31, 107516.	2.9	29
27	Merkel cell polyomavirus activates LSD1-mediated blockade of non-canonical BAF to regulate transformation and tumorigenesis. <i>Nature Cell Biology</i> , 2020, 22, 603-615.	4.6	47
28	The chromatin bound proteome of the human malaria parasite. <i>Microbial Genomics</i> , 2020, 6, .	1.0	13
29	STRIPAK directs PP2A activity toward MAP4K4 to promote oncogenic transformation of human cells. <i>ELife</i> , 2020, 9, .	2.8	46
30	Yeast Nuak1 phosphorylates histone H3 threonine 11 in low glucose stress by the cooperation of AMPK and CK2 signaling. <i>ELife</i> , 2020, 9, .	2.8	7
31	The plasticity of the pyruvate dehydrogenase complex confers a labile structure that is associated with its catalytic activity. <i>PLoS ONE</i> , 2020, 15, e0243489.	1.1	5
32	The <i>Drosophila</i> Dbf4 ortholog Chiffon forms a complex with Gcn5 that is necessary for histone acetylation and viability. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	27
33	The E3 ubiquitin ligase SPOP controls resolution of systemic inflammation by triggering MYD88 degradation. <i>Nature Immunology</i> , 2019, 20, 1196-1207.	7.0	42
34	Biochemical Reduction of the Topology of the Diverse WDR76 Protein Interactome. <i>Journal of Proteome Research</i> , 2019, 18, 3479-3491.	1.8	14
35	BRK phosphorylates SMAD4 for proteasomal degradation and inhibits tumor suppressor FRK to control SNAIL, SLUG, and metastatic potential. <i>Science Advances</i> , 2019, 5, eaaw3113.	4.7	16
36	Characterization of a metazoan ADA acetyltransferase complex. <i>Nucleic Acids Research</i> , 2019, 47, 3383-3394.	6.5	26

#	ARTICLE	IF	CITATIONS
37	Junctional tumor suppressors interact with 14-3-3 proteins to control planar spindle alignment. <i>Journal of Cell Biology</i> , 2019, 218, 1824-1838.	2.3	25
38	Evaluating Chromatographic Approaches for the Quantitative Analysis of a Human Proteome on Orbitrap-Based Mass Spectrometry Systems. <i>Journal of Proteome Research</i> , 2019, 18, 1857-1869.	1.8	7
39	Topological scoring of protein interaction networks. <i>Nature Communications</i> , 2019, 10, 1118.	5.8	32
40	Host Vesicle Fusion Protein VAPB Contributes to the Nuclear Egress Stage of Herpes Simplex Virus Type-1 (HSV-1) Replication. <i>Cells</i> , 2019, 8, 120.	1.8	13
41	DYRK1A regulates the recruitment of 53BP1 to the sites of DNA damage in part through interaction with RNF169. <i>Cell Cycle</i> , 2019, 18, 531-551.	1.3	32
42	RUNX proteins desensitize multiple myeloma to lenalidomide via protecting IKZFs from degradation. <i>Leukemia</i> , 2019, 33, 2006-2021.	3.3	36
43	A chemoproteomic portrait of the oncometabolite fumarate. <i>Nature Chemical Biology</i> , 2019, 15, 391-400.	3.9	77
44	Ataxin-7 and Non-stop coordinate SCAR protein levels, subcellular localization, and actin cytoskeleton organization. <i>ELife</i> , 2019, 8, .	2.8	13
45	dCas9-targeted locus-specific protein isolation method identifies histone gene regulators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2734-E2741.	3.3	44
46	Loss of KLHL6 promotes diffuse large B-cell lymphoma growth and survival by stabilizing the mRNA decay factor roquin2. <i>Nature Cell Biology</i> , 2018, 20, 586-596.	4.6	35
47	A Structured Workflow for Mapping Human Sin3 Histone Deacetylase Complex Interactions Using Halo-MudPIT Affinity-Purification Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1432-1447.	2.5	27
48	Schizosaccharomyces pombe Pol II transcription elongation factor ELL functions as part of a rudimentary super elongation complex. <i>Nucleic Acids Research</i> , 2018, 46, 10095-10105.	6.5	7
49	Probing the Sensitivity of the Orbitrap Lumos Mass Spectrometer Using a Standard Reference Protein in a Complex Background. <i>Journal of Proteome Research</i> , 2018, 17, 3586-3592.	1.8	17
50	Differential HDAC1/2 network analysis reveals a role for prefoldin/CCT in HDAC1/2 complex assembly. <i>Scientific Reports</i> , 2018, 8, 13712.	1.6	32
51	PTPN14 regulates Roquin2 stability by tyrosine dephosphorylation. <i>Cell Cycle</i> , 2018, 17, 2243-2255.	1.3	5
52	FGF2 Antiproliferative Stimulation Induces Proteomic Dynamic Changes and High Expression of FOSB and JUNB in Kâ€Rasâ€Driven Mouse Tumor Cells. <i>Proteomics</i> , 2018, 18, e1800203.	1.3	6
53	DYRK1A interacts with histone acetyl transferase p300 and CBP and localizes to enhancers. <i>Nucleic Acids Research</i> , 2018, 46, 11202-11213.	6.5	26
54	MPTAC Determines APP Fragmentation via Sensing Sulfur Amino Acid Catabolism. <i>Cell Reports</i> , 2018, 24, 1585-1596.	2.9	12

#	ARTICLE	IF	CITATIONS
55	Analysis of RNA-Seq datasets reveals enrichment of tissue-specific splice variants for nuclear envelope proteins. <i>Nucleus</i> , 2018, 9, 410-430.	0.6	10
