

# Charles S Bond

## List of Publications by Year in descending order

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103  
papers

7,917  
citations

61984

43  
h-index

53230

85  
g-index

111  
all docs

111  
docs citations

111  
times ranked

10102  
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp><i>KARRIKIN INSENSITIVE2</i></scp> regulates leaf development, root system architecture and arbuscularâ€”mycorrhizal symbiosis in <i>Brachypodium distachyon</i>. <i>Plant Journal</i> , 2022, 109, 1559-1574.	5.7	15
2	Broad-spectrum <i>in vitro</i> activity of macrophage infectivity potentiator inhibitors against Gram-negative bacteria and <i>Leishmania major</i>. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1625-1634.	3.0	5
3	Single Stranded Fully Modified-Phosphorothioate Oligonucleotides can Induce Structured Nuclear Inclusions, Alter Nuclear Protein Localization and Disturb the Transcriptome In Vitro. <i>Frontiers in Genetics</i> , 2022, 13, 791416.	2.3	10
4	Cofactor-independent RNA editing by a synthetic S-type PPR protein. <i>Synthetic Biology</i> , 2022, 7, ysab034.	2.2	12
5	Structural basis of dimerization and nucleic acid binding of human DBHS proteins NONO and PSCP1. <i>Nucleic Acids Research</i> , 2022, 50, 522-535.	14.5	10
6	An epigenetic switch activates bacterial quorum sensing and horizontal transfer of an integrative and conjugative element. <i>Nucleic Acids Research</i> , 2022, 50, 975-988.	14.5	17
7	Solution NMR and racemic crystallography provide insights into a novel structural class of cyclic plant peptides. <i>RSC Chemical Biology</i> , 2021, 2, 1682-1691.	4.1	1
8	Caveolinâ€”driven membrane remodelling regulates hnRNPKâ€”mediated exosomal microRNA sorting in cancer. <i>Clinical and Translational Medicine</i> , 2021, 11, e381.	4.0	19
9	Structural and biochemical analyses of concanavalin A circular permutation by jack bean asparaginyl endopeptidase. <i>Plant Cell</i> , 2021, 33, 2794-2811.	6.6	9
10	Evolving origin-of-transfer sequences on staphylococcal conjugative and mobilizable plasmidsâ€”whoâ€”s mimicking whom?. <i>Nucleic Acids Research</i> , 2021, 49, 5177-5188.	14.5	8
11	A synthetic RNA editing factor edits its target site in chloroplasts and bacteria. <i>Communications Biology</i> , 2021, 4, 545.	4.4	28
12	The role of G-Quadruplex DNA in Paraspeckle formation in cancer. <i>Biochimie</i> , 2021, 190, 124-131.	2.6	10
13	The Expansion and Diversification of Pentatricopeptide Repeat RNA-Editing Factors in Plants. <i>Molecular Plant</i> , 2020, 13, 215-230.	8.3	71
14	Divergent receptor proteins confer responses to different karrikins in two ephemeral weeds. <i>Nature Communications</i> , 2020, 11, 1264.	12.8	29
15	Amylin and beta amyloid proteins interact to form amorphous heterocomplexes with enhanced toxicity in neuronal cells. <i>Scientific Reports</i> , 2020, 10, 10356.	3.3	44
16	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. <i>Angewandte Chemie</i> , 2019, 131, 16936-16940.	2.0	8
17	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 16780-16784.	13.8	26
18	TGFâ€”induced fibrotic stress increases Gâ€”quadruplex formation in human fibroblasts. <i>FEBS Letters</i> , 2019, 593, 3149-3161.	2.8	8

