

Janosch Hennig

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/102800/publications.pdf>

Version: 2024-02-01

56
papers

2,092
citations

279798

23
h-index

276875

41
g-index

72
all docs

72
docs citations

72
times ranked

2976
citing authors

#	ARTICLE	IF	CITATIONS
1	Vault RNA1 ^Δ 1 riboregulates the autophagic function of p62 by binding to lysine 7 and arginine 21, both of which are critical for p62 oligomerization. <i>Rna</i> , 2022, 28, 742-755.	3.5	9
2	Riboregulation of Enolase 1 activity controls glycolysis and embryonic stem cell differentiation. <i>Molecular Cell</i> , 2022, 82, 2666-2680.e11.	9.7	37
3	Transcriptional regulation of the μ -fructoselysine metabolism in <i>Escherichia coli</i> by global and substrate-specific cues. <i>Molecular Microbiology</i> , 2021, 115, 175-190.	2.5	10
4	Molecular basis of mRNA transport by a kinesin-1 ^Δ atypical tropomyosin complex. <i>Genes and Development</i> , 2021, 35, 976-991.	5.9	29
5	Divergent evolution toward sex chromosome-specific gene regulation in <i>Drosophila</i> . <i>Genes and Development</i> , 2021, 35, 1055-1070.	5.9	12
6	Validation and classification of RNA binding proteins identified by mRNA interactome capture. <i>Rna</i> , 2021, 27, 1173-1185.	3.5	11
7	Structure and dynamics of the quaternary hunchback mRNA translation repression complex. <i>Nucleic Acids Research</i> , 2021, 49, 8866-8885.	14.5	4
8	Structural basis of PETISCO complex assembly during piRNA biogenesis in <i>C. elegans</i> . <i>Genes and Development</i> , 2021, 35, 1304-1323.	5.9	14
9	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , 2021, 597, 533-538.	27.8	159
10	Mechanistic insights into transcription factor cooperativity and its impact on protein-phenotype interactions. <i>Nature Communications</i> , 2020, 11, 124.	12.8	54
11	Integrative Structural Biology of Protein-RNA Complexes. <i>Structure</i> , 2020, 28, 6-28.	3.3	33
12	Pseudo-RNA-Binding Domains Mediate RNA Structure Specificity in Upstream of N-Ras. <i>Cell Reports</i> , 2020, 32, 107930.	6.4	18
13	Molecular dissection of amyloid disaggregation by human HSP70. <i>Nature</i> , 2020, 587, 483-488.	27.8	153
14	Macrocyclic Peptides Uncover a Novel Binding Mode for Reversible Inhibitors of LSD1. <i>ACS Omega</i> , 2020, 5, 3979-3995.	3.5	21
15	Structure-based screening of binding affinities via small-angle X-ray scattering. <i>IUCr</i> , 2020, 7, 644-655.	2.2	9
16	Gain-of-Function Variant p.Pro2555Arg of von Willebrand Factor Increases Aggregate Size through Altering Stem Dynamics. <i>Thrombosis and Haemostasis</i> , 2020, , .	3.4	3
17	Combined Small-Angle X-ray and Neutron Scattering Restraints in Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 4687-4698.	5.3	36
18	Switching the Post-translational Modification of Translation Elongation Factor EF-P. <i>Frontiers in Microbiology</i> , 2019, 10, 1148.	3.5	16

#	ARTICLE	IF	CITATIONS
19	Highlight: Young research groups in Germany – continued. <i>Biological Chemistry</i> , 2019, 400, 1395-1395.	2.5	2
20	Emerging RNA-binding roles in the TRIM family of ubiquitin ligases. <i>Biological Chemistry</i> , 2019, 400, 1443-1464.	2.5	59
21	Structural Basis of an Asymmetric Condensin ATPase Cycle. <i>Molecular Cell</i> , 2019, 74, 1175-1188.e9.	9.7	68
22	Highlight: young research groups in Germany. <i>Biological Chemistry</i> , 2019, 400, 811-812.	2.5	5
23	Structure, dynamics and roX2-lncRNA binding of tandem double-stranded RNA binding domains dsRBD1,2 of <i>Drosophila</i> helicase Maleless. <i>Nucleic Acids Research</i> , 2019, 47, 4319-4333.	14.5	17
24	Structure and dynamics of the platelet integrin-binding C4 domain of von Willebrand factor. <i>Blood</i> , 2019, 133, 366-376.	1.4	22
25	Ab Initio Prediction of NMR Spin Relaxation Parameters from Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 1009-1019.	5.3	23
26	A General Small-Angle X-ray Scattering-Based Screening Protocol Validated for Protein-RNA Interactions. <i>ACS Combinatorial Science</i> , 2018, 20, 197-202.	3.8	18
27	The role of small-angle scattering in structure-based screening applications. <i>Biophysical Reviews</i> , 2018, 10, 1295-1310.	3.2	10
28	Molecular mechanism of influenza A NS1-mediated TRIM25 recognition and inhibition. <i>Nature Communications</i> , 2018, 9, 1820.	12.8	124
29	Segmental, Domain-Selective perdeuteration and Small-Angle Neutron Scattering for Structural Analysis of Multi-Domain Proteins. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 9322-9325.	13.8	52
30	Structural Basis for EarP-Mediated Arginine Glycosylation of Translation Elongation Factor EF-P. <i>MBio</i> , 2017, 8, .	4.1	24
31	Segmental, Domain-Selective perdeuteration and Small-Angle Neutron Scattering for Structural Analysis of Multi-Domain Proteins. <i>Angewandte Chemie</i> , 2017, 129, 9450-9453.	2.0	4
32	Resolving the β -glycosidic linkage of arginine-rhamnosylated translation elongation factor P triggers generation of the first Arg ^{Rha} specific antibody. <i>Chemical Science</i> , 2016, 7, 6995-7001.	7.4	30
33	Improved Accuracy from Joint X-ray and NMR Refinement of a Protein-RNA Complex Structure. <i>Journal of the American Chemical Society</i> , 2016, 138, 1601-1610.	13.7	22
34	The Crystal Structure of the NHL Domain in Complex with RNA Reveals the Molecular Basis of <i>Drosophila</i> Brain-Tumor-Mediated Gene Regulation. <i>Cell Reports</i> , 2015, 13, 1206-1220.	6.4	79
35	Structural basis for cpSRP43 chromodomain selectivity and dynamics in Alb3 insertase interaction. <i>Nature Communications</i> , 2015, 6, 8875.	12.8	24
36	Local Destabilization of the Metal-Binding Region in Human Copper-Zinc Superoxide Dismutase by Remote Mutations Is a Possible Determinant for Progression of ALS. <i>Biochemistry</i> , 2015, 54, 323-333.	2.5	9

