

Garry W Buchko

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Constraint of DNA on Functionalized Graphene Improves its Biostability and Specificity. <i>Small</i> , 2010, 6, 1205-1209.	10.0	342
2	2,2-Diamino-4-[(3,5-di-O-acetyl-2-deoxy- β -D-erythro-pentofuranosyl)amino]-5-(2H)-oxazolone: a Novel and Predominant Radical Oxidation Product of 3',5'-Di-O-acetyl-2'-deoxyguanosine. <i>Journal of the American Chemical Society</i> , 1994, 116, 7403-7404.	13.7	328
3	Accurate de novo design of hyperstable constrained peptides. <i>Nature</i> , 2016, 538, 329-335.	27.8	327
4	Structural and Functional Studies of a Phosphatidic Acid-Binding Antifungal Plant Defensin MtDef4: Identification of an RGFRRR Motif Governing Fungal Cell Entry. <i>PLoS ONE</i> , 2013, 8, e82485.	2.5	120
5	Combining Functional and Structural Genomics to Sample the Essential Burkholderia Structome. <i>PLoS ONE</i> , 2013, 8, e53851.	2.5	113
6	Increasing the structural coverage of tuberculosis drug targets. <i>Tuberculosis</i> , 2015, 95, 142-148.	1.9	103
7	¹ H, ¹³ C and ¹⁵ N nuclear magnetic resonance analysis and chemical features of the two main radical oxidation products of 2- α -deoxyguanosine: oxazolone and imidazolone nucleosides. <i>Journal of the Chemical Society Perkin Transactions II</i> , 1996, , 371-381.	0.9	93
8	Interactions of Human Nucleotide Excision Repair Protein XPA with DNA and RPA70 ¹ C327: Δ Chemical Shift Mapping and ¹⁵ N NMR Relaxation Studies. <i>Biochemistry</i> , 1999, 38, 15116-15128.	2.5	81
9	Conformation of Two Peptides Corresponding to Human Apolipoprotein C-I Residues 7-24 and 35-53 in the Presence of Sodium Dodecyl Sulfate by CD and NMR Spectroscopy. <i>Biochemistry</i> , 1995, 34, 7401-7408.	2.5	70
10	Structural features of the minimal DNA binding domain (M98-F219) of human nucleotide excision repair protein XPA. <i>Nucleic Acids Research</i> , 1998, 26, 2779-2788.	14.5	68
11	Methylene blue-mediated photooxidation of 7,8-dihydro-8-oxo-2- α -deoxyguanosine. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1995, 1263, 17-24.	2.4	56
12	Structural genomics of infectious disease drug targets: the SSGCID. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 979-984.	0.7	55
13	Isolation and Characterization of a New Product Produced by Ionizing Irradiation and Type I Photosensitization of 2- α -deoxyguanosine in Oxygen-saturated aqueous Solution: (2S)-2,5- α -anhydro-1-(2- α -deoxy- β -D-erythro-pentofuranosyl)-5-guanidinylidene-2-hydroxy-4-oxoimidazolidine. <i>International Journal of Radiation Biology</i> , 1993, 63, 669-676.	1.8	53
14	⁶⁷ Zn Solid-State NMR Spectroscopy of the Minimal DNA Binding Domain of Human Nucleotide Excision Repair Protein XPA. <i>Journal of the American Chemical Society</i> , 2001, 123, 992-993.	13.7	52
15	Photooxidation of d(TpG) by phthalocyanines and riboflavin. Isolation and characterization of dinucleoside monophosphates containing the 4R* and 4S* diastereoisomers of 4,8-dihydro-4-hydroxy-8-oxo-2- α -deoxyguanosine. <i>Nucleic Acids Research</i> , 1992, 20, 4847-4851.	14.5	50
16	Achieving Reversible H ₂ /H ⁺ Interconversion at Room Temperature with Enzyme-Inspired Molecular Complexes: A Mechanistic Study. <i>ACS Catalysis</i> , 2016, 6, 6037-6049.	11.2	49
17	Chemical shift changes provide evidence for overlapping single-stranded DNA- and XPA-binding sites on the 70 kDa subunit of human replication protein A. <i>Nucleic Acids Research</i> , 2003, 31, 4176-4183.	14.5	46
18	A multi-pronged search for a common structural motif in the secretion signal of <i>Salmonella enterica</i> serovar Typhimurium type III effector proteins. <i>Molecular BioSystems</i> , 2010, 6, 2448.	2.9	45

