

Andrey Kovalevsky

List of Publications by Year in descending order

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116
papers

4,780
citations

94269

37
h-index

110170

64
g-index

206
all docs

206
docs citations

206
times ranked

5277
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Throughput Virtual Screening and Validation of a SARS-CoV-2 Main Protease Noncovalent Inhibitor. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 116-128.	2.5	54
2	Joint neutron/molecular dynamics vibrational spectroscopy reveals softening of HIV-1 protease upon binding of a tight inhibitor. <i>Physical Chemistry Chemical Physics</i> , 2022, 24, 3586-3597.	1.3	3
3	Hit Expansion of a Noncovalent SARS-CoV-2 Main Protease Inhibitor. <i>ACS Pharmacology and Translational Science</i> , 2022, 5, 255-265.	2.5	17
4	Covalent narpaprevir- and boceprevir-derived hybrid inhibitors of SARS-CoV-2 main protease. <i>Nature Communications</i> , 2022, 13, 2268.	5.8	69
5	Microgravity crystallization of perdeuterated tryptophan synthase for neutron diffraction. <i>Npj Microgravity</i> , 2022, 8, 13.	1.9	5
6	The mechanisms of catalysis and ligand binding for the SARS-CoV-2 NSP3 macrodomain from neutron and x-ray diffraction at room temperature. <i>Science Advances</i> , 2022, 8, .	4.7	24
7	EWALD: A macromolecular diffractometer for the second target station. <i>Review of Scientific Instruments</i> , 2022, 93, .	0.6	4
8	Room temperature crystallography of human acetylcholinesterase bound to a substrate analogue 4K-TMA: Towards a neutron structure. <i>Current Research in Structural Biology</i> , 2021, 3, 206-215.	1.1	6
9	Direct Observation of Protonation State Modulation in SARS-CoV-2 Main Protease upon Inhibitor Binding with Neutron Crystallography. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 4991-5000.	2.9	36
10	Capturing the Catalytic Proton of Dihydrofolate Reductase: Implications for General Acid-Base Catalysis. <i>ACS Catalysis</i> , 2021, 11, 5873-5884.	5.5	8
11	Characterization and structural analysis of a thermophilic GH11 xylanase from compost metatranscriptome. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7757-7767.	1.7	8
12	Covalent inhibition of hAChE by organophosphates causes homodimer dissociation through long-range allosteric effects. <i>Journal of Biological Chemistry</i> , 2021, 297, 101007.	1.6	8
13	Revertant mutation V48G alters conformational dynamics of highly drug resistant HIV protease PRS17. <i>Journal of Molecular Graphics and Modelling</i> , 2021, 108, 108005.	1.3	1
14	Inhibitor binding influences the protonation states of histidines in SARS-CoV-2 main protease. <i>Chemical Science</i> , 2021, 12, 1513-1527.	3.7	47
15	Michaelis-like complex of SARS-CoV-2 main protease visualized by room-temperature X-ray crystallography. <i>IUCr</i> , 2021, 8, 973-979.	1.0	25
16	Structural, Electronic, and Electrostatic Determinants for Inhibitor Binding to Subsites S1 and S2 in SARS-CoV-2 Main Protease. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 17366-17383.	2.9	32
17	Pressure and Temperature Effects on the Formation of Aminoacrylate Intermediates of Tyrosine Phenol-lyase Demonstrate Reaction Dynamics. <i>ACS Catalysis</i> , 2020, 10, 1692-1703.	5.5	6
18	Unusual zwitterionic catalytic site of SARS-CoV-2 main protease revealed by neutron crystallography. <i>Journal of Biological Chemistry</i> , 2020, 295, 17365-17373.	1.6	97