56	The ULK1-FBXW5-SEC23B nexus controls autophagy. <i>ELife</i> , 2018, 7, .	2.8	63
57	Comprehensive Spatial Analysis of the <i>Borrelia burgdorferi</i> Lipoproteome Reveals a Compartmentalization Bias toward the Bacterial Surface. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	60
58	Chromatin remodeller Fun30Ft3 induces nucleosome disassembly to facilitate RNA polymerase II elongation. <i>Nature Communications</i> , 2017, 8, 14527.	5.8	41
59	Identification of Topological Network Modules in Perturbed Protein Interaction Networks. <i>Scientific Reports</i> , 2017, 7, 43845.	1.6	29
60	Mediator structure and rearrangements required for holoenzyme formation. <i>Nature</i> , 2017, 544, 196-201.	13.7	120
61	Cytosolic proteostasis through importing of misfolded proteins into mitochondria. <i>Nature</i> , 2017, 543, 443-446.	13.7	363
62	Composition and Function of Mutant Swi/Snf Complexes. <i>Cell Reports</i> , 2017, 18, 2124-2134.	2.9	71
63	Different phosphoisoforms of RNA polymerase II engage the Rtt103 termination factor in a structurally analogous manner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3944-E3953.	3.3	24
64	PTEN counteracts FBXL2 to promote IP3R3- and Ca ²⁺ -mediated apoptosis limiting tumour growth. <i>Nature</i> , 2017, 546, 554-558.	13.7	182
65	The TDH ^Δ GCN5L1 ^Δ Fbxo15 ^Δ KBP axis limits mitochondrial biogenesis in mouse embryonic stem cells. <i>Nature Cell Biology</i> , 2017, 19, 341-351.	4.6	41
66	Therapeutic Targeting of MLL Degradation Pathways in MLL-Rearranged Leukemia. <i>Cell</i> , 2017, 168, 59-72.e13.	13.5	99
67	The WHHERE coactivator complex is required for retinoic acid-dependent regulation of embryonic symmetry. <i>Nature Communications</i> , 2017, 8, 728.	5.8	27
68	HOXA1 and TALE proteins display cross-regulatory interactions and form a combinatorial binding code on HOXA1 targets. <i>Genome Research</i> , 2017, 27, 1501-1512.	2.4	35
69	Myeloid Leukemia Factor Acts in a Chaperone Complex to Regulate Transcription Factor Stability and Gene Expression. <i>Journal of Molecular Biology</i> , 2017, 429, 2093-2107.	2.0	12
70	Advancement of mass spectrometry-based proteomics technologies to explore triple negative breast cancer. <i>Molecular BioSystems</i> , 2017, 13, 42-55.	2.9	19
71	The human cytoplasmic dynein interactome reveals novel activators of motility. <i>ELife</i> , 2017, 6, .	2.8	120
72	Merkel cell polyomavirus recruits MYCL to the EP400 complex to promote oncogenesis. <i>PLoS Pathogens</i> , 2017, 13, e1006668.	2.1	84

#	ARTICLE	IF	CITATIONS
73	WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. PLoS ONE, 2016, 11, e0155492.	1.1	27
74	The mRNA-bound proteome of the human malaria parasite Plasmodium falciparum. Genome Biology, 2016, 17, 147.	3.8	87
75	The Spliceosomal Protein SF3B5 is a Novel Component of Drosophila SAGA that Functions in Gene Expression Independent of Splicing. Journal of Molecular Biology, 2016, 428, 3632-3649.	2.0	29
76	The Enok acetyltransferase complex interacts with Elg1 and negatively regulates PCNA unloading to promote the G1/S transition. Genes and Development, 2016, 30, 1198-210.	2.7	11
77	Isolation, Proteomic Analysis, and Microscopy Confirmation of the Liver Nuclear Envelope Proteome. Methods in Molecular Biology, 2016, 1411, 3-44.	0.4	7
78	ATXN7L3 and ENY2 Coordinate Activity of Multiple H2B Deubiquitinases Important for Cellular Proliferation and Tumor Growth. Molecular Cell, 2016, 62, 558-571.	4.5	106
79	Cytoplasmic ATXN7L3B Interferes with Nuclear Functions of the SAGA Deubiquitinase Module. Molecular and Cellular Biology, 2016, 36, 2855-2866.	1.1	16
80	SONAR Discovers RNA-Binding Proteins from Analysis of Large-Scale Protein-Protein Interactomes. Molecular Cell, 2016, 64, 282-293.	4.5	155
81	USP44 Is an Integral Component of N-CoR that Contributes to Gene Repression by Deubiquitinating Histone H2B. Cell Reports, 2016, 17, 2382-2393.	2.9	41
82	TNIP2 is a Hub Protein in the NF- κ B Network with Both Protein and RNA Mediated Interactions. Molecular and Cellular Proteomics, 2016, 15, 3435-3449.	2.5	27
83	Role for the MED21-MED7 Hinge in Assembly of the Mediator-RNA Polymerase II Holoenzyme. Journal of Biological Chemistry, 2016, 291, 26886-26898.	1.6	19
84	HIV-1 and HIV-2 exhibit divergent interactions with HLTF and UNG2 DNA repair proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3921-30.	3.3	58
85	Dynamic and Combinatorial Landscape of Histone Modifications during the Intraerythrocytic Developmental Cycle of the Malaria Parasite. Journal of Proteome Research, 2016, 15, 2787-2801.	1.8	49
86	Proteomic and Genomic Analyses of the Rvb1 and Rvb2 Interaction Network upon Deletion of R2TP Complex Components. Molecular and Cellular Proteomics, 2016, 15, 960-974.	2.5	11
