

Paul RÄjsch

List of Publications by Year in descending order

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150
papers

4,401
citations

147726

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153
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153
docs citations

153
times ranked

4169
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of a natural ligand of the hazel allergen Cor a 1. <i>Scientific Reports</i> , 2019, 9, 8714.	1.6	26
2	Reversible fold-switching controls the functional cycle of the antitermination factor RfaH. <i>Nature Communications</i> , 2019, 10, 702.	5.8	50
3	Quality and potency profile of eight recombinant isoallergens, largely mimicking total Bet v 1-specific IgE binding of birch pollen. <i>Clinical and Experimental Allergy</i> , 2019, 49, 712-723.	1.4	12
4	pH and Heat Resistance of the Major Celery Allergen Api-4. <i>Molecular Nutrition and Food Research</i> , 2018, 62, e1700886.	1.5	10
5	Structure and nucleic acid binding properties of KOW domains 4 and 6 of human transcription elongation factor DSIF. <i>Scientific Reports</i> , 2018, 8, 11660.	1.6	9
6	The universally-conserved transcription factor RfaH is recruited to a hairpin structure of the non-template DNA strand. <i>ELife</i> , 2018, 7, .	2.8	45
7	<i>Thermotoga maritima</i> NusG: domain interaction mediates autoinhibition and thermostability. <i>Nucleic Acids Research</i> , 2017, 45, 446-460.	6.5	30
8	Development, synthesis and structure-activity-relationships of inhibitors of the macrophage infectivity potentiator (Mip) proteins of <i>Legionella pneumophila</i> and <i>Burkholderia pseudomallei</i> . <i>Bioorganic and Medicinal Chemistry</i> , 2016, 24, 5134-5147.	1.4	13
9	Transcription is regulated by NusA:NusG interaction. <i>Nucleic Acids Research</i> , 2016, 44, 5971-5982.	6.5	42
10	Resonance assignment of an engineered amino-terminal domain of a major ampullate spider silk with neutralized charge cluster. <i>Biomolecular NMR Assignments</i> , 2016, 10, 199-202.	0.4	2
11	The two domains of <i>Mycobacterium tuberculosis</i> NusG protein are dynamically independent. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 352-361.	2.0	6
12	Exploring RNA polymerase regulation by NMR spectroscopy. <i>Scientific Reports</i> , 2015, 5, 10825.	1.6	14
13	Determination of RNA polymerase binding surfaces of transcription factors by NMR spectroscopy. <i>Scientific Reports</i> , 2015, 5, 16428.	1.6	25
14	Ligand Recognition of the Major Birch Pollen Allergen Bet v 1 is Isoform Dependent. <i>PLoS ONE</i> , 2015, 10, e0128677.	1.1	30
15	Folded or Not? Tracking Bet v 1 Conformation in Recombinant Allergen Preparations. <i>PLoS ONE</i> , 2015, 10, e0132956.	1.1	7
16	AZT resistance alters enzymatic properties and creates an ATP-binding site in SFVmac reverse transcriptase. <i>Retrovirology</i> , 2015, 12, 21.	0.9	2
17	Prosequence switching: An effective strategy to produce biologically active <i>E. coli</i> heat-stable enterotoxin STh. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1537-1545.	2.0	2
18	Inhibition of Foamy Virus Reverse Transcriptase by Human Immunodeficiency Virus Type 1 RNase H Inhibitors. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4086-4093.	1.4	26

