

# Daniel Nietlispach

## List of Publications by Year in descending order

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83  
papers

4,196  
citations

109321

35  
h-index

114465

63  
g-index

89  
all docs

89  
docs citations

89  
times ranked

4979  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Structure of the HP1 chromodomain bound to histone H3 methylated at lysine 9. <i>Nature</i> , 2002, 416, 103-107.   | 27.8 | 594       |
| 2  | Structural basis of HP1/PXVXL motif peptide interactions and HP1 localisation to heterochromatin. <i>EMBO Journal</i> , 2004, 23, 489-499.  | 7.8  | 247       |
| 3  | Fast Multidimensional NMR Spectroscopy Using Compressed Sensing. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 6548-6551.  | 13.8 | 241       |
| 4  | Structure determination of the seven-helix transmembrane receptor sensory rhodopsin II by solution NMR spectroscopy. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 768-774.                                      | 8.2  | 198       |
| 5  | The Structure of Docking Domains in Modular Polyketide Synthases. <i>Chemistry and Biology</i> , 2003, 10, 723-731.   | 6.0  | 185       |
| 6  | Structure of the small G protein Cdc42 bound to the GTPase-binding domain of ACK. <i>Nature</i> , 1999, 399, 384-388.   | 27.8 | 172       |
| 7  | Structure of Cdc42 bound to the GTPase binding domain of PAK. <i>Nature Structural Biology</i> , 2000, 7, 384-388.  | 9.7  | 168       |
| 8  | Detergent-free mass spectrometry of membrane protein complexes. <i>Nature Methods</i> , 2013, 10, 1206-1208.  | 19.0 | 152       |
| 9  | The Vinculin Binding Sites of Talin and $\beta$ -Actinin Are Sufficient to Activate Vinculin. <i>Journal of Biological Chemistry</i> , 2006, 281, 7228-7236.  | 3.4  | 118       |
| 10 | An Approach to the Structure Determination of Larger Proteins Using Triple Resonance NMR Experiments in Conjunction with Random Fractional Deuteration. <i>Journal of the American Chemical Society</i> , 1996, 118, 407-415. | 13.7 | 114       |
| 11 | Insight into partial agonism by observing multiple equilibria for ligand-bound and Gs-mimetic nanobody-bound $\beta$ 21-adrenergic receptor. <i>Nature Communications</i> , 2017, 8, 1795.                                    | 12.8 | 92        |
| 12 | Multienzyme docking in hybrid megasynthetases. <i>Nature Chemical Biology</i> , 2008, 4, 75-81.   | 8.0  | 80        |
| 13 | Ca <sup>2+</sup> -independent binding of an EF-hand domain to a novel motif in the alpha-actinin-titin complex. <i>Nature Structural Biology</i> , 2001, 8, 853-857.  | 9.7  | 76        |
| 14 | Suppression of anti-TROSY lines in a sensitivity enhanced gradient selection TROSY scheme. <i>Journal of Biomolecular NMR</i> , 2005, 31, 161-166.  | 2.8  | 69        |
| 15 | Conformational plasticity of ligand-bound and ternary GPCR complexes studied by <sup>19</sup> F NMR of the $\beta$ 21-adrenergic receptor. <i>Nature Communications</i> , 2020, 11, 669.                                      | 12.8 | 67        |
| 16 | Solution-state NMR Spectroscopy of a Seven-Helix Transmembrane Protein Receptor: Backbone Assignment, Secondary Structure, and Dynamics. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 7297-7300.              | 13.8 | 62        |
| 17 | Structure and solution behavior of a series of classical and nonclassical rhenium hydride complexes. <i>Inorganic Chemistry</i> , 1993, 32, 3628-3636.  | 4.0  | 57        |
| 18 | An approach to global fold determination using limited NMR data from larger proteins selectively protonated at specific residue types. <i>Journal of Biomolecular NMR</i> , 1996, 8, 360-368.                                 | 2.8  | 56        |