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19	A Solution NMR Investigation into the Early Events of Amelogenin Nanosphere Self-Assembly Initiated with Sodium Chloride or Calcium Chloride. <i>Biochemistry</i> , 2008, 47, 13215-13222.	2.5	44
20	Cadmium mutagenicity and human nucleotide excision repair protein XPA: CD, EXAFS and ¹ H/ ¹⁵ N-NMR spectroscopic studies on the zinc(II)- and cadmium(II)-associated minimal DNA-binding domain (M98-F219). <i>Carcinogenesis</i> , 2000, 21, 1051-1057.	2.8	41
21	Influence of nitrogen, oxygen, and nitroimidazole radiosensitizers on DNA damage induced by ionizing radiation. <i>Biochemistry</i> , 1993, 32, 2186-2193.	2.5	40
22	Solution structure of Rv2377c-founding member of the MbtH-like protein family. <i>Tuberculosis</i> , 2010, 90, 245-251.	1.9	37
23	Antifungal symbiotic peptide NCR044 exhibits unique structure and multifaceted mechanisms of action that confer plant protection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16043-16054.	7.1	36
24	Photooxidation of d(TpG) by riboflavin and methylene blue. Isolation and characterization of thymidylyl-(3- ² , 5- ²)-2-amino-5-[(2-deoxy- ¹² -D-erythro-pentofuranosyl)amino]-4H-imidazol-4-one and its primary decomposition product thymidylyl-(3- ² , 5- ²)-2,2-diamino-4-[(2-deoxy- ¹² -D-erythro-pentofuranosyl)amino]-5(2H)-oxazolone. <i>Nucleic Acids Research</i> , 1995, 23, 3954-3961.	14.5	35
25	Influence of nucleic acid base aromaticity on substrate reactivity with enzymes acting on single-stranded DNA. <i>Nucleic Acids Research</i> , 1993, 21, 621-626.	14.5	34
26	Enzyme Design from the Bottom Up: An Active Nickel Electrocatalyst with a Structured Peptide Outer Coordination Sphere. <i>Chemistry - A European Journal</i> , 2014, 20, 1510-1514.	3.3	34
27	Characterization of two potentially universal turn motifs that shape the repeated five-residues fold-Crystal structure of a luminal pentapeptide repeat protein from <i>Cyanospora</i> 51142. <i>Protein Science</i> , 2006, 15, 2579-2595.	7.6	32
28	Structure Determination and Functional Analysis of a Chromate Reductase from <i>Gluconacetobacter hansenii</i> . <i>PLoS ONE</i> , 2012, 7, e42432.	2.5	32
29	Evaluating the role of acidic, basic, and polar amino acids and dipeptides on a molecular electrocatalyst for H ₂ oxidation. <i>Catalysis Science and Technology</i> , 2017, 7, 1108-1121.	4.1	31
30	Protein Scaffold Activates Catalytic CO ₂ Hydrogenation by a Rhodium Bis(diphosphine) Complex. <i>ACS Catalysis</i> , 2019, 9, 620-625.	11.2	30
31	DNA-XPA interactions: a 31P NMR and molecular modeling study of dCCAATAACC association with the minimal DNA-binding domain (M98-F219) of the nucleotide excision repair protein XPA. <i>Nucleic Acids Research</i> , 2001, 29, 2635-2643.	14.5	27
32	High-throughput screening of the ReFRAME, Pandemic Box, and COVID Box drug repurposing libraries against SARS-CoV-2 nsp15 endoribonuclease to identify small-molecule inhibitors of viral activity. <i>PLoS ONE</i> , 2021, 16, e0250019.	2.5	27
33	Conformational studies of the N-terminal lipid-associating domain of human apolipoprotein C-II by CD and ¹ H NMR spectroscopy. <i>Protein Science</i> , 1997, 6, 1858-1868.	7.6	26
34	Spectroscopic Studies of Zinc(II)- and Cobalt(II)-Associated <i>Escherichia coli</i> Formamidopyrimidine-DNA Glycosylase: Extended X-ray Absorption Fine Structure Evidence for a Metal-Binding Domain. <i>Biochemistry</i> , 2000, 39, 12441-12449.	2.5	26
