

Mitchell Guss

List of Publications by Year in descending order

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122
papers

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81743

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128
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docs citations

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times ranked

5003
citing authors

#	ARTICLE	IF	CITATIONS
1	Cyclic peptides can engage a single binding pocket through highly divergent modes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26728-26738.	3.3	27
2	Mutation in a flexible linker modulates binding affinity for modular complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 425-429.	1.5	2
3	The science is in the data. <i>IUCr</i> , 2017, 4, 714-722.	1.0	26
4	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.	1.1	205
5	The structure of haemoglobin bound to the haemoglobin receptor IsdH from <i>Staphylococcus aureus</i> shows disruption of the native α -globin haem pocket. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1295-1306.	2.5	19
6	Structure of the Hemoglobin-IsdH Complex Reveals the Molecular Basis of Iron Capture by <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 6728-6738.	1.6	58
7	How to make deposition of images a reality. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2520-2532.	2.5	19
8	The structure of α -haemoglobin in complex with a haemoglobin-binding domain from <i>Staphylococcus aureus</i> reveals the elusive α -haemoglobin dimerization interface. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1032-1037.	0.4	6
9	New Insights into DNA Recognition by Zinc Fingers Revealed by Structural Analysis of the Oncoprotein ZNF217. <i>Journal of Biological Chemistry</i> , 2013, 288, 10616-10627.	1.6	36
10	A Structural Basis for the Regulation of the LIM-Homeodomain Protein Islet 1 (Isl1) by Intra- and Intermolecular Interactions. <i>Journal of Biological Chemistry</i> , 2013, 288, 21924-21935.	1.6	21
11	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, 31596-31607.	1.6	19
12	The cation-dependent GTP proteins: In a class of their own. <i>FEBS Letters</i> , 2012, 586, 2218-2224.	1.3	37
13	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.	2.3	17
14	Crystallization and diffraction of an Isl1-Ldb1 complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1398-1401.	0.7	1
15	Hans Charles Freeman (1929-2008): A scientific journey from dipole moments to protein crystallography. <i>Journal of Inorganic Biochemistry</i> , 2012, 115, 114-118.	1.5	1
16	The X-ray crystal structure of a pseudoazurin from <i>Sinorhizobium meliloti</i> . <i>Journal of Inorganic Biochemistry</i> , 2012, 115, 148-154.	1.5	9
17	Publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 620-626.	2.5	125
18	Structure and Activity of <i>Aspergillus nidulans</i> Copper Amine Oxidase. <i>Biochemistry</i> , 2011, 50, 5718-5730.	1.2	21

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19	A Novel Structure of an Antikinase and its Inhibitor. <i>Journal of Molecular Biology</i> , 2011, 405, 214-226.	2.0	21
20	The Initiation of GTP Hydrolysis by the G-Domain of FeoB: Insights from a Transition-State Complex Structure. <i>PLoS ONE</i> , 2011, 6, e23355.	1.1	34
21	The structure of TTHA0988 from <i>Thermus thermophilus</i> , a Kipla KipA homologue incorrectly annotated as an allophanate hydrolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 105-111.	2.5	7
22	A suite of Switch I and Switch II mutant structures from the G-protein domain of FeoB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 973-980.	2.5	14
23	The structure of an N11A mutant of the G-protein domain of FeoB. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1511-1515.	0.7	8
24	Structural and enzyme activity studies demonstrate that aryl substituted 2,3-butadienamine analogs inactivate <i>Arthrobacter globiformis</i> amine oxidase (AGAO) by chemical derivatization of the 2,4,5-trihydroxyphenylalanine quinone (TPQ) cofactor. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 638-646.	1.1	2
25	Structural Basis for Hemoglobin Capture by <i>Staphylococcus aureus</i> Cell-surface Protein, IsdH. <i>Journal of Biological Chemistry</i> , 2011, 286, 38439-38447.	1.6	50
26	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, 42971-42980.	1.6	35
27	A new crystal form of human diamine oxidase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 137-142.	0.7	10
28	A new crystal form of human vascular adhesion protein 1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1572-1578.	0.7	16
29	Potassium-activated GTPase Reaction in the G Protein-coupled Ferrous Iron Transporter B. <i>Journal of Biological Chemistry</i> , 2010, 285, 14594-14602.	1.6	51
30	Correlation of Active Site Metal Content in Human Diamine Oxidase with Trihydroxyphenylalanine Quinone Cofactor Biogenesis. <i>Biochemistry</i> , 2010, 49, 8316-8324.	1.2	17
31	Calmodulin Disrupts the Structure of the HIV-1 MA Protein. <i>Journal of Molecular Biology</i> , 2010, 400, 702-714.	2.0	18
32	The zinc fingers of the SR-like protein ZRANB2 are single-stranded RNA-binding domains that recognize 5' splice site-like sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5581-5586.	3.3	75
33	The crystal structure of auracyanin A at 1.85 Å resolution: the structures and functions of auracyanins A and B, two almost identical blue-copper proteins, in the photosynthetic bacterium <i>Chloroflexus aurantiacus</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2009, 14, 329-345.	1.1	21
34	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, 574-581.	2.5	11
35	Crystallization and diffraction of an Lhx4-IsI2 complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 151-153.	0.7	5
36	Structure and Inhibition of Human Diamine Oxidase. <i>Biochemistry</i> , 2009, 48, 9810-9822.	1.2	95

