Marc Graille

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6153730/publications.pdf

Version: 2024-02-01

109321 144013 3,854 87 35 57 h-index citations g-index papers 90 90 90 4914 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	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. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 5399-5404.	7.1	443
2	The human 18S rRNA m6A methyltransferase METTL5 is stabilized by TRMT112. Nucleic Acids Research, 2019, 47, 7719-7733.	14.5	312
3	Complex between Peptostreptococcus magnus Protein L and a Human Antibody Reveals Structural Convergence in the Interaction Modes of Fab Binding Proteins. Structure, 2001, 9, 679-687.	3.3	121
4	Surveillance pathways rescuing eukaryotic ribosomes lost in translation. Nature Reviews Molecular Cell Biology, 2012, 13, 727-735.	37.0	99
5	Structural inhibition of the colicin D tRNase by the tRNA-mimicking immunity protein. EMBO Journal, 2004, 23, 1474-1482.	7.8	85
6	Design, Production and Molecular Structure of a New Family of Artificial Alpha-helicoidal Repeat Proteins ($\hat{1}$ ±Rep) Based on Thermostable HEAT-like Repeats. Journal of Molecular Biology, 2010, 404, 307-327.	4.2	85
7	Structure of Protein Phosphatase Methyltransferase 1 (PPM1), a Leucine Carboxyl Methyltransferase Involved in the Regulation of Protein Phosphatase 2A Activity. Journal of Biological Chemistry, 2004, 279, 8351-8358.	3.4	82
8	Structure of Yeast Dom34. Journal of Biological Chemistry, 2008, 283, 7145-7154.	3.4	81
9	Structural and functional studies of Bud23–Trm112 reveal 18S rRNA <i>N</i> ⁷ -G1575 methylation occurs on late 40S precursor ribosomes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5518-26.	7.1	81
10	Molecular Basis for Bacterial Class I Release Factor Methylation by PrmC. Molecular Cell, 2005, 20, 917-927.	9.7	73
11	Trm112 Is Required for Bud23-Mediated Methylation of the 18S rRNA at Position G1575. Molecular and Cellular Biology, 2012, 32, 2254-2267.	2.3	73
12	Crystal Structure and Functional Characterization of Yeast YLR011wp, an Enzyme with NAD(P)H-FMN and Ferric Iron Reductase Activities. Journal of Biological Chemistry, 2004, 279, 34890-34897.	3.4	71
13	An archaeal orthologue of the universal protein Kae1 is an iron metalloprotein which exhibits atypical DNA-binding properties and apurinic-endonuclease activity in vitro. Nucleic Acids Research, 2007, 35, 6042-6051.	14.5	65
14	Mechanism of activation of methyltransferases involved in translation by the Trm112 â€ [™] hubâ€ [™] protein. Nucleic Acids Research, 2011, 39, 6249-6259.	14.5	65
15	Crystal Structure of the Yeast Phox Homology (PX) Domain Protein Grd19p Complexed to Phosphatidylinositol-3-phosphate. Journal of Biological Chemistry, 2003, 278, 50371-50376.	3.4	64
16	Activation of the LicT Transcriptional Antiterminator Involves a Domain Swing/Lock Mechanism Provoking Massive Structural Changes. Journal of Biological Chemistry, 2005, 280, 14780-14789.	3.4	64
17	Structure of the archaeal Kae1/Bud32 fusion protein MJ1130: a model for the eukaryotic EKC/KEOPS subcomplex. EMBO Journal, 2008, 27, 2340-2351.	7.8	62
18	Crystal Structure of an Intact Type II DNA Topoisomerase: Insights into DNA Transfer Mechanisms. Structure, 2008, 16, 360-370.	3.3	62