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19	Structural requirements for enzymatic activities of foamy virus proteaseâ€reverse transcriptase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 375-385.	1.5	12
20	Identification of the natural ligand of Bet v 1. <i>Clinical and Translational Allergy</i> , 2014, 4, .	1.4	0
21	Analysis of the IgE epitope profile of soybean allergen Gly m 4. <i>Clinical and Translational Allergy</i> , 2014, 4, .	1.4	1
22	Find the match! A tool for residue-specific analysis of epitopes in Bet v 1-like allergens. <i>Clinical and Translational Allergy</i> , 2014, 4, .	1.4	0
23	Secret of the major birch pollen allergen Bet v 1: identification of the physiological ligand. <i>Biochemical Journal</i> , 2014, 457, 379-390.	1.7	80
24	Enlarging the Toolbox for Allergen Epitope Definition with an Allergen-Type Model Protein. <i>PLoS ONE</i> , 2014, 9, e111691.	1.1	18
25	Impact of human immunodeficiency virus type 1 ribonuclease H inhibitors on the polymerase and RNase H function of foamy virus reverse transcriptase. <i>Retrovirology</i> , 2013, 10, .	0.9	0
26	An Autoinhibited State in the Structure of <i>Thermotoga maritima</i> NusG. <i>Structure</i> , 2013, 21, 365-375.	1.6	16
27	Interdomain contacts control folding of transcription factor RfaH. <i>Nucleic Acids Research</i> , 2013, 41, 10077-10085.	6.5	37
28	Solution structure of the strawberry allergen Fra a 1. <i>Bioscience Reports</i> , 2012, 32, 567-575.	1.1	21
29	Transformer proteins. <i>Cell Cycle</i> , 2012, 11, 4289-4290.	1.3	25
30	An Inhibitory Peptide Derived from the α -subunit of the Epithelial Sodium Channel (ENaC) Shows a Helical Conformation. <i>Cellular Physiology and Biochemistry</i> , 2012, 29, 761-774.	1.1	8
31	Transformation. <i>RNA Biology</i> , 2012, 9, 1418-1423.	1.5	11
32	Fast Mapping of Biomolecular Interfaces by Random Spin Labeling (RSL). <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 29, 793-798.	2.0	5
33	An α Helix to β Barrel Domain Switch Transforms the Transcription Factor RfaH into a Translation Factor. <i>Cell</i> , 2012, 150, 291-303.	13.5	201
34	The solution structure of the prototype foamy virus RNase H domain indicates an important role of the basic loop in substrate binding. <i>Retrovirology</i> , 2012, 9, 73.	0.9	8
35	Pipecolic Acid Derivatives As Small-Molecule Inhibitors of the <i>Legionella</i> MIP Protein. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 277-283.	2.9	43
36	Domain interactions of the transcriptionâ€translation coupling factor <i>Escherichia coli</i> NusG are intermolecular and transient. <i>Biochemical Journal</i> , 2011, 435, 783-789.	1.7	38

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37	NusA Interaction with the $\hat{\pm}$ Subunit of E. coli RNA Polymerase Is via the UP Element Site and Releases Autoinhibition. <i>Structure</i> , 2011, 19, 945-954.	1.6	33
38	Regulation of foamy virus protease activity by viral RNA. <i>Retrovirology</i> , 2011, 8, A228.	0.9	0
39	Cross-reactivity of pollen and food allergens: soybean Gly m 4 is a member of the Bet v 1 superfamily and closely resembles yellow lupine proteins. <i>Clinical and Translational Allergy</i> , 2011, 1, .	1.4	0
40	The role of <i>E. coli</i> Nus-Factors in transcription regulation and transcription. <i>Transcription</i> , 2011, 2, 130-134.	1.7	19
41	Regulation of Foamy Virus Protease Activity by Viral RNA: a Novel and Unique Mechanism among Retroviruses. <i>Journal of Virology</i> , 2011, 85, 4462-4469.	1.5	32
42	Formation of transient dimers by a retroviral protease. <i>Biochemical Journal</i> , 2010, 427, 197-203.	1.7	27
43	Crystal structure of the human transcription elongation factor DSIF hSpt4 subunit in complex with the hSpt5 dimerization interface. <i>Biochemical Journal</i> , 2010, 425, 373-380.	1.7	23
44	Fine tuning of the E. coli NusB:NusE complex affinity to BoxA RNA is required for processive antitermination. <i>Nucleic Acids Research</i> , 2010, 38, 314-326.	6.5	22
45	Cure and Curse: E. coli Heat-Stable Enterotoxin and Its Receptor Guanylyl Cyclase C. <i>Toxins</i> , 2010, 2, 2213-2229.	1.5	48
46	The Therapeutically Anti-prion Active Antibody-fragment scFv-W226: Paramagnetic Relaxation-Enhanced NMR Spectroscopy aided Structure Elucidation of the Paratope-epitope Interface. <i>Journal of Biomolecular Structure and Dynamics</i> , 2010, 28, 13-22.	2.0	12
47	A NusE:NusG Complex Links Transcription and Translation. <i>Science</i> , 2010, 328, 501-504.	6.0	294
48	The Membrane Proximal Extracellular Domain of Human hGC-B Folds Independently. <i>Journal of Biomolecular Structure and Dynamics</i> , 2009, 26, 465-472.	2.0	0
49	Binding of TCA to the Prion Protein: Mechanism, Implication for Therapy, and Application as Probe for Complex Formation of Bio-macromolecules. <i>Journal of Biomolecular Structure and Dynamics</i> , 2009, 27, 163-170.	2.0	21
50	RNA-binding specificity of E. coli NusA. <i>Nucleic Acids Research</i> , 2009, 37, 4736-4742.	6.5	31
51	Cross-reactivity of pollen and food allergens: soybean Gly m 4 is a member of the Bet v 1 superfamily and closely resembles yellow lupine proteins. <i>Bioscience Reports</i> , 2009, 29, 183-192.	1.1	40
52	Two Structurally Independent Domains of E. coli NusG Create Regulatory Plasticity via Distinct Interactions with RNA Polymerase and Regulators. <i>Journal of Molecular Biology</i> , 2009, 391, 341-358.	2.0	170
53	SEMPRE: Spectral Editing Mediated by Paramagnetic Relaxation Enhancement. <i>Journal of the American Chemical Society</i> , 2009, 131, 18016-18017.	6.6	11
54	Structural Characterisation of the E. coli Heat Stable Enterotoxin STh. <i>The Open Spectroscopy Journal</i> , 2009, 2, 34-39.	1.0	5