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19	Malleability of the SARS-CoV-2 3CL Mpro Active-Site Cavity Facilitates Binding of Clinical Antivirals. <i>Structure</i> , 2020, 28, 1313-1320.e3.	1.6	108
20	Supercomputer-Based Ensemble Docking Drug Discovery Pipeline with Application to Covid-19. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 5832-5852.	2.5	134
21	Visualizing Tetrahedral Oxyanion Bound in HIV-1 Protease Using Neutrons: Implications for the Catalytic Mechanism and Drug Design. <i>ACS Omega</i> , 2020, 5, 11605-11617.	1.6	6
22	Structural plasticity of SARS-CoV-2 3CL Mpro active site cavity revealed by room temperature X-ray crystallography. <i>Nature Communications</i> , 2020, 11, 3202.	5.8	334
23	Protein kinase A in the neutron beam: Insights for catalysis from directly observing protons. <i>Methods in Enzymology</i> , 2020, 634, 311-331.	0.4	0
24	Rational design, synthesis, and evaluation of uncharged, α -bis-oxime antidotes of organophosphate-inhibited human acetylcholinesterase. <i>Journal of Biological Chemistry</i> , 2020, 295, 4079-4092.	1.6	24
25	Pyridoxal 5 α -phosphate dependent reactions: Analyzing the mechanism of aspartate aminotransferase. <i>Methods in Enzymology</i> , 2020, 634, 333-359.	0.4	10
26	Studying the Role of a Single Mutation of a Family 11 Glycoside Hydrolase Using High-Resolution X-ray Crystallography. <i>Protein Journal</i> , 2020, 39, 671-680.	0.7	2
27	IMAGINE: The neutron protein crystallography beamline at the high flux isotope reactor. <i>Methods in Enzymology</i> , 2020, 634, 69-85.	0.4	21
28	Proton transfer and drug binding details revealed in neutron diffraction studies of wild-type and drug resistant HIV-1 protease. <i>Methods in Enzymology</i> , 2020, 634, 257-279.	0.4	4
29	Substrate Binding Stiffens Aspartate Aminotransferase by Altering the Enzyme Picosecond Vibrational Dynamics. <i>ACS Omega</i> , 2020, 5, 18787-18797.	1.6	7
30	Room-temperature X-ray crystallography reveals the oxidation and reactivity of cysteine residues in SARS-CoV-2 3CL M ^{pro} : insights into enzyme mechanism and drug design. <i>IUCr</i> , 2020, 7, 1028-1035.	1.0	49
31	Room-temperature neutron and X-ray data collection of 3CL M ^{pro} from SARS-CoV-2. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 483-487.	0.4	21
32	A new crystal form of human acetylcholinesterase for exploratory room-temperature crystallography studies. <i>Chemico-Biological Interactions</i> , 2019, 309, 108698.	1.7	82
33	Productive reorientation of a bound oxime reactivator revealed in room temperature X-ray structures of native and VX-inhibited human acetylcholinesterase. <i>Journal of Biological Chemistry</i> , 2019, 294, 10607-10618.	1.6	13
34	Zooming in on protons: Neutron structure of protein kinase A trapped in a product complex. <i>Science Advances</i> , 2019, 5, eaav0482.	4.7	26
35	Room-temperature photo-induced martensitic transformation in a protein crystal. <i>IUCr</i> , 2019, 6, 619-629.	1.0	2
36	Neutron Crystallography Detects Differences in Protein Dynamics: Structure of the PKG II Cyclic Nucleotide Binding Domain in Complex with an Activator. <i>Biochemistry</i> , 2018, 57, 1833-1837.	1.2	1

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37	"To Be or Not to Be" Protonated: Atomic Details of Human Carbonic Anhydrase-Clinical Drug Complexes by Neutron Crystallography and Simulation. <i>Structure</i> , 2018, 26, 383-390.e3.	1.6	40
38	The Neutron Macromolecular Crystallography Instruments at Oak Ridge National Laboratory: Advances, Challenges, and Opportunities. <i>Crystals</i> , 2018, 8, 388.	1.0	26
39	Neutron scattering in the biological sciences: progress and prospects. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1129-1168.	1.1	47
40	Temperature-Induced Replacement of Phosphate Proton with Metal Ion Captured in Neutron Structures of A-DNA. <i>Structure</i> , 2018, 26, 1645-1650.e3.	1.6	4
41	Understanding the pH-Dependent Reaction Mechanism of a Glycoside Hydrolase Using High-Resolution X-ray and Neutron Crystallography. <i>ACS Catalysis</i> , 2018, 8, 8058-8069.	5.5	15
42	IMAGINE: neutrons reveal enzyme chemistry. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 778-786.	1.1	25
43	Hyperconjugation Promotes Catalysis in a Pyridoxal 5'-Phosphate-Dependent Enzyme. <i>ACS Catalysis</i> , 2018, 8, 6733-6737.	5.5	15
44	Room Temperature Neutron Crystallography of Drug Resistant HIV-1 Protease Uncovers Limitations of X-ray Structural Analysis at 100 K. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 2018-2025.	2.9	25
45	Direct evidence that an extended hydrogen-bonding network influences activation of pyridoxal 5'-phosphate in aspartate aminotransferase. <i>Journal of Biological Chemistry</i> , 2017, 292, 5970-5980.	1.6	38
46	Neutron and Atomic Resolution X-ray Structures of a Lytic Polysaccharide Monooxygenase Reveal Copper-Mediated Dioxygen Binding and Evidence for N-Terminal Deprotonation. <i>Biochemistry</i> , 2017, 56, 2529-2532.	1.2	53
47	Direct visualization of critical hydrogen atoms in a pyridoxal 5'-phosphate enzyme. <i>Nature Communications</i> , 2017, 8, 955.	5.8	55
48	Mannobiose Binding Induces Changes in Hydrogen Bonding and Protonation States of Acidic Residues in Concanavalin A As Revealed by Neutron Crystallography. <i>Biochemistry</i> , 2017, 56, 4747-4750.	1.2	25
49	Biological Structures. <i>Experimental Methods in the Physical Sciences</i> , 2017, 49, 1-75.	0.1	10
50	Direct observation of protonation states in a PLP-dependent enzyme by neutron crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a26-a26.	0.0	1
51	Long-Range Electrostatics-Induced Two-Proton Transfer Captured by Neutron Crystallography in an Enzyme Catalytic Site. <i>Angewandte Chemie</i> , 2016, 128, 5008-5011.	1.6	6
52	Long-Range Electrostatics-Induced Two-Proton Transfer Captured by Neutron Crystallography in an Enzyme Catalytic Site. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 4924-4927.	7.2	42
53	Neutron structure of human carbonic anhydrase II in complex with methazolamide: mapping the solvent and hydrogen-bonding patterns of an effective clinical drug. <i>IUCr</i> , 2016, 3, 319-325.	1.0	27
54	Neutron structures of the <i>Helicobacter pylori</i> 5'-methylthioadenosine nucleosidase highlight proton sharing and protonation states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13756-13761.	3.3	31