#	Article	IF	CITATIONS
19	Dissection of Dom34–Hbs1 reveals independent functions in two RNA quality control pathways. Nature Structural and Molecular Biology, 2010, 17, 1446-1452.	8.2	60
20	A new \hat{l} ±-helical extension promotes RNA binding by the dsRBD of Rnt1p RNAse III. EMBO Journal, 2004, 23, 2468-2477.	7.8	56
21	The Zinc Finger Protein Ynr046w Is Plurifunctional and a Component of the eRF1 Methyltransferase in Yeast. Journal of Biological Chemistry, 2006, 281, 36140-36148.	3.4	54
22	The yeast ribosome synthesis factor Emg1 is a novel member of the superfamily of alpha/beta knot fold methyltransferases. Nucleic Acids Research, 2007, 36, 629-639.	14.5	54
23	Structural insights into the dimerization of the response regulator ComE from Streptococcus pneumoniae. Nucleic Acids Research, 2014, 42, 5302-5313.	14.5	54
24	Catalytic Mechanism and Structure of Viral Flavin-dependent Thymidylate Synthase ThyX. Journal of Biological Chemistry, 2006, 281, 24048-24057.	3.4	53
25	Crystal structure of the effector <scp>A</scp> vr <scp>L</scp> m4–7 of <i>Leptosphaeria maculans</i> reveals insights into its translocation into plant cells and recognition by resistance proteins. Plant Journal, 2015, 83, 610-624.	5.7	52
26	The 18S ribosomal <scp>RNA</scp> m ⁶ A methyltransferase Mettl5 is required for normal walking behavior in <i>Drosophila</i> . EMBO Reports, 2020, 21, e49443.	4.5	52
27	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. Journal of Molecular Biology, 2005, 354, 447-458.	4.2	50
28	Structure of the active form of Dcp1–Dcp2 decapping enzyme bound to m7GDP and its Edc3 activator. Nature Structural and Molecular Biology, 2016, 23, 982-986.	8.2	48
29	Trm112, a Protein Activator of Methyltransferases Modifying Actors of the Eukaryotic Translational Apparatus. Biomolecules, 2017, 7, 7.	4.0	48
30	Selection of Specific Protein Binders for Pre-Defined Targets from an Optimized Library of Artificial Helicoidal Repeat Proteins (alphaRep). PLoS ONE, 2013, 8, e71512.	2.5	47
31	A unique surface on Pat1 C-terminal domain directly interacts with Dcp2 decapping enzyme and Xrn1 $5\hat{a}\in^2\hat{a}\in^*3\hat{a}\in^*2$ mRNA exonuclease in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9493-E9501.	7.1	45
32	m6A mRNA Destiny: Chained to the rhYTHm by the YTH-Containing Proteins. Genes, 2019, 10, 49.	2.4	44
33	Crystal structures of the Gon7/Pcc1 and Bud32/Cgi121 complexes provide a model for the complete yeast KEOPS complex. Nucleic Acids Research, 2015, 43, 3358-3372.	14.5	43
34	The universal Kae1 protein and the associated Bud32 kinase (PRPK), a mysterious protein couple probably essential for genome maintenance in Archaea and Eukarya. Biochemical Society Transactions, 2009, 37, 29-35.	3.4	42
35	Evidence for Plasticity and Structural Mimicry at the Immunoglobulin Light Chain-Protein L Interface. Journal of Biological Chemistry, 2002, 277, 47500-47506.	3.4	39
36	Insights into molecular plasticity in protein complexes from Trm9-Trm112 tRNA modifying enzyme crystal structure. Nucleic Acids Research, 2015, 43, 10989-11002.	14.5	38