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55	The Solution Structure of the Simian Foamy Virus Protease Reveals a Monomeric Protein. <i>Journal of Molecular Biology</i> , 2008, 381, 141-149.	2.0	29
56	LEKTI domain 15 is a functional Kazal-type proteinase inhibitor. <i>Protein Expression and Purification</i> , 2008, 57, 45-56.	0.6	9
57	The small hSpt4 subunit of the human transcription elongation factor DSIF is a Zn-finger protein with β/β^2 type topology. <i>Biochemical and Biophysical Research Communications</i> , 2008, 370, 414-418.	1.0	7
58	NELF-E RRM Undergoes Major Structural Changes in Flexible Protein Regions on Target RNA Binding. <i>Biochemistry</i> , 2008, 47, 3756-3761.	1.2	13
59	The Y39A Mutation of HK022 Nun Disrupts a <i>boxB</i> Interaction but Preserves Termination Activity. <i>Biochemistry</i> , 2008, 47, 7335-7341.	1.2	5
60	Solution structure of Phl p 3, a major allergen from timothy grass pollen. <i>Biological Chemistry</i> , 2008, 389, 919-23.	1.2	11
61	Design and characterization of a soluble fragment of the extracellular ligand-binding domain of the peptide hormone receptor guanylyl cyclase-C. <i>Protein Engineering, Design and Selection</i> , 2008, 22, 1-7.	1.0	6
62	Conformation, catalytic site, and enzymatic mechanism of the PR10 allergen-related enzyme norcochlorine synthase. <i>Biochemical Journal</i> , 2008, 413, 281-290.	1.7	31
63	Structural characterization of norcochlorine synthase suggests the enzyme to be a true member of the Bet v 1 protein family. <i>World Allergy Organization Journal</i> , 2007, &NA;, S261.	1.6	0
64	Solution structure of Phl p 3, a major allergen from Timothy grass pollen. <i>World Allergy Organization Journal</i> , 2007, &NA;, S263.	1.6	0
65	High-yield expression and purification of isotopically labeled norcochlorine synthase, a Bet v 1-homologous enzyme, from <i>Thalictrum flavum</i> for NMR studies. <i>Protein Expression and Purification</i> , 2007, 56, 197-204.	0.6	24
66	Mutational epitope analysis and cross-reactivity of two isoforms of Api g 1, the major celery allergen. <i>Molecular Immunology</i> , 2007, 44, 2518-2527.	1.0	31
67	Domain Motions of the Mip Protein from <i>Legionella pneumophila</i> . <i>Biochemistry</i> , 2006, 45, 12303-12311.	1.2	26
68	Interaction of the Intrinsically Unstructured Phage λ N Protein with <i>Escherichia coli</i> NusA. <i>Biochemistry</i> , 2006, 45, 4542-4549.	1.2	26
69	Putative aggregation initiation sites in prion protein. <i>FEBS Letters</i> , 2006, 580, 2033-2040.	1.3	30
70	Structural studies on the RNA-recognition motif of NELF E, a cellular negative transcription elongation factor involved in the regulation of HIV transcription. <i>Biochemical Journal</i> , 2006, 400, 449-456.	1.7	29
71	Structure and stability of 2S albumin-type peanut allergens: implications for the severity of peanut allergic reactions. <i>Biochemical Journal</i> , 2006, 395, 463-472.	1.7	202
72	The <i>E. coli</i> NusA carboxy-terminal domains are structurally similar and show specific RNAP- and λ N interaction. <i>Protein Science</i> , 2005, 14, 2018-2029.	3.1	25