87	Moco biosynthesis and the ATAC acetyltransferase engage translation initiation by inhibiting latent PKR activity. Journal of Molecular Cell Biology, 2016, 8, 44-50.	1.5	11
88	Trio, a Rho Family GEF, Interacts with the Presynaptic Active Zone Proteins Piccolo and Bassoon. PLoS ONE, 2016, 11, e0167535.	1.1	17
89	Proteins interacting with cloning scars: a source of false positive protein-protein interactions. Scientific Reports, 2015, 5, 8530.	1.6	19
90	CyclinA2-Cyclin-dependent Kinase Regulates SAMHD1 Protein Phosphohydrolase Domain. Journal of Biological Chemistry, 2015, 290, 13279-13292.	1.6	84

#	ARTICLE	IF	CITATIONS
91	Amyloidogenic Oligomerization Transforms Drosophila Orb2 from a Translation Repressor to an Activator. <i>Cell</i> , 2015, 163, 1468-1483.	13.5	99
92	Characterization of Human Cyclin-Dependent Kinase 12 (CDK12) and CDK13 Complexes in C-Terminal Domain Phosphorylation, Gene Transcription, and RNA Processing. <i>Molecular and Cellular Biology</i> , 2015, 35, 928-938.	1.1	153
93	Conserved abundance and topological features in chromatin remodeling protein interaction networks. <i>EMBO Reports</i> , 2015, 16, 116-126.	2.0	17
94	Zic2 Is an Enhancer-Binding Factor Required for Embryonic Stem Cell Specification. <i>Molecular Cell</i> , 2015, 57, 685-694.	4.5	92
95	The Integrator complex controls the termination of transcription at diverse classes of gene targets. <i>Cell Research</i> , 2015, 25, 288-305.	5.7	113
96	TRIM29 regulates the assembly of DNA repair proteins into damaged chromatin. <i>Nature Communications</i> , 2015, 6, 7299.	5.8	45
97	Assembly of the Elongin A Ubiquitin Ligase Is Regulated by Genotoxic and Other Stresses. <i>Journal of Biological Chemistry</i> , 2015, 290, 15030-15041.	1.6	24
98	Improving Label-Free Quantitative Proteomics Strategies by Distributing Shared Peptides and Stabilizing Variance. <i>Analytical Chemistry</i> , 2015, 87, 4749-4756.	3.2	36
99	Serine and SAM Responsive Complex SESAME Regulates Histone Modification Crosstalk by Sensing Cellular Metabolism. <i>Molecular Cell</i> , 2015, 60, 408-421.	4.5	136
100	Cyclin-dependent Kinase-mediated Sox2 Phosphorylation Enhances the Ability of Sox2 to Establish the Pluripotent State. <i>Journal of Biological Chemistry</i> , 2015, 290, 22782-22794.	1.6	40
101	Degradation of Cep68 and PCNT cleavage mediate Cep215 removal from the PCM to allow centriole separation, disengagement and licensing. <i>Nature Cell Biology</i> , 2015, 17, 31-43.	4.6	69
102	The multifunctional autophagy pathway in the human malaria parasite, <i>Plasmodium falciparum</i> . <i>Autophagy</i> , 2014, 10, 80-92.	4.3	77
103	Phosphorylation by Casein Kinase 2 Facilitates Psh1 Protein-assisted Degradation of Cse4 Protein. <i>Journal of Biological Chemistry</i> , 2014, 289, 29297-29309.	1.6	23
104	Contribution of Orb2A Stability in Regulated Amyloid-Like Oligomerization of Drosophila Orb2. <i>PLoS Biology</i> , 2014, 12, e1001786.	2.6	48
105	The cohesin acetyltransferase Eco1 coordinates rDNA replication and transcription. <i>EMBO Reports</i> , 2014, 15, 609-617.	2.0	23
106	Loss of <i>Drosophila</i> Ataxin-7, a SAGA subunit, reduces H2B ubiquitination and leads to neural and retinal degeneration. <i>Genes and Development</i> , 2014, 28, 259-272.	2.7	51
107	Suberoylanilide Hydroxamic Acid (SAHA)-Induced Dynamics of a Human Histone Deacetylase Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3114-3125.	2.5	26
108	Gene duplication and neofunctionalization: POLR3G and POLR3GL. <i>Genome Research</i> , 2014, 24, 37-51.	2.4	47

#	ARTICLE	IF	CITATIONS
109	Swi/Snf dynamics on stress-responsive genes is governed by competitive bromodomain interactions. <i>Genes and Development</i> , 2014, 28, 2314-2330.	2.7	41
110	Histone H3 lysine-to-methionine mutants as a paradigm to study chromatin signaling. <i>Science</i> , 2014, 345, 1065-1070.	6.0	163
111	Controlling for Gene Expression Changes in Transcription Factor Protein Networks. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1510-1522.	2.5	23
112	Analysis of the heterochromatin protein 1 (HP1) interactome in <i>Drosophila</i> . <i>Journal of Proteomics</i> , 2014, 102, 137-147.	1.2	28
113	The membrane-associated proteins FCho and SGIP are allosteric activators of the AP2 clathrin adaptor complex. <i>ELife</i> , 2014, 3, .	2.8	75
114	The Little Elongation Complex Functions at Initiation and Elongation Phases of snRNA Gene Transcription. <i>Molecular Cell</i> , 2013, 51, 493-505.	4.5	54
115	Polysome profiling reveals translational control of gene expression in the human malaria parasite <i>Plasmodium falciparum</i> . <i>Genome Biology</i> , 2013, 14, R128.	13.9	131