#	Article	IF	Citations
37	Fine Tuning of the Specificity of an Anti-progesterone Antibody by First and Second Sphere Residue Engineering. Journal of Biological Chemistry, 2005, 280, 24880-24887.	3.4	37
38	Zinc Induces Structural Reorganization of Gelatin Binding Domain from Human Fibronectin and Affects Collagen Binding. Structure, 2010, 18, 710-718.	3.3	37
39	Mechanistic and structural basis for inhibition of thymidylate synthase ThyX. Open Biology, 2012, 2, 120120.	3.6	37
40	Evolutionary insights into Trm112-methyltransferase holoenzymes involved in translation between archaea and eukaryotes. Nucleic Acids Research, 2018, 46, 8483-8499.	14.5	37
41	Immunoglobulin-binding domains: Protein L from Peptostreptococcus magnus. Biochemical Society Transactions, 2003, 31, 716-718.	3.4	36
42	Inhibition of archaeal growth and DNA topoisomerase VI activities by the Hsp90 inhibitor radicicol. Nucleic Acids Research, 2005, 33, 2310-2317.	14.5	33
43	Functional and Structural Characterization of PaeM, a Colicin M-like Bacteriocin Produced by Pseudomonas aeruginosa. Journal of Biological Chemistry, 2012, 287, 37395-37405.	3.4	33
44	Crystal Structure of the YDR533c S. cerevisiae Protein, a Class II Member of the Hsp31 Family. Structure, 2004, 12, 839-847.	3.3	31
45	The structure of the NasR transcription antiterminator reveals a oneâ€component system with a NIT nitrate receptor coupled to an ANTAR RNAâ€binding effector. Molecular Microbiology, 2012, 85, 431-444.	2.5	31
46	Structural and Functional Insights into Saccharomyces cerevisiae Tpa1, a Putative Prolylhydroxylase Influencing Translation Termination and Transcription. Journal of Biological Chemistry, 2010, 285, 30767-30778.	3.4	30
47	Crystal Structure of the Bifunctional Chorismate Synthase from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2004, 279, 619-625.	3.4	29
48	The structure of an archaeal homodimeric ligase which has RNA circularization activity. Protein Science, 2008, 17, 1336-1345.	7.6	28
49	Formation of S. pombe Erh1 homodimer mediates gametogenic gene silencing and meiosis progression. Scientific Reports, 2020, 10, 1034.	3.3	25
50	Structures of in Vitro Evolved Binding Sites on Neocarzinostatin Scaffold Reveal Unanticipated Evolutionary Pathways. Journal of Molecular Biology, 2006, 358, 455-471.	4.2	24
51	Crystal Structure of Yeast Allantoicase Reveals a Repeated Jelly Roll Motif. Journal of Biological Chemistry, 2004, 279, 23447-23452.	3.4	23
52	HalX: an open-source LIMS (Laboratory Information Management System) for small- to large-scale laboratories. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 671-678.	2.5	23
53	Activation mode of the eukaryotic m ² G ₁₀ tRNA methyltransferase Trm11 by its partner protein Trm112. Nucleic Acids Research, 2017, 45, gkw1271.	14.5	23
54	mRNA decapping: finding the right structures. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20180164.	4.0	23

#	Article	IF	CITATIONS
55	Structure-based Functional Annotation. Journal of Biological Chemistry, 2006, 281, 30175-30185.	3.4	22
56	A scaffold IncRNA shapes the mitosis to meiosis switch. Nature Communications, 2021, 12, 770.	12.8	22
57	The X-ray crystallography phase problem solved thanks to <i>AlphaFold</i> and <i>RoseTTAFold</i> models: a case-study report. Acta Crystallographica Section D: Structural Biology, 2022, 78, 517-531.	2.3	22
58	X-Ray Structure and Site-Directed Mutagenesis Analysis of the <i>Escherichia coli </i> Colicin M Immunity Protein. Journal of Bacteriology, 2011, 193, 205-214.	2.2	21
59	Observation and Characterization of the Interaction between a Single Immunoglobulin Binding Domain of Protein L and Two Equivalents of Human κ Light Chains. Journal of Biological Chemistry, 2004, 279, 9370-9378.	3.4	20
60	Crystal structure of yeast YHR049W/FSH1, a member of the serine hydrolase family. Protein Science, 2005, 14, 1350-1356.	7.6	20
61	Identification of the Rps28 binding motif from yeast Edc3 involved in the autoregulatory feedback loop controlling RPS28B mRNA decay. Nucleic Acids Research, 2013, 41, 9514-9523.	14.5	19
62	The Paris-Sud yeast structural genomics pilot-project: from structure to function. Biochimie, 2004, 86, 617-623.	2.6	18
63	The HSP90 and DNA topoisomerase VI inhibitor radicicol also inhibits human type II DNA topoisomerase. Biochemical Pharmacology, 2006, 72, 1207-1216.	4.4	18
64	Protein L mutants for the crystallization of antibody fragments. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1744-1748.	2.5	17
65	Crystal structure of the YGR205w protein from Saccharomyces cerevisiae: Close structural resemblance to E. coli pantothenate kinase. Proteins: Structure, Function and Bioinformatics, 2004, 54, 776-783.	2.6	17
66	Structureâ€"function analysis of Knr4/Smi1, a newly member of intrinsically disordered proteins family, indispensable in the absence of a functional <i>PKC1â€"SLT2</i> pathway in <i>Saccharomyces cerevisiae</i> . Yeast, 2008, 25, 563-576.	1.7	17
67	Structural and functional analysis of the fibronectinâ€binding protein <scp>FNE</scp> from <i>Streptococcus equi</i> spp. <i>equi</i> FEBS Journal, 2014, 281, 5513-5531.	4.7	17
68	Crystal structure of the D-ribose-5-phosphate isomerase: comparison with the archaeal and bacterial enzymes. Biochimie, 2005, 87, 763-769.	2.6	16
69	A Highly Conserved Region Essential for NMD in the Upf2 N-Terminal Domain. Journal of Molecular Biology, 2014, 426, 3689-3702.	4.2	16
70	The DEAH-box RNA helicase Dhr1 contains a remarkable carboxyl terminal domain essential for small ribosomal subunit biogenesis. Nucleic Acids Research, 2019, 47, 7548-7563.	14.5	15
71	High-throughput crystal-optimization strategies in the South Paris Yeast Structural Genomics Project: one size fits all?. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 664-670.	2.5	14
72	Methylation of class I translation termination factors: Structural and functional aspects. Biochimie, 2012, 94, 1533-1543.	2.6	14

