Charles S Bond

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6981512/publications.pdf

Version: 2024-02-01

61984 53230 7,917 103 43 85 citations h-index g-index papers 111 111 111 10102 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	A Combinatorial Amino Acid Code for RNA Recognition by Pentatricopeptide Repeat Proteins. PLoS Genetics, 2012, 8, e1002910.	3.5	455
2	Functional Domains of NEAT1 Architectural IncRNA Induce Paraspeckle Assembly through Phase Separation. Molecular Cell, 2018, 70, 1038-1053.e7.	9.7	429
3	Paraspeckles: nuclear bodies built on long noncoding RNA. Journal of Cell Biology, 2009, 186, 637-644.	5. 2	379
4	<i>ALINE</i> : a WYSIWYG protein-sequence alignment editor for publication-quality alignments. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 510-512.	2.5	369
5	Paraspeckles: Where Long Noncoding RNA Meets Phase Separation. Trends in Biochemical Sciences, 2018, 43, 124-135.	7.5	315
6	Structure of a human lysosomal sulfatase. Structure, 1997, 5, 277-289.	3.3	297
7	Prion-like domains in RNA binding proteins are essential for building subnuclear paraspeckles. Journal of Cell Biology, 2015, 210, 529-539.	5. 2	269
8	Redefining the structural motifs that determine <scp>RNA</scp> binding and <scp>RNA</scp> editing by pentatricopeptide repeat proteins in land plants. Plant Journal, 2016, 85, 532-547.	5.7	267
9	Structural, super-resolution microscopy analysis of paraspeckle nuclear body organization. Journal of Cell Biology, 2016, 214, 817-830.	5. 2	262
10	Convergent evolution of strigolactone perception enabled host detection in parasitic plants. Science, 2015, 349, 540-543.	12.6	255
11	TopDraw: a sketchpad for protein structure topology cartoons. Bioinformatics, 2003, 19, 311-312.	4.1	250
12	Selection patterns on restorer-like genes reveal a conflict between nuclear and mitochondrial genomes throughout angiosperm evolution. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1723-1728.	7.1	236
13	Pentatricopeptide repeat (PPR) proteins as sequence-specificity factors in post-transcriptional processes in organelles. Biochemical Society Transactions, 2007, 35, 1643-1647.	3.4	215
14	P54nrb Forms a Heterodimer with PSP1 That Localizes to Paraspeckles in an RNA-dependent Manner. Molecular Biology of the Cell, 2005, 16, 5304-5315.	2.1	207
15	The DBHS proteins SFPQ, NONO and PSPC1: a multipurpose molecular scaffold. Nucleic Acids Research, 2016, 44, 3989-4004.	14.5	204
16	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
17	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
18	NONO Detects the Nuclear HIV Capsid to Promote cGAS-Mediated Innate Immune Activation. Cell, 2018, 175, 488-501.e22.	28.9	154

#	Article	IF	Citations
19	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
20	Structure of the heterodimer of human NONO and paraspeckle protein component 1 and analysis of its role in subnuclear body formation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4846-4850.	7.1	132
21	The structure of human SFPQ reveals a coiled-coil mediated polymer essential for functional aggregation in gene regulation. Nucleic Acids Research, 2015, 43, 3826-3840.	14.5	115
22	The cytidine deaminase signature <scp>H</scp> x <scp>E</scp> (x) _n <scp>C</scp> xx <scp>C</scp> of <scp>DYW</scp> 1 binds zinc and is necessary for <scp>RNA</scp> editing of <i>ndh<scp>D</scp>â€4</i> New Phytologist, 2014, 203, 1090-1095.	7.3	100
23	Two Interacting Binding Sites for Quinacrine Derivatives in the Active Site of Trypanothione Reductase. Journal of Biological Chemistry, 2004, 279, 29493-29500.	3.4	97
24	The crystal structure of trypanothione reductase from the human pathogen $\langle i \rangle$ Trypanosoma cruzi $\langle i \rangle$ at 2.3 \tilde{A} resolution. Protein Science, 1996, 5, 52-61.	7.6	89
25	Structure of 2C-methyl-D-erythritol 2,4- cyclodiphosphate synthase: An essential enzyme for isoprenoid biosynthesis and target for antimicrobial drug development. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6591-6596.	7.1	82
26	Exploring the molecular mechanism of karrikins and strigolactones. Bioorganic and Medicinal Chemistry Letters, 2012, 22, 3743-3746.	2.2	78
27	Specificity of the trypanothione-dependent Leishmania major glyoxalase I: structure and biochemical comparison with the human enzyme. Molecular Microbiology, 2006, 59, 1239-1248.	2.5	76
28	Predictable Alteration of Sequence Recognition by RNA Editing Factors from Arabidopsis. Plant Cell, 2015, 27, 403-416.	6.6	75
29	The ins and outs of IncRNA structure: How, why and what comes next?. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 46-58.	1.9	71
30	The Expansion and Diversification of Pentatricopeptide Repeat RNA-Editing Factors in Plants. Molecular Plant, 2020, 13, 215-230.	8.3	71
31	Quantitative Variation in Effector Activity of ToxA Isoforms from <i>Stagonospora nodorum</i> and <i>Pyrenophora tritici-repentis</i> Molecular Plant-Microbe Interactions, 2012, 25, 515-522.	2.6	70
32	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
33	Non-nuclear Pool of Splicing Factor SFPQ Regulates Axonal Transcripts Required for Normal Motor Development. Neuron, 2017, 94, 322-336.e5.	8.1	61
34	The macrocyclizing protease butelase 1 remains autocatalytic and reveals the structural basis for ligase activity. Plant Journal, 2019, 98, 988-999.	5.7	57
35	Mechanistic implications for Escherichia coli cofactor-dependent phosphoglycerate mutase based on the high-resolution crystal structure of a vanadate complex. Journal of Molecular Biology, 2002, 316, 1071-1081.	4.2	56
36	The solution structure of the pentatricopeptide repeat protein PPR10 upon binding atpH RNA. Nucleic Acids Research, 2015, 43, 1918-1926.	14.5	56

