

List of Publications by Citations

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

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|--------------------|-------------------------|----------------|-----------------|
| 137 papers | 5,388 citations | 43 h-index | 67 g-index |
| 161 ext. papers | 5,892 ext. citations | 5.4 avg, IF | 5.47 L-index |

| # | Paper | IF | Citations |
|-----|---|------|-----------|
| 137 | Comparison of the crystal and solution structures of calmodulin and troponin C. <i>Biochemistry</i> , 1988 , 27, 909-15 | 3.2 | 317 |
| 136 | Small-angle scattering for structural biology--expanding the frontier while avoiding the pitfalls. <i>Protein Science</i> , 2010 , 19, 642-57 | 6.3 | 298 |
| 135 | Refinement of multidomain protein structures by combination of solution small-angle X-ray scattering and NMR data. <i>Journal of the American Chemical Society</i> , 2005 , 127, 16621-8 | 16.4 | 185 |
| 134 | 2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 710-728 | 5.5 | 145 |
| 133 | Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015 , 23, 1156-67 | 5.2 | 131 |
| 132 | MULCh: modules for the analysis of small-angle neutron contrast variation data from biomolecular assemblies. <i>Journal of Applied Crystallography</i> , 2008 , 41, 222-226 | 3.8 | 128 |
| 131 | Changes in the structure of calmodulin induced by a peptide based on the calmodulin-binding domain of myosin light chain kinase. <i>Biochemistry</i> , 1989 , 28, 6757-64 | 3.2 | 118 |
| 130 | A model structure of the muscle protein complex 4Ca ²⁺ .troponin C.troponin I derived from small-angle scattering data: implications for regulation. <i>Biochemistry</i> , 1994 , 33, 12800-6 | 3.2 | 111 |
| 129 | Publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 620-6 | | 107 |
| 128 | Cardiac myosin-binding protein C decorates F-actin: implications for cardiac function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18360-5 | 11.5 | 99 |
| 127 | Calmodulin and troponin C structures studied by Fourier transform infrared spectroscopy: effects of Ca ²⁺ and Mg ²⁺ binding. <i>Biochemistry</i> , 1989 , 28, 1294-301 | 3.2 | 94 |
| 126 | Refined solution structure of the 82-kDa enzyme malate synthase G from joint NMR and synchrotron SAXS restraints. <i>Journal of Biomolecular NMR</i> , 2008 , 40, 95-106 | 3 | 93 |
| 125 | Troponin I encompasses an extended troponin C in the Ca(2+)-bound complex: a small-angle X-ray and neutron scattering study. <i>Biochemistry</i> , 1994 , 33, 8233-9 | 3.2 | 89 |
| 124 | The structure of human SFPQ reveals a coiled-coil mediated polymer essential for functional aggregation in gene regulation. <i>Nucleic Acids Research</i> , 2015 , 43, 3826-40 | 20.1 | 81 |
| 123 | The relative orientation of Gla and EGF domains in coagulation factor X is altered by Ca ²⁺ binding to the first EGF domain. A combined NMR-small angle X-ray scattering study. <i>Biochemistry</i> , 1996 , 35, 11547-59 | 3.2 | 76 |
| 122 | The assembly of immunoglobulin-like modules in titin: implications for muscle elasticity. <i>Journal of Molecular Biology</i> , 1998 , 284, 761-77 | 6.5 | 75 |
| 121 | Phosphorylation-dependent conformational transition of the cardiac specific N-extension of troponin I in cardiac troponin. <i>Journal of Molecular Biology</i> , 2007 , 373, 706-22 | 6.5 | 73 |

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|-----|--|------|----|
| 120 | Functional dynamics of the hydrophobic cleft in the N-domain of calmodulin. <i>Biophysical Journal</i> , 2001 , 80, 2082-92 | 2.9 | 71 |