35	The use of sodium dodecyl sulfate to model the apolipoprotein environment. Evidence for peptide-SDS complexes using pulsed-field-gradient NMR spectroscopy. <i>Lipids and Lipid Metabolism</i> , 1998, 1392, 101-108.	2.6	25
36	Mineral Association Changes the Secondary Structure and Dynamics of Murine Amelogenin. <i>Journal of Dental Research</i> , 2013, 92, 1000-1004.	5.2	25

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37	Sequence-Defined Energetic Shifts Control the Disassembly Kinetics and Microstructure of Amelogenin Adsorbed onto Hydroxyapatite (100). <i>Langmuir</i> , 2015, 31, 10451-10460.	3.5	24
38	Using MbH ⁺ -Like Proteins to Alter the Substrate Profile of a Nonribosomal Peptide Adenylation Enzyme. <i>ChemBioChem</i> , 2018, 19, 2186-2194.	2.6	23
39	Identification of 2-deoxy-D-ribo-1,4-lactone at the site of benzophenone photosensitized release of guanine in 2 ^{â€²} -deoxyguanosine and thymidyl-(3 ^{â€²} -5 ^{â€²})-2 ^{â€²} -deoxyguanosine. <i>Canadian Journal of Chemistry</i> , 1992, 70, 1827-1832.	1.1	22
40	Human nucleotide excision repair protein XPA: Extended X ^{â€²} -ray absorption fine ^{â€²} structure evidence for a metal ^{â€²} -binding domain. <i>Protein Science</i> , 1998, 7, 1970-1975.	7.6	22
41	Solution-state NMR investigation of DNA binding interactions in <i>Escherichia coli</i> formamidopyrimidine-DNA glycosylase (Fpg): a dynamic description of the DNA/protein interface. <i>DNA Repair</i> , 2005, 4, 327-339.	2.8	22
42	Crystal structure of the receptor binding domain of the botulinum C ^{â€²} D mosaic neurotoxin reveals potential roles of lysines 1118 and 1136 in membrane interactions. <i>Biochemical and Biophysical Research Communications</i> , 2011, 404, 407-412.	2.1	21
43	Structural Studies of a Peptide Activator of Human Lecithin-Cholesterol Acyltransferase. <i>Journal of Biological Chemistry</i> , 1996, 271, 3039-3045.	3.4	20
44	The energetic basis for hydroxyapatite mineralization by amelogenin variants provides insights into the origin of <i>amelogenesis imperfecta</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13867-13872.	7.1	20
45	Compensating bends in a 16-base-pair DNA oligomer containing a T3A3 segment: A NMR study of global DNA curvature. <i>Biopolymers</i> , 2004, 75, 497-511.	2.4	19
46	A Positive Charge in the Outer Coordination Sphere of an Artificial Enzyme Increases CO ₂ Hydrogenation. <i>Organometallics</i> , 2020, 39, 1532-1544.	2.3	19
47	Recent contributions of structure-based drug design to the development of antibacterial compounds. <i>Current Opinion in Microbiology</i> , 2015, 27, 133-138.	5.1	18
48	Photooxydation sensibilis ^{â€²} de la d ^{â€²} soxy-2 ^{â€²} guanosine par des phtalocyanines et naphtalocyanines. D ^{â€²} termination de l ^{â€²} importance des m ^{â€²} canismes de type I et de type II. <i>Journal De Chimie Physique Et De Physico-Chimie Biologique</i> , 1991, 88, 1069-1076.	0.2	18
49	¹ H, ¹³ C, and ¹⁵ N resonance assignments of murine amelogenin, an enamel biomineralization protein. <i>Biomolecular NMR Assignments</i> , 2008, 2, 89-91.	0.8	17
50	Controls of nature: Secondary, tertiary, and quaternary structure of the enamel protein amelogenin in solution and on hydroxyapatite. <i>Journal of Structural Biology</i> , 2020, 212, 107630.	2.8	16
51	Extended X-Ray Absorption Fine Structure Evidence for a Single Metal Binding Domain in <i>Xenopus laevis</i> Nucleotide Excision Repair Protein XPA. <i>Biochemical and Biophysical Research Communications</i> , 1999, 254, 109-113.	2.1	15
52	Insights into the structural variation between pentapeptide repeat proteins ^{â€²} Crystal structure of Rfr23 from <i>Cyanothece</i> 51142. <i>Journal of Structural Biology</i> , 2008, 162, 184-192.	2.8	15
