

Quan Hao

List of Publications by Year in descending order

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134
papers

6,969
citations

61984

43
h-index

62596

80
g-index

137
all docs

137
docs citations

137
times ranked

8668
citing authors

#	ARTICLE	IF	CITATIONS
1	Binding of ruthenium and osmium at non-iron sites of transferrin accounts for their iron-independent cellular uptake. <i>Journal of Inorganic Biochemistry</i> , 2022, 234, 111885.	3.5	7
2	Structure-guided optimization of D-captopril for discovery of potent NDM-1 inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2021, 29, 115902.	3.0	14
3	Weblinks for the Daresbury Laue software source code and information. Addendum. <i>Journal of Synchrotron Radiation</i> , 2021, 28, 666-666.	2.4	3
4	Single-step fluorescent probes to detect decrotonylation activity of HDACs through intramolecular reactions. <i>European Journal of Medicinal Chemistry</i> , 2021, 212, 113120.	5.5	9
5	Desuccinylation-Triggered Peptide Self-Assembly: Live Cell Imaging of SIRT5 Activity and Mitochondrial Activity Modulation. <i>Journal of the American Chemical Society</i> , 2020, 142, 18150-18159.	13.7	84
6	Resensitizing carbapenem- and colistin-resistant bacteria to antibiotics using auranofin. <i>Nature Communications</i> , 2020, 11, 5263.	12.8	70
7	Crystal structure of the rice acyl-CoA-binding protein OsACBP2 in complex with C18:3-CoA reveals a novel pattern of binding to acyl-CoA esters. <i>FEBS Letters</i> , 2020, 594, 3568-3575.	2.8	6
8	<i>IPCAS</i> : a direct-method-based pipeline from phasing to model building and refinement for macromolecular structure determination. <i>Journal of Applied Crystallography</i> , 2020, 53, 253-261.	4.5	7
9	Using cryo-electron microscopy maps for X-ray structure determination of homologues. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 63-72.	2.3	1
10	Crystal structure of human APPL BAR-PH heterodimer reveals a flexible dimeric BAR curve: implication in mutual regulation of endosomal targeting. <i>Biochemical Journal</i> , 2020, 477, 4769-4783.	3.7	0
11	Chemical Probes Reveal Sirt2's New Function as a Robust "Eraser" of Lysine Lipoylation. <i>Journal of the American Chemical Society</i> , 2019, 141, 18428-18436.	13.7	37
12	<i>Talaromyces marneffeii</i> Mp1 Protein, a Novel Virulence Factor, Carries Two Arachidonic Acid-Binding Domains To Suppress Inflammatory Responses in Hosts. <i>Infection and Immunity</i> , 2019, 87, .	2.2	13
13	Identification of the YEATS domain of GAS41 as a pH-dependent reader of histone succinylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2365-2370.	7.1	53
14	Mp1p homologues as virulence factors in <i>Aspergillus fumigatus</i> . <i>Medical Mycology</i> , 2018, 56, 350-360.	0.7	5
15	Active-Site Conformational Fluctuations Promote the Enzymatic Activity of NDM-1. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	58
16	Lysine benzoylation is a histone mark regulated by SIRT2. <i>Nature Communications</i> , 2018, 9, 3374.	12.8	150
17	Using cryo-electron microscopy maps for X-ray structure determination. <i>IUCr</i> , 2018, 5, 382-389.	2.2	8
18	Haploinsufficiency of Trp53 dramatically extends the lifespan of Sirt6-deficient mice. <i>ELife</i> , 2018, 7, .	6.0	36

