

Gert E Folkers

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/7693436/gert-e-folkers-publications-by-year.pdf>

Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

69 papers	2,377 citations	29 h-index	47 g-index
72 ext. papers	2,626 ext. citations	8.2 avg, IF	4.48 L-index

#	Paper	IF	Citations
69	Characterization of nucleosome sediments for protein interaction studies by solid-state NMR spectroscopy. <i>Magnetic Resonance</i> , 2021 , 2, 187-202	2.9	4
68	Characterizing proteins in a native bacterial environment using solid-state NMR spectroscopy. <i>Nature Protocols</i> , 2021 , 16, 893-918	18.8	16
67	When Small becomes Too Big: Expanding the Use of In-Cell Solid-State NMR Spectroscopy. <i>ChemPlusChem</i> , 2020 , 85, 760-768	2.8	9
66	DNP-Supported Solid-State NMR Spectroscopy of Proteins Inside Mammalian Cells. <i>Angewandte Chemie - International Edition</i> , 2019 , 58, 12969-12973	16.4	53
65	DNP-Supported Solid-State NMR Spectroscopy of Proteins Inside Mammalian Cells. <i>Angewandte Chemie</i> , 2019 , 131, 13103-13107	3.6	16
64	R&Ktitelbild: DNP-Supported Solid-State NMR Spectroscopy of Proteins Inside Mammalian Cells (Angew. Chem. 37/2019). <i>Angewandte Chemie</i> , 2019 , 131, 13296-13296	3.6	
63	iSEE: Interface structure, evolution, and energy-based machine learning predictor of binding affinity changes upon mutations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 110-119	4.2	33
62	Function and Interactions of ERCC1-XPF in DNA Damage Response. <i>Molecules</i> , 2018 , 23,	4.8	31
61	Efficient switching of mCherry fluorescence using chemical caging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 7013-7018	11.5	13
60	Single-stranded DNA Binding by the Helix-Hairpin-Helix Domain of XPF Protein Contributes to the Substrate Specificity of the ERCC1-XPF Protein Complex. <i>Journal of Biological Chemistry</i> , 2017 , 292, 2842-2853	5.4	10
59	EGFR Dynamics Change during Activation in Native Membranes as Revealed by NMR. <i>Cell</i> , 2016 , 167, 1241-1251.e11	56.2	110
58	A model for the interaction of the G3-subdomain of Geobacillus stearothermophilus IF2 with the 30S ribosomal subunit. <i>Protein Science</i> , 2016 , 25, 1722-33	6.3	2
57	Magic-angle-spinning solid-state NMR of membrane proteins. <i>Methods in Enzymology</i> , 2015 , 557, 307-281	1.7	17
56	Efficient cellular solid-state NMR of membrane proteins by targeted protein labeling. <i>Journal of Biomolecular NMR</i> , 2015 , 62, 199-208	3	30
55	The Cerebro-oculo-facio-skeletal Syndrome Point Mutation F231L in the ERCC1 DNA Repair Protein Causes Dissociation of the ERCC1-XPF Complex. <i>Journal of Biological Chemistry</i> , 2015 , 290, 20541-55	5.4	10
54	Probing a cell-embedded megadalton protein complex by DNP-supported solid-state NMR. <i>Nature Methods</i> , 2015 , 12, 649-52	21.6	103
53	Structural basis of nucleic acid binding by Nicotiana tabacum glycine-rich RNA-binding protein: implications for its RNA chaperone function. <i>Nucleic Acids Research</i> , 2014 , 42, 8705-18	20.1	13

