Janosch Hennig

List of Publications by Year
in descending order

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56	2,092	279487	276539
papers	citations	23 h-index	41 g-index

72	72	72	2976
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Bioaccumulation of therapeutic drugs by human gut bacteria. Nature, 2021, 597, 533-538.	13.7	159
2	Molecular dissection of amyloid disaggregation by human HSP70. Nature, 2020, 587, 483-488.	13.7	153
3	Molecular mechanism of influenza A NS1-mediated TRIM25 recognition and inhibition. Nature Communications, 2018, 9, 1820.	5.8	124
4	Structural basis for the assembly of the Sxlâ€“Unr translation regulatory complex. Nature, 2014, 515, 287-290.	13.7	102
5	Structural features of Argonauteâ€“GW182 protein interactions. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3770-9.	3.3	98
6	The Crystal Structure of the NHL Domain in Complex with RNA Reveals the Molecular Basis of Drosophila Brain-Tumor-Mediated Gene Regulation. Cell Reports, 2015, 13, 1206-1220.	2.9	79
7	Efficient segmental isotope labeling of multi-domain proteins using Sortase A. Journal of Biomolecular NMR, 2015, 63, 1-8.	1.6	79
8	Structure, dynamics and RNA binding of the multi-domain splicing factor TIA-1. Nucleic Acids Research, 2014, 42, 5949-5966.	6.5	77
9	The NHL domain of BRAT is an RNA-binding domain that directly contacts the hunchback mRNA for regulation. Genes and Development, 2014, 28, 749-764.	2.7	74
10	Structural Basis of an Asymmetric Condensin ATPase Cycle. Molecular Cell, 2019, 74, 1175-1188.e9.	4.5	68
11	The structural analysis of shark IgNAR antibodies reveals evolutionary principles of immunoglobulins. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8155-8160.	3.3	67
12	Anti-Ro52 Autoantibodies from Patients with SjÃ¶gren's Syndrome Inhibit the Ro52 E3 Ligase Activity by Blocking the E3/E2 Interface. Journal of Biological Chemistry, 2011, 286, 36478-36491.	1.6	64
13	Emerging RNA-binding roles in the TRIM family of ubiquitin ligases. Biological Chemistry, 2019, 400, 1443-1464.	1.2	59
14	Mechanistic insights into transcription factor cooperativity and its impact on protein-phenotype interactions. Nature Communications, 2020, 11, 124.	5.8	54
15	Segmental, Domainâ€Selective Perdeuteration and Smallâ€Angle Neutron Scattering for Structural Analysis of Multiâ€Domain Proteins. Angewandte Chemie - International Edition, 2017, 56, 9322-9325.	7.2	52
16	Combining NMR and small angle X-ray and neutron scattering in the structural analysis of a ternary protein-RNA complex. Journal of Biomolecular NMR, 2013, 56, 17-30.	1.6	48
17	The dynamic duo: Combining NMR and small angle scattering in structural biology. Protein Science, 2014, 23, 669-682.	3.1	45
18	Structural, functional and immunologic characterization of folded subdomains in the Ro52 protein targeted in SjÃ¶gren's syndrome. Molecular Immunology, 2006, 43, 588-598.	1.0	40

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19	Riboregulation of Enolase 1 activity controls glycolysis and embryonic stem cell differentiation. Molecular Cell, 2022, 82, 2666-2680.e11.	4.5	37
20	Combined Small-Angle X-ray and Neutron Scattering Restraints in Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2019, 15, 4687-4698.	2.3	36
21	Integrative Structural Biology of Protein-RNA Complexes. Structure, 2020, 28, 6-28.	1.6	33
22	Resolving the Î±-glycosidic linkage of arginine-rhamnosylated translation elongation factor P triggers generation of the first Arg^{Rha} specific antibody. Chemical Science, 2016, 7, 6995-7001.	3.7	30
23	Molecular basis of mRNA transport by a kinesin-1â€“atypical tropomyosin complex. Genes and Development, 2021, 35, 976-991.	2.7	29
24	Deciphering the proteinâ€RNA recognition code: Combining largeâ€scale quantitative methods with structural biology. BioEssays, 2015, 37, 899-908.	1.2	26
25	Structural basis for cpSRP43 chromodomain selectivity and dynamics in Alb3 insertase interaction. Nature Communications, 2015, 6, 8875.	5.8	24
26	Structural Basis for EarP-Mediated Arginine Glycosylation of Translation Elongation Factor EF-P. MBio, 2017, 8, .	1.8	24
27	The Fellowship of the RING: The RINGâ€“B-Box Linker Region Interacts with the RING in TRIM21/Ro52, Contains a Native Autoantigenic Epitope in SjÃ¶gren Syndrome, and is an Integral and Conserved Region in TRIM Proteins. Journal of Molecular Biology, 2008, 377, 431-449.	2.0	23
28	Ab Initio Prediction of NMR Spin Relaxation Parameters from Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2018, 14, 1009-1019.	2.3	23
29	Structural Organization and Zn2+-dependent Subdomain Interactions Involving Autoantigenic Epitopes in the Ring-B-box-Coiled-coil (RBCC) Region of Ro52. Journal of Biological Chemistry, 2005, 280, 33250-33261.	1.6	22
30	Improved Accuracy from Joint X-ray and NMR Refinement of a Proteinâ€“RNA Complex Structure. Journal of the American Chemical Society, 2016, 138, 1601-1610.	6.6	22
31	Structure and dynamics of the platelet integrin-binding C4 domain of von Willebrand factor. Blood, 2019, 133, 366-376.	0.6	22
32	Macrocyclic Peptides Uncover a Novel Binding Mode for Reversible Inhibitors of LSD1. ACS Omega, 2020, 5, 3979-3995.	1.6	21
33	Protein conformational exchange measured by 1H R1Ï•relaxation dispersion of methyl groups. Journal of Biomolecular NMR, 2013, 57, 47-55.	1.6	19
34	A General Small-Angle X-ray Scattering-Based Screening Protocol Validated for Proteinâ€“RNA Interactions. ACS Combinatorial Science, 2018, 20, 197-202.	3.8	18
35	Pseudo-RNA-Binding Domains Mediate RNA Structure Specificity in Upstream of N-Ras. Cell Reports, 2020, 32, 107930.	2.9	18
36	Structure, dynamics and roX2-lncRNA binding of tandem double-stranded RNA binding domains dsRBD1,2 of Drosophila helicase Maleless. Nucleic Acids Research, 2019, 47, 4319-4333.	6.5	17