#	ARTICLE	IF	CITATIONS
37	Deciphering the protein-RNA recognition code: Combining large-scale quantitative methods with structural biology. <i>BioEssays</i> , 2015, 37, 899-908.	2.5	26
38	The EBNA-2 N-Terminal Transactivation Domain Folds into a Dimeric Structure Required for Target Gene Activation. <i>PLoS Pathogens</i> , 2015, 11, e1004910.	4.7	10
39	Structural Analysis of Protein-RNA Complexes in Solution Using NMR Paramagnetic Relaxation Enhancements. <i>Methods in Enzymology</i> , 2015, 558, 333-362.	1.0	16
40	Efficient segmental isotope labeling of multi-domain proteins using Sortase A. <i>Journal of Biomolecular NMR</i> , 2015, 63, 1-8.	2.8	79
41	Breaking the protein-RNA recognition code. <i>Cell Cycle</i> , 2014, 13, 3619-3620.	2.6	14
42	Structure, dynamics and RNA binding of the multi-domain splicing factor TIA-1. <i>Nucleic Acids Research</i> , 2014, 42, 5949-5966.	14.5	77
43	The dynamic duo: Combining NMR and small angle scattering in structural biology. <i>Protein Science</i> , 2014, 23, 669-682.	7.6	45
44	The structural analysis of shark IgNAR antibodies reveals evolutionary principles of immunoglobulins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8155-8160.	7.1	67
45	The NHL domain of BRAT is an RNA-binding domain that directly contacts the <i>hunchback</i> mRNA for regulation. <i>Genes and Development</i> , 2014, 28, 749-764.	5.9	74
46	Structural basis for the assembly of the Sxl-Unr translation regulatory complex. <i>Nature</i> , 2014, 515, 287-290.	27.8	102
47	Protein conformational exchange measured by ¹ H R ₁ ρ-relaxation dispersion of methyl groups. <i>Journal of Biomolecular NMR</i> , 2013, 57, 47-55.	2.8	19
48	Combining NMR and small angle X-ray and neutron scattering in the structural analysis of a ternary protein-RNA complex. <i>Journal of Biomolecular NMR</i> , 2013, 56, 17-30.	2.8	48
49	Structural features of Argonaute-GW182 protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3770-9.	7.1	98
50	MTMDAT-HADDOCK: High-throughput, protein complex structure modeling based on limited proteolysis and mass spectrometry. <i>BMC Structural Biology</i> , 2012, 12, 29.	2.3	11
51	Structural Characteristics Determine the Cause of the Low Enzyme Activity of Two Thiopurine S-Methyltransferase Allelic Variants: A Biophysical Characterization of TPMT*2 and TPMT*5. <i>Biochemistry</i> , 2012, 51, 5912-5920.	2.5	7
52	Anti-Ro52 Autoantibodies from Patients with Sjögren's Syndrome Inhibit the Ro52 E3 Ligase Activity by Blocking the E3/E2 Interface. <i>Journal of Biological Chemistry</i> , 2011, 286, 36478-36491.	3.4	64
53	The Fellowship of the RING: The RING-B-Box Linker Region Interacts with the RING in TRIM21/Ro52, Contains a Native Autoantigenic Epitope in Sjögren Syndrome, and is an Integral and Conserved Region in TRIM Proteins. <i>Journal of Molecular Biology</i> , 2008, 377, 431-449.	4.2	23
54	MTMDAT: Automated analysis and visualization of mass spectrometry data for tertiary and quaternary structure probing of proteins. <i>Bioinformatics</i> , 2008, 24, 1310-1312.	4.1	10

#	ARTICLE	IF	CITATIONS
55	Structural, functional and immunologic characterization of folded subdomains in the Ro52 protein targeted in Sjögren's syndrome. <i>Molecular Immunology</i> , 2006, 43, 588-598.	2.2	40
56	Structural Organization and Zn ²⁺ -dependent Subdomain Interactions Involving Autoantigenic Epitopes in the Ring-B-box-Coiled-coil (RBCC) Region of Ro52. <i>Journal of Biological Chemistry</i> , 2005, 280, 33250-33261.	3.4	22