53	The leucine-rich amelogenin protein (LRAP) is primarily monomeric and unstructured in physiological solution. <i>Journal of Structural Biology</i> , 2015, 190, 81-91.	2.8	15
54	Investigating the role of chain and linker length on the catalytic activity of an H ₂ production catalyst containing a ^{â€²} 2-hairpin peptide. <i>Journal of Coordination Chemistry</i> , 2016, 69, 1730-1747.	2.2	15

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55	Backbone chemical shift assignments for the SARS-CoV-2 non-structural protein Nsp9: intermediate (ms $\hat{\epsilon}$ $\hat{1}/4s$) dynamics in the C-terminal helix at the dimer interface. <i>Biomolecular NMR Assignments</i> , 2021, 15, 107-116.	0.8	15
56	Structural analysis of the receptor binding domain of botulinum neurotoxin serotype D. <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 498-503.	2.1	14
57	Active Hydrogenation Catalyst with a Structured, Peptide-Based Outer-Coordination Sphere. <i>ACS Catalysis</i> , 2012, 2, 2114-2118.	11.2	14
58	A solution NMR investigation into the impaired self-assembly properties of two murine amelogenins containing the point mutations T21 $\hat{\epsilon}$ 'I or P41 $\hat{\epsilon}$ 'T. <i>Archives of Biochemistry and Biophysics</i> , 2013, 537, 217-224.	3.0	14
59	Structural characterization of a $\hat{1}^2$ -hydroxyacid dehydrogenase from <i>Geobacter sulfurreducens</i> and <i>Geobacter metallireducens</i> with succinic semialdehyde reductase activity. <i>Biochimie</i> , 2014, 104, 61-69.	2.6	14
60	Cytosolic expression, solution structures, and molecular dynamics simulation of genetically encodable disulfide $\hat{\epsilon}$ rich $\langle i \rangle$ de novo $\langle /i \rangle$ designed peptides. <i>Protein Science</i> , 2018, 27, 1611-1623.	7.6	14
61	A solution NMR investigation into the murine amelogenin splice-variant LRAP (Leucine-Rich Amelogenin) Tj ETQq1 1,0,784314.rgBT /Ove	2.3	13
62	Crystal structure of a macrophage migration inhibitory factor from <i>Giardia lamblia</i> . <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 47-57.	1.2	13
63	Infrared Spectroscopy of Human Apolipoprotein Fragments in SDS/D ₂ O: \hat{A} Relative Lipid-Binding Affinities and a Novel Amide I Assignment $\hat{\epsilon}$. <i>Biochemistry</i> , 1997, 36, 14531-14538.	2.5	12
64	Human nucleotide excision repair protein XPA: NMR spectroscopic studies of an XPA fragment containing the ERCC1-binding region and the minimal DNA-binding domain (M59-F219). <i>Mutation Research DNA Repair</i> , 2001, 486, 1-10.	3.7	12
65	Backbone chemical shift assignments for <i>Xanthomonas campestris</i> peroxiredoxin Q in the reduced and oxidized states: a dramatic change in backbone dynamics. <i>Biomolecular NMR Assignments</i> , 2016, 10, 57-61.	0.8	12
66	Solid-State NMR Identification of Intermolecular Interactions in Amelogenin Bound to Hydroxyapatite. <i>Biophysical Journal</i> , 2018, 115, 1666-1672.	0.5	12
67	Functional and Structural Characterization of DR_0079 from $\langle i \rangle$ <i>Deinococcus radiodurans</i> $\langle /i \rangle$, a Novel Nudix Hydrolase with a Preference for Cytosine (Deoxy)ribonucleoside 5 $\hat{\epsilon}$ ² -Di- and Triphosphates. <i>Biochemistry</i> , 2008, 47, 6571-6582.	2.5	11
68	The flexible structure of the K24S28 region of Leucine-Rich Amelogenin Protein (LRAP) bound to apatites as a function of surface type, calcium, mutation, and ionic strength. <i>Frontiers in Physiology</i> , 2014, 5, 254.	2.8	11
69	Backbone chemical shift assignments and secondary structure analysis of the U1 protein from the Bas-Congo virus. <i>Biomolecular NMR Assignments</i> , 2017, 11, 51-56.	0.8	11
