

# Jiri Novacek

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9102522/publications.pdf>

Version: 2024-02-01

26  
papers

850  
citations

471509

17  
h-index

526287

27  
g-index

29  
all docs

29  
docs citations

29  
times ranked

1265  
citing authors

#	ARTICLE	IF	CITATIONS
1	A switch from $\alpha$ -helical to $\beta$ -strand conformation during co-translational protein folding. EMBO Journal, 2022, 41, e109175.	7.8	21
2	Virion Structure and <i>In Vitro</i> Genome Release Mechanism of Dicistrovirus Kashmir Bee Virus. Journal of Virology, 2021, 95, .	3.4	4
3	Lipoprotein Particles Interact with Membranes and Transfer Their Cargo without Receptors. Biochemistry, 2020, 59, 4421-4428.	2.5	18
4	Receptor-Independent Transfer of Low Density Lipoprotein Cargo to Biomembranes. Nano Letters, 2019, 19, 2562-2567.	9.1	23
5	A role for the <i>Saccharomyces cerevisiae</i> ABCF protein New1 in translation termination/recycling. Nucleic Acids Research, 2019, 47, 8807-8820.	14.5	26
6	Role of SH3b binding domain in a natural deletion mutant of Kayvirus endolysin LysF1 with a broad range of lytic activity. Virus Genes, 2018, 54, 130-139.	1.6	40
7	Structural basis for antibiotic resistance mediated by the <i>Bacillus subtilis</i> ABCF ATPase VmlR. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8978-8983.	7.1	78
8	The Structural Properties in Solution of the Intrinsically Mixed Folded Protein Ataxin-3. Biophysical Journal, 2018, 115, 59-71.	0.5	10
9	Functionally specific binding regions of microtubule-associated protein 2c exhibit distinct conformations and dynamics. Journal of Biological Chemistry, 2018, 293, 13297-13309.	3.4	13
10	Multivalency regulates activity in an intrinsically disordered transcription factor. ELife, 2018, 7, .	6.0	34
11	Phosphorylation of the regulatory domain of human tyrosine hydroxylase 1 monitored using non-uniformly sampled NMR. Biophysical Chemistry, 2017, 223, 25-29.	2.8	13
12	Structure of deformed wing virus, a major honey bee pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3210-3215.	7.1	43
13	Quantitative mapping of microtubule-associated protein 2c (MAP2c) phosphorylation and regulatory protein 14-3-3 $\sigma$ -binding sites reveals key differences between MAP2c and its homolog Tau. Journal of Biological Chemistry, 2017, 292, 6715-6727.	3.4	16
14	Triple resonance $^{15}\text{N}$ NMR relaxation experiments for studies of intrinsically disordered proteins. Journal of Biomolecular NMR, 2017, 69, 133-146.	2.8	11
15	Structure and genome release of Twort-like Myoviridae phage with a double-layered baseplate. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9351-9356.	7.1	77
16	NMR assignment of intrinsically disordered self-processing module of the FrpC protein of <i>Neisseria meningitidis</i> . Biomolecular NMR Assignments, 2015, 9, 435-440.	0.8	5
17	Conformational Dynamics and Antigenicity in the Disordered Malaria Antigen Merozoite Surface Protein 2. PLoS ONE, 2015, 10, e0119899.	2.5	27
18	Toward optimal-resolution NMR of intrinsically disordered proteins. Journal of Magnetic Resonance, 2014, 241, 41-52.	2.1	29

#	ARTICLE	IF	CITATIONS
19	NMR Determines Transient Structure and Dynamics in the Disordered C-Terminal Domain of WASp Interacting Protein. <i>Biophysical Journal</i> , 2013, 105, 481-493.	0.5	25
20	Multiple Recognition Motifs in Nucleoporin Nup159 Provide a Stable and Rigid Nup159-Dyn2 Assembly. <i>Journal of Biological Chemistry</i> , 2013, 288, 2614-2622.	3.4	35
21	Efficient protocol for backbone and side-chain assignments of large, intrinsically disordered proteins: transient secondary structure analysis of 49.2 kDa microtubule associated protein 2c. <i>Journal of Biomolecular NMR</i> , 2013, 56, 291-301.	2.8	38
22	Structural Study of the Partially Disordered Full-Length $\hat{\nu}$ Subunit of RNA Polymerase from <i>Bacillus subtilis</i> . <i>ChemBioChem</i> , 2013, 14, 1772-1779.	2.6	18
23	4D Non-uniformly sampled HCBCACON and $1J(NC^{\alpha})$ -selective HCBCANCO experiments for the sequential assignment and chemical shift analysis of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2012, 53, 139-148.	2.8	40
24	5D $^{13}C$ -detected experiments for backbone assignment of unstructured proteins with a very low signal dispersion. <i>Journal of Biomolecular NMR</i> , 2011, 50, 1-11.	2.8	77
25	Strategy for complete NMR assignment of disordered proteins with highly repetitive sequences based on resolution-enhanced 5D experiments. <i>Journal of Biomolecular NMR</i> , 2010, 48, 169-177.	2.8	99
26	Solution structure of the N-terminal domain of <i>Bacillus subtilis</i> $\hat{\nu}$ subunit of RNA polymerase and its classification based on structural homologs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1807-1810.	2.6	24