52	Proteins feel more than they see: fine-tuning of binding affinity by properties of the non-interacting surface. <i>Journal of Molecular Biology</i> , 2014 , 426, 2632-52	6.5	69
51	The Fanconi anemia associated protein FAAP24 uses two substrate specific binding surfaces for DNA recognition. <i>Nucleic Acids Research</i> , 2013 , 41, 6739-49	20.1	4
50	The structure of the XPF-ssDNA complex underscores the distinct roles of the XPF and ERCC1 helix-hairpin-helix domains in ss/ds DNA recognition. <i>Structure</i> , 2012 , 20, 667-75	5.2	24
49	Structural dynamics of bacterial translation initiation factor IF2. <i>Journal of Biological Chemistry</i> , 2012 , 287, 10922-32	5.4	20
48	Expression of protein complexes using multiple Escherichia coli protein co-expression systems: a benchmarking study. <i>Journal of Structural Biology</i> , 2011 , 175, 159-70	3.4	34
47	Structural insights into transcription complexes. <i>Journal of Structural Biology</i> , 2011 , 175, 135-46	3.4	13
46	NMR characterization of foldedness for the production of E3 RING domains. <i>Journal of Structural Biology</i> , 2010 , 172, 120-7	3.4	5
45	Novel structural features in two ZHX homeodomains derived from a systematic study of single and multiple domains. <i>BMC Structural Biology</i> , 2010 , 10, 13	2.7	9
44	Phosphatidylethanolamine-binding proteins, including RKIP, exhibit affinity for phosphodiesterase-5 inhibitors. <i>ChemBioChem</i> , 2009 , 10, 2654-62	3.8	11
43	The tandem zinc-finger region of human ZHX adopts a novel C2H2 zinc finger structure with a C-terminal extension. <i>Biochemistry</i> , 2009 , 48, 4431-9	3.2	9
42	Novel strategies to overcome expression problems encountered with toxic proteins: application to the production of Lac repressor proteins for NMR studies. <i>Protein Expression and Purification</i> , 2009 , 67, 104-12	2	8
41	Specificity and affinity of Lac repressor for the auxiliary operators O2 and O3 are explained by the structures of their protein-DNA complexes. <i>Journal of Molecular Biology</i> , 2009 , 390, 478-89	6.5	41
40	Structure and DNA binding of the human Rtf1 Plus3 domain. <i>Structure</i> , 2008 , 16, 149-59	5.2	36
39	Solution structure and characterization of the DNA-binding activity of the B3BP-Smr domain. <i>Journal of Molecular Biology</i> , 2008 , 383, 1156-70	6.5	17
38	The HhH domain of the human DNA repair protein XPF forms stable homodimers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 1551-63	4.2	18
37	Interactions between the toxin Kid of the bacterial parD system and the antitoxins Kis and MazE. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 67, 219-31	4.2	29
36	Analysis of the XPA and ssDNA-binding surfaces on the central domain of human ERCC1 reveals evidence for subfunctionalization. <i>Nucleic Acids Research</i> , 2007 , 35, 5789-98	20.1	36
35	Structural characterization of Spo0E-like protein-aspartic acid phosphatases that regulate sporulation in bacilli. <i>Journal of Biological Chemistry</i> , 2006 , 281, 37993-8003	5.4	13

34	The nucleotide-binding site of bacterial translation initiation factor 2 (IF2) as a metabolic sensor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 13962-7	11.5	135
33	Solution structure of the human ubiquitin-specific protease 15 DUSP domain. <i>Journal of Biological Chemistry</i> , 2006 , 281, 5026-31	5.4	28
32	The intrinsically unstructured domain of PC4 modulates the activity of the structured core through inter- and intramolecular interactions. <i>Biochemistry</i> , 2006 , 45, 5067-81	3.2	18
31	RING Domain Proteins 2006 ,		1
30	Implementation of semi-automated cloning and prokaryotic expression screening: the impact of SPINE. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1103-13		49
29	Recombinant protein expression and solubility screening in <i>Escherichia coli</i> : a comparative study. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1218-26		108
28	NMR in the SPINE Structural Proteomics project. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1150-61		10
27	Application of high-throughput technologies to a structural proteomics-type analysis of <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1267-75		22
26	Gradual phosphorylation regulates PC4 coactivator function. <i>FEBS Journal</i> , 2006 , 273, 1430-44	5.7	23
25	Enzyme free cloning for high throughput gene cloning and expression. <i>Journal of Structural and Functional Genomics</i> , 2006 , 7, 109-18		36
24	Structural properties of the promiscuous VP16 activation domain. <i>Biochemistry</i> , 2005 , 44, 827-39	3.2	57
23	The structure of the human ERCC1/XPF interaction domains reveals a complementary role for the two proteins in nucleotide excision repair. <i>Structure</i> , 2005 , 13, 1849-58	5.2	103
22	Altered specificity in DNA binding by the lac repressor: a mutant lac headpiece that mimics the gal repressor. <i>ChemBioChem</i> , 2005 , 6, 1628-37	3.8	14
21	The structure of bypass of forespore C, an intercompartmental signaling factor during sporulation in <i>Bacillus</i> . <i>Journal of Biological Chemistry</i> , 2005 , 280, 36214-20	5.4	2
20	Expression screening, protein purification and NMR analysis of human protein domains for structural genomics. <i>Journal of Structural and Functional Genomics</i> , 2004 , 5, 119-31		41
19	Solution structure and DNA-binding properties of the C-terminal domain of UvrC from <i>E. coli</i> . <i>EMBO Journal</i> , 2002 , 21, 6257-66	13	39
18	Strong DNA binding by covalently linked dimeric Lac headpiece: evidence for the crucial role of the hinge helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 6039-44	11.5	55
17	Changes in dynamical behavior of the retinoid X receptor DNA-binding domain upon binding to a 14 base-pair DNA half site. <i>Biochemistry</i> , 2000 , 39, 8747-57	3.2	15