| 119 | Small-angle scattering studies show distinct conformations of calmodulin in its complexes with two peptides based on the regulatory domain of the catalytic subunit of phosphorylase kinase. <i>Biochemistry</i> , 1990 , 29, 9316-24 | 3.2 | 71 |
| 118 | Evolution of quaternary structure in a homotetrameric enzyme. <i>Journal of Molecular Biology</i> , 2008 , 380, 691-703 | 6.5 | 70 |
| 117 | Structures of calmodulin and a functional myosin light chain kinase in the activated complex: a neutron scattering study. <i>Biochemistry</i> , 1997 , 36, 6017-23 | 3.2 | 66 |
| 116 | Report of the wwPDB Small-Angle Scattering Task Force: data requirements for biomolecular modeling and the PDB. <i>Structure</i> , 2013 , 21, 875-81 | 5.2 | 65 |
| 115 | Large-scale shape changes in proteins and macromolecular complexes. <i>Annual Review of Physical Chemistry</i> , 2000 , 51, 355-80 | 15.7 | 64 |
| 114 | Assignment of segments of the bacteriorhodopsin sequence to positions in the structural map. <i>Biophysical Journal</i> , 1983 , 42, 233-41 | 2.9 | 64 |
| 113 | Effects of macromolecular crowding on an intrinsically disordered protein characterized by small-angle neutron scattering with contrast matching. <i>Biophysical Journal</i> , 2011 , 100, 1120-8 | 2.9 | 62 |
| 112 | Myosin light chain kinase: functional domains and structural motifs. <i>Acta Physiologica Scandinavica</i> , 1998 , 164, 471-82 | | 61 |
| 111 | Synaptic arrangement of the neuroligin/beta-neurexin complex revealed by X-ray and neutron scattering. <i>Structure</i> , 2007 , 15, 693-705 | 5.2 | 60 |
| 110 | The structure of the KinA-Sda complex suggests an allosteric mechanism of histidine kinase inhibition. <i>Journal of Molecular Biology</i> , 2007 , 368, 407-20 | 6.5 | 59 |
| 109 | Mechanisms associated with cGMP binding and activation of cGMP-dependent protein kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 2380-5 | 11.5 | 59 |
| 108 | PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. <i>Structure</i> , 2017 , 25, 1317-1318 | 5.2 | 58 |
| 107 | Small-angle X-ray scattering reveals the N-terminal domain organization of cardiac myosin binding protein C. <i>Journal of Molecular Biology</i> , 2008 , 377, 1186-99 | 6.5 | 55 |
| 106 | The solution structure of a cardiac troponin C-troponin I-troponin T complex shows a somewhat compact troponin C interacting with an extended troponin I-troponin T component. <i>Biochemistry</i> , 2002 , 41, 15654-63 | 3.2 | 53 |
| 105 | Conformational differences among solution structures of the type Ialpha, IIalpha and IIbeta protein kinase A regulatory subunit homodimers: role of the linker regions. <i>Journal of Molecular Biology</i> , 2004 , 337, 1183-94 | 6.5 | 50 |
| 104 | Neutron-scattering studies reveal further details of the Ca ²⁺ /calmodulin-dependent activation mechanism of myosin light chain kinase. <i>Biochemistry</i> , 1998 , 37, 13997-4004 | 3.2 | 50 |
| 103 | Ligand-induced conformational changes and conformational dynamics in the solution structure of the lactose repressor protein. <i>Journal of Molecular Biology</i> , 2008 , 376, 466-81 | 6.5 | 49 |

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|-----|---|-----|----|
| 102 | Differential effects of substrate on type I and type II PKA holoenzyme dissociation. <i>Biochemistry</i> , 2004 , 43, 5629-36 | 3.2 | 49 |
| 101 | The N-terminal domains of myosin binding protein C can bind polymorphically to F-actin. <i>Journal of Molecular Biology</i> , 2011 , 412, 379-86 | 6.5 | 45 |
| 100 | A model of troponin-I in complex with troponin-C using hybrid experimental data: the inhibitory region is a beta-hairpin. <i>Protein Science</i> , 2000 , 9, 1312-26 | 6.3 | 45 |