#	Article	IF	CITATIONS
37	The glycoforms of a Trypanosoma brucei variant surface glycoprotein and molecular modeling of a glycosylated surface coat. Glycobiology, 2002, 12, 607-612.	2.5	55
38	Structure of Tagatose-1,6-bisphosphate Aldolase. Journal of Biological Chemistry, 2002, 277, 22018-22024.	3.4	55
39	High-resolution crystal structure of Trypanosoma brucei UDP-galactose 4′-epimerase: a potential target for structure-based development of novel trypanocides. Molecular and Biochemical Parasitology, 2003, 126, 173-180.	1.1	55
40	The Structure of the Karrikin-Insensitive Protein (KAI2) in Arabidopsis thaliana. PLoS ONE, 2013, 8, e54758.	2.5	54
41	Structural basis of ribosomal peptide macrocyclization in plants. ELife, 2018, 7, .	6.0	52
42	Determinants of affinity and specificity in RNA-binding proteins. Current Opinion in Structural Biology, 2016, 38, 83-91.	5.7	51
43	Crystal structure of auracyanin, a "blue―copper protein from the green thermophilic photosynthetic bacterium Chloroflexus aurantiacus11Edited by R Huber. Journal of Molecular Biology, 2001, 306, 47-67.	4.2	50
44	Amylin and beta amyloid proteins interact to form amorphous heterocomplexes with enhanced toxicity in neuronal cells. Scientific Reports, 2020, 10, 10356.	3.3	44
45	Tryparedoxins from Crithidia fasciculata and Trypanosoma brucei. Journal of Biological Chemistry, 2003, 278, 25919-25925.	3.4	43
46	Hexameric Assembly of the Bifunctional Methylerythritol 2,4-Cyclodiphosphate Synthase and Protein-Protein Associations in the Deoxy-xylulose-dependent Pathway of Isoprenoid Precursor Biosynthesis. Journal of Biological Chemistry, 2004, 279, 52753-52761.	3.4	43
47	Substrate recognition and catalysis by the Holliday junction resolving enzyme Hje. Nucleic Acids Research, 2004, 32, 5442-5451.	14.5	41
48	Structural and Functional Implications of Metal Ion Selection in Aminopeptidase P, a Metalloprotease with a Dinuclear Metal Centerâ€. Biochemistry, 2005, 44, 13820-13836.	2.5	41
49	Catalytically-inactive \hat{I}^2 -amylase BAM4 required for starch breakdown in Arabidopsis leaves is a starch-binding-protein. Archives of Biochemistry and Biophysics, 2009, 489, 92-98.	3.0	41
50	The design and structural characterization of a synthetic pentatricopeptide repeat protein. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 196-208.	2.5	41
51	Structure of the macrocycle thiostrepton solved using the anomalous dispersion contribution of sulfur. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 755-758.	2.5	39
52	The identification of isoprenoids that bind in the intersubunit cavity of Escherichia coli 2C-methyl-D-erythritol-2,4-cyclodiphosphate synthase by complementary biophysical methods. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 45-52.	2.5	38
53	Conformational flexibility revealed by the crystal structure of a crenarchaeal RadA. Nucleic Acids Research, 2005, 33, 1465-1473.	14.5	32
54	Crystal structure of a SFPQ/PSPC1 heterodimer provides insights into preferential heterodimerization of human DBHS family proteins. Journal of Biological Chemistry, 2018, 293, 6593-6602.	3.4	32