70	A Phenotarget Approach for Identifying an Alkaloid Interacting with the Tuberculosis Protein Rv1466. <i>Marine Drugs</i> , 2020, 18, 149.	4.6	11
71	Structural characterization of the model amphipathic peptide Ac-LKKLLKLLKLLK-NH ₂ in aqueous solution and with 2,2,2-trifluoroethanol and 1,1,1,3,3,3-hexafluoroisopropanol. <i>Canadian Journal of Chemistry</i> , 2013, 91, 406-413.	1.1	10
72	Improved protocol to purify untagged amelogenin $\hat{\epsilon}$ Application to murine amelogenin containing the equivalent P70 $\hat{\epsilon}$ ' T point mutation observed in human amelogenesis imperfecta. <i>Protein Expression and Purification</i> , 2015, 105, 14-22.	1.3	10

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73	Characterization of \hat{I}^3 -Radiation Induced Decomposition Products of Thymidine-Containing Dinucleoside Monophosphates by Nuclear Magnetic Resonance Spectroscopy. <i>Journal of Biomolecular Structure and Dynamics</i> , 1993, 10, 747-762.	3.5	9
74	Identification of the \hat{I}^1 and \hat{I}^2 Anomers of 1-(2-Deoxy-d-Erythro-Pentofuranosyl)-Oxaluric Acid at the Site of Riboflavin-mediated Photooxidation of Guanine in 2-Deoxyguanosine and Thymidyl-(3-Deoxy-5-Deoxy)-2-Deoxyguanosine. <i>Photochemistry and Photobiology</i> , 2006, 82, 191.	2.5	9
75	Solution-state NMR structure and biophysical characterization of zinc-substituted rubredoxin B (Rv3250c) from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1148-1153.	0.7	9
76	Structural insights into the functional role of the Hcn sub-domain of the receptor-binding domain of the botulinum neurotoxin mosaic serotype C/D. <i>Biochimie</i> , 2013, 95, 1379-1385.	2.6	8
77	Crystal structure of a hemerythrin-like protein from <i>Mycobacterium kansasii</i> and homology model of the orthologous Rv2633c protein of <i>M. tuberculosis</i> . <i>Biochemical Journal</i> , 2020, 477, 567-581.	3.7	8
78	Solution Structure of the Conserved Hypothetical Protein Rv2302 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2006, 188, 5993-6001.	2.2	7
79	NMR resonance assignments of the human high mobility group protein HMGA1. <i>Journal of Biomolecular NMR</i> , 2007, 38, 185-185.	2.8	7
80	Identification of major matrix metalloproteinase-20 proteolytic processing products of murine amelogenin and tyrosine-rich amelogenin peptide using a nuclear magnetic resonance spectroscopy based method. <i>Archives of Oral Biology</i> , 2018, 93, 187-194.	1.8	7
81	Human Nucleotide Excision Repair Protein XPA:1H NMR and CD Solution Studies of a Synthetic Peptide Fragment Corresponding to the Zinc-Binding Domain (101-141). <i>Journal of Biomolecular Structure and Dynamics</i> , 1997, 14, 677-690.	3.5	6
82	A BAYESIAN INTEGRATION MODEL OF HIGH-THROUGHPUT PROTEOMICS AND METABOLOMICS DATA FOR IMPROVED EARLY DETECTION OF MICROBIAL INFECTIONS. , 2008, , .		6
83	Conformational studies of an amphipathic peptide corresponding to human apolipoprotein A-II residues 18-30 with a C-terminal lipid binding motif EWLNS. <i>International Journal of Peptide and Protein Research</i> , 1996, 48, 21-30.	0.1	6
84	Inaugural structure from the DUF3349 superfamily of proteins, <i>Mycobacterium tuberculosis</i> Rv0543c. <i>Archives of Biochemistry and Biophysics</i> , 2011, 506, 150-156.	3.0	6
85	Human nucleotide excision repair protein XPA: expression and NMR backbone assignments of the 14.7 kDa minimal damaged DNA binding domain (Met98-Phe219). <i>Journal of Biomolecular NMR</i> , 1997, 10, 313-314.	2.8	5