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37	Crystals on the cover. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 1-1.	0.7	0
38	Validation of macromolecular structures: updating standards for publication of NMR structures in an IUCr journal. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 63-63.	0.7	1
39	A new service for preparing enhanced figures in IUCr journals. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 154-155.	0.7	1
40	Crystallization of an Lhx3-Is1 complex. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 297-299.	0.7	13
41	Deposition of diffraction images to be discussed at the Open Meeting of the Commission on Biological Macromolecules of the IUCr in Osaka. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 231-232.	0.7	2
42	Complexes of the copper-containing amine oxidase from <i>Arthrobacter globiformis</i> with the inhibitors benzylhydrazine and tranlylcypromine. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 577-583.	0.7	13
43	Crystallization of a ZRANB2-RNA complex. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 1175-1177.	0.7	5
44	Implementing the LIM code: the structural basis for cell type-specific assembly of LIM-homeodomain complexes. EMBO Journal, 2008, 27, 2018-2029.	3.5	68
45	Structure of N-acetyl-1 ² -D-glucosaminidase (GcnA) from the Endocarditis Pathogen <i>Streptococcus gordonii</i> and its Complex with the Mechanism-based Inhibitor NAG-thiazoline. Journal of Molecular Biology, 2008, 377, 104-116.	2.0	37
46	Histidine Kinase Regulation by a Cyclophilin-like Inhibitor. Journal of Molecular Biology, 2008, 384, 422-435.	2.0	29
47	Complexes of mutants of <i>Escherichia coli</i> aminopeptidase P and the tripeptide substrate ValProLeu. Archives of Biochemistry and Biophysics, 2008, 469, 200-208.	1.4	19
48	Structure and Inhibition of Orotidine 5 ² -Monophosphate Decarboxylase from <i>Plasmodium falciparum</i> . Biochemistry, 2008, 47, 3842-3854.	1.2	21
49	Enantiomer-Specific Binding of Ruthenium(II) Molecular Wires by the Amine Oxidase of <i>Arthrobacter globiformis</i> . Journal of the American Chemical Society, 2008, 130, 8069-8078.	6.6	18
50	The Structure of the KinA-Sda Complex Suggests an Allosteric Mechanism of Histidine Kinase Inhibition. Journal of Molecular Biology, 2007, 368, 407-420.	2.0	77
51	Structures of Ligand-free and Inhibitor Complexes of Dihydroorotase from <i>Escherichia coli</i> : Implications for Loop Movement in Inhibitor Design. Journal of Molecular Biology, 2007, 370, 812-825.	2.0	35
52	Kinetic and Structural Analysis of Mutant <i>Escherichia coli</i> Dihydroorotases: A Flexible Loop Stabilizes the Transition State. Biochemistry, 2007, 46, 10538-10550.	1.2	16
53	Structure of the T109S mutant of <i>Escherichia coli</i> dihydroorotase complexed with the inhibitor 5-fluoroorotate: catalytic activity is reflected by the crystal form. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 154-161.	0.7	11
54	Kinetic and Crystallographic Analysis of Mutant <i>Escherichia coli</i> Aminopeptidase P: Insights into Substrate Recognition and the Mechanism of Catalysis. Biochemistry, 2006, 45, 964-975.	1.2	41