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55	Limitations in current acetylcholinesterase structure-based design of oxime antidotes for organophosphate poisoning. <i>Annals of the New York Academy of Sciences</i> , 2016, 1378, 41-49.	1.8	17
56	Visualizing the Bohr effect in hemoglobin: neutron structure of equine cyanomethemoglobin in the R state and comparison with human deoxyhemoglobin in the T state. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 892-903.	1.1	7
57	Evolution and characterization of a new reversibly photoswitching chromogenic protein, Dathail. <i>Journal of Molecular Biology</i> , 2016, 428, 1776-1789.	2.0	20
58	Joint neutron crystallographic and NMR solution studies of Tyr residue ionization and hydrogen bonding: Implications for enzyme-mediated proton transfer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5673-5678.	3.3	36
59	Phosphoryl Transfer Reaction Snapshots in Crystals. <i>Journal of Biological Chemistry</i> , 2015, 290, 15538-15548.	1.6	22
60	Neutron and high-resolution room-temperature X-ray data collection from crystallized lytic polysaccharide monooxygenase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1448-1452.	0.4	8
61	Direct determination of protonation states and visualization of hydrogen bonding in a glycoside hydrolase with neutron crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12384-12389.	3.3	35
62	Protein Kinase A Catalytic Subunit Primed for Action: Time-Lapse Crystallography of Michaelis Complex Formation. <i>Structure</i> , 2015, 23, 2331-2340.	1.6	22
63	Novel complex MAD phasing and RNase H structural insights using selenium oligonucleotides. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 354-361.	2.5	17
64	Toward resolving the catalytic mechanism of dihydrofolate reductase using neutron and ultrahigh-resolution X-ray crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18225-18230.	3.3	72
65	Preliminary joint X-ray and neutron protein crystallographic studies of ecDHFR complexed with folate and NADP. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 814-818.	0.4	7
66	Neutron Diffraction Reveals Hydrogen Bonds Critical for cGMP-Selective Activation: Insights for cGMP-Dependent Protein Kinase Agonist Design. <i>Biochemistry</i> , 2014, 53, 6725-6727.	1.2	31
67	L-Arabinose Binding, Isomerization, and Epimerization by D-Xylose Isomerase: X-Ray/Neutron Crystallographic and Molecular Simulation Study. <i>Structure</i> , 2014, 22, 1287-1300.	1.6	22
68	Metal-Free cAMP-Dependent Protein Kinase Can Catalyze Phosphoryl Transfer. <i>Biochemistry</i> , 2014, 53, 3179-3186.	1.2	18
69	Engineering acidic <i>Streptomyces rubiginosus</i> D-xylose isomerase by rational enzyme design. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 59-64.	1.0	19
70	X-ray crystallographic studies of family 11 xylanase Michaelis and product complexes: implications for the catalytic mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 11-23.	2.5	34
71	The IMAGINE instrument: first neutron protein structure and new capabilities for neutron macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2157-2160.	2.5	73
72	Insights into the Phosphoryl Transfer Catalyzed by cAMP-Dependent Protein Kinase: An X-ray Crystallographic Study of Complexes with Various Metals and Peptide Substrate SP20. <i>Biochemistry</i> , 2013, 52, 3721-3727.	1.2	24

