

Marc Graille

List of Publications by Year in descending order

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87
papers

3,854
citations

109321

35
h-index

144013

57
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90
all docs

90
docs citations

90
times ranked

4914
citing authors

#	ARTICLE	IF	CITATIONS
1	Division of labor in epitranscriptomics: What have we learnt from the structures of eukaryotic and viral multimeric <i>RNA</i> methyltransferases?. <i>Wiley Interdisciplinary Reviews RNA</i> , 2022, 13, e1673.	6.4	5
2	The X-ray crystallography phase problem solved thanks to <i>AlphaFold</i> and <i>RoseTTAFold</i> models: a case-study report. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 517-531.	2.3	22
3	Cg1246, a new player in mycolic acid biosynthesis in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , 2022, 168, .	1.8	0
4	A scaffold lncRNA shapes the mitosis to meiosis switch. <i>Nature Communications</i> , 2021, 12, 770.	12.8	22
5	Structural and functional insights into <i>Archaeoglobus fulgidus</i> m ² G ¹⁰ tRNA methyltransferase Trm11 and its Trm112 activator. <i>Nucleic Acids Research</i> , 2020, 48, 11068-11082.	14.5	8
6	The catalytic activity of the translation termination factor methyltransferase Mtq2-Trm112 complex is required for large ribosomal subunit biogenesis. <i>Nucleic Acids Research</i> , 2020, 48, 12310-12325.	14.5	9
7	Pby1 is a direct partner of the Dcp2 decapping enzyme. <i>Nucleic Acids Research</i> , 2020, 48, 6353-6366.	14.5	4
8	The 18S ribosomal <i>RNA</i> m ⁶ A methyltransferase Mettl5 is required for normal walking behavior in <i>Drosophila</i> . <i>EMBO Reports</i> , 2020, 21, e49443.	4.5	52
9	ERH proteins: connecting RNA processing to tumorigenesis?. <i>Current Genetics</i> , 2020, 66, 689-692.	1.7	8
10	Formation of <i>S. pombe</i> Erh1 homodimer mediates gametogenic gene silencing and meiosis progression. <i>Scientific Reports</i> , 2020, 10, 1034.	3.3	25
11	The human 18S rRNA m ⁶ A methyltransferase METTL5 is stabilized by TRMT112. <i>Nucleic Acids Research</i> , 2019, 47, 7719-7733.	14.5	312
12	m ⁶ A mRNA Destiny: Chained to the rYTHm by the YTH-Containing Proteins. <i>Genes</i> , 2019, 10, 49.	2.4	44
13	The DEAH-box RNA helicase Dhr1 contains a remarkable carboxyl terminal domain essential for small ribosomal subunit biogenesis. <i>Nucleic Acids Research</i> , 2019, 47, 7548-7563.	14.5	15
14	mRNA decapping: finding the right structures. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20180164.	4.0	23
15	Evolutionary insights into Trm112-methyltransferase holoenzymes involved in translation between archaea and eukaryotes. <i>Nucleic Acids Research</i> , 2018, 46, 8483-8499.	14.5	37
16	Activation mode of the eukaryotic m ² G ¹⁰ tRNA methyltransferase Trm11 by its partner protein Trm112. <i>Nucleic Acids Research</i> , 2017, 45, gkw1271.	14.5	23
17	A unique surface on Pat1 C-terminal domain directly interacts with Dcp2 decapping enzyme and Xrn1 5' mRNA exonuclease in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9493-E9501.	7.1	45
18	Trm112, a Protein Activator of Methyltransferases Modifying Actors of the Eukaryotic Translational Apparatus. <i>Biomolecules</i> , 2017, 7, 7.	4.0	48

