

Wladek Minor

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/993383/publications.pdf>

Version: 2024-02-01

246
papers

42,693
citations

31902

53
h-index

2071

204
g-index

283
all docs

283
docs citations

283
times ranked

39472
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Optimal structure determination from sub-optimal diffraction data. <i>Protein Science</i> , 2022, 31, 259-268. | 3.1 | 6 |
| 2 | Group depositions to the Protein Data Bank need adequate presentation and different archiving protocol. <i>Protein Science</i> , 2022, 31, 784-786. | 3.1 | 6 |
| 3 | New ligand-binding sites identified in the crystal structures of β^2 -lactoglobulin complexes with desipramine. <i>IUCr</i> , 2022, 9, 386-398. | 1.0 | 3 |
| 4 | Organism-specific differences in the binding of ketoprofen to serum albumin. <i>IUCr</i> , 2022, 9, 551-561. | 1.0 | 6 |
| 5 | A study on the structure, mechanism, and biochemistry of kanamycin B dioxygenase (Kan) β an enzyme with a broad range of substrates. <i>FEBS Journal</i> , 2021, 288, 1366-1386. | 2.2 | 5 |
| 6 | Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2-related structural models. <i>Protein Science</i> , 2021, 30, 115-124. | 3.1 | 15 |
| 7 | Synchrotron radiation as a tool for macromolecular X-Ray Crystallography: A XXI century perspective. <i>Nuclear Instruments & Methods in Physics Research B</i> , 2021, 489, 30-40. | 0.6 | 3 |
| 8 | Rapid response to emerging biomedical challenges and threats. <i>IUCr</i> , 2021, 8, 395-407. | 1.0 | 5 |
| 9 | Gcn5-Related N-Acetyltransferases (GNATs) With a Catalytic Serine Residue Can Play Ping-Pong Too. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 646046. | 1.6 | 8 |
| 10 | Recognizing and validating ligands with CheckMyBlob. <i>Nucleic Acids Research</i> , 2021, 49, W86-W92. | 6.5 | 9 |
| 11 | Dr. Alexander Wlodawer celebrating five decades of service to the structural biology community. <i>FEBS Journal</i> , 2021, 288, 4160-4164. | 2.2 | 0 |
| 12 | Detecting anomalies in X-ray diffraction images using convolutional neural networks. <i>Expert Systems With Applications</i> , 2021, 174, 114740. | 4.4 | 9 |
| 13 | virusMED: an atlas of hotspots of viral proteins. <i>IUCr</i> , 2021, 8, 931-942. | 1.0 | 5 |
| 14 | State-of-the-Art Data Management: Improving the Reproducibility, Consistency, and Traceability of Structural Biology and in Vitro Biochemical Experiments. <i>Methods in Molecular Biology</i> , 2021, 2199, 209-236. | 0.4 | 5 |
| 15 | The Integrated Resource for Reproducibility in Molecular Crystallography: experiences of the first five years. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2021, 77, a187-a187. | 0.0 | 0 |
| 16 | Rapid response to biomedical challenges and threats. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2021, 77, a268-a268. | 0.0 | 0 |
| 17 | Molstack: A platform for interactive presentations of electron density and cryo-EM maps and their interpretations. <i>Protein Science</i> , 2020, 29, 120-127. | 3.1 | 9 |
| 18 | Structural and biochemical analysis of <i>Bacillus Anthracis</i> prephenate dehydrogenase reveals an unusual mode of inhibition by tyrosine via the ACT domain. <i>FEBS Journal</i> , 2020, 287, 2235-2255. | 2.2 | 3 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Structure of the Complex of an Iminopyridinedione Protein Tyrosine Phosphatase 4A3 Phosphatase Inhibitor with Human Serum Albumin. <i>Molecular Pharmacology</i> , 2020, 98, 648-657. | 1.0 | 7 |
| 20 | Ligand-centered assessment of SARS-CoV-2 drug target models in the Protein Data Bank. <i>FEBS Journal</i> , 2020, 287, 3703-3718. | 2.2 | 35 |
| 21 | Albumin-Based Transport of Nonsteroidal Anti-Inflammatory Drugs in Mammalian Blood Plasma. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 6847-6862. | 2.9 | 37 |
| 22 | Regioselectivity of hyoscyamine 6 β -hydroxylase-catalysed hydroxylation as revealed by high-resolution structural information and QM/MM calculations. <i>Dalton Transactions</i> , 2020, 49, 4454-4469. | 1.6 | 15 |
| 23 | Structural Basis of Non-Steroidal Anti-Inflammatory Drug (NSAID) Transport by Serum Albumin. <i>Biophysical Journal</i> , 2020, 118, 323a-324a. | 0.2 | 0 |
| 24 | Comparison of metal-bound and unbound structures of aminopeptidase B proteins from <i>Escherichia coli</i> and <i>Yersinia pestis</i> . <i>Protein Science</i> , 2020, 29, 1618-1628. | 3.1 | 3 |
| 25 | On the evolution of the quality of macromolecular models in the PDB. <i>FEBS Journal</i> , 2020, 287, 2685-2698. | 2.2 | 15 |
| 26 | Molecular determinants of vascular transport of dexamethasone in COVID-19 therapy. <i>IUCr</i> , 2020, 7, 1048-1058. | 1.0 | 12 |
