

Jean Cavarelli

List of Publications by Year in descending order

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papers

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218677

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#	ARTICLE	IF	CITATIONS
1	Turning Nonselective Inhibitors of Type I Protein Arginine Methyltransferases into Potent and Selective Inhibitors of Protein Arginine Methyltransferase 4 through a Deconstruction–Reconstruction and Fragment-Growing Approach. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 11574-11606.	6.4	15
2	A Direct Assay for Measuring the Activity and Inhibition of Coactivator-Associated Arginine Methyltransferase 1. <i>Biochemistry</i> , 2022, 61, 1055-1063.	2.5	1
3	Structural studies provide new insights into the role of lysine acetylation on substrate recognition by CARM1 and inform the design of potent peptidomimetic inhibitors. <i>ChemBioChem</i> , 2021, 22, 3469-3476.	2.6	3
4	Structure, Activity and Function of the PRMT2 Protein Arginine Methyltransferase. <i>Life</i> , 2021, 11, 1263.	2.4	21
5	Aminobenzosuberone derivatives as PfA-M1 inhibitors: Molecular recognition and antiplasmodial evaluation. <i>Bioorganic Chemistry</i> , 2020, 98, 103750.	4.1	10
6	Hijacking DNA methyltransferase transition state analogues to produce chemical scaffolds for PRMT inhibitors. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170072.	4.0	24
7	Transition state mimics are valuable mechanistic probes for structural studies with the arginine methyltransferase CARM1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3625-3630.	7.1	31
8	Insight into the remarkable affinity and selectivity of the aminobenzosuberone scaffold for the M1 aminopeptidases family based on structure analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1413-1421.	2.6	8
9	SECIS-binding protein 2 interacts with the SMN complex and the methylosome for selenoprotein mRNA assembly and translation. <i>Nucleic Acids Research</i> , 2017, 45, gkx031.	14.5	13
10	Structural studies of protein arginine methyltransferase 2 reveal its interactions with potential substrates and inhibitors. <i>FEBS Journal</i> , 2017, 284, 77-96.	4.7	25
11	TCTP contains a BH3-like domain, which instead of inhibiting, activates Bcl-xL. <i>Scientific Reports</i> , 2016, 6, 19725.	3.3	39
12	Structure of the Elongator cofactor complex Kti11/Kti13 provides insight into the role of Kti13 in Elongator-dependent tRNA modification. <i>FEBS Journal</i> , 2015, 282, 819-833.	4.7	20
13	Functional insights from high resolution structures of mouse protein arginine methyltransferase 6. <i>Journal of Structural Biology</i> , 2015, 191, 175-183.	2.8	23
14	Structural insight into arginine methylation by the mouse protein arginine methyltransferase 7: a zinc finger freezes the mimic of the dimeric state into a single active site. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2401-2412.	2.5	32
15	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.	4.2	60
16	Cloning, expression, purification and preliminary X-ray crystallographic analysis of mouse protein arginine methyltransferase 7. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 80-86.	0.8	8
17	Structural Basis for Hijacking of Cellular LxxLL Motifs by Papillomavirus E6 Oncoproteins. <i>Science</i> , 2013, 339, 694-698.	12.6	167
18	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.	4.7	136