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19	Structure of the active form of Dcp1â€“Dcp2 decapping enzyme bound to m7GDP and its Edc3 activator. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 982-986.	8.2	48
20	Crystal structure of the effector <i>vrL</i> of <i>Leptosphaeria maculans</i> reveals insights into its translocation into plant cells and recognition by resistance proteins. <i>Plant Journal</i> , 2015, 83, 610-624.	5.7	52
21	Insights into molecular plasticity in protein complexes from Trm9-Trm112 tRNA modifying enzyme crystal structure. <i>Nucleic Acids Research</i> , 2015, 43, 10989-11002.	14.5	38
22	Crystal structures of the Gon7/Pcc1 and Bud32/Cgi121 complexes provide a model for the complete yeast KEOPS complex. <i>Nucleic Acids Research</i> , 2015, 43, 3358-3372.	14.5	43
23	Structural and functional studies of Bud23â€“Trm112 reveal 18S rRNA ⁷ -G1575 methylation occurs on late 40S precursor ribosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5518-26.	7.1	81
24	A Highly Conserved Region Essential for NMD in the Upf2 N-Terminal Domain. <i>Journal of Molecular Biology</i> , 2014, 426, 3689-3702.	4.2	16
25	Structural and functional analysis of the fibronectinâ€“binding protein <i>FNE</i> from <i>Streptococcus equi</i> spp. <i>FEBS Journal</i> , 2014, 281, 5513-5531.	4.7	17
26	Structural insights into the dimerization of the response regulator ComE from <i>Streptococcus pneumoniae</i> . <i>Nucleic Acids Research</i> , 2014, 42, 5302-5313.	14.5	54
27	The C-Terminal Domain from <i>S. cerevisiae</i> Pat1 Displays Two Conserved Regions Involved in Decapping Factor Recruitment. <i>PLoS ONE</i> , 2014, 9, e96828.	2.5	14
28	Cytoplasmic mRNA Surveillance Pathways. , 2014, , 195-216.		0
29	Identification of the Rps28 binding motif from yeast Edc3 involved in the autoregulatory feedback loop controlling RPS28B mRNA decay. <i>Nucleic Acids Research</i> , 2013, 41, 9514-9523.	14.5	19
30	Selection of Specific Protein Binders for Pre-Defined Targets from an Optimized Library of Artificial Helicoidal Repeat Proteins (alphaRep). <i>PLoS ONE</i> , 2013, 8, e71512.	2.5	47
31	Trm112 Is Required for Bud23-Mediated Methylation of the 18S rRNA at Position G1575. <i>Molecular and Cellular Biology</i> , 2012, 32, 2254-2267.	2.3	73
32	Mechanistic and structural basis for inhibition of thymidylate synthase ThyX. <i>Open Biology</i> , 2012, 2, 120120.	3.6	37
33	Functional and Structural Characterization of PaeM, a Colicin M-like Bacteriocin Produced by <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 37395-37405.	3.4	33
34	Methylation of class I translation termination factors: Structural and functional aspects. <i>Biochimie</i> , 2012, 94, 1533-1543.	2.6	14
35	Surveillance pathways rescuing eukaryotic ribosomes lost in translation. <i>Nature Reviews Molecular Cell Biology</i> , 2012, 13, 727-735.	37.0	99
36	The structure of the NasR transcription antiterminator reveals a oneâ€“component system with a NIT nitrate receptor coupled to an ANTAR RNAâ€“binding effector. <i>Molecular Microbiology</i> , 2012, 85, 431-444.	2.5	31