86	Structural studies of a baboon (<i>Papio sp.</i>) plasma protein inhibitor of cholesteryl ester transferase. <i>Protein Science</i> , 2000, 9, 1548-1558.	7.6	5
87	Solution structure of hypothetical nudix hydrolase DR0079 from extremely radiation-resistant <i>Deinococcus radiodurans</i> bacterium. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 28-39.	2.6	5
88	Cloning, expression, crystallization and preliminary crystallographic analysis of a pentapeptide-repeat protein (Rfr23) from the bacterium <i>Cyanothece</i> A51142. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1251-1254.	0.7	5
89	The structure and purity of a reference dye standard used for quantification of C.I. Solvent Red 164 in fuels. <i>Dyes and Pigments</i> , 2009, 82, 307-315.	3.7	5
90	High-level expression, purification, crystallization and preliminary X-ray crystallographic studies of the receptor-binding domain of botulinum neurotoxin serotype D. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1610-1613.	0.7	5

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91	Solution structure of an arsenate reductase-related protein, YffB, from <i>Brucella melitensis</i> , the etiological agent responsible for brucellosis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1129-1136.	0.7	5
92	Chemical shift assignments for Rv0577, a putative glyoxylase associated with virulence from <i>Mycobacterium tuberculosis</i> . <i>Biomolecular NMR Assignments</i> , 2012, 6, 43-46.	0.8	5
93	DNA-Targeted 2-Nitroimidazoles: Studies of the Influence of the Phenanthridine-Linked Nitroimidazoles, 2-NLP-3 and 2-NLP-4, on DNA Damage Induced by Ionizing Radiation. <i>Radiation Research</i> , 2002, 158, 302-310.	1.5	4
94	Base excision repair: NMR backbone assignments of <i>Escherichia coli</i> formamidopyrimidine-DNA glycosylase. <i>Journal of Biomolecular NMR</i> , 2002, 22, 301-302.	2.8	4
95	Structural characterization of the protein cce_0567 from <i>Cyanotheca 51142</i> , a metalloprotein associated with nitrogen fixation in the DUF683 family. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 627-633.	2.3	4
96	Structure of a Nudix hydrolase (MutT) in the Mg ²⁺ -bound state from <i>Bartonella henselae</i> , the bacterium responsible for cat scratch fever. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1078-1083.	0.7	4
97	Solution-state NMR structure of the putative morphogene protein BolA (PFE0790c) from <i>Plasmodium falciparum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 514-521.	0.8	4
98	Structural and Biophysical Characterization of the <i>Mycobacterium tuberculosis</i> Protein Rv0577, a Protein Associated with Neutral Red Staining of Virulent <i>Tuberculosis</i> Strains and Homologue of the <i>Streptomyces coelicolor</i> Protein KbpA. <i>Biochemistry</i> , 2017, 56, 4015-4027.	2.5	4
99	Carcinogenic alkylation of nucleic acid bases. Solid state and solution studies of O ² -isopropyl-2'-deoxythymidine. <i>Canadian Journal of Chemistry</i> , 1988, 66, 1628-1634.	1.1	3
100	Time-of-Flight Secondary Ion Mass Spectrometry of Isomeric O-Alkylthymidines. <i>Nucleosides & Nucleotides</i> , 1992, 11, 1305-1324.	0.5	3
101	¹ H, ¹³ C, and ¹⁵ N NMR assignments of the hypothetical Nudix protein DR0079 from the extremely radiation-resistant bacterium <i>Deinococcus radiodurans</i> . <i>Journal of Biomolecular NMR</i> , 2003, 25, 169-170.	2.8	3
102	Structural characterization of <i>Burkholderia pseudomallei</i> adenylate kinase (Adk): Profound asymmetry in the crystal structure of the "open" state. <i>Biochemical and Biophysical Research Communications</i> , 2010, 394, 1012-1017.	2.1	3