| 99 | Quaternary structures of a catalytic subunit-regulatory subunit dimeric complex and the holoenzyme of the cAMP-dependent protein kinase by neutron contrast variation. <i>Journal of Biological Chemistry</i> , 1998 , 273, 30448-59 | 5.4 | 45 |
| 98 | Progressive cyclic nucleotide-induced conformational changes in the cGMP-dependent protein kinase studied by small angle X-ray scattering in solution. <i>Journal of Biological Chemistry</i> , 1997 , 272, 31929-36 | 5.4 | 44 |
| 97 | Insights into biomolecular function from small-angle scattering. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 702-8 | 8.1 | 44 |
| 96 | Small-angle neutron scattering with contrast variation reveals spatial relationships between the three subunits in the ternary cardiac troponin complex and the effects of troponin I phosphorylation. <i>Biochemistry</i> , 2003 , 42, 7790-800 | 3.2 | 44 |
| 95 | Ligand-induced conformational changes via flexible linkers in the amino-terminal region of the inositol 1,4,5-trisphosphate receptor. <i>Journal of Molecular Biology</i> , 2007 , 373, 1269-80 | 6.5 | 43 |
| 94 | Further insights into calmodulin-myosin light chain kinase interaction from solution scattering and shape restoration. <i>Biochemistry</i> , 2003 , 42, 10579-88 | 3.2 | 43 |
| 93 | An optimized SEC-SAXS system enabling high X-ray dose for rapid SAXS assessment with correlated UV measurements for biomolecular structure analysis. <i>Journal of Applied Crystallography</i> , 2018 , 51, 97-111 | 3.8 | 41 |
| 92 | Coassembling Peptide-Based Biomaterials: Effects of Pairing Equal and Unequal Chain Length Oligopeptides. <i>Chemistry of Materials</i> , 2006 , 18, 6157-6162 | 9.6 | 41 |
| 91 | A novel approach for enhancing the catalytic efficiency of a protease at low temperature: reduction in substrate inhibition by chemical modification. <i>Biotechnology and Bioengineering</i> , 2009 , 103, 676-86 | 4.9 | 40 |
| 90 | Small-angle scattering and neutron contrast variation for studying bio-molecular complexes. <i>Methods in Molecular Biology</i> , 2009 , 544, 307-23 | 1.4 | 40 |
| 89 | Global conformational changes control the reactivity of methane monooxygenase. <i>Biochemistry</i> , 1999 , 38, 6752-60 | 3.2 | 39 |
| 88 | Activation of the retroviral budding factor ALIX. <i>Journal of Virology</i> , 2011 , 85, 9222-6 | 6.6 | 38 |
| 87 | Stability of transmembrane regions in bacteriorhodopsin studied by progressive proteolysis. <i>Journal of Membrane Biology</i> , 1985 , 88, 233-47 | 2.3 | 37 |
| 86 | The outer-membrane export signal of <i>Porphyromonas gingivalis</i> type IX secretion system (T9SS) is a conserved C-terminal Eandwich domain. <i>Scientific Reports</i> , 2016 , 6, 23123 | 4.9 | 37 |
| 85 | Small-angle X-ray scattering of reduced ribonuclease A: effects of solution conditions and comparisons with a computational model of unfolded proteins. <i>Journal of Molecular Biology</i> , 2008 , 377, 1576-92 | 6.5 | 36 |

| | | | |
|----|---|------|----|
| 84 | C subunits binding to the protein kinase A RI alpha dimer induce a large conformational change. <i>Journal of Biological Chemistry</i> , 2004 , 279, 19084-90 | 5.4 | 36 |
| 83 | Structures of fd gene 5 protein.nucleic acid complexes: a combined solution scattering and electron microscopy study. <i>Journal of Molecular Biology</i> , 1995 , 249, 576-94 | 6.5 | 36 |
| 82 | The solution structures of calmodulin and its complexes with synthetic peptides based on target enzyme binding domains. <i>Cell Calcium</i> , 1992 , 13, 377-90 | 4 | 36 |
| 81 | Calmodulin binding to myosin light chain kinase begins at substoichiometric Ca ²⁺ concentrations: a small-angle scattering study of binding and conformational transitions. <i>Biochemistry</i> , 1998 , 37, 17810-7 | 3.2 | 35 |