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|----|--|------|-----------|
| 19 | Local Cooperativity in an Amyloidogenic State of Human Lysozyme Observed at Atomic Resolution. <i>Journal of the American Chemical Society</i> , 2010, 132, 15580-15588.   | 13.7 | 55        |
| 20 | Synthesis and NMR T1 relaxation study of rhenium and manganese hydride complexes. <i>Inorganic Chemistry</i> , 1993, 32, 3270-3276.  | 4.0  | 54        |
| 21 | Compressed sensing reconstruction of undersampled 3D NOESY spectra: application to large membrane proteins. <i>Journal of Biomolecular NMR</i> , 2012, 54, 15-32.  | 2.8  | 51        |
| 22 | Deuterium quadrupole coupling constants and ionic bond character in transition metal hydride complexes from <sup>2</sup> H NMR T1 relaxation data in solution. <i>Journal of the American Chemical Society</i> , 1993, 115, 9191-9195.   | 13.7 | 49        |
| 23 | Molecular Dissection of the Interaction between the Small G Proteins Rac1 and RhoA and Protein Kinase C-related Kinase 1 (PRK1). <i>Journal of Biological Chemistry</i> , 2003, 278, 50578-50587.  | 3.4  | 49        |
| 24 | Structure of the Chromo Barrel Domain from the MOF Acetyltransferase. <i>Journal of Biological Chemistry</i> , 2005, 280, 32326-32331.   | 3.4  | 49        |
| 25 | The Rac1 Polybasic Region Is Required for Interaction with Its Effector PRK1. <i>Journal of Biological Chemistry</i> , 2008, 283, 1492-1500.   | 3.4  | 46        |
| 26 | NMR Analysis of the Structure, Dynamics, and Unique Oligomerization Properties of the Chemokine CCL27. <i>Journal of Biological Chemistry</i> , 2010, 285, 14424-14437.  | 3.4  | 46        |
| 27 | A Novel Approach for the Sequential Backbone Assignment of Larger Proteins: Selective Intra-HNCA and DQ-HNCA. <i>Journal of the American Chemical Society</i> , 2002, 124, 11199-11207.  | 13.7 | 45        |
| 28 | Solution NMR studies of polytopic $\alpha$ -helical membrane proteins. <i>Current Opinion in Structural Biology</i> , 2011, 21, 497-508.   | 5.7  | 43        |
| 29 | The role of NMR spectroscopy in mapping the conformational landscape of GPCRs. <i>Current Opinion in Structural Biology</i> , 2019, 57, 145-156.   | 5.7  | 43        |
| 30 | Structure of the Sterile $\alpha$ Motif (SAM) Domain of the <i>Saccharomyces cerevisiae</i> Mitogen-activated Protein Kinase Pathway-modulating Protein STE50 and Analysis of Its Interaction with the STE11 SAM. <i>Journal of Biological Chemistry</i> , 2004, 279, 2192-2201. | 3.4  | 42        |
| 31 | Structure of the C-terminal Domain from <i>Trypanosoma brucei</i> Variant Surface Glycoprotein MITat1.2. <i>Journal of Biological Chemistry</i> , 2005, 280, 7228-7235.  | 3.4  | 42        |
| 32 | NMR protein structure determination in living <i>E. coli</i> cells using nonlinear sampling. <i>Nature Protocols</i> , 2010, 5, 1051-1060.   | 12.0 | 42        |
| 33 | Solution Structure and Dynamics of the Small GTPase RalB in Its Active Conformation: Significance for Effector Protein Binding. <i>Biochemistry</i> , 2009, 48, 2192-2206.   | 2.5  | 41        |
| 34 | The RalB-RLIP76 Complex Reveals a Novel Mode of Ral-Effector Interaction. <i>Structure</i> , 2010, 18, 985-995.  | 3.3  | 40        |
| 35 | Structure and Dynamics of GPCRs in Lipid Membranes: Physical Principles and Experimental Approaches. <i>Molecules</i> , 2020, 25, 4729.  | 3.8  | 38        |
| 36 | The Sodium Channel $\beta$ 3-Subunit Induces Multiphasic Gating in NaV1.3 and Affects Fast Inactivation via Distinct Intracellular Regions. <i>Journal of Biological Chemistry</i> , 2010, 285, 33404-33412.   | 3.4  | 34        |