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19	Identification of Small-Molecule Enhancers of Arginine Methylation Catalyzed by Coactivator-Associated Arginine Methyltransferase 1. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 9875-9890.	6.4	22
20	On the Structure and Function of the Phytoene Desaturase CRTI from <i>Pantoea ananatis</i> , a Membrane-Peripheral and FAD-Dependent Oxidase/Isomerase. <i>PLoS ONE</i> , 2012, 7, e39550.	2.5	87
21	Structural insights into transcription complexes. <i>Journal of Structural Biology</i> , 2011, 175, 135-146.	2.8	14
22	Acyl derivatives of p-aminosulfonamides and dapsone as new inhibitors of the arginine methyltransferase hPRMT1. <i>Bioorganic and Medicinal Chemistry</i> , 2011, 19, 3717-3731.	3.0	85
23	Structure determination of the minimal complex between Tfb5 and Tfb2, two subunits of the yeast transcription/DNA-repair factor TFIIH: a retrospective study. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 745-755.	2.5	4
24	Crystallization and preliminary crystallographic analysis of eukaryotic transcription and mRNA export factor lws1 from <i>Encephalitozoon cuniculi</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 207-210.	0.7	2
25	The structure of an lws1/Spt6 complex reveals an interaction domain conserved in TFIIS, Elongin A and Med26. <i>EMBO Journal</i> , 2010, 29, 3979-3991.	7.8	58
26	Noncanonical Tandem SH2 Enables Interaction of Elongation Factor Spt6 with RNA Polymerase II. <i>Journal of Biological Chemistry</i> , 2010, 285, 38389-38398.	3.4	52
27	TCTP protects from apoptotic cell death by antagonizing bax function. <i>Cell Death and Differentiation</i> , 2008, 15, 1211-1220.	11.2	184
28	Structural basis for group A trichothiodystrophy. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 980-984.	8.2	54
29	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.	4.2	21
30	Expression, purification, crystallization and preliminary crystallographic study of isolated modules of the mouse coactivator-associated arginine methyltransferase 1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 330-333.	0.7	9
31	Functional insights from structures of coactivator-associated arginine methyltransferase 1 domains. <i>EMBO Journal</i> , 2007, 26, 4391-4401.	7.8	131
32	Expression, purification, and characterization of a new heterotetramer structure of leucyl-tRNA synthetase from <i>Aquifex aeolicus</i> in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2006, 47, 1-9.	1.3	2
33	Crystallization and preliminary X-ray crystallographic study of the wild type and two mutants of the CP1 hydrolytic domain from <i>Aquifex aeolicus</i> leucyl-tRNA synthetase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 899-901.	0.7	0
34	Cloning, purification and crystallization of a Walker-type <i>Pyrococcus abyssi</i> ATPase family member. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 925-927.	0.7	0
35	Biochemical and NMR Mapping of the Interface between CREB-binding Protein and Ligand Binding Domains of Nuclear Receptor. <i>Journal of Biological Chemistry</i> , 2005, 280, 5682-5692.	3.4	17
36	Translationally controlled tumor protein is a target of tumor reversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15364-15369.	7.1	208