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19	Evolution of a 72-Kilobase Cointegrant, Conjugative Multiresistance Plasmid in Community-Associated Methicillin-Resistant Staphylococcus aureus Isolates from the Early 1990s. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	12
20	Delineation of the integrase-attachment and origin-of-transfer regions of the symbiosis island ICEMISymR7A. <i>Plasmid</i> , 2019, 104, 102416.	1.4	4
21	The macrocyclizing protease butelase 1 remains autocatalytic and reveals the structural basis for ligase activity. <i>Plant Journal</i> , 2019, 98, 988-999.	5.7	57
22	Structure of <i>Aspergillus fumigatus</i> Cytosolic Thiolase: Trapped Tetrahedral Reaction Intermediates and Activation by Monovalent Cations. <i>ACS Catalysis</i> , 2018, 8, 1973-1989.	11.2	4
23	Paraspeckles: Where Long Noncoding RNA Meets Phase Separation. <i>Trends in Biochemical Sciences</i> , 2018, 43, 124-135.	7.5	315
24	Crystal structure of a SFPQ/PSPC1 heterodimer provides insights into preferential heterodimerization of human DBHS family proteins. <i>Journal of Biological Chemistry</i> , 2018, 293, 6593-6602.	3.4	32
25	Intracellular speciation of gold nanorods alters the conformational dynamics of genomic DNA. <i>Nature Nanotechnology</i> , 2018, 13, 1148-1153.	31.5	16
26	NONO Detects the Nuclear HIV Capsid to Promote cGAS-Mediated Innate Immune Activation. <i>Cell</i> , 2018, 175, 488-501.e22.	28.9	154
27	Functional Domains of NEAT1 Architectural lncRNA Induce Paraspeckle Assembly through Phase Separation. <i>Molecular Cell</i> , 2018, 70, 1038-1053.e7.	9.7	429
28	Structural basis of ribosomal peptide macrocyclization in plants. <i>ELife</i> , 2018, 7, .	6.0	52
29	Whaddaya Know: A Guide to Uncertainty and Subjectivity in Structural Biology. <i>Trends in Biochemical Sciences</i> , 2017, 42, 155-167.	7.5	14
30	Non-nuclear Pool of Splicing Factor SFPQ Regulates Axonal Transcripts Required for Normal Motor Development. <i>Neuron</i> , 2017, 94, 322-336.e5.	8.1	61
31	Evidence for Ancient Origins of Bowman-Birk Inhibitors from <i>Selaginella moellendorffii</i> . <i>Plant Cell</i> , 2017, 29, 461-473.	6.6	18
32	Redefining the structural motifs that determine <i>scp</i> RNA binding and <i>scp</i> RNA editing by pentatricopeptide repeat proteins in land plants. <i>Plant Journal</i> , 2016, 85, 532-547.	5.7	267
33	Structural, super-resolution microscopy analysis of paraspeckle nuclear body organization. <i>Journal of Cell Biology</i> , 2016, 214, 817-830.	5.2	262
34	Determinants of affinity and specificity in RNA-binding proteins. <i>Current Opinion in Structural Biology</i> , 2016, 38, 83-91.	5.7	51
35	A crystallographic study of human NONO (p54 <sup>nrb</sup> ): overcoming pathological problems with purification, data collection and noncrystallographic symmetry. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 761-769.	2.3	11
36	The DBHS proteins SFPQ, NONO and PSPC1: a multipurpose molecular scaffold. <i>Nucleic Acids Research</i> , 2016, 44, 3989-4004.	14.5	204

