

Robert Kaptein

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10706018/publications.pdf>

Version: 2024-02-01

62
papers

9,384
citations

136740

32
h-index

123241

61
g-index

72
all docs

72
docs citations

72
times ranked

11031
citing authors

#	ARTICLE	IF	CITATIONS
1	AQUA and PROCHECK-NMR: Programs for checking the quality of protein structures solved by NMR. <i>Journal of Biomolecular NMR</i> , 1996, 8, 477-86.	1.6	4,736
2	Structure and Flexibility Adaptation in Nonspecific and Specific Protein-DNA Complexes. <i>Science</i> , 2004, 305, 386-389.	6.0	506
3	The nisin-lipid II complex reveals a pyrophosphate cage that provides a blueprint for novel antibiotics. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 963-967.	3.6	505
4	Recommendations for the presentation of NMR structures of proteins and nucleic acids. IUPAC-IUBMB-IUPAB Inter-Union Task Group on the Standardization of Data Bases of Protein and Nucleic Acid Structures Determined by NMR Spectroscopy. <i>Journal of Biomolecular NMR</i> , 1998, 12, 1-23.	1.6	347
5	RECOORD: A recalculated coordinate database of 500+ proteins from the PDB using restraints from the BioMagResBank. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 662-672.	1.5	323
6	Recommendations for the presentation of NMR structures of proteins and nucleic acids. <i>Journal of Molecular Biology</i> , 1998, 280, 933-952.	2.0	217
7	Structure of Arc repressor in solution: evidence for a family of β -sheet DNA-binding proteins. <i>Nature</i> , 1990, 346, 586-589.	13.7	180
8	Recommendations for the presentation of NMR structures of proteins and nucleic acids. IUPAC-IUBMB-IUPAB inter-union task group on the standardization of data bases of protein and nucleic acid structures determined by NMR spectroscopy. <i>FEBS Journal</i> , 1998, 256, 1-15.	0.2	137
9	The solution structure of the amino-terminal HHCC domain of HIV-2 integrase: a three-helix bundle stabilized by zinc. <i>Current Biology</i> , 1997, 7, 739-746.	1.8	134
10	Solution Structure and Backbone Dynamics of the Photoactive Yellow Protein. <i>Biochemistry</i> , 1998, 37, 12689-12699.	1.2	129
11	Plasticity in protein-DNA recognition: lac repressor interacts with its natural operator O1 through alternative conformations of its DNA-binding domain. <i>EMBO Journal</i> , 2002, 21, 2866-2876.	3.5	117
12	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, 1849-1858.	1.6	116
13	The Solution Structure of the AppA BLUF Domain: Insight into the Mechanism of Light-Induced Signaling. <i>ChemBioChem</i> , 2006, 7, 187-193.	1.3	111
14	NMR analysis of protein interactions. <i>Current Opinion in Chemical Biology</i> , 2005, 9, 501-508.	2.8	109
15	Quality assessment of NMR structures: a statistical survey. <i>Journal of Molecular Biology</i> , 1998, 281, 149-164.	2.0	106
16	Solution Structure of the HU Protein from <i>Bacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 1995, 254, 692-703.	2.0	103
17	Quantitative Measurement of Relaxation Interference Effects between ^1H NCSA and ^1H - ^{15}N Dipolar Interaction: A Correlation with Secondary Structure. <i>Journal of the American Chemical Society</i> , 1997, 119, 8985-8990.	6.6	94
18	The solution structure of Lac repressor headpiece 62 complexed to a symmetrical lac operator. <i>Structure</i> , 1999, 7, 1483-53.	1.6	84