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19	Talaromyces marneffeii Mp1p Is a Virulence Factor that Binds and Sequesters a Key Proinflammatory Lipid to Dampen Host Innate Immune Response. Cell Chemical Biology, 2017, 24, 182-194.	5.2	26
20	Deacylation Mechanism by SIRT2 Revealed in the 1â€²-SH-2â€²-O-Myristoyl Intermediate Structure. Cell Chemical Biology, 2017, 24, 339-345.	5.2	40
21	The first plant acyl-CoA-binding protein structures: the close homologues OsACBP1 and OsACBP2 from rice. Acta Crystallographica Section D: Structural Biology, 2017, 73, 438-448.	2.3	29
22	Histone Ketoamide Adduction by 4-Oxo-2-nonenal Is a Reversible Posttranslational Modification Regulated by Sirt2. ACS Chemical Biology, 2017, 12, 47-51.	3.4	24
23	SIRT7 Is an RNA-Activated Protein Lysine Deacylase. ACS Chemical Biology, 2017, 12, 300-310.	3.4	83
24	Porcine <sc>CD</sc>38 exhibits prominent secondary <sc>NAD</sc> ⁺ cyclase activity. Protein Science, 2016, 25, 650-661.	7.6	4
25	Structural Characterization of H1N1 Nucleoprotein-Nucleozin Binding Sites. Scientific Reports, 2016, 6, 29684.	3.3	16
26	Crystal Structure of Escherichia coli originated MCR-1, a phosphoethanolamine transferase for Colistin Resistance. Scientific Reports, 2016, 6, 38793.	3.3	60
27	Structural Basis for Human PECAM-1-Mediated Trans-homophilic Cell Adhesion. Scientific Reports, 2016, 6, 38655.	3.3	24
28	SIRT7 Is Activated by DNA and Deacetylates Histone H3 in the Chromatin Context. ACS Chemical Biology, 2016, 11, 742-747.	3.4	57
29	Immuno-targeting the multifunctional CD38 using nanobody. Scientific Reports, 2016, 6, 27055.	3.3	61
30	Fluorescent Probes for Single-Step Detection and Proteomic Profiling of Histone Deacetylases. Journal of the American Chemical Society, 2016, 138, 15596-15604.	13.7	67
31	Mechanistic study of TRPM2-Ca²⁺-CAMK2-BECN1 signaling in oxidative stress-induced autophagy inhibition. Autophagy, 2016, 12, 1340-1354.	9.1	72
32	Mp1p Is a Virulence Factor in Talaromyces (Penicillium) marneffeii. PLoS Neglected Tropical Diseases, 2016, 10, e0004907.	3.0	29
33	De novo phasing with optimized XFEL data. IUCr, 2016, 3, 161-162.	2.2	0
34	Lamin A Is an Endogenous SIRT6 Activator and Promotes SIRT6-Mediated DNA Repair. Cell Reports, 2015, 13, 1396-1406.	6.4	117
35	Protein-complex structure completion using IPCAS (Iterative Protein Crystal structure Automatic) Tj ETQq1 1 0.784314 rgBT /Overlock 2.5 6	2.5	6
36	Efficient Demyristoylase Activity of SIRT2 Revealed by Kinetic and Structural Studies. Scientific Reports, 2015, 5, 8529.	3.3	143