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73	Structural characterization of Lyn-SH3 domain in complex with a herpesviral protein reveals an extended recognition motif that enhances binding affinity. <i>Protein Science</i> , 2005, 14, 2487-2498.	3.1	43
74	Letter to the Editor: 1H, 13C, 15N backbone and sidechain resonance assignment of Mip(77?213) the PPlase domain of the Legionella pneumophila Mip protein. <i>Journal of Biomolecular NMR</i> , 2005, 31, 77-78.	1.6	7
75	Binding, Domain Orientation, and Dynamics of the Lck SH3~SH2 Domain Pair and Comparison with Other Src-Family Kinases. <i>Biochemistry</i> , 2005, 44, 13043-13050.	1.2	23
76	Letter to the Editor: Sequence-Specific 1H, 13C, 15N Resonance Assignments and Secondary Structure of the Carboxyterminal Domain of the E. Coli Transcription Factor NusA. <i>Journal of Biomolecular NMR</i> , 2004, 28, 193-194.	1.6	4
77	Letter to the Editor: Sequence-specific 1H, 13C and 15N resonance assignments of Ara h 6, an allergenic 2S albumin from peanut. <i>Journal of Biomolecular NMR</i> , 2004, 29, 93-94.	1.6	8
78	Treatment of Peak Intensity Uncertainties in NMR Relaxation Data Analysis Can Lead to Severe Artifacts. <i>Monatshefte für Chemie</i> , 2004, 135, 1089.	0.9	0
79	The Solution Structure of a Chimeric LEKTI Domain Reveals a Chameleon Sequence. <i>Biochemistry</i> , 2004, 43, 11238-11247.	1.2	21
80	Characterization of Lck-Binding Elements in the Herpesviral Regulatory Tip Protein. <i>Biochemistry</i> , 2004, 43, 14932-14939.	1.2	24
81	Role of Disulfide Bonds for the Structure and Folding of Proguanylin. <i>Biochemistry</i> , 2004, 43, 10050-10057.	1.2	6
82	Solution Structure, Dynamics, and Hydrodynamics of the Calcium-bound Cross-reactive Birch Pollen Allergen Bet v 4 Reveal a Canonical Monomeric Two EF-Hand Assembly with a Regulatory Function. <i>Journal of Molecular Biology</i> , 2004, 336, 1141-1157.	2.0	45
83	Sequence-specific 1H, 13C and 15N resonance assignments of SAM22, an allergenic stress-induced protein from soy bean. <i>Journal of Biomolecular NMR</i> , 2003, 26, 191-192.	1.6	7
84	Sequence-specific 1H, 13C and 15N resonance assignments of the SH3-SH2 domain pair from the human tyrosine kinase Lck. <i>Journal of Biomolecular NMR</i> , 2003, 27, 405-406.	1.6	2
85	High-yield expression in Escherichia coli, purification, and characterization of properly folded major peanut allergen Ara h 2. <i>Protein Expression and Purification</i> , 2003, 31, 250-259.	0.6	53
86	Mutational epitope analysis of Pru av 1 and Api g 1, the major allergens of cherry (Prunus avium) and celery (Apium graveolens): correlating IgE reactivity with three-dimensional structure. <i>Biochemical Journal</i> , 2003, 376, 97-107.	1.7	113
87	CD and NMR Studies of Prion Protein (PrP) Helix 1. <i>Journal of Biological Chemistry</i> , 2003, 278, 50175-50181.	1.6	66
88	Solution Structure of Human Proguanylin. <i>Journal of Biological Chemistry</i> , 2003, 278, 24118-24124.	1.6	18
89	Structure and activity of human parathyroid hormone N-terminal fragments in solution. , 2002, , 645-646.		0
90	Accurate Disulfide Formation in Escherichia coli: Overexpression and Characterization of the First Domain (HF6478) of the Multiple Kazal-Type Inhibitor LEKTI. <i>Protein Expression and Purification</i> , 2001, 22, 108-112.	0.6	28