103	Backbone chemical shift assignments for the sensor domain of the <i>Burkholderia pseudomallei</i> histidine kinase RisS: ¹⁵ N-missing resonances at the dimer interface. <i>Biomolecular NMR Assignments</i> , 2015, 9, 381-385.	0.8	3
104	Solution NMR structures of oxidized and reduced <i>Ehrlichia chaffeensis</i> thioredoxin: NMR-invisible structure owing to backbone dynamics. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 46-56.	0.8	3
105	An NMR study of dinucleoside monophosphates with an O ⁴ -ethylated thymine. d(e ⁴ TpT) and d(Tpe ⁴ T). <i>Canadian Journal of Chemistry</i> , 1989, 67, 109-119.	1.1	2
106	Structural studies of oligonucleotides with an O ⁴ -isopropylated thymine. d(i ⁴ TpT), d(Tpi ⁴ T), and d(Tpi ⁴ TpT). <i>Canadian Journal of Chemistry</i> , 1989, 67, 1344-1353.	1.1	2
107	Synthesis and properties of DNA oligomers containing an O ⁴ -ethylated thymine. d(e ⁴ TpA), d(Ape ⁴ T), d(Ape ⁴ TpA), and d(Tpe ⁴ TpT). <i>Canadian Journal of Chemistry</i> , 1990, 68, 2011-2021.	1.1	2
108	Purification, crystallization and preliminary X-ray analysis of two nudix hydrolases from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 737-740.	2.5	2

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109	Backbone 1H, 13C, and 15N NMR assignments for the Cyanothecce 51142 protein cce_0567: a protein associated with nitrogen fixation in the DUF683 family. <i>Biomolecular NMR Assignments</i> , 2008, 2, 25-28.	0.8	2
110	Circular Dichroism Studies on the <i>Deinococcus radiodurans</i> Nudix Hydrolase DR_0079: An Atypical Thermal Melt. <i>Protein and Peptide Letters</i> , 2010, 17, 831-835.	0.9	2
111	Secondary structure and dynamics study of the intrinsically disordered silica-mineralizing peptide P ₅ S ₃ during silicic acid condensation and silica decondensation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 2111-2126.	2.6	2
112	Solution structure for an <i>Encephalitozoon cuniculi</i> adrenodoxin-like protein in the oxidized state. <i>Protein Science</i> , 2020, 29, 809-817.	7.6	2
113	Structural Genomics-A Goldmine of Blueprints for Structure-Based Drug Design. <i>Metabolomics: Open Access</i> , 2011, 01, .	0.1	2
114	Backbone and side chain 1H, 13C, and 15N NMR assignments for the organic hydroperoxide resistance protein (Ohr) from <i>Burkholderia pseudomallei</i> . <i>Biomolecular NMR Assignments</i> , 2009, 3, 163-166.	0.8	1
115	Crystal structure of cce_0566 from <i>Cyanothecce 51142</i> , a protein associated with nitrogen fixation in the DUF269 family. <i>FEBS Letters</i> , 2012, 586, 350-355.	2.8	1
116	Solution structure of a putative FKBP-type peptidyl-propyl cis-trans isomerase from <i>Giardia lamblia</i> . <i>Journal of Biomolecular NMR</i> , 2013, 57, 369-374.	2.8	1
117	Structure of a CutA1 divalent-cation tolerance protein from <i>Cryptosporidium parvum</i> , the protozoal parasite responsible for cryptosporidiosis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 522-530.	0.8	1
118	Structural diversity in the Mycobacteria DUF3349 superfamily. <i>Protein Science</i> , 2020, 29, 670-685.	7.6	1
119	3D Nanoscale Analysis of Protein-Mineral Nanoparticle Interfaces Using Atom Probe Tomography for Understanding Amelogenesis. <i>Microscopy and Microanalysis</i> , 2021, 27, 1268-1269.	0.4	1
120	Synthesis and characterization of oligodeoxyribonucleotides containing O4-ethylthymine: d(e4TpApe4TpA), d(e4TpApTpA) and (TpApe4TpA). <i>Collection of Czechoslovak Chemical Communications</i> , 1990, 55, 209-212.	1.0	1
121	Hydroxyapatite Elution Behavior of Human Nucleotide Excision Repair Protein XPA and Fragments of XPA. <i>Protein and Peptide Letters</i> , 2001, 8, 357-365.	0.9	0