#	Article	IF	CITATIONS
55	The structure of plastocyanin from the cyanobacterium Phormidium laminosum. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 414-421.	2.5	29
56	Structure of a tetragonal crystal form of Escherichia coli2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 607-610.	2.5	29
57	Divergent receptor proteins confer responses to different karrikins in two ephemeral weeds. Nature Communications, 2020, 11, 1264.	12.8	29
58	The crystal structure of a plant 2C-methyl-D-erythritol 4-phosphate cytidylyltransferase exhibits a distinct quaternary structure compared to bacterial homologues and a possible role in feedback regulation for cytidine monophosphate. FEBS Journal, 2006, 273, 1065-1073.	4.7	28
59	A synthetic RNA editing factor edits its target site in chloroplasts and bacteria. Communications Biology, 2021, 4, 545.	4.4	28
60	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. Angewandte Chemie - International Edition, 2019, 58, 16780-16784.	13.8	26
61	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
62	<i>Caenorhabditis elegans</i> <scp>NONO</scp> â€1: Insights into <scp>DBHS</scp> protein structure, architecture, and function. Protein Science, 2015, 24, 2033-2043.	7.6	22
63	Operation of the Australian Store.Synchrotron for macromolecular crystallography. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2510-2519.	2.5	21
64	Holliday Junction Resolution Is Modulated by Archaeal Chromatin Components in Vitro. Journal of Biological Chemistry, 2002, 277, 2992-2996.	3.4	20
65	Caveolinâ€1â€driven membrane remodelling regulates hnRNPKâ€mediated exosomal microRNA sorting in cancer. Clinical and Translational Medicine, 2021, 11, e381.	4.0	19
66	Construct optimization for studying protein complexes: obtaining diffraction-quality crystals of the pseudosymmetric PSPC1–NONO heterodimer. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 981-987.	2.5	18
67	Evidence for Ancient Origins of Bowman-Birk Inhibitors from <i>Selaginella moellendorffii</i> Cell, 2017, 29, 461-473.	6.6	18
68	An epigenetic switch activates bacterial quorum sensing and horizontal transfer of an integrative and conjugative element. Nucleic Acids Research, 2022, 50, 975-988.	14.5	17
69	Intracellular speciation of gold nanorods alters the conformational dynamics of genomic DNA. Nature Nanotechnology, 2018, 13, 1148-1153.	31.5	16
70	<scp><i>KARRIKIN INSENSITIVE2</i></scp> regulates leaf development, root system architecture and arbuscularâ€mycorrhizal symbiosis in <i>Brachypodium distachyon</i> . Plant Journal, 2022, 109, 1559-1574.	5.7	15
71	Crystallization of a paraspeckle protein PSPC1–NONO heterodimer. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1231-1234.	0.7	14
72	Invariom refinement of a new monoclinic solvate of thiostrepton at 0.64â€Ã resolution. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1530-1539.	2.5	14