| 80 | Human cardiac myosin binding protein C: structural flexibility within an extended modular architecture. <i>Journal of Molecular Biology</i> , 2011 , 414, 735-48 | 6.5 | 34 |
| 79 | Fractal dimension of an intrinsically disordered protein: small-angle X-ray scattering and computational study of the bacteriophage IN protein. <i>Protein Science</i> , 2011 , 20, 1955-70 | 6.3 | 33 |
| 78 | LIM domain binding proteins 1 and 2 have different oligomeric states. <i>Journal of Molecular Biology</i> , 2010 , 399, 133-44 | 6.5 | 33 |
| 77 | Domain organization of the monomeric form of the Tom70 mitochondrial import receptor. <i>Journal of Molecular Biology</i> , 2009 , 388, 1043-58 | 6.5 | 33 |
| 76 | Solution scattering reveals large differences in the global structures of type II protein kinase A isoforms. <i>Journal of Molecular Biology</i> , 2006 , 357, 880-9 | 6.5 | 32 |
| 75 | Structural basis for partial redundancy in a class of transcription factors, the LIM homeodomain proteins, in neural cell type specification. <i>Journal of Biological Chemistry</i> , 2011 , 286, 42971-80 | 5.4 | 31 |
| 74 | Small-angle scattering and 3D structure interpretation. <i>Current Opinion in Structural Biology</i> , 2016 , 40, 1-7 | 8.1 | 29 |
| 73 | K7del is a common TPM2 gene mutation associated with nemaline myopathy and raised myofibre calcium sensitivity. <i>Brain</i> , 2013 , 136, 494-507 | 11.2 | 29 |
| 72 | The C0C1 fragment of human cardiac myosin binding protein C has common binding determinants for both actin and myosin. <i>Journal of Molecular Biology</i> , 2011 , 413, 908-13 | 6.5 | 29 |
| 71 | A chemically modified alpha-amylase with a molten-globule state has entropically driven enhanced thermal stability. <i>Protein Engineering, Design and Selection</i> , 2010 , 23, 769-80 | 1.9 | 29 |
| 70 | There is communication between all four Ca(2+)-bindings sites of calcineurin B. <i>Biochemistry</i> , 2001 , 40, 12094-102 | 3.2 | 29 |
| 69 | The solution structure of the Sac7d/DNA complex: a small-angle X-ray scattering study. <i>Biochemistry</i> , 1999 , 38, 10247-55 | 3.2 | 29 |
| 68 | Ordered macromolecular structures in ferrofluid mixtures. <i>Physical Review Letters</i> , 1989 , 62, 1667-1670 | 7.4 | 29 |
| 67 | Solution structure of ectodomains of the insulin receptor family: the ectodomain of the type 1 insulin-like growth factor receptor displays asymmetry of ligand binding accompanied by limited conformational change. <i>Journal of Molecular Biology</i> , 2009 , 394, 878-92 | 6.5 | 28 |

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|----|--|------|----|
| 66 | The macromolecular architecture of extracellular domain of alphaNRXN1: domain organization, flexibility, and insights into trans-synaptic disposition. <i>Structure</i> , 2010 , 18, 1044-53 | 5.2 | 28 |
| 65 | Histidine kinase regulation by a cyclophilin-like inhibitor. <i>Journal of Molecular Biology</i> , 2008 , 384, 422-356 | 5.5 | 26 |
| 64 | Activation of myosin light chain kinase requires translocation of bound calmodulin. <i>Journal of Biological Chemistry</i> , 2001 , 276, 4535-8 | 5.4 | 26 |
| 63 | A structural model of the catalytic subunit-regulatory subunit dimeric complex of the cAMP-dependent protein kinase. <i>Journal of Biological Chemistry</i> , 2002 , 277, 12423-31 | 5.4 | 26 |
| 62 | 1H-NMR studies of ferric soybean leghemoglobin: assignment of hyperfine shifted resonances of complexes with cyanide, nicotinate, pyridine and azide. <i>Biochimica Et Biophysica Acta (BBA) - Protein Structure</i> , 1980 , 625, 202-20 | | 26 |