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91	Nuclear magnetic resonance studies of allergens. Biomedical Applications, 2001, 756, 165-177.	1.7	3
92	Improving the efficiency of the Gaussian conformational database potential for the refinement of protein and nucleic acid structures. Journal of Biomolecular NMR, 2001, 21, 373-375.	1.6	11
93	Allergic Cross-reactivity Made Visible. Journal of Biological Chemistry, 2001, 276, 22756-22763.	1.6	151
94	The Structure of the Coliphage HK022 Nun Protein- ϕ -phage boxB RNA Complex. Journal of Biological Chemistry, 2001, 276, 32064-32070.	1.6	25
95	Antitermination in bacteriophage ϕ . FEBS Journal, 2000, 267, 2397-2408.	0.2	72
96	Sequence-specific ^1H , ^{13}C and ^{15}N resonance assignments of the major cherry allergen Pru a 1. Journal of Biomolecular NMR, 2000, 18, 71-72.	1.6	5
97	Sequence-specific ^1H , ^{13}C and ^{15}N resonance assignments and secondary structure of [2Fe-2S] ferredoxin from Halobacterium salinarum. Journal of Biomolecular NMR, 2000, 16, 347-348.	1.6	5
98	Solution structure of a zinc substituted eukaryotic rubredoxin from the cryptomonad alga <i>Guillardia theta</i> . Protein Science, 2000, 9, 1474-1486.	3.1	10
99	Structural Rearrangements of HIV-1 Tat-responsive RNA upon Binding of Neomycin B. Journal of Biological Chemistry, 2000, 275, 20660-20666.	1.6	131
100	Solution Structures of Human Parathyroid Hormone Fragments hPTH(1-34) and hPTH(1-39) and Bovine Parathyroid Hormone Fragment bPTH(1-37). Biochemical and Biophysical Research Communications, 2000, 267, 213-220.	1.0	70
101	Structure of the Cytoplasmic Domain of p23 in Solution: Implications for the Formation of COPI Vesicles. Biochemical and Biophysical Research Communications, 2000, 271, 401-408.	1.0	9
102	Identification and characterization of a eukaryotically encoded rubredoxin in a cryptomonad alga. FEBS Letters, 2000, 471, 191-196.	1.3	19
103	Role of the prosequence of guanylin. Protein Science, 1999, 8, 1850-1859.	3.1	27
104	The structure of human parathyroid hormone-related protein(1-34) in near-physiological solution. FEBS Letters, 1999, 444, 239-244.	1.3	27
105	Solution Structure of the Human CC Chemokine 2: A Monomeric Representative of the CC Chemokine Subtype ϵ . Biochemistry, 1999, 38, 5995-6002.	1.2	33
106	The structure of iron-sulfur proteins. Progress in Biophysics and Molecular Biology, 1998, 70, 95-136.	1.4	131
107	Structural Model of the HIV-1 Tat(46-58)-TAR Complex. Journal of Biomolecular Structure and Dynamics, 1998, 16, 683-692.	2.0	15
108	Equine infectious anemia virus transactivator is a homeodomain-type protein 1 Edited by J. Karn. Journal of Molecular Biology, 1998, 277, 749-755.	2.0	8