#	Article	IF	CITATIONS
73	Whaddaya Know: A Guide to Uncertainty and Subjectivity in Structural Biology. Trends in Biochemical Sciences, 2017, 42, 155-167.	7.5	14
74	Revised electrostatics from invariom refinement of the 18-residue peptaibol antibiotic trichotoxin A50E. CrystEngComm, 2010, 12, 2419.	2.6	12
75	The Crystal Structure of a Homodimeric <i>Pseudomonas</i> Glyoxalaseâ€I Enzyme Reveals Asymmetric Metallation Commensurate with Halfâ€ofâ€Sites Activity. Chemistry - A European Journal, 2015, 21, 541-544.	3.3	12
76	Evolution of a 72-Kilobase Cointegrant, Conjugative Multiresistance Plasmid in Community-Associated Methicillin-Resistant Staphylococcus aureus Isolates from the Early 1990s. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	12
77	Cofactor-independent RNA editing by a synthetic S-type PPR protein. Synthetic Biology, 2022, 7, ysab034.	2.2	12
78	<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. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 2998-3002.	3.6	11
79	Colloidal graphenes as heterogeneous additives to enhance protein crystal yield. Nanoscale, 2012, 4, 5321.	5.6	11
80	A crystallographic study of human NONO (p54 ^{nrb}): overcoming pathological problems with purification, data collection and noncrystallographic symmetry. Acta Crystallographica Section D: Structural Biology, 2016, 72, 761-769.	2.3	11
81	Trypanosoma cruzi Trypanothione Reductase Crystallization, Unit Cell Dimensions and Structure Solution. Journal of Molecular Biology, 1993, 232, 1217-1220.	4.2	10
82	Crystallization and preliminary X-ray diffraction studies of recombinantEscherichia coli4-diphosphocytidyl-2-C-methyl-D-erythritol synthetase. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1189-1191.	2.5	10
83	Crystallization and preliminary X-ray analysis ofLeishmania majorglyoxalase I. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 769-772.	0.7	10
84	Electrostatic complementarity in pseudoreceptor modeling based on drug molecule crystal structures: the case of loxistatin acid (E64c). New Journal of Chemistry, 2015, 39, 1628-1633.	2.8	10
85	The role of G-Quadruplex DNA in Paraspeckle formation in cancer. Biochimie, 2021, 190, 124-131.	2.6	10
86	Single Stranded Fully Modified-Phosphorothioate Oligonucleotides can Induce Structured Nuclear Inclusions, Alter Nuclear Protein Localization and Disturb the Transcriptome In Vitro. Frontiers in Genetics, 2022, 13, 791416.	2.3	10
87	Structural basis of dimerization and nucleic acid binding of human DBHS proteins NONO and PSPC1. Nucleic Acids Research, 2022, 50, 522-535.	14.5	10
88	Easy editing of Protein Data Bank formatted files with EMACS. Journal of Applied Crystallography, 2003, 36, 350-351.	4.5	9
89	Confinement of Silver Triangles in Silver Nanoplates Templated by Duplex DNA. Crystal Growth and Design, 2008, 8, 1451-1453.	3.0	9
90	The Peroxisomal Targeting Signal 1 in sterol carrier protein 2 is autonomous and essential for receptor recognition. BMC Biochemistry, 2011, 12, 12.	4.4	9

#	Article	IF	Citations
91	Structural and biochemical analyses of concanavalin A circular permutation by jack bean asparaginyl endopeptidase. Plant Cell, 2021, 33, 2794-2811.	6.6	9
92	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. Angewandte Chemie, 2019, 131, 16936-16940.	2.0	8
93	TGFâ€Î²â€induced fibrotic stress increases Gâ€quadruplex formation in human fibroblasts. FEBS Letters, 2019, 593, 3149-3161.	2.8	8
94	Evolving origin-of-transfer sequences on staphylococcal conjugative and mobilizable plasmidsâ€"who's mimicking whom?. Nucleic Acids Research, 2021, 49, 5177-5188.	14.5	8
95	Crystallization and preliminary X-ray diffraction studies of Hje, a Holliday junction resolving enzyme fromSulfolobus solfataricus. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 171-173.	2.5	7
96	Solar irradiation of the seed germination stimulant karrikinolide produces two novel head-to-head cage dimers. Organic and Biomolecular Chemistry, 2012, 10, 4069.	2.8	7
97	Broad-spectrum <i>in vitro</i> activity of macrophage infectivity potentiator inhibitors against Gram-negative bacteria and <i>Leishmania major</i> Journal of Antimicrobial Chemotherapy, 2022, 77, 1625-1634.	3.0	5
98	Structure of Aspergillus fumigatus Cytosolic Thiolase: Trapped Tetrahedral Reaction Intermediates and Activation by Monovalent Cations. ACS Catalysis, 2018, 8, 1973-1989.	11.2	4
99	Delineation of the integrase-attachment and origin-of-transfer regions of the symbiosis island ICEMISymR7A. Plasmid, 2019, 104, 102416.	1.4	4
100	Sodium ion association via bridging water molecules for different charged p-phosphonated calix[4] arene bilayers. CrystEngComm, 2012, 14, 8541.	2.6	3
101	Solvent and hydrogen confinement in molecular capsules—Hirshfeld surface and molecular simulation analysis. Chemical Communications, 2011, 47, 9882.	4.1	2
102	Crystal â€~Unengineering': Reducing the Crystallisability of Sulfolobus solfataricus Hjc. Australian Journal of Chemistry, 2014, 67, 1818.	0.9	2
103	Solution NMR and racemic crystallography provide insights into a novel structural class of cyclic plant peptides. RSC Chemical Biology, 2021, 2, 1682-1691.	4.1	1