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37	The ins and outs of lncRNA structure: How, why and what comes next?. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 46-58.	1.9	71
38	<i>Caenorhabditis elegans</i> NONO: Insights into DBHS protein structure, architecture, and function. <i>Protein Science</i> , 2015, 24, 2033-2043.	7.6	22
39	The design and structural characterization of a synthetic pentatricopeptide repeat protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 196-208.	2.5	41
40	The solution structure of the pentatricopeptide repeat protein PPR10 upon binding atpH RNA. <i>Nucleic Acids Research</i> , 2015, 43, 1918-1926.	14.5	56
41	Convergent evolution of strigolactone perception enabled host detection in parasitic plants. <i>Science</i> , 2015, 349, 540-543.	12.6	255
42	Predictable Alteration of Sequence Recognition by RNA Editing Factors from Arabidopsis. <i>Plant Cell</i> , 2015, 27, 403-416.	6.6	75
43	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, 3826-3840.	14.5	115
44	Prion-like domains in RNA binding proteins are essential for building subnuclear paraspeckles. <i>Journal of Cell Biology</i> , 2015, 210, 529-539.	5.2	269
45	Electrostatic complementarity in pseudoreceptor modeling based on drug molecule crystal structures: the case of loxistatin acid (E64c). <i>New Journal of Chemistry</i> , 2015, 39, 1628-1633.	2.8	10
46	The Crystal Structure of a Homodimeric <i>Pseudomonas</i> Glyoxalase...I Enzyme Reveals Asymmetric Metallation Commensurate with Half-of-Sites Activity. <i>Chemistry - A European Journal</i> , 2015, 21, 541-544.	3.3	12
47	Crystal "Unengineering": Reducing the Crystallisability of <i>Sulfolobus solfataricus</i> Hjc. <i>Australian Journal of Chemistry</i> , 2014, 67, 1818.	0.9	2
48	The cytidine deaminase signature HxxEx(x)nCx of DYW1 binds zinc and is necessary for RNA editing of ndhD. <i>New Phytologist</i> , 2014, 203, 1090-1095.	7.3	100
49	Operation of the Australian Synchrotron for macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2510-2519.	2.5	21
50	Invariom refinement of a new monoclinic solvate of thiostrepton at 0.64 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1530-1539.	2.5	14
51	The Structure of the Karrikin-Insensitive Protein (KAI2) in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2013, 8, e54758.	2.5	54
52	A Combinatorial Amino Acid Code for RNA Recognition by Pentatricopeptide Repeat Proteins. <i>PLoS Genetics</i> , 2012, 8, e1002910.	3.5	455
53	Structure of the heterodimer of human NONO and paraspeckle protein component 1 and analysis of its role in subnuclear body formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4846-4850.	7.1	132
54	Solar irradiation of the seed germination stimulant karrikinolide produces two novel head-to-head cage dimers. <i>Organic and Biomolecular Chemistry</i> , 2012, 10, 4069.	2.8	7