#	ARTICLE	IF	CITATIONS
19	Refined solution structure of the c-terminal DNA-binding domain of human immunovirus-1 integrase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 36, 556-564.	1.5	83
20	Formation of the hinge helix in the lac repressor is induced upon binding to the lac operator. <i>Nature Structural Biology</i> , 1996, 3, 916-919.	9.7	77
21	Rapid and simple approach for the NMR resonance assignment of the carbohydrate chains of an intact glycoprotein Application of gradient-enhanced natural abundance ¹ H- ¹³ C HSQC and HSQC-TOCSY to the β -subunit of human chorionic gonadotropin. <i>FEBS Letters</i> , 1994, 348, 1-6.	1.3	75
22	NMR Studies of the Free α Subunit of Human Chorionic Gonadotropin. Structural Influences of N-Glycosylation and the β Subunit on the Conformation of the α Subunit. <i>FEBS Journal</i> , 1996, 241, 229-242.	0.2	75
23	Toward an Integrated Model of Protein-DNA Recognition as Inferred from NMR Studies on the Lac Repressor System. <i>Chemical Reviews</i> , 2004, 104, 3567-3586.	23.0	74
24	The Solution Structure of a Transient Photoreceptor Intermediate: ¹⁵ N Photoactive Yellow Protein. <i>Structure</i> , 2005, 13, 953-962.	1.6	71
25	Mapping the Targeted Membrane Pore Formation Mechanism by Solution NMR: The Nisin Z and Lipid II Interaction in SDS Micelles. <i>Biochemistry</i> , 2002, 41, 7670-7676.	1.2	68
26	Completeness of NOEs in protein structure: a statistical analysis of NMR. <i>Journal of Biomolecular NMR</i> , 1999, 14, 123-132.	1.6	66
27	BioMagResBank databases DOCR and FRED containing converted and filtered sets of experimental NMR restraints and coordinates from over 500 protein PDB structures. <i>Journal of Biomolecular NMR</i> , 2005, 32, 1-12.	1.6	50
28	The tetramerization domain of the Mnt repressor consists of two right-handed coiled coils. <i>Nature Structural Biology</i> , 1999, 6, 755-759.	9.7	49
29	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, 478-489.	2.0	46
30	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, 5789-5798.	6.5	39
31	Measurement of (¹⁵ N)-(¹ H) coupling constants in uniformly (¹⁵ N)-labeled proteins: Application to the photoactive yellow protein. <i>Journal of Biomolecular NMR</i> , 1997, 10, 301-306.	1.6	38
32	Solution Structure of the Human Ubiquitin-specific Protease 15 DUSP Domain. <i>Journal of Biological Chemistry</i> , 2006, 281, 5026-5031.	1.6	33
33	NMR studies of bipyrimidine cyclobutane photodimers. <i>FEBS Journal</i> , 1991, 195, 29-40.	0.2	31
34	Two-dimensional NMR studies on des-pentapeptide-insulin. Proton resonance assignments and secondary structure analysis. <i>FEBS Journal</i> , 1990, 191, 147-153.	0.2	29
35	Assignment of the ¹ H-NMR spectrum of a lac repressor headpiece-operator complex in H ₂ O and identification of NOEs. Consequences for protein-DNA interaction. <i>FEBS Journal</i> , 1990, 194, 629-637.	0.2	28
36	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, 667-675.	1.6	28