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73	Neutron protein crystallography reveals unique details of clinical drug binding to a human target enzyme. <i>Neutron News</i> , 2013, 24, 20-23.	0.1	0
74	Joint X-ray/Neutron Crystallographic Study of HIV-1 Protease with Clinical Inhibitor Amprenavir: Insights for Drug Design. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 5631-5635.	2.9	61
75	Heterologous expression, purification, crystallization and preliminary X-ray analysis of <i>Trichoderma reesei</i> xylanase II and four variants. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 320-323.	0.7	2
76	Direct observation of hydrogen atom dynamics and interactions by ultrahigh resolution neutron protein crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15301-15306.	3.3	51
77	Inhibition of D-xylose isomerase by polyols: atomic details by joint X-ray/neutron crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1201-1206.	2.5	18
78	Capturing the Reaction Pathway in Near-Atomic-Resolution Crystal Structures of HIV-1 Protease. <i>Biochemistry</i> , 2012, 51, 7726-7732.	1.2	13
79	Neutron Diffraction of Acetazolamide-Bound Human Carbonic Anhydrase II Reveals Atomic Details of Drug Binding. <i>Journal of the American Chemical Society</i> , 2012, 134, 14726-14729.	6.6	100
80	Inorganic pyrophosphatase crystals from <i>Thermococcus thioreducens</i> for X-ray and neutron diffraction. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1482-1487.	0.7	19
81	Room-temperature ultrahigh-resolution time-of-flight neutron and X-ray diffraction studies of H/D-exchanged crambin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 119-123.	0.7	9
82	Low- and room-temperature X-ray structures of protein kinase A ternary complexes shed new light on its activity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 854-860.	2.5	26
83	Neutron Structure of Human Carbonic Anhydrase II: A Hydrogen-Bonded Water Network Observed between pH 7.8 and 10.0. <i>Biochemistry</i> , 2011, 50, 9421-9423.	1.2	52
84	High-resolution neutron crystallographic studies of the hydration of the coenzyme cob(II)alamin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 584-591.	2.5	30
85	Preliminary joint X-ray and neutron protein crystallographic studies of endoxylanase II from the fungus <i>Trichoderma longibrachiatum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 283-286.	0.7	6
86	Preliminary joint neutron time-of-flight and X-ray crystallographic study of human ABO(H) blood group A glycosyltransferase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 258-262.	0.7	4
87	Time-of-flight neutron diffraction study of bovine $\hat{3}$ -chymotrypsin at the Protein Crystallography Station. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 587-590.	0.7	1
88	Identification of the Elusive Hydronium Ion Exchanging Roles with a Proton in an Enzyme at Lower pH...Values. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 7520-7523.	7.2	62
89	Metal Ion Roles and the Movement of Hydrogen during Reaction Catalyzed by D-Xylose Isomerase: A Joint X-Ray and Neutron Diffraction Study. <i>Structure</i> , 2010, 18, 688-699.	1.6	139
90	Protonation states of histidine and other key residues in deoxy normal human adult hemoglobin by neutron protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1144-1152.	2.5	6