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|----|---|------|-----------|
| 37 | An Adaptable Phospholipid Membrane Mimetic System for Solution NMR Studies of Membrane Proteins. <i>Journal of the American Chemical Society</i> , 2017, 139, 14829-14832.                                  | 13.7 | 34        |
| 38 | A Comparative Study of the Reactivity of Mn(no) <sub>2</sub> L <sub>2</sub> H and Mn(CO) <sub>3</sub> L <sub>2</sub> H Complexes (L = Phosphorus Donor). <i>Chemische Berichte</i> , 1994, 127, 2403-2415.  | 0.2  | 33        |
| 39 | A novel method for the biosynthesis of deuterated proteins with selective protonation at the aromatic rings of Phe, Tyr and Trp. <i>Journal of Biomolecular NMR</i> , 2003, 27, 81-86.                      | 2.8  | 32        |
| 40 | Structural Analysis of the SH3 Domain of Î²-PIX and Its Interaction with Î±-p21 Activated Kinase (PAK)â€¦. <i>Biochemistry</i> , 2005, 44, 10977-10983.   | 2.5  | 32        |
| 41 | Structure of the GTPase-binding Domain of Sec5 and Elucidation of its Ral Binding Site. <i>Journal of Biological Chemistry</i> , 2003, 278, 17053-17059.  | 3.4  | 31        |
| 42 | Integral membrane protein structure determination using pseudocontact shifts. <i>Journal of Biomolecular NMR</i> , 2015, 61, 197-207.   | 2.8  | 30        |
| 43 | Insertion Reactions of [ReH(CO)5-n(PMe3)n] Complexes (n = 2-4) with aldehydes, CO2, and activated acetylenes. <i>Helvetica Chimica Acta</i> , 1994, 77, 2197-2208.  | 1.6  | 29        |
| 44 | Solution Structure and Backbone Dynamics of the KH-QUA2 Region of the Xenopus STAR/GSG Quaking Protein. <i>Journal of Molecular Biology</i> , 2005, 348, 265-279.   | 4.2  | 29        |
| 45 | Structure of a Glycosylphosphatidylinositol-anchored Domain from a Trypanosome Variant Surface Glycoprotein. <i>Journal of Biological Chemistry</i> , 2008, 283, 3584-3593.                                 | 3.4  | 29        |
| 46 | Investigation of the Interaction between Cdc42 and Its Effector TOCA1. <i>Journal of Biological Chemistry</i> , 2016, 291, 13875-13890.   | 3.4  | 27        |
| 47 | Rapid Synthesis of a Register-specific Heterotrimeric Type I Collagen Helix Encompassing the Integrin Î±2Î²1 Binding Site. <i>Journal of Molecular Biology</i> , 2006, 359, 289-298.                        | 4.2  | 22        |
| 48 | Ultra-high resolution 3D NMR spectra from limited-size data sets. <i>Journal of Magnetic Resonance</i> , 2004, 169, 215-224.  | 2.1  | 21        |
| 49 | Investigations into Protein Crystallization in the Presence of a Strong Magnetic Field. <i>Crystal Growth and Design</i> , 2010, 10, 691-699.   | 3.0  | 21        |
| 50 | Compressed sensing: Reconstruction of nonâ€¦uniformly sampled multidimensional NMR data. <i>Concepts in Magnetic Resonance Part A: Bridging Education and Research</i> , 2017, 46A, .                       | 0.5  | 20        |
| 51 | Sticky swinging arm dynamics: studies of an acyl carrier protein domain from the mycolactone polyketide synthase. <i>Biochemical Journal</i> , 2016, 473, 1097-1110.  | 3.7  | 19        |
| 52 | NMR assignment of human chemerin, a novel chemoattractant. <i>Biomolecular NMR Assignments</i> , 2007, 1, 171-173.  | 0.8  | 18        |
| 53 | Mechanistic Aspects of the Covalent Flavoprotein Dimethylglycine Oxidase of <i>Arthrobacter globiformis</i> Studied by Stopped-Flow Spectrophotometry. <i>Biochemistry</i> , 2002, 41, 4733-4743.           | 2.5  | 16        |
| 54 | <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments and secondary structure of the human protein tyrosine phosphatase, PRL-2. <i>Journal of Biomolecular NMR</i> , 2003, 27, 397-398. | 2.8  | 16        |