#	Article	IF	Citations
73	The C-Terminal Domain from S. cerevisiae Pat1 Displays Two Conserved Regions Involved in Decapping Factor Recruitment. PLoS ONE, 2014, 9, e96828.	2.5	14
74	Crystal structure of the YML079w protein from Saccharomyces cerevisiae reveals a new sequence family of the jelly-roll fold. Protein Science, 2009, 14, 209-215.	7.6	13
75	Crystallization of macromolecular complexes: combinatorial complex crystallization. Journal of Crystal Growth, 2001, 232, 573-579.	1.5	12
76	Structural and functional analysis of Nro1/Ett1: a protein involved in translation termination in S. cerevisiae and in O2-mediated gene control in S. pombe. Rna, 2011, 17, 1213-1224.	3.5	11
77	A B-Cell Superantigen that Targets B-1 Lymphocytes. Current Topics in Microbiology and Immunology, 2000, 252, 251-263.	1.1	11
78	The catalytic activity of the translation termination factor methyltransferase Mtq2-Trm112 complex is required for large ribosomal subunit biogenesis. Nucleic Acids Research, 2020, 48, 12310-12325.	14.5	9
79	Crystallization of macromolecular complexes:. Journal of Crystal Growth, 2001, 232, 580-590.	1.5	8
80	Crystal structure of the yeast His6 enzyme suggests a reaction mechanism. Protein Science, 2006, 15, 1516-1521.	7.6	8
81	Structural and functional insights into Archaeoglobus fulgidus m2G10 tRNA methyltransferase Trm11 and its Trm112 activator. Nucleic Acids Research, 2020, 48, 11068-11082.	14.5	8
82	ERH proteins: connecting RNA processing to tumorigenesis?. Current Genetics, 2020, 66, 689-692.	1.7	8
83	Crystal structure of yeast YER010Cp, aknotable member of the RraA protein family. Protein Science, 2005, 14, 2751-2758.	7.6	5
84	Division of labor in epitranscriptomics: What have we learnt from the structures of eukaryotic and viral multimeric <scp>RNA</scp> methyltransferases?. Wiley Interdisciplinary Reviews RNA, 2022, 13, e1673.	6.4	5
85	Pby1 is a direct partner of the Dcp2 decapping enzyme. Nucleic Acids Research, 2020, 48, 6353-6366.	14.5	4
86	Cytoplasmic mRNA Surveillance Pathways. , 2014, , 195-216.		0
87	Cg1246, a new player in mycolic acid biosynthesis in Corynebacterium glutamicum. Microbiology (United Kingdom), 2022, 168, .	1.8	0