| 61 | Calmodulin remains extended upon binding to smooth muscle caldesmon: a combined small-angle scattering and fourier transform infrared spectroscopy study. <i>Biochemistry</i> , 2000 , 39, 3979-87 | 3.2 | 25 |
| 60 | Effect of temperature during assembly on the structure and mechanical properties of peptide-based materials. <i>Biomacromolecules</i> , 2010 , 11, 1502-6 | 6.9 | 24 |
| 59 | Subdividing repressor function: DNA binding affinity, selectivity, and allostery can be altered by amino acid substitution of nonconserved residues in a LacI/GalR homologue. <i>Biochemistry</i> , 2008 , 47, 8058-69 | 3.2 | 23 |
| 58 | Ca ²⁺ -induced structural changes in phosphorylase kinase detected by small-angle X-ray scattering. <i>Protein Science</i> , 2005 , 14, 1039-48 | 6.3 | 22 |
| 57 | Troponin I inhibitory peptide (96-115) has an extended conformation when bound to skeletal muscle troponin C. <i>Biochemistry</i> , 1999 , 38, 6911-7 | 3.2 | 22 |
| 56 | Molecular basis for proton-dependent anion binding by soybean leghaemoglobin a. <i>Nature</i> , 1979 , 280, 87-88 | 50.4 | 22 |
| 55 | Structural Characterization of the Extracellular Domain of CASPR2 and Insights into Its Association with the Novel Ligand Contactin1. <i>Journal of Biological Chemistry</i> , 2016 , 291, 5788-5802 | 5.4 | 21 |
| 54 | Bayesian inference of protein conformational ensembles from limited structural data. <i>PLoS Computational Biology</i> , 2018 , 14, e1006641 | 5 | 20 |
| 53 | The C-Terminal Zinc Fingers of ZBTB38 are Novel Selective Readers of DNA Methylation. <i>Journal of Molecular Biology</i> , 2018 , 430, 258-271 | 6.5 | 18 |
| 52 | Neutron Resonance Scattering Shows Specific Binding of Plutonium to the Calcium-Binding Sites of the Protein Calmodulin and Yields Precise Distance Information. <i>Journal of the American Chemical Society</i> , 1997 , 119, 5118-5125 | 16.4 | 18 |
| 51 | The conformationally dynamic C helix of the RIalpha subunit of protein kinase A mediates isoform-specific domain reorganization upon C subunit binding. <i>Journal of Biological Chemistry</i> , 2005 , 280, 35521-7 | 5.4 | 18 |
| 50 | A novel structure of an antikinase and its inhibitor. <i>Journal of Molecular Biology</i> , 2011 , 405, 214-26 | 6.5 | 17 |
| 49 | Calmodulin disrupts the structure of the HIV-1 MA protein. <i>Journal of Molecular Biology</i> , 2010 , 400, 702-14 | 6.5 | 17 |

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|----|--|------|----|
| 48 | The role of heme binding by DNA-protective protein from starved cells (Dps) in the Tolerance of <i>Porphyromonas gingivalis</i> to heme toxicity. <i>Journal of Biological Chemistry</i> , 2012 , 287, 42243-58 | 5.4 | 16 |
| 47 | A picornaviral loop-to-loop replication complex. <i>Journal of Structural Biology</i> , 2009 , 166, 251-62 | 3.4 | 16 |
| 46 | The different views from small angles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 4967-8 | 11.5 | 15 |
| 45 | The solution structure of the DNA double-stranded break repair protein Ku and its complex with DNA: a neutron contrast variation study. <i>Biochemistry</i> , 1999 , 38, 2152-9 | 3.2 | 15 |
| 44 | Structural properties of a haemophore facilitate targeted elimination of the pathogen <i>Porphyromonas gingivalis</i> . <i>Nature Communications</i> , 2018 , 9, 4097 | 17.4 | 15 |
| 43 | Reliable structural interpretation of small-angle scattering data from bio-molecules in solution—the importance of quality control and a standard reporting framework. <i>BMC Structural Biology</i> , 2012 , 12, 9 | 2.7 | 14 |