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37	Powder to become crystal clear. IUCrj, 2015, 2, 307-308.	2.2	1
38	Identification of "erasers"™ for lysine crotonylated histone marks using a chemical proteomics approach. ELife, 2014, 3, .	6.0	237
39	Cyclic Adenosine 5'-Diphosphate Ribose Analogs without a "Southern" Ribose Inhibit ADP-ribosyl Cyclase "Hydrolase CD38. Journal of Medicinal Chemistry, 2014, 57, 8517-8529.	6.4	19
40	Crystallographic phasing with NMR models: an envelope approach. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1977-1982.	2.5	3
41	Revealing CD38 Cellular Localization Using a Cell Permeable, Mechanism-Based Fluorescent Small-Molecule Probe. Journal of the American Chemical Society, 2014, 136, 5656-5663.	13.7	41
42	SIRT6 regulates TNF- α secretion through hydrolysis of long-chain fatty acyl lysine. Nature, 2013, 496, 110-113.	27.8	611
43	Identification of ADP-ribosylation sites of CD38 mutants by precursor ion scanning mass spectrometry. Analytical Biochemistry, 2013, 433, 218-226.	2.4	7
44	Crystal Structures of Human CD38 in Complex with NAADP and ADPRP. Messenger (Los Angeles, Calif.): Tj ETQq0 0.0 rgBT /Overlock 10 0.3	0.3	0
45	CD38 Structure-Based Inhibitor Design Using the N1-Cyclic Inosine 5'-Diphosphate Ribose Template. PLoS ONE, 2013, 8, e66247.	2.5	24
46	Iron and bismuth bound human serum transferrin reveals a partially-opened conformation in the N-lobe. Scientific Reports, 2012, 2, 999.	3.3	91
47	The Bicyclic Intermediate Structure Provides Insights into the Desuccinylation Mechanism of Human Sirtuin 5 (SIRT5). Journal of Biological Chemistry, 2012, 287, 28307-28314.	3.4	77
48	Structure of Crimean-Congo Hemorrhagic Fever Virus Nucleoprotein: Superhelical Homo-Oligomers and the Role of Caspase-3 Cleavage. Journal of Virology, 2012, 86, 12294-12303.	3.4	71
49	Analysis of surface structures of hydrogen bonding in protein-ligand interactions using the alpha shape model. Chemical Physics Letters, 2012, 545, 125-131.	2.6	22
50	<i>Plasmodium falciparum</i> Sir2A Preferentially Hydrolyzes Medium and Long Chain Fatty Acyl Lysine. ACS Chemical Biology, 2012, 7, 155-159.	3.4	70
51	Structural Studies of Intermediates along the Cyclization Pathway of Aplysia ADP-Ribosyl Cyclase. Journal of Molecular Biology, 2012, 415, 514-526.	4.2	14
52	Catalysis-Based Inhibitors of the Calcium Signaling Function of CD38. Biochemistry, 2012, 51, 555-564.	2.5	31
53	Expression, purification, crystallization and preliminary X-ray analysis of <i>Plasmodium falciparum</i> GTP:AMP phosphotransferase. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 671-674.	0.7	0
54	Crystal structure of NDM-1 reveals a common β -lactam hydrolysis mechanism. FASEB Journal, 2011, 25, 2574-2582.	0.5	218

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55	Cytosolic CD38 Protein Forms Intact Disulfides and Is Active in Elevating Intracellular Cyclic ADP-ribose. <i>Journal of Biological Chemistry</i> , 2011, 286, 22170-22177.	3.4	28
56	Sirt5 Is a NAD-Dependent Protein Lysine Demalonylase and Desuccinylase. <i>Science</i> , 2011, 334, 806-809.	12.6	1,165
57	Dynamic Conformations of the CD38-Mediated NAD Cyclization Captured in a Single Crystal. <i>Journal of Molecular Biology</i> , 2011, 405, 1070-1078.	4.2	21
58	Design, synthesis and biological characterization of novel inhibitors of CD38. <i>Organic and Biomolecular Chemistry</i> , 2011, 9, 3246.	2.8	35
59	Prediction of Protein-protein Interactions Using Alpha Shape Modeling. , 2011, , .		4
60	Feasibility of one-shot-per-crystal structure determination using Laue diffraction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 2-11.	2.5	19
61	High resolution pair-distance distribution function P(r) of protein solutions. <i>Applied Physics Letters</i> , 2009, 94, .	3.3	10
62	Measurements of accurate x-ray scattering data of protein solutions using small stationary sample cells. <i>Review of Scientific Instruments</i> , 2009, 80, 014303.	1.3	9
63	Mechanism of Cyclizing NAD to Cyclic ADP-ribose by ADP-ribosyl Cyclase and CD38. <i>Journal of Biological Chemistry</i> , 2009, 284, 27629-27636.	3.4	70
64	Structural Basis for Enzymatic Evolution from a Dedicated ADP-ribosyl Cyclase to a Multifunctional NAD Hydrolase. <i>Journal of Biological Chemistry</i> , 2009, 284, 27637-27645.	3.4	53
65	Combining solution wide-angle X-ray scattering and crystallography: determination of molecular envelope and heavy-atom sites. <i>Journal of Applied Crystallography</i> , 2009, 42, 259-264.	4.5	3
66	Mechanism-Based Small Molecule Probes for Labeling CD38 on Live Cells. <i>Journal of the American Chemical Society</i> , 2009, 131, 1658-1659.	13.7	29
67	Covalent and Noncovalent Intermediates of an NAD Utilizing Enzyme, Human CD38. <i>Chemistry and Biology</i> , 2008, 15, 1068-1078.	6.0	38
68	SNAP ²⁵ is also an iron-sulfur protein. <i>FEBS Letters</i> , 2008, 582, 1431-1436.	2.8	10
69	Mapping Nanostructure: A Systematic Enumeration of Nanomaterials by Assembling Nanobuilding Blocks at Crystallographic Positions. <i>ACS Nano</i> , 2008, 2, 1237-1251.	14.6	50
70	Conformational Closure of the Catalytic Site of Human CD38 Induced by Calcium. <i>Biochemistry</i> , 2008, 47, 13966-13973.	2.5	12
71	Hierarchical and Helical Self-Assembly of ADP-Ribosyl Cyclase into Large-Scale Protein Microtubes. <i>Journal of Physical Chemistry B</i> , 2008, 112, 14682-14686.	2.6	8
72	Conformational Closure of the Catalytic Site of Human CD38 Induced by Calcium. <i>Biochemistry</i> , 2008, 47, 13966-73.	2.5	0