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55	Colloidal graphenes as heterogeneous additives to enhance protein crystal yield. <i>Nanoscale</i> , 2012, 4, 5321.	5.6	11
56	Sodium ion association via bridging water molecules for different charged p-phosphonated calix[4]arene bilayers. <i>CrystEngComm</i> , 2012, 14, 8541.	2.6	3
57	Quantitative Variation in Effector Activity of ToxA Isoforms from <i>Stagonospora nodorum</i> and <i>Pyrenophora tritici-repentis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 515-522.	2.6	70
58	Exploring the molecular mechanism of karrikins and strigolactones. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2012, 22, 3743-3746.	2.2	78
59	Solvent and hydrogen confinement in molecular capsules—Hirshfeld surface and molecular simulation analysis. <i>Chemical Communications</i> , 2011, 47, 9882.	4.1	2
60	Construct optimization for studying protein complexes: obtaining diffraction-quality crystals of the pseudosymmetric PSPC1–NONO heterodimer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 981-987.	2.5	18
61	Crystallization of a paraspeckle protein PSPC1–NONO heterodimer. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1231-1234.	0.7	14
62	The Peroxisomal Targeting Signal 1 in sterol carrier protein 2 is autonomous and essential for receptor recognition. <i>BMC Biochemistry</i> , 2011, 12, 12.	4.4	9
63	Selection patterns on restorer-like genes reveal a conflict between nuclear and mitochondrial genomes throughout angiosperm evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1723-1728.	7.1	236
64	Revised electrostatics from invariom refinement of the 18-residue peptaibol antibiotic trichotoxin A50E. <i>CrystEngComm</i> , 2010, 12, 2419.	2.6	12
65	<i>In Vitro</i> Kinetic Properties of the Thr201Met Variant of Human Aromatase Gene CYP19A1: Functional Responses to Substrate and Product Inhibition and Enzyme Inhibitors. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2009, 94, 2998-3002.	3.6	11
66	<i>ALINE</i> : a WYSIWYG protein-sequence alignment editor for publication-quality alignments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 510-512.	2.5	369
67	Paraspeckles: nuclear bodies built on long noncoding RNA. <i>Journal of Cell Biology</i> , 2009, 186, 637-644.	5.2	379
68	Catalytically-inactive Î <sup>2</sup> -amylase BAM4 required for starch breakdown in Arabidopsis leaves is a starch-binding-protein. <i>Archives of Biochemistry and Biophysics</i> , 2009, 489, 92-98.	3.0	41
69	Confinement of Silver Triangles in Silver Nanoplates Templated by Duplex DNA. <i>Crystal Growth and Design</i> , 2008, 8, 1451-1453.	3.0	9
70	Pentatricopeptide repeat (PPR) proteins as sequence-specificity factors in post-transcriptional processes in organelles. <i>Biochemical Society Transactions</i> , 2007, 35, 1643-1647.	3.4	215
71	The crystal structure of a plant 2C-methyl-D-erythritol 4-phosphate cytidyltransferase exhibits a distinct quaternary structure compared to bacterial homologues and a possible role in feedback regulation for cytidine monophosphate. <i>FEBS Journal</i> , 2006, 273, 1065-1073.	4.7	28
72	Specificity of the trypanothione-dependent <i>Leishmania major</i> glyoxalase I: structure and biochemical comparison with the human enzyme. <i>Molecular Microbiology</i> , 2006, 59, 1239-1248.	2.5	76

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73	The identification of isoprenoids that bind in the intersubunit cavity of <i>Escherichia coli</i> 2C-methyl-D-erythritol-2,4-cyclodiphosphate synthase by complementary biophysical methods. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 45-52.	2.5	38
74	Crystallization and preliminary X-ray analysis of <i>Leishmania major</i> glyoxalase I. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 769-772.	0.7	10
75	Conformational flexibility revealed by the crystal structure of a crenarchaeal RadA. <i>Nucleic Acids Research</i> , 2005, 33, 1465-1473.	14.5	32
76	P54 <sup>nrb</sup> Forms a Heterodimer with PSP1 That Localizes to Paraspeckles in an RNA-dependent Manner. <i>Molecular Biology of the Cell</i> , 2005, 16, 5304-5315.	2.1	207
77	Structural and Functional Implications of Metal Ion Selection in Aminopeptidase P, a Metalloprotease with a Dinuclear Metal Center. <i>Biochemistry</i> , 2005, 44, 13820-13836.	2.5	41
78	Substrate recognition and catalysis by the Holliday junction resolving enzyme Hje. <i>Nucleic Acids Research</i> , 2004, 32, 5442-5451.	14.5	41
79	Hexameric Assembly of the Bifunctional Methylerythritol 2,4-Cyclodiphosphate Synthase and Protein-Protein Associations in the Deoxy-xylulose-dependent Pathway of Isoprenoid Precursor Biosynthesis. <i>Journal of Biological Chemistry</i> , 2004, 279, 52753-52761.	3.4	43
80	Two Interacting Binding Sites for Quinacrine Derivatives in the Active Site of Trypanothione Reductase. <i>Journal of Biological Chemistry</i> , 2004, 279, 29493-29500.	3.4	97
81	High-resolution crystal structure of <i>Trypanosoma brucei</i> UDP-galactose 4-epimerase: a potential target for structure-based development of novel trypanocides. <i>Molecular and Biochemical Parasitology</i> , 2003, 126, 173-180.	1.1	55
82	Easy editing of Protein Data Bank formatted files with EMACS. <i>Journal of Applied Crystallography</i> , 2003, 36, 350-351.	4.5	9
83	Crystallization and preliminary X-ray diffraction studies of Hje, a Holliday junction resolving enzyme from <i>Sulfolobus solfataricus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 171-173.	2.5	7
84	Structure of a tetragonal crystal form of <i>Escherichia coli</i> 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 607-610.	2.5	29
85	Tryparedoxins from <i>Crithidia fasciculata</i> and <i>Trypanosoma brucei</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 25919-25925.	3.4	43
86	TopDraw: a sketchpad for protein structure topology cartoons. <i>Bioinformatics</i> , 2003, 19, 311-312.	4.1	250
87	Structure of 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase: An essential enzyme for isoprenoid biosynthesis and target for antimicrobial drug development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6591-6596.	7.1	82
88	The glycoforms of a <i>Trypanosoma brucei</i> variant surface glycoprotein and molecular modeling of a glycosylated surface coat. <i>Glycobiology</i> , 2002, 12, 607-612.	2.5	55
89	Holliday Junction Resolution Is Modulated by Archaeal Chromatin Components in Vitro. <i>Journal of Biological Chemistry</i> , 2002, 277, 2992-2996.	3.4	20
90	Mechanistic implications for <i>Escherichia coli</i> cofactor-dependent phosphoglycerate mutase based on the high-resolution crystal structure of a vanadate complex. <i>Journal of Molecular Biology</i> , 2002, 316, 1071-1081.	4.2	56