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55	The 1.23 Å structure of <i>Pichia pastoris</i> lysyl oxidase reveals a lysine-lysine cross-link. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1073-1084.	2.5	18
56	<i>Acta Crystallographica Section F: developments in the first year. Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 314-314.	0.7	0
57	The copper-containing amine oxidase from <i>Arthrobacter globiformis</i> : refinement at 1.55 and 2.20 Å resolution in two crystal forms. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1052-1057.	0.7	8
58	A C-terminal disulfide bond in the copper-containing amine oxidase from pea seedlings violates the twofold symmetry of the molecular dimer. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1168-1173.	0.7	6
59	Stabilization of a binary protein complex by intein-mediated cyclization. <i>Protein Science</i> , 2006, 15, 2612-2618.	3.1	29
60	Structures of two minor-groove-binding quinolinium quaternary salts complexed with d(CGCGAATTCGCG) ₂ at 1.6 and 1.8 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1348-1353.	2.5	5
61	Reversible inhibition of copper amine oxidase activity by channel-blocking ruthenium(II) and rhenium(I) molecular wires. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13451-13456.	3.3	34
62	Dihydroorotase from <i>Escherichia coli</i> : Loop Movement and Cooperativity between Subunits. <i>Journal of Molecular Biology</i> , 2005, 348, 523-533.	2.0	30
63	Crystal Structures of Recombinant Human Purple Acid Phosphatase With and Without an Inhibitory Conformation of the Repression Loop. <i>Journal of Molecular Biology</i> , 2005, 351, 233-246.	2.0	73
64	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.	1.2	41
65	Tandem LIM domains provide synergistic binding in the LMO4:Ldb1 complex. <i>EMBO Journal</i> , 2004, 23, 3589-3598.	3.5	84
66	Metal-substituted derivatives of the rubredoxin from <i>Clostridium pasteurianum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 298-303.	2.5	35
67	Structure of 9-amino-[N-(2-dimethylamino)propyl]acridine-4-carboxamide bound to d(CGACG) ₂ : a comparison of structures of d(CGACG) ₂ complexed with intercalators in the presence of cobalt. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 823-828.	2.5	11
68	Structure of <i>Escherichia coli</i> aminopeptidase P in complex with the inhibitor apstatin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1770-1779.	2.5	29
69	Crystallization of GcnA, an N-acetyl-β-D-glucosaminidase, from <i>Streptococcus gordonii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1910-1911.	2.5	1
70	Differential Inhibition of Six Copper Amine Oxidases by a Family of 4-(Aryloxy)-2-butylnamines: Evidence for a New Mode of Inactivation. <i>Biochemistry</i> , 2004, 43, 10965-10978.	1.2	23
71	Structure of the Prolidase from <i>Pyrococcus furiosus</i> . <i>Biochemistry</i> , 2004, 43, 2771-2783.	1.2	87
72	Using Xenon as a Probe for Dioxygen-binding Sites in Copper Amine Oxidases. <i>Journal of Molecular Biology</i> , 2004, 344, 599-607.	2.0	61

