Gert E Folkers

List of Publications by Citations

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	The retinoid ligand 4-oxo-retinoic acid is a highly active modulator of positional specification. *Nature*, **1993**, 366, 340-4	50.4	249
68	Molecular cloning, genetic mapping, and developmental expression of bovine POU5F1. *Biology of Reproduction*, **1999**, 60, 1093-103	3.9	159
67	The nucleotide-binding site of bacterial translation initiation factor 2 (IF2) as a metabolic sensor. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 13962-7	11.5	135
66	EGFR Dynamics Change during Activation in Native Membranes as Revealed by NMR. *Cell*, **2016**, 167, 1241-1251.e11	56.2	110
65	Recombinant protein expression and solubility screening in Escherichia coli: a comparative study. *Acta Crystallographica Section D: Biological Crystallography*, **2006**, 62, 1218-26		108
64	Probing a cell-embedded megadalton protein complex by DNP-supported solid-state NMR. *Nature Methods*, **2015**, 12, 649-52	21.6	103
63	The structure of the human ERCC1/XPF interaction domains reveals a complementary role for the two proteins in nucleotide excision repair. *Structure*, **2005**, 13, 1849-58	5.2	103
62	Proteins feel more than they see: fine-tuning of binding affinity by properties of the non-interacting surface. *Journal of Molecular Biology*, **2014**, 426, 2632-52	6.5	69
61	Structural properties of the promiscuous VP16 activation domain. *Biochemistry*, **2005**, 44, 827-39	3.2	57
60	Strong DNA binding by covalently linked dimeric Lac headpiece: evidence for the crucial role of the hinge helices. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 6039-44	11.5	55
59	Retinoic acid receptor alpha 1 isoform is induced by estradiol and confers retinoic acid sensitivity in human breast cancer cells. *Molecular and Cellular Endocrinology*, **1995**, 109, 77-86	4.4	55
58	DNP-Supported Solid-State NMR Spectroscopy of Proteins Inside Mammalian Cells. *Angewandte Chemie - International Edition*, **2019**, 58, 12969-12973	16.4	53
57	Implementation of semi-automated cloning and prokaryotic expression screening: the impact of SPINE. *Acta Crystallographica Section D: Biological Crystallography*, **2006**, 62, 1103-13		49
56	A cyclic AMP response element is involved in retinoic acid-dependent RAR beta 2 promoter activation. *Nucleic Acids Research*, **1992**, 20, 6393-9	20.1	47
55	Hinge-helix formation and DNA bending in various lac repressor-operator complexes. *EMBO Journal* , **1999**, 18, 6472-80	13	46
54	Specificity and affinity of Lac repressor for the auxiliary operators O2 and O3 are explained by the structures of their protein-DNA complexes. *Journal of Molecular Biology*, **2009**, 390, 478-89	6.5	41
53	Expression screening, protein purification and NMR analysis of human protein domains for structural genomics. *Journal of Structural and Functional Genomics*, **2004**, 5, 119-31		41