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73	Structural Basis for Formation and Hydrolysis of the Calcium Messenger Cyclic ADP-ribose by Human CD38. <i>Journal of Biological Chemistry</i> , 2007, 282, 5853-5861.	3.4	48
74	Catalysis-associated Conformational Changes Revealed by Human CD38 Complexed with a Non-hydrolyzable Substrate Analog*. <i>Journal of Biological Chemistry</i> , 2007, 282, 24825-24832.	3.4	24
75	Crystal Structure of Uroporphyrinogen Decarboxylase from <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2007, 189, 3573-3580.	2.2	20
76	High-pressure cryocooling for capillary sample cryoprotection and diffraction phasing at long wavelengths. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 653-659.	2.5	23
77	Structure of human upstream binding factor HMG box 5 and site for binding of the cell-cycle regulatory factor TAF1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 730-737.	2.5	8
78	Structural basis for modulation of Kv4 K ⁺ channels by auxiliary KChIP subunits. <i>Nature Neuroscience</i> , 2007, 10, 32-39.	14.8	135
79	The structural basis for activation of plant immunity by bacterial effector protein AvrPto. <i>Nature</i> , 2007, 449, 243-247.	27.8	162
80	Crystal structure of 3-hydroxyanthranilic acid 3,4-dioxygenase from <i>Saccharomyces cerevisiae</i> : A special subgroup of the type III extradiol dioxygenases. <i>Protein Science</i> , 2006, 15, 761-773.	7.6	34
81	Macromolecular phasing. <i>Physics Today</i> , 2006, 59, 46-52.	0.3	10
82	Macromolecular envelope determination and envelope-based phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 909-914.	2.5	10
83	Solution of protein crystallographic structures by high-pressure cryocooling and noble-gas phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 687-694.	2.5	26
84	Multilayer X-ray optics at CHESS. <i>Journal of Synchrotron Radiation</i> , 2006, 13, 204-210.	2.4	45
85	Structure of human MRG15 chromo domain and its binding to Lys36-methylated histone H3. <i>Nucleic Acids Research</i> , 2006, 34, 6621-6628.	14.5	138
86	Structural Basis for the Mechanistic Understanding of Human CD38-controlled Multiple Catalysis. <i>Journal of Biological Chemistry</i> , 2006, 281, 32861-32869.	3.4	54
87	Crystal Structure of Mammalian Cysteine Dioxygenase. <i>Journal of Biological Chemistry</i> , 2006, 281, 18723-18733.	3.4	148
88	Acidic Residues at the Active Sites of CD38 and ADP-ribosyl Cyclase Determine Nicotinic Acid Adenine Dinucleotide Phosphate (NAADP) Synthesis and Hydrolysis Activities. <i>Journal of Biological Chemistry</i> , 2006, 281, 28951-28957.	3.4	81
89	Crystal Structures of Native and Ligand Bound Cysteine Dioxygenase. <i>FASEB Journal</i> , 2006, 20, A476.	0.5	0
90	Structure of the CED-4/CED-9 complex provides insights into programmed cell death in <i>Caenorhabditis elegans</i> . <i>Nature</i> , 2005, 437, 831-837.	27.8	207