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73	Crystallization of hamster dihydroorotase: involvement of a disulfide-linked tetrameric form. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 381-384.	2.5	5
74	An orthorhombic form of Escherichia coli aminopeptidase P at 2.4 Å... resolution. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 897-902.	2.5	19
75	Crystallization of FLINC4, an intramolecular LMO4-Idb1 complex. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1484-1486.	2.5	10
76	Auracyanin B structure in space group P65. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1545-1550.	2.5	7
77	The Crystal Structure of Pichia pastoris Lysyl Oxidase. Biochemistry, 2003, 42, 15148-15157.	1.2	99
78	Crystallization of Pichia pastoris lysyl oxidase. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2177-2179.	2.5	4
79	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.	2.0	50
80	The Binding Site of Acetylcholine Receptor as Visualized in the X-Ray Structure of a Complex between α -Bungarotoxin and a Mimotope Peptide. Neuron, 2001, 32, 265-275.	3.8	125
81	Crystallization and characterization of the prolidase from Pyrococcus furiosus. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 428-430.	2.5	15
82	Guidelines for the deposition and release of macromolecular coordinate and experimental data. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 2-2.	2.5	6
83	Rubredoxin from Clostridium pasteurianum. Structures of G10A, G43A and G10VG43A mutant proteins. Mutation of conserved glycine 10 to valine causes the 9-10 peptide link to invert. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 962-968.	2.5	8
84	Crystal Structure of the Topoisomerase II Poison 9-Amino-[N-(2-dimethylamino)ethyl]acridine-4-carboxamide Bound to the DNA Hexanucleotide d(CGTACG) ₂ . Biochemistry, 1999, 38, 9221-9233.	1.2	88
85	The Rubredoxin from Clostridium pasteurianum: Mutation of the Iron Cysteine Ligands to Serine. Crystal and Molecular Structures of Oxidized and Dithionite-Treated Forms of the Cys42Ser Mutant. Journal of the American Chemical Society, 1998, 120, 4135-4150.	6.6	81
86	The crystal structure of bikunin from the inter- α -inhibitor complex: A serine protease inhibitor with two kunitz domains. Edited by R. Huber. Journal of Molecular Biology, 1998, 276, 955-966.	2.0	69
87	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.	3.3	180
88	Crystal Structures of the Copper-Containing Amine Oxidase from Arthrobacter globiformis in the Holo and Apo Forms: Implications for the Biogenesis of Topaquinone. Biochemistry, 1997, 36, 16116-16133.	1.2	258
89	Structure of the Calcium-Binding Echidna Milk Lysozyme at 1.9 Å... Resolution. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 355-363.	2.5	14
90	Structure of Ferric Soybean Leghemoglobin Nicotinate at 2.3 Å... Resolution. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 302-310.	2.5	15

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91	Structure of the calcium-binding echidna milk lysozyme at 1.9 Å... Resolution. Erratum. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 805-805.	2.5	0
92	The Structure of a Phycocyanin, the Basic Blue Protein from Cucumber, Refined at 1.8 Å... Resolution. Journal of Molecular Biology, 1996, 262, 686-705.	2.0	122
93	Crystal structure of a eukaryotic (pea seedling) copper-containing amine oxidase at 2.2 Å resolution. Structure, 1996, 4, 943-955.	1.6	256
94	Crystallization and preliminary characterization of human recombinant N-acetylgalactosamine-4-sulfatase. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 1082-1083.	2.5	3
95	ASIR: an automatic procedure for determining solvent structure in protein crystallography. Journal of Applied Crystallography, 1994, 27, 421-426.	1.9	11
96	Accuracy and precision in protein crystal structure analysis: two independent refinements of the structure of poplar plastocyanin at 173 K. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 709-730.	2.5	44
97	The expression, purification and crystallization of the $\hat{\mu}$ subunit of the F1 portion of the ATPase of Escherichia coli. Journal of Molecular Biology, 1992, 228, 306-309.	2.0	4
98	The Weissenberg method for the collection of X-ray diffraction data from macromolecular crystals: modifications to the data-processing program WEIS. Journal of Applied Crystallography, 1992, 25, 809-811.	1.9	8
99	Accuracy and precision in protein structure analysis: restrained least-squares refinement of the structure of poplar plastocyanin at 1.33 Å... resolution. Acta Crystallographica Section B: Structural Science, 1992, 48, 790-811.	1.8	202
100	Three-dimensional model for stellacyanin, a "blue" copper-protein. Journal of Molecular Biology, 1991, 222, 1053-1065.	2.0	79
101	Crystal structure of plastocyanin from a green alga, Enteromorpha prolifera. Journal of Molecular Biology, 1990, 211, 617-632.	2.0	140
102	Crystal structure analyses of reduced (CuI) poplar plastocyanin at six pH values. Journal of Molecular Biology, 1986, 192, 361-387.	2.0	404
103	Cluster chemistry. Journal of Organometallic Chemistry, 1983, 251, 261-271.	0.8	31
104	Preliminary crystallographic data for plastocyanins from an alga (Enteromorpha prolifera) and from cucumber (Cucumis sativus). Journal of Molecular Biology, 1983, 164, 351-353.	2.0	5
105	X-ray crystal structure analysis of plastocyanin at 2.7 Å... resolution. Nature, 1978, 272, 319-324.	13.7	769
106	Preliminary crystallographic data for a copper-containing protein, plastocyanin. Journal of Molecular Biology, 1977, 110, 187-189.	2.0	23
107	Preliminary crystallographic data for a basic copper-containing protein from cucumber seedlings. Journal of Molecular Biology, 1977, 112, 649-650.	2.0	30
108	Crystal and molecular structure of the dimer of variable domains of the Bence-Jones protein ROY. Journal of Molecular Biology, 1977, 116, 73-79.	2.0	39