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109	Structure-Activity Relation of NH ₂ -terminal Human Parathyroid Hormone Fragments. <i>Journal of Biological Chemistry</i> , 1998, 273, 4308-4316.	1.6	25
110	Carboxy-terminal extension stabilizes the topological stereoisomers of guanylin. <i>Chemical Biology and Drug Design</i> , 1998, 52, 518-525.	1.2	15
111	One peptide, two topologies: structure and interconversion dynamics of human uroguanylin isomers. <i>Chemical Biology and Drug Design</i> , 1998, 52, 229-240.	1.2	23
112	Homology Modeling of Adenylosuccinate Synthetase from <i>Saccharomyces Cerevisiae</i> Reveals a Possible Binding Region for Single-Stranded ARS Sequences. <i>Journal of Biomolecular Structure and Dynamics</i> , 1997, 14, 667-675.	2.0	4
113	Expression in <i>Escherichia coli</i> , Purification, and Spectroscopic Characterization of Two Mutant Bet v 1 Proteins. <i>Biological Chemistry</i> , 1997, 378, 687-95.	1.2	11
114	Solution Structure of Porcine Delta Sleep-inducing Peptide Immunoreactive Peptide A Homolog of the Short-sighted Gene Product. <i>Journal of Biological Chemistry</i> , 1997, 272, 30918-30927.	1.6	11
115	The Interaction of HIV-1 Tat(32-72) with its Target RNA: A Fluorescence and Nuclear Magnetic Resonance Study. <i>Biochemical and Biophysical Research Communications</i> , 1997, 241, 31-36.	1.0	20
116	Secondary Structure and Tertiary Fold of the Human Immunodeficiency Virus Protein U (Vpu) Cytoplasmic Domain in Solution. <i>FEBS Journal</i> , 1997, 245, 581-588.	0.2	73
117	Spectroscopic investigations of HIV-1 trans-activator and related peptides in aqueous solutions. <i>Biophysical Chemistry</i> , 1997, 63, 87-96.	1.5	8
118	Structure of the LAV6 peptide: A nucleation site for the correct receptor-induced refolding of the CD4-binding domain of HIV1 gp 120. , 1997, 29, 203-211.		6
119	Synthesis, biological activity and isomerism of guanylate cyclase C-activating peptides guanylin and uroguanylin. <i>Chemical Biology and Drug Design</i> , 1997, 50, 222-230.	1.2	26
120	Structure of <i>Synechococcus elongatus</i> [Fe2S2] Ferredoxin in Solution. <i>Biochemistry</i> , 1996, 35, 12831-12841.	1.2	48
121	Structural rearrangements on HIV-1 Tat (32-72) TAR complex formation. <i>FEBS Letters</i> , 1996, 384, 255-259.	1.3	28
122	Cloning, High-Yield Expression in <i>Escherichia coli</i> , and Purification of Biologically Active HIV-1 Tat Protein. <i>Protein Expression and Purification</i> , 1996, 8, 75-84.	0.6	21
123	Solution structure of the human CD4 (403-419) receptor peptide. <i>Journal of Biomedical Science</i> , 1996, 3, 435-441.	2.6	13
124	Structure and Activity of a Chimeric Interleukin-8-Melanoma-Growth-Stimulatory-Activity Protein. <i>FEBS Journal</i> , 1996, 235, 26-35.	0.2	6
125	Structural Studies of the Equine Infectious Anemia Virus trans-Activator Protein. <i>FEBS Journal</i> , 1996, 240, 45-52.	0.2	3
126	Sequence-Specific Resonance Assignments of the 1H-NMR Spectra and Structural Characterization in Solution of the HIV-1 Transframe Protein p6*. <i>FEBS Journal</i> , 1996, 237, 383-392.	0.2	29