116	FBH1 promotes DNA double-strand breakage and apoptosis in response to DNA replication stress. <i>Journal of Cell Biology</i> , 2013, 200, 141-149.	2.3	50
117	Regulation of the CRL4Cdt2 Ubiquitin Ligase and Cell-Cycle Exit by the SCFFbxo11 Ubiquitin Ligase. <i>Molecular Cell</i> , 2013, 49, 1159-1166.	4.5	67
118	Role for Human Mediator Subunit MED25 in Recruitment of Mediator to Promoters by Endoplasmic Reticulum Stress-responsive Transcription Factor ATF6 β . <i>Journal of Biological Chemistry</i> , 2013, 288, 26179-26187.	1.6	33
119	Novel Thioredoxin-Like Proteins Are Components of a Protein Complex Coating the Cortical Microtubules of <i>Toxoplasma gondii</i> . <i>Eukaryotic Cell</i> , 2013, 12, 1588-1599.	3.4	48
120	Quantitative Proteomics Demonstrates That the RNA Polymerase II Subunits Rpb4 and Rpb7 Dissociate during Transcriptional Elongation. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1530-1538.	2.5	45
121	FBXL2- and PTPL1-mediated degradation of p110-free p85 β regulatory subunit controls the PI(3)K signalling cascade. <i>Nature Cell Biology</i> , 2013, 15, 472-480.	4.6	98
122	Binding of <i>Drosophila</i> Polo kinase to its regulator Matrimony is noncanonical and involves two separate functional domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1222-31.	3.3	27
123	The nuclear envelope proteome differs notably between tissues. <i>Nucleus</i> , 2012, 3, 552-564.	0.6	177
124	Identification of FAM111A as an SV40 Host Range Restriction and Adenovirus Helper Factor. <i>PLoS Pathogens</i> , 2012, 8, e1002949.	2.1	58
125	Polycomb Repressive Complex 2-Dependent and -Independent Functions of Jarid2 in Transcriptional Regulation in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2012, 32, 1683-1693.	1.1	66
126	Human Family with Sequence Similarity 60 Member A (FAM60A) Protein: a New Subunit of the Sin3 Deacetylase Complex. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1815-1828.	2.5	47

#	ARTICLE	IF	CITATIONS
127	Shaggy/glycogen synthase kinase 3 ^Δ and phosphorylation of Sarah/regulator of calcineurin are essential for completion of <i>Drosophila</i> female meiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6382-6389.	3.3	44
128	Endoplasmic Reticulum Stress-responsive Transcription Factor ATF6 ^Δ Directs Recruitment of the Mediator of RNA Polymerase II Transcription and Multiple Histone Acetyltransferase Complexes. <i>Journal of Biological Chemistry</i> , 2012, 287, 23035-23045.	1.6	22
129	The RDE-10/RDE-11 complex triggers RNAi-induced mRNA degradation by association with target mRNA in <i>C. elegans</i> . <i>Genes and Development</i> , 2012, 26, 846-856.	2.7	27
130	The Super Elongation Complex Family of RNA Polymerase II Elongation Factors: Gene Target Specificity and Transcriptional Output. <i>Molecular and Cellular Biology</i> , 2012, 32, 2608-2617.	1.1	150
131	Characterization of a Highly Conserved Histone Related Protein, Ydl156w, and Its Functional Associations Using Quantitative Proteomic Analyses. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011544.	2.5	28
132	Cyclin F-Mediated Degradation of Ribonucleotide Reductase M2 Controls Genome Integrity and DNA Repair. <i>Cell</i> , 2012, 149, 1023-1034.	13.5	313
133	Chromatin remodelers Isw1 and Chd1 maintain chromatin structure during transcription by preventing histone exchange. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 884-892.	3.6	256
134	A Metazoan ATAC Acetyltransferase Subunit That Regulates Mitogen-activated Protein Kinase Signaling Is Related to an Ancient Molybdopterin Synthase Component. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 90-99.	2.5	6
135	Improving Proteomics Mass Accuracy by Dynamic Offline Lock Mass. <i>Analytical Chemistry</i> , 2011, 83, 9344-9351.	3.2	46
136	Human Mediator Subunit MED26 Functions as a Docking Site for Transcription Elongation Factors. <i>Cell</i> , 2011, 146, 92-104.	13.5	293
137	The Little Elongation Complex Regulates Small Nuclear RNA Transcription. <i>Molecular Cell</i> , 2011, 44, 954-965.	4.5	75
138	Temporal Regulation of Gene Expression of the <i>Thermus thermophilus</i> Bacteriophage P23-45. <i>Journal of Molecular Biology</i> , 2011, 405, 125-142.	2.0	33
139	Post-transcription initiation function of the ubiquitous SAGA complex in tissue-specific gene activation. <i>Genes and Development</i> , 2011, 25, 1499-1509.	2.7	60
140	Combinatorial depletion analysis to assemble the network architecture of the SAGA and ADA chromatin remodeling complexes. <i>Molecular Systems Biology</i> , 2011, 7, 503.	3.2	140
141	Vpx relieves inhibition of HIV-1 infection of macrophages mediated by the SAMHD1 protein. <i>Nature</i> , 2011, 474, 658-661.	13.7	1,060