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37	Mechanism of activation of methyltransferases involved in translation by the Trm112 \hat{c} hub \hat{c} ™ protein. <i>Nucleic Acids Research</i> , 2011, 39, 6249-6259.	14.5	65
38	Structural and functional analysis of Nro1/Ett1: a protein involved in translation termination in <i>S. cerevisiae</i> and in O ₂ -mediated gene control in <i>S. pombe</i> . <i>Rna</i> , 2011, 17, 1213-1224.	3.5	11
39	X-Ray Structure and Site-Directed Mutagenesis Analysis of the <i>Escherichia coli</i> Colicin M Immunity Protein. <i>Journal of Bacteriology</i> , 2011, 193, 205-214.	2.2	21
40	Zinc Induces Structural Reorganization of Gelatin Binding Domain from Human Fibronectin and Affects Collagen Binding. <i>Structure</i> , 2010, 18, 710-718.	3.3	37
41	Dissection of Dom34 \hat{c} Hbs1 reveals independent functions in two RNA quality control pathways. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1446-1452.	8.2	60
42	Structural and Functional Insights into <i>Saccharomyces cerevisiae</i> Tpa1, a Putative Prolylhydroxylase Influencing Translation Termination and Transcription. <i>Journal of Biological Chemistry</i> , 2010, 285, 30767-30778.	3.4	30
43	Design, Production and Molecular Structure of a New Family of Artificial Alpha-helical Repeat Proteins (\hat{c} Rep) Based on Thermostable HEAT-like Repeats. <i>Journal of Molecular Biology</i> , 2010, 404, 307-327.	4.2	85
44	Crystal structure of the YML079w protein from <i>Saccharomyces cerevisiae</i> reveals a new sequence family of the jelly-roll fold. <i>Protein Science</i> , 2009, 14, 209-215.	7.6	13
45	The universal Kae1 protein and the associated Bud32 kinase (PRPK), a mysterious protein couple probably essential for genome maintenance in Archaea and Eukarya. <i>Biochemical Society Transactions</i> , 2009, 37, 29-35.	3.4	42
46	Structure \hat{c} function analysis of Knr4/Smi1, a newly member of intrinsically disordered proteins family, indispensable in the absence of a functional <i>PKC1\hat{c}SLT2</i> pathway in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2008, 25, 563-576.	1.7	17
47	The structure of an archaeal homodimeric ligase which has RNA circularization activity. <i>Protein Science</i> , 2008, 17, 1336-1345.	7.6	28
48	Structure of the archaeal Kae1/Bud32 fusion protein MJ1130: a model for the eukaryotic EKC/KEOPS subcomplex. <i>EMBO Journal</i> , 2008, 27, 2340-2351.	7.8	62
49	Crystal Structure of an Intact Type II DNA Topoisomerase: Insights into DNA Transfer Mechanisms. <i>Structure</i> , 2008, 16, 360-370.	3.3	62
50	Structure of Yeast Dom34. <i>Journal of Biological Chemistry</i> , 2008, 283, 7145-7154.	3.4	81
51	An archaeal orthologue of the universal protein Kae1 is an iron metalloprotein which exhibits atypical DNA-binding properties and apurinic-endonuclease activity in vitro. <i>Nucleic Acids Research</i> , 2007, 35, 6042-6051.	14.5	65
52	The yeast ribosome synthesis factor Emg1 is a novel member of the superfamily of alpha/beta knot fold methyltransferases. <i>Nucleic Acids Research</i> , 2007, 36, 629-639.	14.5	54
53	Structures of in Vitro Evolved Binding Sites on Neocarzinostatin Scaffold Reveal Unanticipated Evolutionary Pathways. <i>Journal of Molecular Biology</i> , 2006, 358, 455-471.	4.2	24
54	Crystal structure of the yeast His6 enzyme suggests a reaction mechanism. <i>Protein Science</i> , 2006, 15, 1516-1521.	7.6	8

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55	The HSP90 and DNA topoisomerase VI inhibitor radicicol also inhibits human type II DNA topoisomerase. <i>Biochemical Pharmacology</i> , 2006, 72, 1207-1216.	4.4	18
56	Structure-based Functional Annotation. <i>Journal of Biological Chemistry</i> , 2006, 281, 30175-30185.	3.4	22
57	The Zinc Finger Protein Ynr046w Is Plurifunctional and a Component of the eRF1 Methyltransferase in Yeast. <i>Journal of Biological Chemistry</i> , 2006, 281, 36140-36148.	3.4	54
58	Catalytic Mechanism and Structure of Viral Flavin-dependent Thymidylate Synthase ThyX. <i>Journal of Biological Chemistry</i> , 2006, 281, 24048-24057.	3.4	53
59	Crystal structure of yeast YHR049W/FSH1, a member of the serine hydrolase family. <i>Protein Science</i> , 2005, 14, 1350-1356.	7.6	20
60	Crystal structure of yeast YER010Cp, aknotable member of the RraA protein family. <i>Protein Science</i> , 2005, 14, 2751-2758.	7.6	5
61	High-throughput crystal-optimization strategies in the South Paris Yeast Structural Genomics Project: one size fits all?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 664-670.	2.5	14
62	HalX: an open-source LIMS (Laboratory Information Management System) for small- to large-scale laboratories. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 671-678.	2.5	23
63	Activation of the LicT Transcriptional Antiterminator Involves a Domain Swing/Lock Mechanism Provoking Massive Structural Changes. <i>Journal of Biological Chemistry</i> , 2005, 280, 14780-14789.	3.4	64
64	Fine Tuning of the Specificity of an Anti-progesterone Antibody by First and Second Sphere Residue Engineering. <i>Journal of Biological Chemistry</i> , 2005, 280, 24880-24887.	3.4	37
65	Inhibition of archaeal growth and DNA topoisomerase VI activities by the Hsp90 inhibitor radicicol. <i>Nucleic Acids Research</i> , 2005, 33, 2310-2317.	14.5	33
66	Crystal Structure of the Complex between the Monomeric Form of Toxoplasma gondii Surface Antigen 1 (SAG1) and a Monoclonal Antibody that Mimics the Human Immune Response. <i>Journal of Molecular Biology</i> , 2005, 354, 447-458.	4.2	50
67	Molecular Basis for Bacterial Class I Release Factor Methylation by PrmC. <i>Molecular Cell</i> , 2005, 20, 917-927.	9.7	73
68	Crystal structure of the D-ribose-5-phosphate isomerase: comparison with the archaeal and bacterial enzymes. <i>Biochimie</i> , 2005, 87, 763-769.	2.6	16
69	Crystal Structure of the Bifunctional Chorismate Synthase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 619-625.	3.4	29
70	Crystal Structure of Yeast Allantoicase Reveals a Repeated Jelly Roll Motif. <i>Journal of Biological Chemistry</i> , 2004, 279, 23447-23452.	3.4	23
71	Observation and Characterization of the Interaction between a Single Immunoglobulin Binding Domain of Protein L and Two Equivalents of Human I κ Light Chains. <i>Journal of Biological Chemistry</i> , 2004, 279, 9370-9378.	3.4	20
72	Structure of Protein Phosphatase Methyltransferase 1 (PPM1), a Leucine Carboxyl Methyltransferase Involved in the Regulation of Protein Phosphatase 2A Activity. <i>Journal of Biological Chemistry</i> , 2004, 279, 8351-8358.	3.4	82