#	ARTICLE	IF	CITATIONS
37	Refined solution structure of the dimeric N-terminal HHCC domain of HIV-2 integrase. <i>Journal of Biomolecular NMR</i> , 2000, 18, 119-128.	1.6	27
38	The solution structure of a monomeric insulin. A two-dimensional ¹ H-NMR study of des-(B26-B30)-insulin in combination with distance geometry and restrained molecular dynamics. <i>FEBS Journal</i> , 1991, 202, 447-458.	0.2	25
39	The auto-orientation in high magnetic fields of oxidized cytochrome b562 as source of constraints for solution structure determination. <i>Journal of Biomolecular NMR</i> , 2000, 17, 295-304.	1.6	25
40	Use of very long-distance NOEs in a fully deuterated protein: an approach for rapid protein fold determination. <i>Journal of Magnetic Resonance</i> , 2003, 163, 228-235.	1.2	25
41	Rapid protein fold determination using secondary chemical shifts and cross-hydrogen bond ¹⁵ N- ¹³ C' scalar couplings (3hbJNC'). <i>Journal of Biomolecular NMR</i> , 2001, 21, 221-233.	1.6	23
42	Structure of the LexA Repressor-DNA Complex Probed by Affinity Cleavage and Affinity Photo-Cross-Linking. <i>Biochemistry</i> , 1996, 35, 4279-4286.	1.2	22
43	Validation of nuclear magnetic resonance structures of proteins and nucleic acids: Hydrogen geometry and nomenclature. , 1999, 37, 404-416.		21
44	The HhH domain of the human DNA repair protein XPF forms stable homodimers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1551-1563.	1.5	19
45	Solution Structure and Characterization of the DNA-Binding Activity of the B3BP-Smr Domain. <i>Journal of Molecular Biology</i> , 2008, 383, 1156-1170.	2.0	18
46	Describing Partially Unfolded States of Proteins from Sparse NMR Ddata. <i>Journal of Biomolecular NMR</i> , 2005, 33, 175-186.	1.6	17
47	Joint refinement as a tool for thorough comparison between NMR and X-ray data and structures of HU protein. <i>Journal of Biomolecular NMR</i> , 2001, 21, 235-248.	1.6	16
48	Direct Use of Unassigned Resonances in NMR Structure Calculations with Proxy Residues. <i>Journal of the American Chemical Society</i> , 2006, 128, 7566-7571.	6.6	15
49	Altered Specificity in DNA Binding by the lac Repressor: A Mutant lac Headpiece that Mimics the gal Repressor. <i>ChemBioChem</i> , 2005, 6, 1628-1637.	1.3	14
50	Structural Characterization of SpoOE-like Protein-aspartic Acid Phosphatases That Regulate Sporulation in Bacilli. <i>Journal of Biological Chemistry</i> , 2006, 281, 37993-38003.	1.6	14
51	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, 20541-20555.	1.6	14
52	Applications of Two-Dimensional ¹ H NMR Methods to Photochemically Induced Dynamic Nuclear Polarisation Spectroscopy. <i>Israel Journal of Chemistry</i> , 1988, 28, 319-327.	1.0	11
53	¹ H-NMR Investigation of the Interaction of the Amino Terminal Domain of the LexA Repressor with a Synthetic Half-Operator. <i>Journal of Biomolecular Structure and Dynamics</i> , 1991, 9, 447-461.	2.0	11
54	NMR investigation of the interaction of the inhibitor protein Im9 with its partner DNase. <i>Protein Science</i> , 2000, 9, 1709-1718.	3.1	11

#	ARTICLE	IF	CITATIONS
55	Sliding and target location of DNA-binding proteins:an NMR view of the lac repressor system. Journal of Biomolecular NMR, 2013, 56, 41-49.	1.6	10
56	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, 104-112.	0.6	9
57	The Structure of Bypass of Forespore C, an Intercompartmental Signaling Factor during Sporulation in Bacillus. Journal of Biological Chemistry, 2005, 280, 36214-36220.	1.6	7
58	NMR structure determination of the tetramerization domain of the Mnt repressor: An asymmetric alpha-helical assembly in slow exchange. Journal of Biomolecular NMR, 1999, 15, 39-53.	1.6	4
59	The Fanconi anemia associated protein FAAP24 uses two substrate specific binding surfaces for DNA recognition. Nucleic Acids Research, 2013, 41, 6739-6749.	6.5	4
60	Proton NMR resonance assignments and surface accessibility of tryptophan residues of a dimeric phospholipase A2fromTrimeresurus flavoviridis. FEBS Letters, 1988, 230, 57-60.	1.3	3
61	Solution Structure of Porcine Pancreatic Procolipase as Determined from ¹ H Homonuclear Twoâ€Dimensional and Threeâ€Dimensional NMR. FEBS Journal, 1995, 227, 663-672.	0.2	3
62	Structure and Dynamics of the Tetrameric Mnt Repressor and a Model for its DNA Complex. Journal of Biomolecular Structure and Dynamics, 2000, 17, 113-122.	2.0	2