142	Unraveling the Ubiquitome of the Human Malaria Parasite. <i>Journal of Biological Chemistry</i> , 2011, 286, 40320-40330.	1.6	66
143	The COMPASS Family of H3K4 Methylases in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 4310-4318.	1.1	195
144	Subunit Organization of the Human INO80 Chromatin Remodeling Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 11283-11289.	1.6	93

#	ARTICLE	IF	CITATIONS
145	Several Novel Nuclear Envelope Transmembrane Proteins Identified in Skeletal Muscle Have Cytoskeletal Associations. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003129.	2.5	118
146	DYRK1A protein kinase promotes quiescence and senescence through DREAM complex assembly. <i>Genes and Development</i> , 2011, 25, 801-813.	2.7	231
147	Highly Reproducible Label Free Quantitative Proteomic Analysis of RNA Polymerase Complexes. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S13.	2.5	78
148	Nuclear cGMP-Dependent Kinase Regulates Gene Expression via Activity-Dependent Recruitment of a Conserved Histone Deacetylase Complex. <i>PLoS Genetics</i> , 2011, 7, e1002065.	1.5	41
149	The tumour antigen PRAME is a subunit of a Cul2 ubiquitin ligase and associates with active NFY promoters. <i>EMBO Journal</i> , 2011, 30, 3786-3798.	3.5	59
150	The Leukocyte Nuclear Envelope Proteome Varies with Cell Activation and Contains Novel Transmembrane Proteins That Affect Genome Architecture. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2571-2585.	2.5	120
151	Deacetylase Inhibitors Dissociate the Histone-Targeting ING2 Subunit from the Sin3 Complex. <i>Chemistry and Biology</i> , 2010, 17, 65-74.	6.2	79
152	SCFCyclin F controls centrosome homeostasis and mitotic fidelity through CP110 degradation. <i>Nature</i> , 2010, 466, 138-142.	13.7	235
153	Aneuploidy confers quantitative proteome changes and phenotypic variation in budding yeast. <i>Nature</i> , 2010, 468, 321-325.	13.7	521
154	Gcn5 regulates the dissociation of SWI/SNF from chromatin by acetylation of Swi2/Snf2. <i>Genes and Development</i> , 2010, 24, 2766-2771.	2.7	67
155	Delayed Correlation of mRNA and Protein Expression in Rapamycin-treated Cells and a Role for Ggc1 in Cellular Sensitivity to Rapamycin. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 271-284.	2.5	134
156	Subunit Composition and Substrate Specificity of a MOF-containing Histone Acetyltransferase Distinct from the Male-specific Lethal (MSL) Complex. <i>Journal of Biological Chemistry</i> , 2010, 285, 4268-4272.	1.6	211
157	Linking H3K79 trimethylation to Wnt signaling through a novel Dot1-containing complex (DotCom). <i>Genes and Development</i> , 2010, 24, 574-589.	2.7	272
158	Heterochromatin protein 1 (HP1) connects the FACT histone chaperone complex to the phosphorylated CTD of RNA polymerase II. <i>Genes and Development</i> , 2010, 24, 2133-2145.	2.7	90
159	AFF4, a Component of the ELL/P-TEFb Elongation Complex and a Shared Subunit of MLL Chimeras, Can Link Transcription Elongation to Leukemia. <i>Molecular Cell</i> , 2010, 37, 429-437.	4.5	504
160	Psh1 Is an E3 Ubiquitin Ligase that Targets the Centromeric Histone Variant Cse4. <i>Molecular Cell</i> , 2010, 40, 444-454.	4.5	159
161	The ATAC Acetyltransferase Complex Coordinates MAP Kinases to Regulate JNK Target Genes. <i>Cell</i> , 2010, 142, 726-736.	13.5	66
162	Refinements to Label Free Proteome Quantitation: How to Deal with Peptides Shared by Multiple Proteins. <i>Analytical Chemistry</i> , 2010, 82, 2272-2281.	3.2	366

#	ARTICLE	IF	CITATIONS
163	Determining Protein Complex Connectivity Using a Probabilistic Deletion Network Derived from Quantitative Proteomics. PLoS ONE, 2009, 4, e7310.	1.1	35
164	Poly(ADP-ribosyl)ation directs recruitment and activation of an ATP-dependent chromatin remodeler. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13770-13774.	3.3	322
165	Proteomics Reveals a Physical and Functional Link between Hepatocyte Nuclear Factor 4 α and Transcription Factor IID. Journal of Biological Chemistry, 2009, 284, 32405-32412.	1.6	9
166	A novel histone fold domain-containing protein that replaces TAF6 in <i>Drosophila</i> SAGA is required for SAGA-dependent gene expression. Genes and Development, 2009, 23, 2818-2823.	2.7	34
167	INTS3 controls the hSSB1-mediated DNA damage response. Journal of Cell Biology, 2009, 187, 25-32.	2.3	80
168	Regulation of H3K4 Trimethylation via Cps40 (Spp1) of COMPASS Is Monoubiquitination Independent: Implication for a Phe/Tyr Switch by the Catalytic Domain of Set1. Molecular and Cellular Biology, 2009, 29, 3478-3486.	1.1	54
169	Yeast Sgf73/Ataxin-7 serves to anchor the deubiquitination module into both SAGA and Slik(SALSA) HAT complexes. Epigenetics and Chromatin, 2009, 2, 2.	1.8	84
