Mark D Carr

List of Publications by Year
in descending order

57 papers	2,695 citations	201674 27 h-index	189892 50 g-index
59 all docs	59 docs citations	59 times ranked	3491 citing authors

#	Article	IF	Citations
1	Conclusive Evidence That the Major T-cell Antigens of theMycobacterium tuberculosis Complex ESAT-6 and CFP-10 Form a Tight, 1:1 Complex and Characterization of the Structural Properties of ESAT-6, CFP-10, and the ESAT-6Â·CFP-10 Complex. Journal of Biological Chemistry, 2002, 277, 21598-21603.	3.4	288
2	Structure and function of the complex formed by the tuberculosis virulence factors CFP-10 and ESAT-6. EMBO Journal, 2005, 24, 2491-2498.	7.8	282
3	Structure and Interactions of the Human Programmed Cell Death 1 Receptor. Journal of Biological Chemistry, 2013, 288, 11771-11785.	3.4	256
4	Characterization of the Structural Features and Interactions of Sclerostin. Journal of Biological Chemistry, 2009, 284, 10890-10900.	3.4	206
5	Structural characterization of the interaction of mTOR with phosphatidic acid and a novel class of inhibitor: compelling evidence for a central role of the FRB domain in small molecule-mediated regulation of mTOR. Oncogene, 2008, 27, 585-595.	5.9	138
6	Mapping the Binding Site for Matrix Metalloproteinase on the N-Terminal Domain of the Tissue Inhibitor of Metalloproteinases-2 by NMR Chemical Shift Perturbationâ€. Biochemistry, 1997, 36, 13882-13889.	2.5	119
7	Solution structure of the active domain of tissue inhibitor of metalloproteinases-2. A new member of the OB fold protein family. Biochemistry, 1994, 33, 11745-11759.	2.5	106
8	High Resolution Structure of the N-terminal Domain of Tissue Inhibitor of Metalloproteinases-2 and Characterization of Its Interaction Site with Matrix Metalloproteinase-3. Journal of Biological Chemistry, 1998, 273, 21736-21743.	3.4	80
9	Solution Structure of the Mycobacterium tuberculosis EsxGÂ·EsxH Complex. Journal of Biological Chemistry, 2011, 286, 29993-30002.	3.4	77
10	Characterization of the Interaction of Sclerostin with the Low Density Lipoprotein Receptor-related Protein (LRP) Family of Wnt Co-receptors. Journal of Biological Chemistry, 2012, 287, 26464-26477.	3.4	77
11	Structural Diversity in p160/CREB-binding Protein Coactivator Complexes. Journal of Biological Chemistry, 2006, 281, 14787-14795.	3.4	67
12	Proton NMR-based determination of the secondary structure of porcine pancreatic spasmolytic polypeptide: one of a new family of "trefoil" motif containing cell growth factors. Biochemistry, 1992, 31, 1998-2004.	2.5	49
13	Solution Structure of the Mycobacterium tuberculosis Complex Protein MPB70. Journal of Biological Chemistry, 2003, 278, 43736-43743.	3.4	48
14	Molecular Features Governing the Stability and Specificity of Functional Complex Formation by Mycobacterium tuberculosis CFP-10/ESAT-6 Family Proteins. Journal of Biological Chemistry, 2008, 283, 17681-17690.	3.4	48
15	Structure of the C-terminal MA-3 domain of the tumour suppressor protein Pdcd4 and characterization of its interaction with eIF4A. Oncogene, 2007, 26, 4941-4950.	5.9	45
16	Mycobacterium tuberculosis RNA Polymerase-binding Protein A (RbpA) and Its Interactions with Sigma Factors. Journal of Biological Chemistry, 2013, 288, 14438-14450.	3.4	44
17	Characterisation of complex formation between members of theMycobacterium tuberculosiscomplex CFP-10/ESAT-6 protein family: towards an understanding of the rules governing complex formation and thereby functional flexibility. FEMS Microbiology Letters, 2004, 238, 255-262.	1.8	42
18	High Resolution NMR-based Model for the Structure of a scFv-IL-1Î² Complex. Journal of Biological Chemistry, 2009, 284, 31928-31935.	3.4	40