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37	Structural Analysis of Proteinâ€“RNA Complexes in Solution Using NMR Paramagnetic Relaxation Enhancements. Methods in Enzymology, 2015, 558, 333-362.	0.4	16
38	Switching the Post-translational Modification of Translation Elongation Factor EF-P. Frontiers in Microbiology, 2019, 10, 1148.	1.5	16
39	Breaking the protein-RNA recognition code. Cell Cycle, 2014, 13, 3619-3620.	1.3	14
40	Structural basis of PETISCO complex assembly during piRNA biogenesis in C. elegans. Genes and Development, 2021, 35, 1304-1323.	2.7	14
41	Divergent evolution toward sex chromosome-specific gene regulation inDrosophila. Genes and Development, 2021, 35, 1055-1070.	2.7	12
42	MTMDAT-HADDOCK: High-throughput, protein complex structure modeling based on limited proteolysis and mass spectrometry. BMC Structural Biology, 2012, 12, 29.	2.3	11
43	Validation and classification of RNA binding proteins identified by mRNA interactome capture. Rna, 2021, 27, 1173-1185.	1.6	11
44	MTMDAT: Automated analysis and visualization of mass spectrometry data for tertiary and quaternary structure probing of proteins. Bioinformatics, 2008, 24, 1310-1312.	1.8	10
45	The EBNA-2 N-Terminal Transactivation Domain Folds into a Dimeric Structure Required for Target Gene Activation. PLoS Pathogens, 2015, 11, e1004910.	2.1	10
46	The role of small-angle scattering in structure-based screening applications. Biophysical Reviews, 2018, 10, 1295-1310.	1.5	10
47	Transcriptional regulation of the N_{Îµ}â€fructoselysine metabolism in Escherichia coli by global and substrateâ€specific cues. Molecular Microbiology, 2021, 115, 175-190.	1.2	10
48	Local Destabilization of the Metal-Binding Region in Human Copperâ€“Zinc Superoxide Dismutase by Remote Mutations Is a Possible Determinant for Progression of ALS. Biochemistry, 2015, 54, 323-333.	1.2	9
49	Structure-based screening of binding affinities via small-angle X-ray scattering. IUCrJ, 2020, 7, 644-655.	1.0	9
50	Vault RNA1â€“1 riboregulates the autophagic function of p62 by binding to lysine 7 and arginine 21, both of which are critical for p62 oligomerization. Rna, 2022, 28, 742-755.	1.6	9
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. Biochemistry, 2012, 51, 5912-5920.	1.2	7
52	Highlight: young research groups in Germany. Biological Chemistry, 2019, 400, 811-812.	1.2	5
53	Segmental, Domainâ€Selective Perdeuteration and Smallâ€Angle Neutron Scattering for Structural Analysis of Multiâ€Domain Proteins. Angewandte Chemie, 2017, 129, 9450-9453.	1.6	4
54	Structure and dynamics of the quaternary hunchback mRNA translation repression complex. Nucleic Acids Research, 2021, 49, 8866-8885.	6.5	4

#	Article	IF	Citations
55	Gain-of-Function Variant p.Pro2555Arg of von Willebrand Factor Increases Aggregate Size through Altering Stem Dynamics. Thrombosis and Haemostasis, 2020, , .	1.8	3
56	Highlight: Young research groups in Germany â€“ continued. Biological Chemistry, 2019, 400, 1395-1395.	1.2	2