170	A label free quantitative proteomic analysis of the Saccharomyces cerevisiae nucleus. Journal of Proteomics, 2009, 72, 110-120.	1.2	65
171	The Anopheles gambiae adult midgut peritrophic matrix proteome. Insect Biochemistry and Molecular Biology, 2009, 39, 125-134.	1.2	112
172	Rtr1 Is a CTD Phosphatase that Regulates RNA Polymerase II during the Transition from Serine 5 to Serine 2 Phosphorylation. Molecular Cell, 2009, 34, 168-178.	4.5	125
173	Evaluation of Clustering Algorithms for Protein Complex and Protein Interaction Network Assembly. Journal of Proteome Research, 2009, 8, 2944-2952.	1.8	44
174	Effect of Dynamic Exclusion Duration on Spectral Count Based Quantitative Proteomics. Analytical Chemistry, 2009, 81, 6317-6326.	3.2	167
175	Generation and Analysis of Multidimensional Protein Identification Technology Datasets. Methods in Molecular Biology, 2009, 492, 1-20.	0.4	24
176	Use of Sequential Chemical Extractions to Purify Nuclear Membrane Proteins for Proteomics Identification. Methods in Molecular Biology, 2009, 528, 201-225.	0.4	20
177	Interaction of Hepatocyte nuclear factor 4 α (HNF4 α) with the TATA box binding protein (TBP) contributes to TFIID recruitment and HNF4 α dependent transcription. FASEB Journal, 2009, 23, 660.12.	0.2	0
178	Functions of the Uch37 deubiquitinating enzyme in the proteasome and the INO80 chromatin remodeling complex. FASEB Journal, 2009, 23, 669.1.	0.2	0
179	ALC1: A Chromatin Remodeling Enzyme Activated by Poly(ADP-ribose) Polymerase (PARP) and NAD. FASEB Journal, 2009, 23, 488.2.	0.2	0
180	ATAC is a double histone acetyltransferase complex that stimulates nucleosome sliding. Nature Structural and Molecular Biology, 2008, 15, 364-372.	3.6	171

#	ARTICLE	IF	CITATIONS
181	Genomic and Proteomic Analysis of phiEco32, a Novel Escherichia coli Bacteriophage. <i>Journal of Molecular Biology</i> , 2008, 377, 774-789.	2.0	61
182	Genome Comparison and Proteomic Characterization of Thermus thermophilus Bacteriophages P23-45 and P74-26: Siphoviruses with Triplex-forming Sequences and the Longest Known Tails. <i>Journal of Molecular Biology</i> , 2008, 378, 468-480.	2.0	56
183	Structural Changes in TAF4b-TFIID Correlate with Promoter Selectivity. <i>Molecular Cell</i> , 2008, 29, 81-91.	4.5	55
184	Distinct Modes of Regulation of the Uch37 Deubiquitinating Enzyme in the Proteasome and in the Ino80 Chromatin-Remodeling Complex. <i>Molecular Cell</i> , 2008, 31, 909-917.	4.5	132
185	Heterochromatin Protein 1a Stimulates Histone H3 Lysine 36 Demethylation by the Drosophila KDM4A Demethylase. <i>Molecular Cell</i> , 2008, 32, 696-706.	4.5	97
186	Drosophila ELMO/CED-12 interacts with Myoblast city to direct myoblast fusion and ommatidial organization. <i>Developmental Biology</i> , 2008, 314, 137-149.	0.9	83
187	Probabilistic assembly of human protein interaction networks from label-free quantitative proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1454-1459.	3.3	220
188	Characterization of Cullin-box Sequences That Direct Recruitment of Cul2-Rbx1 and Cul5-Rbx2 Modules to Elongin BC-based Ubiquitin Ligases. <i>Journal of Biological Chemistry</i> , 2008, 283, 8005-8013.	1.6	147
189	Neuralized-like 1 (Neurl1) Targeted to the Plasma Membrane by N-Myristoylation Regulates the Notch Ligand Jagged1. <i>Journal of Biological Chemistry</i> , 2008, 283, 3846-3853.	1.6	69
190	Molecular Regulation of H3K4 Trimethylation by Wdr82, a Component of Human Set1/COMPASS. <i>Molecular and Cellular Biology</i> , 2008, 28, 7337-7344.	1.1	281
191	Lentiviral Vpx Accessory Factor Targets VprBP/DCAF1 Substrate Adaptor for Cullin 4 E3 Ubiquitin Ligase to Enable Macrophage Infection. <i>PLoS Pathogens</i> , 2008, 4, e1000059.	2.1	192
192	Statistical Similarities between Transcriptomics and Quantitative Shotgun Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 631-644.	2.5	146
193	Identification of Novel Integral Membrane Proteins of the Nuclear Envelope with Potential Disease Links Using Subtractive Proteomics. <i>Novartis Foundation Symposium</i> , 2008, , 63-80.	1.2	11
194	Intrinsic Capability of Budding Yeast Cofilin to Promote Turnover of Tropomyosin-Bound Actin Filaments. <i>PLoS ONE</i> , 2008, 3, e3641.	1.1	13
195	Subcellular Fractionation and Proteomics of Nuclear Envelopes. <i>Methods in Molecular Biology</i> , 2008, 432, 117-137.	0.4	16
196	PARC and CUL7 Form Atypical Cullin RING Ligase Complexes. <i>Cancer Research</i> , 2007, 67, 2006-2014.	0.4	56
197	Lentiviral Vpr usurps Cul4-DDB1[VprBP] E3 ubiquitin ligase to modulate cell cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11778-11783.	3.3	209