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19	Chemically and Conformationally Authentic Active Domain of Human Tissue Inhibitor of Metalloproteinases-2 Refolded from Bacterial Inclusion Bodies. FEBS Journal, 1996, 241, 476-483.	0.2	39
20	Tyrosine 36 Plays a Critical Role in the Interaction of the AB Loop of Tissue Inhibitor of Metalloproteinases-2 with Matrix Metalloproteinase-14. Journal of Biological Chemistry, 2001, 276, 32966-32970.	3.4	39
21	Characterisation of complex formation between members of the complex CFP-10/ESAT-6 protein family: towards an understanding of the rules governing complex formation and thereby functional flexibility. FEMS Microbiology Letters, 2004, 238, 255-262.	1.8	39
22	1H NMR structure of an antifungal Î³-thionin protein SIÎ±1: Similarity to scorpion toxins. , 1998, 32, 334-349.		36
23	Letter to the Editor: Sequence-specific assignment and secondary structure determination of the 195-residue complex formed by the Mycobacterium tuberculosis proteins CFP-10 and ESAT-6. Journal of Biomolecular NMR, 2004, 30, 225-226.	2.8	33
24	The Discovery, Engineering and Characterisation of a Highly Potent Anti-Human IL-13 Fab Fragment Designed for Administration by Inhalation. Journal of Molecular Biology, 2013, 425, 577-593.	4.2	33
25	NMR Assignment of the mTOR Domain Responsible for Rapamycin Binding. Journal of Biomolecular NMR, 2006, 36, 3-3.	2.8	31
26	Insight into small molecule binding to the neonatal Fc receptor by X-ray crystallography and 100 kHz magic-angle-spinning NMR. PLoS Biology, 2018, 16, e2006192.	5.6	31
27	Structure of the Tandem MA-3 Region of Pdcd4 Protein and Characterization of Its Interactions with eIF4A and eIF4G. Journal of Biological Chemistry, 2011, 286, 17270-17280.	3.4	29
28	Structure of the B-Myb DNA-binding Domain in Solution and Evidence for Multiple Conformations in the Region of Repeat-2 Involved in DNA Binding. Implications for Sequence-Specific DNA Binding by Myb Proteins. FEBS Journal, 1996, 235, 721-735.	0.2	28
29	Superior T cell activation by ESAT-6 as compared with the ESAT-6â€“CFP-10 complex. International Immunology, 2005, 17, 1439-1446.	4.0	26
30	Structural and functional analysis of Dickkopf 4 (Dkk4): New insights into Dkk evolution and regulation of Wnt signaling by Dkk and Kremen proteins. Journal of Biological Chemistry, 2018, 293, 12149-12166.	3.4	26
31	Solution Structure of the B-Myb DNA-Binding Domain:Â A Possible Role for Conformational Instability of the Protein in DNA Binding and Control of Gene Expressionâ€,â€¡. Biochemistry, 1998, 37, 9619-9629.	2.5	24
32	High-Resolution Solution Structure of Human Intestinal Trefoil Factor and Functional Insights from Detailed Structural Comparisons with the Other Members of the Trefoil Family of Mammalian Cell Motility Factorsâ€,â€¡. Biochemistry, 2001, 40, 9552-9559.	2.5	23
33	In Vitro Assessment of Putative PD-1/PD-L1 Inhibitors: Suggestions of an Alternative Mode of Action. ACS Medicinal Chemistry Letters, 2019, 10, 1187-1192.	2.8	22
34	The Effect of Matrix Metalloproteinase Complex Formation on the Conformational Mobility of Tissue Inhibitor of Metalloproteinases-2 (TIMP-2). Journal of Biological Chemistry, 1999, 274, 37226-37232.	3.4	21
35	Conservation of Functional Sites on Interleukin-6 and Implications for Evolution of Signaling Complex Assembly and Therapeutic Intervention. Journal of Biological Chemistry, 2012, 287, 40043-40050.	3.4	20
36	NMR and molecular dynamics studies of the mKr2 'zinc finger'. FEBS Journal, 1990, 188, 455-461.	0.2	19