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91	Structure of Tagatose-1,6-bisphosphate Aldolase. Journal of Biological Chemistry, 2002, 277, 22018-22024.	3.4	55
92	Crystal structure of auracyanin, a blue-copper protein from the green thermophilic photosynthetic bacterium Chloroflexus aurantiacus Edited by R Huber. Journal of Molecular Biology, 2001, 306, 47-67.	4.2	50
93	Structure of the macrocycle thioestrepton solved using the anomalous dispersion contribution of sulfur. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 755-758.	2.5	39
94	Crystallization and preliminary X-ray diffraction studies of recombinant Escherichia coli 4-diphosphocytidyl-2-C-methyl-D-erythritol synthetase. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1189-1191.	2.5	10
95	High Resolution Structure of the Phosphohistidine-activated Form of Escherichia coli Cofactor-dependent Phosphoglycerate Mutase. Journal of Biological Chemistry, 2001, 276, 3247-3253.	3.4	63
96	The Structure of Reduced Tryparedoxin Peroxidase Reveals a Decamer and Insight into Reactivity of 2Cys-peroxiredoxins. Journal of Molecular Biology, 2000, 300, 903-916.	4.2	152
97	The structure of plastocyanin from the cyanobacterium Phormidium laminosum. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 414-421.	2.5	29
98	Crystal structure of Trypanosoma cruzi trypanothione reductase in complex with trypanothione, and the structure-based discovery of new natural product inhibitors. Structure, 1999, 7, 81-89.	3.3	197
99	Immune Response to Enzyme Replacement Therapy: 4-Sulfatase Epitope Reactivity of Plasma Antibodies from MPS VI Cats. Molecular Genetics and Metabolism, 1999, 67, 194-205.	1.1	22
100	Structure and mechanism of a proline-specific aminopeptidase from Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 3472-3477.	7.1	180
101	Structure of a human lysosomal sulfatase. Structure, 1997, 5, 277-289.	3.3	297
102	The crystal structure of trypanothione reductase from the human pathogen Trypanosoma cruzi at 2.3 Å resolution. Protein Science, 1996, 5, 52-61.	7.6	89
103	Trypanosoma cruzi Trypanothione Reductase Crystallization, Unit Cell Dimensions and Structure Solution. Journal of Molecular Biology, 1993, 232, 1217-1220.	4.2	10