198	CHD8 Associates with Human Staf and Contributes to Efficient U6 RNA Polymerase III Transcription. <i>Molecular and Cellular Biology</i> , 2007, 27, 8729-8738.	1.1	67

#	ARTICLE	IF	CITATIONS
199	Identification and Characterization of a Schizosaccharomyces pombe RNA Polymerase II Elongation Factor with Similarity to the Metazoan Transcription Factor ELL. <i>Journal of Biological Chemistry</i> , 2007, 282, 5761-5769.	1.6	25
200	Ctk Complex-Mediated Regulation of Histone Methylation by COMPASS. <i>Molecular and Cellular Biology</i> , 2007, 27, 709-720.	1.1	59
201	Histone Crosstalk between H2B Monoubiquitination and H3 Methylation Mediated by COMPASS. <i>Cell</i> , 2007, 131, 1084-1096.	13.5	373
202	Evolutionarily Conserved Multisubunit RBL2/p130 and E2F4 Protein Complex Represses Human Cell Cycle-Dependent Genes in Quiescence. <i>Molecular Cell</i> , 2007, 26, 539-551.	4.5	347
203	Scm3 Is Essential to Recruit the Histone H3 Variant Cse4 to Centromeres and to Maintain a Functional Kinetochores. <i>Molecular Cell</i> , 2007, 26, 853-865.	4.5	222
204	Quantitative shotgun proteomics using a protease with broad specificity and normalized spectral abundance factors. <i>Molecular BioSystems</i> , 2007, 3, 354.	2.9	144
205	The Inhibition of Polo Kinase by Matrimony Maintains G2 Arrest in the Meiotic Cell Cycle. <i>PLoS Biology</i> , 2007, 5, e323.	2.6	68
206	YY1 functions with INO80 to activate transcription. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 872-874.	3.6	178
207	Purification of a Human SRCAP Complex That Remodels Chromatin by Incorporating the Histone Variant H2A.Z into Nucleosomes. <i>Biochemistry</i> , 2006, 45, 5671-5677.	1.2	211
208	Statistical Analysis of Membrane Proteome Expression Changes in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2006, 5, 2339-2347.	1.8	1,042
209	A role for Yin Yang-1 (YY1) in the assembly of snRNA transcription complexes. <i>Gene</i> , 2006, 377, 96-108.	1.0	10
210	<i>Thermus thermophilus</i> Bacteriophage ϕ YS40 Genome and Proteomic Characterization of Virions. <i>Journal of Molecular Biology</i> , 2006, 364, 667-677.	2.0	60
211	Analyzing chromatin remodeling complexes using shotgun proteomics and normalized spectral abundance factors. <i>Methods</i> , 2006, 40, 303-311.	1.9	293
212	Proteasome recruitment and activation of the Uch37 deubiquitinating enzyme by Adrm1. <i>Nature Cell Biology</i> , 2006, 8, 994-1002.	4.6	282
213	Proteomic Analysis by Multidimensional Protein Identification Technology. , 2006, 328, 159-176.		211
214	Cytoskeletal Components of an Invasion Machine—The Apical Complex of <i>Toxoplasma gondii</i> . <i>PLoS Pathogens</i> , 2006, 2, e13.	2.1	251
215	Host Cell Factor and an Uncharacterized SANT Domain Protein Are Stable Components of ATAC, a Novel dAda2A/dGcn5-Containing Histone Acetyltransferase Complex in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2006, 26, 871-882.	1.1	107
216	Quantitative proteomic analysis of distinct mammalian Mediator complexes using normalized spectral abundance factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18928-18933.	3.3	495

#	ARTICLE	IF	CITATIONS
217	Mnd1/Hop2 Facilitates Dmc1-Dependent Interhomolog Crossover Formation in Meiosis of Budding Yeast. <i>Molecular and Cellular Biology</i> , 2006, 26, 2913-2923.	1.1	49
218	The Essential Gene <i>wda</i> Encodes a WD40 Repeat Subunit of Drosophila SAGA Required for Histone H3 Acetylation. <i>Molecular and Cellular Biology</i> , 2006, 26, 7178-7189.	1.1	30
219	Stable incorporation of sequence specific repressors Ash1 and Ume6 into the Rpd3L complex. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2005, 1731, 77-87.	2.4	131
220	Proteomic comparison of two fractions derived from the transsynaptic scaffold. <i>Journal of Neuroscience Research</i> , 2005, 81, 762-775.	1.3	70
221	The Deubiquitylation Activity of Ubp8 Is Dependent upon Sgf11 and Its Association with the SAGA Complex. <i>Molecular and Cellular Biology</i> , 2005, 25, 1173-1182.	1.1	143
222	A Mammalian Chromatin Remodeling Complex with Similarities to the Yeast INO80 Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 41207-41212.	1.6	211
223	Characterization of the Yeast Trimeric-SAS Acetyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 11987-11994.	1.6	76
224	Maspin alters the carcinoma proteome. <i>FASEB Journal</i> , 2005, 19, 1123-1124.	0.2	34
225	The Mammalian YL1 Protein Is a Shared Subunit of the TRRAP/TIP60 Histone Acetyltransferase and SRCAP Complexes. <i>Journal of Biological Chemistry</i> , 2005, 280, 13665-13670.	1.6	185
226	The HIR corepressor complex binds to nucleosomes generating a distinct protein/DNA complex resistant to remodeling by SWI/SNF. <i>Genes and Development</i> , 2005, 19, 2534-2539.	2.7	89