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37	NMR-Based Structural Studies of the pNR-2/pS2 Single Domain Trefoil Peptide. Similarities to Porcine Spasmolytic Peptide and Evidence for a Monomeric Structure. FEBS Journal, 1995, 233, 847-855.	0.2	18
38	Cross-Reactive SARS-CoV-2 Neutralizing Antibodies From Deep Mining of Early Patient Responses. Frontiers in Immunology, 2021, 12, 678570.	4.8	16
39	The transcriptional control proteins c-Myb and v-Myb contain a basic region DNA binding motif. FEBS Letters, 1991, 282, 293-294.	2.8	14
40	Allosteric activation of MALT1 by its ubiquitin-binding Ig3 domain. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3093-3102.	7.1	14
41	Conformational Heterogeneity in Antibody-Protein Antigen Recognition. Journal of Biological Chemistry, 2014, 289, 7200-7210.	3.4	13
42	Structure of a Potential Therapeutic Antibody Bound to Interleukin-16 (IL-16). Journal of Biological Chemistry, 2016, 291, 16840-16848.	3.4	11
43	Discovery of a novel pseudo Î²-hairpin structure of N-truncated amyloid-Î² for use as a vaccine against Alzheimerâ€™s disease. Molecular Psychiatry, 2021, , .	7.9	11
44	The 1H-NMR assignments of the aromatic resonances in complexes of Lactobacillus casei dihydrofolate reductase and the origins of their chemical shifts. FEBS Journal, 1990, 191, 659-668.	0.2	10
45	Extensive sequence and structural evolution of Arginase 2 inhibitory antibodies enabled by an unbiased approach to affinity maturation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16949-16960.	7.1	10
46	NMR Assignment and Secondary Structure Determination of the C-terminal MA-3 Domain of the Tumour Suppressor Protein Pdcd4. Journal of Biomolecular NMR, 2006, 36, 18-18.	2.8	8
47	Interaction of the Transactivation Domain of B-Myb with the TAZ2 Domain of the Coactivator p300: Molecular Features and Properties of the Complex. PLoS ONE, 2012, 7, e52906.	2.5	7
48	15N, 13C and 1H resonance assignments and secondary structure determination of the Mycobacterium tuberculosis Rv0287â€“Rv0288 protein complex. Biomolecular NMR Assignments, 2009, 3, 171-174.	0.8	6
49	Nucleotide binding to active and 4-chloro-7-nitrobenzofurazan-inhibited forms of chloroplast F1-ATPase â€” an NMR study. Biochimica Et Biophysica Acta - Bioenergetics, 1990, 1015, 79-86.	1.0	5
50	The statistical significance of selected senseâ€“antisense peptide interactions. Journal of Computational Chemistry, 2012, 33, 1440-1447.	3.3	5
51	Conformational dynamics in interleukin 17A and 17F functional complexes is a key determinant of receptor A affinity and specificity. Cytokine, 2021, 142, 155476.	3.2	4
52	Sequence-specific assignment and determination of the secondary structure of the 163-residue M. tuberculosis and M. bovis antigenic protein mpb70. Journal of Biomolecular NMR, 2001, 20, 185-186.	2.8	2
53	Resonance assignment and secondary structure of the middle MA-3 domain and complete tandem MA-3 region of the tumour suppressor protein Pdcd4. Biomolecular NMR Assignments, 2010, 4, 49-53.	0.8	2
54	15N, 13C and 1H resonance assignments and secondary structure determination of a variable heavy domain of a heavy chain antibody. Biomolecular NMR Assignments, 2014, 8, 113-116.	0.8	2

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55	Resonance assignment and secondary structure determination of full length human Dickkopf 4 (hDkk4), a secreted, disulphide-rich Wnt inhibitor protein. Biomolecular NMR Assignments, 2015, 9, 147-151.	0.8	2
56	Structural and functional characterization of C0021158, a high-affinity monoclonal antibody that inhibits Arginase 2 function via a novel non-competitive mechanism of action. MAbs, 2020, 12, 1801230.	5.2	2
57	Sequence-specific assignment of the B-Myb DNA-binding domain (B-MybR2R3) bound to a 16 base-pair DNA target site corresponding to a regulatory site from the tom-1 gene. Journal of Biomolecular NMR, 2003, 26, 375-376.	2.8	0