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91	Hemoglobin redux: combining neutron and X-ray diffraction with mass spectrometry to analyse the quaternary state of oxidized hemoglobins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1249-1256.	2.5	1
92	Macromolecular neutron crystallography at the Protein Crystallography Station (PCS). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1206-1212.	2.5	11
93	Using neutron protein crystallography to understand enzyme mechanisms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1257-1261.	2.5	5
94	Amprenavir complexes with HIV-1 protease and its drug-resistant mutants altering hydrophobic clusters. <i>FEBS Journal</i> , 2010, 277, 3699-3714.	2.2	116
95	Neutron Structure of Human Carbonic Anhydrase II: Implications for Proton Transfer. <i>Biochemistry</i> , 2010, 49, 415-421.	1.2	82
96	Direct Determination of Protonation States of Histidine Residues in a 2.2 Å... Neutron Structure of Deoxy-Human Normal Adult Hemoglobin and Implications for the Bohr Effect. <i>Journal of Molecular Biology</i> , 2010, 398, 276-291.	2.0	35
97	Design, Synthesis, Protein-Ligand X-ray Structure, and Biological Evaluation of a Series of Novel Macrocyclic Human Immunodeficiency Virus-1 Protease Inhibitors to Combat Drug Resistance. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 7689-7705.	2.9	40
98	The Catalytic Mechanism of an Aspartic Proteinase Explored with Neutron and X-ray Diffraction. <i>Journal of the American Chemical Society</i> , 2008, 130, 7235-7237.	6.6	106
99	Effect of Flap Mutations on Structure of HIV-1 Protease and Inhibition by Saquinavir and Darunavir. <i>Journal of Molecular Biology</i> , 2008, 381, 102-115.	2.0	81
100	Structural Evidence for Effectiveness of Darunavir and Two Related Antiviral Inhibitors against HIV-2 Protease. <i>Journal of Molecular Biology</i> , 2008, 384, 178-192.	2.0	44
101	Potent HIV-1 protease inhibitors incorporating meso-bicyclic urethanes as P2-ligands: structure-based design, synthesis, biological evaluation and protein-ligand X-ray studies. <i>Organic and Biomolecular Chemistry</i> , 2008, 6, 3703.	1.5	17
102	Solution Kinetics Measurements Suggest HIV-1 Protease Has Two Binding Sites for Darunavir and Amprenavir. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 6599-6603.	2.9	30
103	Hydrogen Location in Stages of an Enzyme-Catalyzed Reaction: Time-of-Flight Neutron Structure of d-Xylose Isomerase with Bound d-Xylulose. <i>Biochemistry</i> , 2008, 47, 7595-7597.	1.2	42
104	Caught in the Act: The 1.5 Å... Resolution Crystal Structures of the HIV-1 Protease and the I54V Mutant Reveal a Tetrahedral Reaction Intermediate. <i>Biochemistry</i> , 2007, 46, 14854-14864.	1.2	44
105	Anion Chain Structure Controlled Behavior of Phase Transition in Quasi-Two-Dimensional Organic Metal (EDT-TTF) ₄ [Hg ₃ I ₈]. <i>Crystal Growth and Design</i> , 2007, 7, 2768-2773.	1.4	7
106	Atomic resolution crystal structures of HIV-1 protease and mutants V82A and I84V with saquinavir. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 232-242.	1.5	84
107	Structural aspects of two-stage dimerization in an ionic C ₆₀ complex with bis(benzene)chromium: Cr(C ₆ H ₆) ₂ ·C ₆₀ ·C ₆ H ₄ Cl ₂ . <i>Dalton Transactions</i> , 2006, , 3716-3720.	1.6	36
108	Mechanism of Drug Resistance Revealed by the Crystal Structure of the Unliganded HIV-1 Protease with F53L Mutation. <i>Journal of Molecular Biology</i> , 2006, 358, 1191-1199.	2.0	48

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109	Ultra-high Resolution Crystal Structure of HIV-1 Protease Mutant Reveals Two Binding Sites for Clinical Inhibitor TMC114. <i>Journal of Molecular Biology</i> , 2006, 363, 161-173.	2.0	136
110	Bis[bis(3-phenylpyrazol-1-yl)(pyrazol-1-yl)methane]copper(II) bis(perchlorate) acetonitrile disolvate. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2006, 62, m30-m32.	0.4	0
111	Synthesis, Crystal Structures, Magnetic Properties and Photoconductivity of C60 and C70 Complexes with Metal Dialkyldithiocarbamates M(R2dte)x, where M = CuII, CuI, AgI, ZnII, CdII, HgII, MnII, NiII, and PtII; R = Me, Et, and nPr. <i>European Journal of Inorganic Chemistry</i> , 2006, 2006, 1881-1895.	1.0	44
112	Synthesis, crystal structure and photoconductivity of the first [60]fullerene complex with metal diethyldithiocarbamate: {CuII(dedtc)2}2·C60. <i>Dalton Transactions</i> , 2005, , 1821.	1.6	20
113	Physical and Kinetic Analysis of the Cooperative Role of Metal Ions in Catalysis of Phosphodiester Cleavage by a Dinuclear Zn(II) Complex. <i>Journal of the American Chemical Society</i> , 2003, 125, 1988-1993.	6.6	224
114	Creating nanocavities of tunable sizes: Hollow helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11583-11588.	3.3	149
115	Photoinduced Linkage Isomers of Transition-Metal Nitrosyl Compounds and Related Complexes. <i>Chemical Reviews</i> , 2002, 102, 861-884.	23.0	411
116	First Observation of Photoinduced Nitrosyl Linkage Isomers of Iron Nitrosyl Porphyrins. <i>Journal of the American Chemical Society</i> , 2000, 122, 7142-7143.	6.6	75