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127	An NMR-Derived Model for the Solution Structure of Oxidized <i>Thermotoga maritima</i> 1 [Fe4-S4] Ferredoxin. <i>FEBS Journal</i> , 1996, 237, 726-735.	0.2	21
128	Secondary Structure and Tertiary Fold of the Birch Pollen Allergen Bet v 1 in Solution. <i>Journal of Biological Chemistry</i> , 1996, 271, 19243-19250.	1.6	28
129	Structure of Amyloid A4-(1-40)-Peptide of Alzheimer's Disease. <i>FEBS Journal</i> , 1995, 233, 293-298.	0.2	273
130	Structure of Human Parathyroid Hormone 1-37 in Solution. <i>Journal of Biological Chemistry</i> , 1995, 270, 15194-15202.	1.6	66
131	¹ H Nuclear-Magnetic-Resonance Investigation of Oxidized Fe4S4 Ferredoxin from <i>Thermotoga maritima</i> . Hyperfine-Shifted Resonances, Sequence-Specific Assignments and Secondary Structure. <i>FEBS Journal</i> , 1995, 229, 658-668.	0.2	18
132	Trifluoroethanol Stabilizes a Helix-Turn-Helix Motif in Equine Infectious-Anemia-Virus Trans-Activator Protein. <i>FEBS Journal</i> , 1994, 225, 855-861.	0.2	24
133	Generation of a Non-prolyl cis Peptide Bond in Ribonuclease T1. <i>Journal of Molecular Biology</i> , 1994, 240, 288-293.	2.0	43
134	Biological activity and intracellular location of the Tat protein of equine infectious anemia virus. <i>Gene</i> , 1994, 150, 307-311.	1.0	8
135	Equine infectious anemia virus Tat is a predominantly helical protein. <i>FEBS Journal</i> , 1993, 218, 973-976.	0.2	24
136	Proton NMR studies of the GDP.Mg ²⁺ complex of the Ha-ras oncogene product p21. <i>Biochemical and Biophysical Research Communications</i> , 1988, 150, 444-448.	1.0	15
137	Proton-nuclear magnetic resonance studies of the aromatic spin systems of <i>Escherichia coli</i> adenylate kinase. <i>Journal of Molecular Biology</i> , 1988, 200, 745-748.	2.0	6
138	Simulation of the cross-peak fine structure in 2D NMR spectroscopy by analytical calculation of the density operator in a product operator basis. <i>Journal of Magnetic Resonance</i> , 1987, 74, 177-183.	0.5	4
139	NMR-studies of phosphoryl transferring enzymes. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 1986, 18, 123-169.	3.9	13
140	Nuclear magnetic resonance: Protein structure determination. <i>Nature</i> , 1986, 321, 469-470.	13.7	7
141	Biophysics: Use of deuterated proteins in nuclear magnetic resonance. <i>Nature</i> , 1986, 323, 670-670.	13.7	1
142	³¹ P-NMR Studies on ATP-Mg ²⁺ , p21-Nucleotide, and Adenylate Kinase-Nucleotide Complexes. <i>Chemical Shifts, Rate and Equilibrium Constants. Biological Chemistry Hoppe-Seyler</i> , 1986, 367, 781-786.	1.4	4
143	Assignment of aromatic spin systems in the ¹ H nuclear magnetic resonance spectrum of adenylate kinase. <i>Journal of Molecular Biology</i> , 1985, 182, 341-345.	2.0	6
144	THE INFLUENCE OF METAL ION COMPLEXATION ON ³¹ P-NMR PARAMETERS OF PHOSPHOROTHIOATES OF GUANOSINE NUCLEOTIDES. <i>Phosphorous and Sulfur and the Related Elements</i> , 1984, 21, 9-16.	0.2	5

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145	The Structural Isomerisation of Human-Muscle Adenylate Kinase as Studied by ¹ H-Nuclear Magnetic Resonance. FEBS Journal, 1982, 126, 531-536.	0.2	23
146	The interaction of myosine S1 with phosphorothioates of ADP: An ¹⁸ O exchange study by ³¹ P NMR. Archives of Biochemistry and Biophysics, 1981, 211, 622-627.	1.4	10
147	The effect of phosphorylation of the histidyl residue in the tetrapeptide Gly-Gly-His-Ala. Changes of chemical shift and pK values in ¹ H- and ³¹ P-NMR spectra. Magnetic Resonance in Chemistry, 1981, 17, 88-91.	0.7	15
148	³¹ P NMR spectra of thiophosphate analogues of guanosine nucleotides. FEBS Letters, 1980, 121, 211-214.	1.3	14
149	The Phosphoenolpyruvate-Dependent Phosphotransferase System of Staphylococcus aureus. Complete Tyrosine Assignments in the ¹ H Nuclear-Magnetic-Resonance Spectrum of the Phosphocarrier Protein HPr. FEBS Journal, 1979, 96, 43-48.	0.2	15
150	Studies on the Cellular Factors NELF and DSIF Involved in the Regulation of HIV Transcription. , 0, 2007, .		0