| 42 | Changes in small-angle X-ray scattering parameters observed upon binding of ligand to rabbit muscle pyruvate kinase are not correlated with allosteric transitions. <i>Biochemistry</i> , 2010 , 49, 7202-9 | 3.2 | 14 |
| 41 | The motif of human cardiac myosin-binding protein C is required for its Ca ²⁺ -dependent interaction with calmodulin. <i>Journal of Biological Chemistry</i> , 2012 , 287, 31596-607 | 5.4 | 14 |
| 40 | Orienting rigid and flexible biological assemblies in ferrofluids for small-angle neutron scattering studies. <i>Biophysical Journal</i> , 1991 , 60, 1178-89 | 2.9 | 14 |
| 39 | Structural basis of interprotein electron transfer in bacterial sulfite oxidation. <i>ELife</i> , 2015 , 4, e09066 | 8.9 | 14 |
| 38 | Calmodulin binds a highly extended HIV-1 MA protein that refolds upon its release. <i>Biophysical Journal</i> , 2012 , 103, 541-549 | 2.9 | 12 |
| 37 | A Highly Conserved Yet Flexible Linker Is Part of a Polymorphic Protein-Binding Domain in Myosin-Binding Protein C. <i>Structure</i> , 2016 , 24, 2000-2007 | 5.2 | 12 |
| 36 | Solution structure studies of monomeric human TIP47/perilipin-3 reveal a highly extended conformation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 2046-55 | 4.2 | 11 |
| 35 | Clinically Linked Mutations in the Central Domains of Cardiac Myosin-Binding Protein C with Distinct Phenotypes Show Differential Structural Effects. <i>Structure</i> , 2016 , 24, 105-115 | 5.2 | 10 |
| 34 | Sol and gel states in peptide hydrogels visualized by Gd(III)-enhanced magnetic resonance imaging. <i>Biopolymers</i> , 2011 , 96, 734-43 | 2.2 | 10 |
| 33 | Mutation-Induced Population Shift in the MexR Conformational Ensemble Disengages DNA Binding: A Novel Mechanism for MarR Family Derepression. <i>Structure</i> , 2016 , 24, 1311-1321 | 5.2 | 10 |
| 32 | Structure of the sporulation histidine kinase inhibitor Sda from <i>Bacillus subtilis</i> and insights into its solution state. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009 , 65, 574-81 | | 9 |
| 31 | Solution structure of heavy meromyosin by small-angle scattering. <i>Journal of Biological Chemistry</i> , 2003 , 278, 6034-40 | 5.4 | 8 |

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|----|---|-----|---|
| 30 | Spin state equilibria in soybean ferric leghemoglobin and its complexes with formate and acetate. <i>Biochemical and Biophysical Research Communications</i> , 1979 , 88, 713-21 | 3.4 | 8 |
| 29 | The structure of TTHA0988 from <i>Thermus thermophilus</i> , a Kipl-KipA homologue incorrectly annotated as an allophanate hydrolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 105-11 | | 7 |
| 28 | Effects of chain length on oligopeptide hydrogelation. <i>Soft Matter</i> , 2011 , 7, 2624-2631 | 3.6 | 7 |
| 27 | Characterization of the solution structure of a neuroligin/beta-neurexin complex. <i>Chemico-Biological Interactions</i> , 2008 , 175, 150-5 | 5 | 7 |
| 26 | Differences in the heme environment of soybean leghemoglobin components shown by ¹ H-NMR spectroscopy. <i>BBA - Proteins and Proteomics</i> , 1982 , 700, 171-177 | | 7 |
| 25 | Solution structure of the LIM-homeodomain transcription factor complex Lhx3/Ldb1 and the effects of a pituitary mutation on key Lhx3 interactions. <i>PLoS ONE</i> , 2012 , 7, e40719 | 3.7 | 7 |
| 24 | Neutrons reveal how nature uses structural themes and variation in biological regulation. <i>Physica B: Condensed Matter</i> , 2006 , 385-386, 825-830 | 2.8 | 6 |
| 23 | Recent advances in small-angle scattering and its expanding impact in structural biology.. <i>Structure</i> , 2022 , 30, 15-23 | 5.2 | 6 |
| 22 | E3 ubiquitin-protein ligase TRIM21-mediated lysine capture by UBE2E1 reveals substrate-targeting mode of a ubiquitin-conjugating E2. <i>Journal of Biological Chemistry</i> , 2019 , 294, 11404-11419 | 5.4 | 5 |