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|----|--|-----|-----------|
| 55 | Improving resolution in multidimensional NMR using random quadrature detection with compressed sensing reconstruction. <i>Journal of Biomolecular NMR</i> , 2017, 68, 67-77.   | 2.8 | 13        |
| 56 | A Selective Intra-HN(CA)CO Experiment for the Backbone Assignment of Deuterated Proteins. <i>Journal of Biomolecular NMR</i> , 2004, 28, 131-136.  | 2.8 | 12        |
| 57 | Structure Determination of Protein Complexes by NMR. , 2004, 278, 255-288.   |     | 11        |
| 58 | The Structure of the RLIP76 RhoGAP-Ral Binding Domain Dyad: Fixed Position of the Domains Leads to Dual Engagement of Small G Proteins at the Membrane. <i>Structure</i> , 2013, 21, 2131-2142.  | 3.3 | 10        |
| 59 | The Structure of Binder of Arl2 (BART) Reveals a Novel G Protein Binding Domain. <i>Journal of Biological Chemistry</i> , 2009, 284, 992-999.  | 3.4 | 9         |
| 60 | <sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N resonance assignments for the small G protein RalB in its active conformation. <i>Biomolecular NMR Assignments</i> , 2007, 1, 147-149.  | 0.8 | 7         |
| 61 | NMR backbone resonance assignment and solution secondary structure determination of human NSD1 and NSD2. <i>Biomolecular NMR Assignments</i> , 2016, 10, 315-320.  | 0.8 | 7         |
| 62 | NUScon: a community-driven platform for quantitative evaluation of nonuniform sampling in NMR. <i>Magnetic Resonance</i> , 2021, 2, 843-861.   | 1.9 | 7         |
| 63 | Solution NMR Studies of Integral Polytopic $\alpha$ -Helical Membrane Proteins: The Structure Determination of the Seven-Helix Transmembrane Receptor Sensory Rhodopsin II, pSRII. <i>Methods in Molecular Biology</i> , 2012, 914, 25-45. | 0.9 | 6         |
| 64 | In support of the BMRB. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 854-860.  | 8.2 | 6         |
| 65 | Letter to the Editor: Backbone <sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N Assignments of a 42 kDa RecR Homodimer. <i>Journal of Biomolecular NMR</i> , 2004, 28, 199-200.  | 2.8 | 4         |
| 66 | Characterization of Denatured States and Reversible Unfolding of Sensory Rhodopsin II. <i>Journal of Molecular Biology</i> , 2018, 430, 4068-4086.   | 4.2 | 4         |
| 67 | Structural and Functional Consequences of the Weak Binding of Chlorin e6 to Bovine Rhodopsin. <i>Photochemistry and Photobiology</i> , 2019, 95, 787-802.  | 2.5 | 4         |
| 68 | Backbone <sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N E. coli nickel binding protein NikA. <i>Journal of Biomolecular NMR</i> , 2005, 32, 177-177.   | 2.8 | 3         |
| 69 | <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments for the active conformation of the small G protein RalB in complex with its effector RLIP76. <i>Biomolecular NMR Assignments</i> , 2008, 2, 179-182.             | 0.8 | 3         |
| 70 | Resonance assignments for the RLIP76 Ral binding domain in its free form and in complex with the small G protein RalB. <i>Biomolecular NMR Assignments</i> , 2008, 2, 191-194.   | 0.8 | 3         |
| 71 | <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments of the GTPase-activating (GAP) and Ral binding domains (GBD) of RLIP76 (RalBP1). <i>Biomolecular NMR Assignments</i> , 2012, 6, 119-122.                         | 0.8 | 3         |
| 72 | <sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C backbone assignments of GDP-bound human H-Ras mutant G12V. <i>Biomolecular NMR Assignments</i> , 2016, 10, 121-123.  | 0.8 | 3         |

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|----|--|------|-----------|
| 73 | Characterisation of denatured states of sensory rhodopsin II by solution-state NMR. <i>Journal of Molecular Biology</i> , 2019, 431, 2790-2809.  | 4.2  | 2         |
| 74 | Time-domain signal modelling in multidimensional NMR experiments for estimation of relaxation parameters. <i>Journal of Biomolecular NMR</i> , 2019, 73, 93-104.   | 2.8  | 2         |
| 75 | <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments for Binder of Arl2, BART. <i>Biomolecular NMR Assignments</i> , 2009, 3, 33-36.  | 0.8  | 1         |
| 76 | <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments of the Cdc42-binding domain of TOCA1. <i>Biomolecular NMR Assignments</i> , 2016, 10, 407-411.   | 0.8  | 1         |
| 77 | A generalized approach for NMR studies of lipid-protein interactions based on sparse fluorination of acyl chains. <i>Chemical Communications</i> , 2018, 54, 7306-7309.  | 4.1  | 1         |
| 78 | Chapter 10. Compressed Sensing and $\ell_1$ -Norm Minimisation in Multidimensional NMR Spectroscopy. <i>New Developments in NMR</i> , 0, , 267-303.  | 0.1  | 1         |
| 79 | 1P060 Applications of nonlinear sampling scheme for four dimensional triple resonance NMR spectroscopy(Proteins-methodology,Poster Presentations). <i>Seibutsu Butsuri</i> , 2007, 47, S38.  | 0.1  | 0         |
| 80 | Inside Cover: Solution-State NMR Spectroscopy of a Seven-Helix Transmembrane Protein Receptor: Backbone Assignment, Secondary Structure, and Dynamics ( <i>Angew. Chem. Int. Ed.</i> 38/2008). <i>Angewandte Chemie - International Edition</i> , 2008, 47, 7142-7142. | 13.8 | 0         |
| 81 | Innentitelbild: Solution-State NMR Spectroscopy of a Seven-Helix Transmembrane Protein Receptor: Backbone Assignment, Secondary Structure, and Dynamics ( <i>Angew. Chem.</i> 38/2008). <i>Angewandte Chemie</i> , 2008, 120, 7252-7252.                               | 2.0  | 0         |
| 82 | 3P-051 Applications of nonlinear sampling scheme to four dimensional triple resonance NMR spectroscopy(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008, 48, S135.   | 0.1  | 0         |
| 83 | Application of random coherence order selection in gradient-enhanced multidimensional NMR. <i>Journal of Physics: Conference Series</i> , 2016, 699, 012004.   | 0.4  | 0         |