227	Molecular Regulation of Histone H3 Trimethylation by COMPASS and the Regulation of Gene Expression. <i>Molecular Cell</i> , 2005, 19, 849-856.	4.5	263
228	Histone H3 Methylation by Set2 Directs Deacetylation of Coding Regions by Rpd3S to Suppress Spurious Intragenic Transcription. <i>Cell</i> , 2005, 123, 581-592.	13.5	1,154
229	The mammalian Mediator complex. <i>FEBS Letters</i> , 2005, 579, 904-908.	1.3	43
230	Glial Membranes at the Node of Ranvier Prevent Neurite Outgrowth. <i>Science</i> , 2005, 310, 1813-1817.	6.0	147
231	A Comprehensive Survey of the Plasmodium Life Cycle by Genomic, Transcriptomic, and Proteomic Analyses. <i>Science</i> , 2005, 307, 82-86.	6.0	743
232	Correlation of Relative Abundance Ratios Derived from Peptide Ion Chromatograms and Spectrum Counting for Quantitative Proteomic Analysis Using Stable Isotope Labeling. <i>Analytical Chemistry</i> , 2005, 77, 6218-6224.	3.2	324
233	A Mammalian Mediator Subunit that Shares Properties with <i>Saccharomyces cerevisiae</i> Mediator Subunit Cse2. <i>Journal of Biological Chemistry</i> , 2004, 279, 5846-5851.	1.6	24
234	A Plasmodium Gene Family Encoding Maurer's Cleft Membrane Proteins: Structural Properties and Expression Profiling. <i>Genome Research</i> , 2004, 14, 1052-1059.	2.4	133

#	ARTICLE	IF	CITATIONS
235	Global analysis of transcript and protein levels across the Plasmodium falciparum life cycle. <i>Genome Research</i> , 2004, 14, 2308-2318.	2.4	394
236	The Plasmodium falciparum clag9 gene encodes a rhoptry protein that is transferred to the host erythrocyte upon invasion. <i>Molecular Microbiology</i> , 2004, 52, 107-118.	1.2	78
237	Proteomics approach reveals novel proteins on the surface of malaria-infected erythrocytes. <i>Molecular and Biochemical Parasitology</i> , 2004, 135, 1-11.	0.5	168
238	Acetylation by Tip60 Is Required for Selective Histone Variant Exchange at DNA Lesions. <i>Science</i> , 2004, 306, 2084-2087.	6.0	602
239	Actin-binding proteins in a postsynaptic preparation: Lasp-1 is a component of central nervous system synapses and dendritic spines. <i>Journal of Neuroscience Research</i> , 2004, 78, 38-48.	1.3	45
240	FUNCTIONAL CHARACTERIZATION OF AN LCCL-LECTIN DOMAIN CONTAINING PROTEIN FAMILY IN PLASMODIUM BERGHEI. <i>Journal of Parasitology</i> , 2004, 90, 1062-1071.	0.3	42
241	Proteome Analysis of Rhoptry-Enriched Fractions Isolated from Plasmodium Merozoites. <i>Journal of Proteome Research</i> , 2004, 3, 995-1001.	1.8	84
242	Proteomics in Malaria. <i>Journal of Proteome Research</i> , 2004, 3, 296-306.	1.8	30
243	A Set of Consensus Mammalian Mediator Subunits Identified by Multidimensional Protein Identification Technology. <i>Molecular Cell</i> , 2004, 14, 685-691.	4.5	270
244	Proteomic analysis of chromatin-modifying complexes in Saccharomyces cerevisiae identifies novel subunits. <i>Biochemical Society Transactions</i> , 2004, 32, 899-903.	1.6	33
245	Nuclear Membrane Proteins with Potential Disease Links Found by Subtractive Proteomics. <i>Science</i> , 2003, 301, 1380-1382.	6.0	604
246	Identification of Plasmodium falciparum antigens by antigenic analysis of genomic and proteomic data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9952-9957.	3.3	227
247	Exploring the proteome of Plasmodium. <i>International Journal for Parasitology</i> , 2002, 32, 1539-1542.	1.3	28
248	Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii. <i>Nature</i> , 2002, 419, 512-519.	13.7	666
249	A proteomic view of the Plasmodium falciparum life cycle. <i>Nature</i> , 2002, 419, 520-526.	13.7	1,184
250	Where is "outside" in cytochrome c oxidase and how and when do protons get there?. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2000, 1458, 180-187.	0.5	53
251	Structure function relationships within the multihemic cytochrome C3 superfamily. <i>Journal of Inorganic Biochemistry</i> , 1997, 67, 398.	1.5	0
252	Interfacial Properties of the Polyheme Cytochrome C3 Superfamily from Desulfovibrio. <i>Biochemistry</i> , 1995, 34, 11327-11334.	1.2	12

#	ARTICLE	IF	CITATIONS
253	Drastic Influence of a Single Heme Axial Ligand Replacement on the Thermostability of Cytochrome c3. Biochemical and Biophysical Research Communications, 1995, 211, 742-747.	1.0	12
254	Thermal stability of the polyheme cytochromec3superfamily. FEBS Letters, 1995, 373, 280-284.	1.3	13
255	Recent advances in the characterization of the hexadecahemic cytochrome c from Desulfovibrio. Biochimie, 1994, 76, 561-568.	1.3	7
256	Characterization and oxidoreduction properties of cytochrome c3 after heme axial ligand replacements. Journal of Biological Chemistry, 1994, 269, 6340-6.	1.6	37