| 21 | Conformationally constrained analogs of protein kinase inhibitor (6-22)amide: effect of turn structures in the center of the peptide on inhibition of cAMP-dependent protein kinase. <i>Protein Science</i> , 1995 , 4, 405-15 | 6.3 | 5 |
| 20 | Protein kinase A targeting and activation as seen by small-angle solution scattering. <i>European Journal of Cell Biology</i> , 2006 , 85, 655-62 | 6.1 | 5 |
| 19 | Small-angle solution scattering reveals information on conformational dynamics in calcium-binding proteins and in their interactions with regulatory targets. <i>Methods in Molecular Biology</i> , 2002 , 173, 137-55 | 1.4 | 5 |
| 18 | ¹ H N.M.R Studies of High-Spin Complexes of Soybean Leghemoglobin. Interactions Between the Distal Histidine and Acetate, Formate and Fluoride Ligands. <i>Australian Journal of Chemistry</i> , 1986 , 39, 317 | 1.2 | 5 |
| 17 | Effects of gadolinium chelate on the evolution of the nanoscale structure in peptide hydrogels. <i>Biopolymers</i> , 2012 , 98, 50-8 | 2.2 | 4 |
| 16 | Invited review: probing the structures of muscle regulatory proteins using small-angle solution scattering. <i>Biopolymers</i> , 2011 , 95, 505-16 | 2.2 | 4 |
| 15 | Archiving of Integrative Structural Models. <i>Advances in Experimental Medicine and Biology</i> , 2018 , 1105, 261-272 | 3.6 | 4 |
| 14 | Binding of N-Terminus Fragments of Cardiac Myosin-Binding C-protein to Actin. <i>Biophysical Journal</i> , 2010 , 98, 157a | 2.9 | 3 |
| 13 | Structural themes and variations in protein kinase A as seen by small-angle scattering and neutron contrast variation. <i>European Biophysics Journal</i> , 2006 , 35, 585-9 | 1.9 | 2 |

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|----|---|------|---|
| 12 | Potential biophysical application of the Los Alamos infrared free electron laser: DNA spectroscopy. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 1990 , 296, 809-813 | 1.2 | 2 |
| 11 | Small Angle Scattering and Structural Biology: Data Quality and Model Validation. <i>Advances in Experimental Medicine and Biology</i> , 2018 , 1105, 77-100 | 3.6 | 2 |
| 10 | Growing a thriving international community for small-angle scattering through collaboration. <i>Journal of Applied Crystallography</i> , 2021 , 54, 1029-1033 | 3.8 | 2 |
| 9 | Mutation in a flexible linker modulates binding affinity for modular complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 425-429 | 4.2 | 1 |
| 8 | ¹ H, ¹³ C and ¹⁵ N backbone and side chain resonance assignments of the N-terminal domain of the histidine kinase inhibitor Kipl from <i>Bacillus subtilis</i> . <i>Biomolecular NMR Assignments</i> , 2010 , 4, 167-9 | 0.7 | 1 |
| 7 | Nanoscale Science and Technology at Los Alamos National Laboratory. <i>Journal of Nanoparticle Research</i> , 2000 , 2, 249-266 | 2.3 | 1 |
| 6 | Reflections of a Woman Scientist in the Year 2011. <i>Australian Journal of Chemistry</i> , 2011 , 64, 666 | 1.2 | |
| 5 | A Day in the World Science Alliance. <i>Science</i> , 1999 , 286, 2104-2106 | 33.3 | |
| 4 | Neutron diffraction studies of bacteriorhodopsin. <i>Physica B: Physics of Condensed Matter & C: Atomic, Molecular and Plasma Physics, Optics</i> , 1986 , 136, 249-251 | | |
| 3 | The Structure of the Muscle Protein Complex 4Ca ²⁺ -Troponin C-Troponin I 1996 , 137-147 | | |
| 2 | Small-Angle Scattering of Neutrons and X-Rays 1-11 | | |
| 1 | Contrasting DNA-binding behaviour by ISL1 and LHX3 underpins differential gene targeting in neuronal cell specification. <i>Journal of Structural Biology: X</i> , 2021 , 5, 100043 | 2.9 | |