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109	Prepatent periods of a tropical strain of Plasmodium vivax after inoculations of tenfold dilutions of sporozoites. Transactions of the Royal Society of Tropical Medicine and Hygiene, 1976, 70, 482-483.	0.7	65
110	Hyaluronic acid: Molecular conformations and interactions in two sodium salts. Journal of Molecular Biology, 1975, 95, 359-384.	2.0	176
111	The dimer of heptafulveneiron tricarbonyl. Journal of Organometallic Chemistry, 1974, 80, 245-256.	0.8	25
112	Conformation of keratan sulphate. Journal of Molecular Biology, 1974, 88, 175-184.	2.0	61
113	Dermatan sulfate and chondroitin 6-sulfate conformations. Biochemical and Biophysical Research Communications, 1973, 54, 1377-1383.	1.0	51
114	Reactions of [14]annulene and dehydro[14]annulene with organotricarbonylchromium complexes: crystal and molecular structures of hexacarbonyl-trans-6a,12a-dihydro-octalenedichromium(0), tricarbonyl-1,4-dihydrophenanthrenechromium(0), and tricarbonylphenanthrenechromium(0). Journal of the Chemical Society Dalton Transactions, 1973, , 1834-1840.	1.1	12
115	Crystal and molecular structure of chlorobis-[2-(diphenoxyphosphino-oxy)phenyl](triphenyl) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10 Chemical Society Dalton Transactions, 1972, , 2193.	1.1	14
116	Oxidative addition reactions of triphenylphosphine with dodecacarbonyltriosmium(0) : benzyne-, phenyl-, and related complexes of osmium. Journal of the Chemical Society Chemical Communications, 1972, , 87.	2.0	102
117	A tetranuclear cluster complex of copper(I) with bridging aryl ligands: the crystal structure of (4-methyl-2-cupriobenzyl)dimethylamine. Journal of the Chemical Society Chemical Communications, 1972, , 446-447.	2.0	49
118	Oxidative addition reactions in cluster complexes of osmium: Intracluster reactions of benzyne and a novel 'phenyl' complex. Journal of Organometallic Chemistry, 1972, 40, C70-C72.	0.8	75
119	Copper(II)-aryl bonds in cluster complexes: The structure of [Cu(2-Me2NH6H4)]4(CuBr)2·1.5C6H6. Journal of Organometallic Chemistry, 1972, 40, C79-C80.	0.8	57
120	Carbon-hydrogen bond cleavage in metal complexes: X-ray study of the geometry of iridium-ortho-carbon (aryl) bonds in IrCl[P(OPh)2(OC6H4)]2P(OPh)3. Challenge, 1971, .	0.4	11
121	The structure of a mixed amino-acid complex: L-histidinato-L-threoninatoaquocopper(II) hydrate. Challenge, 1969, , 225.	0.4	65
122	Crystal structures of four nickel complexes of glycine and glycine peptides. Chemical Communications / Chemical Society, London, 1968, , 485.	0.1	6