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73	Crystal Structure and Functional Characterization of Yeast YLR011wp, an Enzyme with NAD(P)H-FMN and Ferric Iron Reductase Activities. <i>Journal of Biological Chemistry</i> , 2004, 279, 34890-34897.	3.4	71
74	Structural inhibition of the colicin D tRNase by the tRNA-mimicking immunity protein. <i>EMBO Journal</i> , 2004, 23, 1474-1482.	7.8	85
75	A new α -helical extension promotes RNA binding by the dsRBD of Rnt1p RNase III. <i>EMBO Journal</i> , 2004, 23, 2468-2477.	7.8	56
76	Crystal Structure of the YDR533c <i>S. cerevisiae</i> Protein, a Class II Member of the Hsp31 Family. <i>Structure</i> , 2004, 12, 839-847.	3.3	31
77	Crystal structure of the YGR205w protein from <i>Saccharomyces cerevisiae</i> : Close structural resemblance to <i>E. coli</i> pantothenate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 54, 776-783.	2.6	17
78	The Paris-Sud yeast structural genomics pilot-project: from structure to function. <i>Biochimie</i> , 2004, 86, 617-623.	2.6	18
79	Crystal Structure of the Yeast Phox Homology (PX) Domain Protein Grd19p Complexed to Phosphatidylinositol-3-phosphate. <i>Journal of Biological Chemistry</i> , 2003, 278, 50371-50376.	3.4	64
80	Immunoglobulin-binding domains: Protein L from <i>Peptostreptococcus magnus</i> . <i>Biochemical Society Transactions</i> , 2003, 31, 716-718.	3.4	36
81	Evidence for Plasticity and Structural Mimicry at the Immunoglobulin Light Chain-Protein L Interface. <i>Journal of Biological Chemistry</i> , 2002, 277, 47500-47506.	3.4	39
82	Protein L mutants for the crystallization of antibody fragments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1744-1748.	2.5	17
83	Crystallization of macromolecular complexes. <i>Journal of Crystal Growth</i> , 2001, 232, 580-590.	1.5	8
84	Crystallization of macromolecular complexes: combinatorial complex crystallization. <i>Journal of Crystal Growth</i> , 2001, 232, 573-579.	1.5	12
85	Complex between <i>Peptostreptococcus magnus</i> Protein L and a Human Antibody Reveals Structural Convergence in the Interaction Modes of Fab Binding Proteins. <i>Structure</i> , 2001, 9, 679-687.	3.3	121
86	Crystal structure of a <i>Staphylococcus aureus</i> protein A domain complexed with the Fab fragment of a human IgM antibody: Structural basis for recognition of B-cell receptors and superantigen activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 5399-5404.	7.1	443
87	A B-Cell Superantigen that Targets B-1 Lymphocytes. <i>Current Topics in Microbiology and Immunology</i> , 2000, 252, 251-263.	1.1	11