52	Solution structure and DNA-binding properties of the C-terminal domain of UvrC from E.coli. *EMBO Journal*, **2002**, 21, 6257-66	13	39
51	Structure and DNA binding of the human Rtf1 Plus3 domain. *Structure*, **2008**, 16, 149-59	5.2	36
50	Analysis of the XPA and ssDNA-binding surfaces on the central domain of human ERCC1 reveals evidence for subfunctionalization. *Nucleic Acids Research*, **2007**, 35, 5789-98	20.1	36
49	Enzyme free cloning for high throughput gene cloning and expression. *Journal of Structural and Functional Genomics*, **2006**, 7, 109-18		36
48	Genes from Bacillus thuringiensis entomocidus 60.5 coding for insect-specific crystal proteins. *Molecular Genetics and Genomics*, **1988**, 212, 219-224		36
47	Expression of protein complexes using multiple Escherichia coli protein co-expression systems: a benchmarking study. *Journal of Structural Biology*, **2011**, 175, 159-70	3.4	34
46	iSEE: Interface structure, evolution, and energy-based machine learning predictor of binding affinity changes upon mutations. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 110-119	4.2	33
45	Function and Interactions of ERCC1-XPF in DNA Damage Response. *Molecules*, **2018**, 23,	4.8	31
44	Efficient cellular solid-state NMR of membrane proteins by targeted protein labeling. *Journal of Biomolecular NMR*, **2015**, 62, 199-208	3	30
43	Millisecond to microsecond time scale dynamics of the retinoid X and retinoic acid receptor DNA-binding domains and dimeric complex formation. *Biochemistry*, **1999**, 38, 1951-6	3.2	30
42	Interactions between the toxin Kid of the bacterial parD system and the antitoxins Kis and MazE. *Proteins: Structure, Function and Bioinformatics*, **2007**, 67, 219-31	4.2	29
41	Promoter architecture, cofactors, and orphan receptors contribute to cell-specific activation of the retinoic acid receptor beta2 promoter. *Journal of Biological Chemistry*, **1998**, 273, 32200-12	5.4	29
40	Solution structure of the human ubiquitin-specific protease 15 DUSP domain. *Journal of Biological Chemistry*, **2006**, 281, 5026-31	5.4	28
39	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. *Structure*, **2012**, 20, 667-75	5.2	24
38	Gradual phosphorylation regulates PC4 coactivator function. *FEBS Journal*, **2006**, 273, 1430-44	5.7	23
37	Metabolism to a response pathway selective retinoid ligand during axial pattern formation. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 15424-9	11.5	23
36	Application of high-throughput technologies to a structural proteomics-type analysis of Bacillus anthracis. *Acta Crystallographica Section D: Biological Crystallography*, **2006**, 62, 1267-75		22
35	The retinoic acid receptor-beta 2 contains two separate cell-specific transactivation domains, at the N-terminus and in the ligand-binding domain. *Molecular Endocrinology*, **1993**, 7, 616-627		21

34	Structural dynamics of bacterial translation initiation factor IF2. *Journal of Biological Chemistry*, **2012**, 287, 10922-32	5.4	20
33	Activation function 1 of retinoic acid receptor beta 2 is an acidic activator resembling VP16. *Journal of Biological Chemistry*, **1995**, 270, 23552-9	5.4	20
32	The HhH domain of the human DNA repair protein XPF forms stable homodimers. *Proteins: Structure, Function and Bioinformatics*, **2008**, 70, 1551-63	4.2	18
31	The intrinsically unstructured domain of PC4 modulates the activity of the structured core through inter- and intramolecular interactions. *Biochemistry*, **2006**, 45, 5067-81	3.2	18
30	Magic-angle-spinning solid-state NMR of membrane proteins. *Methods in Enzymology*, **2015**, 557, 307-28	1.7	17
29	Solution structure and characterization of the DNA-binding activity of the B3BP-Smr domain. *Journal of Molecular Biology*, **2008**, 383, 1156-70	6.5	17
28	Genomic organization of the human retinoic acid receptor beta 2. *Biochemical and Biophysical Research Communications*, **1992**, 188, 695-702	3.4	17
27	DNP-Supported Solid-State NMR Spectroscopy of Proteins Inside Mammalian Cells. *Angewandte Chemie*, **2019**, 131, 13103-13107	3.6	16
26	Characterizing proteins in a native bacterial environment using solid-state NMR spectroscopy. *Nature Protocols*, **2021**, 16, 893-918	18.8	16
25	Changes in dynamical behavior of the retinoid X receptor DNA-binding domain upon binding to a 14 base-pair DNA half site. *Biochemistry*, **2000**, 39, 8747-57	3.2	15
24	Altered specificity in DNA binding by the lac repressor: a mutant lac headpiece that mimics the gal repressor. *ChemBioChem*, **2005**, 6, 1628-37	3.8	14
23	Efficient switching of mCherry fluorescence using chemical caging. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 7013-7018	11.5	13
22	Structural basis of nucleic acid binding by Nicotiana tabacum glycine-rich RNA-binding protein: implications for its RNA chaperone function. *Nucleic Acids Research*, **2014**, 42, 8705-18	20.1	13
21	Structural insights into transcription complexes. *Journal of Structural Biology*, **2011**, 175, 135-46	3.4	13
20	Structural characterization of Spo0E-like protein-aspartic acid phosphatases that regulate sporulation in bacilli. *Journal of Biological Chemistry*, **2006**, 281, 37993-8003	5.4	13
19	E1A functions as a coactivator of retinoic acid-dependent retinoic acid receptor-beta 2 promoter activation. *Molecular Endocrinology*, **1993**, 7, 604-615		12
18	Phosphatidylethanolamine-binding proteins, including RKIP, exhibit affinity for phosphodiesterase-5 inhibitors. *ChemBioChem*, **2009**, 10, 2654-62	3.8	11
17	Single-stranded DNA Binding by the Helix-Hairpin-Helix Domain of XPF Protein Contributes to the Substrate Specificity of the ERCC1-XPF Protein Complex. *Journal of Biological Chemistry*, **2017**, 292, 2842-2853	5.4	10