16	Structure and dynamics of the tetrameric mnt repressor and a model for its DNA complex. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000 , 17 Suppl 1, 113-22	3.6	2
15	Molecular cloning, genetic mapping, and developmental expression of bovine POU5F1. <i>Biology of Reproduction</i> , 1999 , 60, 1093-103	3.9	159
14	Hinge-helix formation and DNA bending in various lac repressor-operator complexes. <i>EMBO Journal</i> , 1999 , 18, 6472-80	13	46
13	Millisecond to microsecond time scale dynamics of the retinoid X and retinoic acid receptor DNA-binding domains and dimeric complex formation. <i>Biochemistry</i> , 1999 , 38, 1951-6	3.2	30
12	Promoter architecture, cofactors, and orphan receptors contribute to cell-specific activation of the retinoic acid receptor beta2 promoter. <i>Journal of Biological Chemistry</i> , 1998 , 273, 32200-12	5.4	29
11	Metabolism to a response pathway selective retinoid ligand during axial pattern formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 15424-9	11.5	23
10	A role for cofactors in synergistic and cell-specific activation by retinoic acid receptors and retinoid X receptor. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 1996 , 56, 119-29	5.1	3
9	Activation function 1 of retinoic acid receptor beta 2 is an acidic activator resembling VP16. <i>Journal of Biological Chemistry</i> , 1995 , 270, 23552-9	5.4	20
8	Retinoic acid receptor alpha 1 isoform is induced by estradiol and confers retinoic acid sensitivity in human breast cancer cells. <i>Molecular and Cellular Endocrinology</i> , 1995 , 109, 77-86	4.4	55
7	The retinoid ligand 4-oxo-retinoic acid is a highly active modulator of positional specification. <i>Nature</i> , 1993 , 366, 340-4	50.4	249
6	E1A functions as a coactivator of retinoic acid-dependent retinoic acid receptor-beta 2 promoter activation. <i>Molecular Endocrinology</i> , 1993 , 7, 604-615		12
5	The retinoic acid receptor-beta 2 contains two separate cell-specific transactivation domains, at the N-terminus and in the ligand-binding domain. <i>Molecular Endocrinology</i> , 1993 , 7, 616-627		21
4	A cyclic AMP response element is involved in retinoic acid-dependent RAR beta 2 promoter activation. <i>Nucleic Acids Research</i> , 1992 , 20, 6393-9	20.1	47
3	Genomic organization of the human retinoic acid receptor beta 2. <i>Biochemical and Biophysical Research Communications</i> , 1992 , 188, 695-702	3.4	17
2	The use of a two-liquid-phase electron removal system for culture of proton-reducing bacteria. <i>Journal of Microbiological Methods</i> , 1991 , 13, 223-230	2.8	6
1	Genes from <i>Bacillus thuringiensis entomocidus</i> 60.5 coding for insect-specific crystal proteins. <i>Molecular Genetics and Genomics</i> , 1988 , 212, 219-224		36