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37	Mutation and Evolution of the Magnesium-Binding Site of a Class II Aminoacyl-tRNA Synthetase. <i>Biochemistry</i> , 2004, 43, 7028-7037.	2.5	12
38	Pushing Induced Fit to Its Limits. <i>Structure</i> , 2003, 11, 484-486.	3.3	3
39	Evidence for assembly-dependent folding of protein and RNA in an icosahedral virus. <i>Virology</i> , 2003, 314, 26-33.	2.4	20
40	Limited Set of Amino Acid Residues in a Class Ia Aminoacyl-tRNA Synthetase Is Crucial for tRNA Binding. <i>Biochemistry</i> , 2003, 42, 15092-15101.	2.5	14
41	Crystal Structure of the V-region of <i>Streptococcus mutans</i> Antigen I/II at 2.4Å... Resolution Suggests a Sugar Preformed Binding Site. <i>Journal of Molecular Biology</i> , 2002, 318, 179-188.	4.2	55
42	Crucial Role of the HIGH-loop Lysine for the Catalytic Activity of Arginyl-tRNA Synthetase. <i>Journal of Biological Chemistry</i> , 2001, 276, 3723-3726.	3.4	15
43	Crystallization and preliminary X-ray crystallographic analysis of yeast arginyl-tRNA synthetase-yeast tRNA ^{Arg} complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 492-494.	2.5	6
44	tRNA aminoacylation by arginyl-tRNA synthetase: induced conformations during substrates binding. <i>EMBO Journal</i> , 2000, 19, 5599-5610.	7.8	159
45	In vivo selection of lethal mutations reveals two functional domains in arginyl-tRNA synthetase. <i>Rna</i> , 2000, 6, 434-448.	3.5	15
46	The free yeast aspartyl-tRNA synthetase differs from the tRNA ^{Asp} -complexed enzyme by structural changes in the catalytic site, hinge region, and anticodon-binding domain. <i>Journal of Molecular Biology</i> , 2000, 299, 1313-1324.	4.2	67
47	Crystallogensis studies on yeast aspartyl-tRNA synthetase: use of phase diagram to improve crystal quality. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 149-156.	2.5	17
48	Aminoacyl-tRNA synthetases: A new image for a classical family. <i>Biochimie</i> , 1999, 81, 683-700.	2.6	81
49	Active site mapping of yeast aspartyl-tRNA synthetase by in vivo selection of enzyme mutations lethal for cell growth. <i>Journal of Molecular Biology</i> , 1999, 288, 231-242.	4.2	19
50	L-Arginine recognition by yeast arginyl-tRNA synthetase. <i>EMBO Journal</i> , 1998, 17, 5438-5448.	7.8	101
51	Structures of RNA-binding proteins. <i>Quarterly Reviews of Biophysics</i> , 1997, 30, 195-240.	5.7	19
52	The structure of <i>Staphylococcus aureus</i> epidermolytic toxin A, an atypic serine protease, at 1.7 Å... resolution. <i>Structure</i> , 1997, 5, 813-824.	3.3	88
53	The 2.8 Å... Structure of a T=4 Animal Virus and its Implications for Membrane Translocation of RNA. <i>Journal of Molecular Biology</i> , 1996, 261, 1-10.	4.2	103
54	Conformational flexibility of tRNA: structural changes in yeast tRNA ^{Asp} upon binding to aspartyl-tRNA synthetase. <i>Biochimie</i> , 1996, 78, 624-631.	2.6	26

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55	Genomic organization of the rat aspartyl-tRNA synthetase gene family: A single active gene and several retropseudogenes. <i>Gene</i> , 1996, 180, 197-205.	2.2	2
56	The class II aminoacyl-tRNA synthetases and their active site: Evolutionary conservation of an ATP binding site. <i>Journal of Molecular Evolution</i> , 1995, 40, 499-508.	1.8	44
57	Yeast tRNA ^{Asp} recognition by its cognate class II aminoacyl-tRNA synthetase. <i>Nature</i> , 1993, 362, 181-184.	27.8	316
58	Yeast aspartyl-tRNA synthetase: A structural view of the aminoacylation reaction. <i>Biochimie</i> , 1993, 75, 1117-1123.	2.6	19
59	Role of dimerization in yeast aspartyl-tRNA synthetase and importance of the class II invariant proline.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 10816-10820.	7.1	63
60	Recognition of tRNAs by aminoacyl-tRNA synthetases.. <i>FASEB Journal</i> , 1993, 7, 79-86.	0.5	93
61	Crystallization and preliminary structure analysis of an insect virus with T=4 quasi-symmetry: <i>Nudaurelia capensis</i> 1% virus. <i>Acta Crystallographica Section B: Structural Science</i> , 1991, 47, 23-29.	1.8	22
62	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, 235-236.	4.2	55
63	Yeast tRNA ^{Asp} -Aspartyl-tRNA Synthetase Complex: Low Resolution Crystal Structure. <i>Journal of Biomolecular Structure and Dynamics</i> , 1987, 5, 187-198.	3.5	29
64	Preliminary crystallographic data for exfoliative toxin B from <i>Staphylococcus aureus</i> . <i>Journal of Molecular Biology</i> , 1984, 175, 89-91.	4.2	5
65	The Aspartic Acid tRNA System: Recognition by a Class II Aminoacyl-tRNA Synthetase. , 0, , 411-422.		1