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91	Crystal Structure of Human CD38 Extracellular Domain. <i>Structure</i> , 2005, 13, 1331-1339.	3.3	155
92	Crystallographic data collection using a 0.22% bandwidth multilayer. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 345-348.	2.4	8
93	Preparation, crystallization and X-ray diffraction analysis to 1.5Å resolution of rat cysteine dioxygenase, a mononuclear iron enzyme responsible for cysteine thiol oxidation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 1013-1016.	0.7	9
94	Crystal structure of a new class of glutathione transferase from the model human hookworm nematode <i>Heligmosomoides polygyrus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 1024-1031.	2.6	29
95	Crystal Structure of the Cysteine-rich Secretory Protein Stecrisp Reveals That the Cysteine-rich Domain Has a K ⁺ Channel Inhibitor-like Fold. <i>Journal of Biological Chemistry</i> , 2005, 280, 12405-12412.	3.4	132
96	Blocking Effect and Crystal Structure of Natrin Toxin, a Cysteine-Rich Secretory Protein from <i>Naja atra</i> Venom that Targets the BKCa Channel. <i>Biochemistry</i> , 2005, 44, 10145-10152.	2.5	99
97	Crystal Structures of Fms1 and its Complex with Spermine Reveal Substrate Specificity. <i>Journal of Molecular Biology</i> , 2005, 348, 951-959.	4.2	49
98	The Atomic Resolution Crystal Structure of Atratoxin Determined by Single Wavelength Anomalous Diffraction Phasing. <i>Journal of Biological Chemistry</i> , 2004, 279, 39094-39104.	3.4	11
99	ADP-Ribosyl Cyclase. <i>Structure</i> , 2004, 12, 477-486.	3.3	24
100	Crystallographic Snapshots of <i>Aspergillus fumigatus</i> Phytase, Revealing Its Enzymatic Dynamics. <i>Structure</i> , 2004, 12, 1575-1583.	3.3	30
101	Purification, partial characterization, crystallization and structural determination of AHP-LAAO, a novel L-amino-acid oxidase with cell apoptosis-inducing activity from <i>Agkistrodon halys pallasvenom</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 974-977.	2.5	52
102	Purification, partial characterization, crystallization and preliminary X-ray diffraction of two cysteine-rich secretory proteins from <i>Naja atra</i> and <i>Trimeresurus stejnegeri</i> venoms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1108-1111.	2.5	7
103	SAD phasing by combination of direct methods with the SOLVE/RESOLVE procedure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1244-1253.	2.5	32
104	Purification, characterization, crystallization and preliminary X-ray crystallographic analysis of two novel C-type lectin-like proteins: Aall-A and Aall-B from <i>Deinagkistrodon acutus</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2035-2037.	2.5	3
105	ABS: a program to determine absolute configuration and evaluate anomalous scatterer substructure. <i>Journal of Applied Crystallography</i> , 2004, 37, 498-499.	4.5	67
106	Crystal Structure of a Heat-resilient Phytase from <i>Aspergillus fumigatus</i> , Carrying a Phosphorylated Histidine. <i>Journal of Molecular Biology</i> , 2004, 339, 437-445.	4.2	52
107	MacCHESS: A resource for macromolecular diffraction at the Cornell high-energy synchrotron source. <i>Synchrotron Radiation News</i> , 2004, 17, 38-43.	0.8	0
108	SAPI: a direct-methods program for finding heavy-atom sites with SAD or SIR data. <i>Journal of Applied Crystallography</i> , 2003, 36, 1274-1276.	4.5	8