16	The Cerebro-oculo-facio-skeletal Syndrome Point Mutation F231L in the ERCC1 DNA Repair Protein Causes Dissociation of the ERCC1-XPF Complex. *Journal of Biological Chemistry*, **2015**, 290, 20541-55	5.4	10
15	NMR in the SPINE Structural Proteomics project. *Acta Crystallographica Section D: Biological Crystallography*, **2006**, 62, 1150-61		10
14	When Small becomes Too Big: Expanding the Use of In-Cell Solid-State NMR Spectroscopy. *ChemPlusChem*, **2020**, 85, 760-768	2.8	9
13	The tandem zinc-finger region of human ZHX adopts a novel C2H2 zinc finger structure with a C-terminal extension. *Biochemistry*, **2009**, 48, 4431-9	3.2	9
12	Novel structural features in two ZHX homeodomains derived from a systematic study of single and multiple domains. *BMC Structural Biology*, **2010**, 10, 13	2.7	9
11	Novel strategies to overcome expression problems encountered with toxic proteins: application to the production of Lac repressor proteins for NMR studies. *Protein Expression and Purification*, **2009**, 67, 104-12	2	8
10	The use of a two-liquid-phase electron removal system for culture of proton-reducing bacteria. *Journal of Microbiological Methods*, **1991**, 13, 223-230	2.8	6
9	NMR characterization of foldedness for the production of E3 RING domains. *Journal of Structural Biology*, **2010**, 172, 120-7	3.4	5
8	The Fanconi anemia associated protein FAAP24 uses two substrate specific binding surfaces for DNA recognition. *Nucleic Acids Research*, **2013**, 41, 6739-49	20.1	4
7	Characterization of nucleosome sediments for protein interaction studies by solid-state NMR spectroscopy. *Magnetic Resonance*, **2021**, 2, 187-202	2.9	4
6	A role for cofactors in synergistic and cell-specific activation by retinoic acid receptors and retinoid X receptor. *Journal of Steroid Biochemistry and Molecular Biology*, **1996**, 56, 119-29	5.1	3
5	A model for the interaction of the G3-subdomain of Geobacillus stearothermophilus IF2 with the 30S ribosomal subunit. *Protein Science*, **2016**, 25, 1722-33	6.3	2
4	The structure of bypass of forespore C, an intercompartmental signaling factor during sporulation in Bacillus. *Journal of Biological Chemistry*, **2005**, 280, 36214-20	5.4	2
3	Structure and dynamics of the tetrameric mnt repressor and a model for its DNA complex. *Journal of Biomolecular Structure and Dynamics*, **2000**, 17 Suppl 1, 113-22	3.6	2
2	RING Domain Proteins **2006**,		1
1	R□ktitelbild: DNP-Supported Solid-State NMR Spectroscopy of Proteins Inside Mammalian Cells (Angew. Chem. 37/2019). *Angewandte Chemie*, **2019**, 131, 13296-13296	3.6	