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109	S-SWAT (softer single-wavelength anomalous technique): potential in high-throughput protein crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2003, 59, 327-334.	0.3	38
110	Low-resolution molecular replacement using a six-dimensional search. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1016-1019.	2.5	7
111	Crystallization and preliminary crystallographic analysis of a new class of glutathione transferase from nematodes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1262-1264.	2.5	1
112	Purification, partial characterization and crystallization of acucetin, a protein containing both disintegrin-like and cysteine-rich domains released by auto-proteolysis of a P-III-type metalloproteinase AaH-IV from <i>Agkistrodon acutus</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2310-2312.	2.5	12
113	Direct-method-aided phasing of MAD data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 250-253.	2.5	0
114	Phasing from an envelope. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1410-1414.	2.5	13
115	OASIS: a computer program for breaking phase ambiguity in one-wavelength anomalous scattering or single isomorphous substitution (replacement) data. <i>Journal of Applied Crystallography</i> , 2000, 33, 980-981.	4.5	58
116	Implementation of cluster analysis for ab initio phasing using the molecular envelope from solution X-ray scattering. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1002-1006.	2.5	5
117	Direct phasing of one-wavelength anomalous-scattering data. <i>Journal of Synchrotron Radiation</i> , 2000, 7, 148-151.	2.4	2
118	LSCALE – the new normalization, scaling and absorption correction program in the Daresbury Laue software suite. <i>Journal of Applied Crystallography</i> , 1999, 32, 554-562.	4.5	102
119	Estimating unobserved reflection intensities in Laue diffraction by the maximum-entropy method. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 238-242.	2.5	4
120	Ab initio phasing using molecular envelope from solution X-ray scattering. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 243-246.	2.5	16
121	Combining direct methods with isomorphous replacement or anomalous scattering data. VIII. Phasing experimental SIR data with the replacing atoms in a centrosymmetric arrangement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 846-848.	2.5	3
122	Is single-wavelength anomalous scattering sufficient for solving phases? A comparison of different methods for a 2.1 Å structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1620-1622.	2.5	4
123	Accurate and highly complete synchrotron protein crystal Laue diffraction data using the ESRF CCD and the Daresbury Laue software. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 995-1006.	2.4	15
124	LAUEGEN version 6.0 and INTLDM. <i>Journal of Applied Crystallography</i> , 1998, 31, 496-502.	4.5	164
125	Structure Determination of a 16.8 kDa Copper Protein at 2.1 Å Resolution Using Anomalous Scattering Data with Direct Methods. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 629-635.	2.5	17
126	Use of Single Isomorphous Replacement Data of Proteins – Resolving the Phase Ambiguity and a New Procedure for Phase Extension. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 49-55.	2.5	4

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127	Structure Solution of Azurin II from <i>Alcaligenes xylosoxidans</i> using the Laue Method: Possibility of Studying In Situ Redox Changes using X-rays. <i>Journal of Synchrotron Radiation</i> , 1996, 3, 14-19.	2.4	4
128	Direct-Method Structure Determination of the Native Azurin II Protein Using One-Wavelength Anomalous Scattering Data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 937-941.	2.5	2
129	Determination of d_{min} and λ_{min} from the Intensity Distributions of Laue Patterns. <i>Journal of Applied Crystallography</i> , 1995, 28, 447-450.	4.5	7
130	The Laue Data Module (LDM) – a software development for Laue X-ray diffraction data processing. <i>Journal of Applied Crystallography</i> , 1995, 28, 635-640.	4.5	5
131	Evaluation of Reflection Intensities for the Components of Multiple Laue Diffraction Spots. III. Using a Real-Space Density Modification Method. <i>Journal of Synchrotron Radiation</i> , 1995, 2, 27-30.	2.4	2
132	Structure determination with Laue diffraction data – including refinement when anomalous scatterers are present. <i>Acta Crystallographica Section B: Structural Science</i> , 1994, 50, 441-447.	1.8	5
133	Crystal Structure of a 1:1:1 Molecular Complex of (R)-(+)-2,2-Dihydroxy-1,1-binaphthyl,N,N,N-Tetra(2-butyl)terephthalamide, and Methanol. <i>Chemistry Letters</i> , 1986, 15, 1913-1916.		1
134	A dual-function chemical probe for detecting erasers of lysine lipoylation. <i>Frontiers of Chemical Science and Engineering</i> , 0, , 1.	4.4	3