| 27 | Automatic recognition of ligands in electron density by machine learning. <i>Bioinformatics</i> , 2019, 35, 452-461. | 1.8 | 22 |
| 28 | Testosterone meets albumin – the molecular mechanism of sex hormone transport by serum albumins. <i>Chemical Science</i> , 2019, 10, 1607-1618. | 3.7 | 38 |
| 29 | Pyrimidine biosynthesis in pathogens – Structures and analysis of dihydroorotases from <i>Yersinia pestis</i> and <i>Vibrio cholerae</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 136, 1176-1187. | 3.6 | 17 |
| 30 | The Integrated Resource for Reproducibility in Macromolecular Crystallography: Experiences of the first four years. <i>Structural Dynamics</i> , 2019, 6, 064301. | 0.9 | 25 |
| 31 | Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>Journal of Applied Crystallography</i> , 2019, 52, 495-497. | 1.9 | 1 |
| 32 | Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>IUCr</i> , 2019, 6, 341-343. | 1.0 | 8 |
| 33 | Energetics of interactions in the solid state of 2-hydroxy-8-quinoline derivatives ($X = N$). <i>Tj ETQq1</i> 1 0.784314 rgBT /Overton, 2019, 6, 868-883. | 1.0 | 11 |
| 34 | Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 321-323. | 0.4 | 3 |
| 35 | Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 455-457. | 1.1 | 10 |
| 36 | Credible measures of resolution limits. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, a326-a326. | 0.0 | 0 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | The Integrated Resource for Reproducibility in Macromolecular Crystallography (IRRMCM). Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a259-a259. | 0.0 | 0 |
| 38 | ACT domain of Bacillus anthracis prephenate dehydrogenase acts as tyrosine sensor and inhibits the enzyme via a mechanical switch. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a341-a341. | 0.0 | 0 |
| 39 | Decomposition methods for analysis of specific radiation damage. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a330-a330. | 0.0 | 0 |
| 40 | Comparison of X-ray wavefunction refinement and multipole refinement based on the energetic analysis of the crystal structures of 2-hydroxy-8-X-quinoline derivatives (X = Cl, Br, I, S-Ph). Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e454-e454. | 0.0 | 0 |
| 41 | Characterizing metal-binding sites in proteins with X-ray crystallography. Nature Protocols, 2018, 13, 1062-1090. | 5.5 | 86 |
| 42 | Structural, Biochemical, and Evolutionary Characterizations of Glyoxylate/Hydroxypyruvate Reductases Show Their Division into Two Distinct Subfamilies. Biochemistry, 2018, 57, 963-977. | 1.2 | 12 |
| 43 | Detect, correct, retract: How to manage incorrect structural models. FEBS Journal, 2018, 285, 444-466. | 2.2 | 49 |
| 44 | Molstackâ€”Interactive visualization tool for presentation, interpretation, and validation of macromolecules and electron density maps. Protein Science, 2018, 27, 86-94. | 3.1 | 31 |
| 45 | Classification, substrate specificity and structural features of D-2-hydroxyacid dehydrogenases: 2HADH knowledgebase. BMC Evolutionary Biology, 2018, 18, 199. | 3.2 | 21 |
| 46 | A Gcn5-Related N-Acetyltransferase (GNAT) Capable of Acetylating Polymyxin B and Colistin Antibiotics in Vitro. Biochemistry, 2018, 57, 7011-7020. | 1.2 | 11 |
| 47 | Refining the macromolecular model â€” achieving the best agreement with the data from X-ray diffraction experiment. Crystallography Reviews, 2018, 24, 236-262. | 0.4 | 43 |
| 48 | A transient post-translational modification of active site cysteine alters binding properties of the parkinsonism protein DJ-1. Biochemical and Biophysical Research Communications, 2018, 504, 328-333. | 1.0 | 12 |
| 49 | A close look onto structural models and primary ligands of metallo-Î²-lactamases. Drug Resistance Updates, 2018, 40, 1-12. | 6.5 | 47 |
| 50 | Differences in substrate specificity of <i>V. cholerae</i> FabH enzymes suggest new approaches for the development of novel antibiotics and biofuels. FEBS Journal, 2018, 285, 2900-2921. | 2.2 | 3 |
| 51 | Antigenic Determinants of Der p 1: Specificity and Cross-Reactivity Associated with IgE Antibody Recognition. Journal of Immunology, 2017, 198, 1334-1344. | 0.4 | 20 |
| 52 | Optimization of overexpression of a chaperone protein of steroid C25 dehydrogenase for biochemical and biophysical characterization. Protein Expression and Purification, 2017, 134, 47-62. | 0.6 | 5 |
| 53 | Data mining of iron(II) and iron(III) bond-valence parameters, and their relevance for macromolecular crystallography. Acta Crystallographica Section D: Structural Biology, 2017, 73, 316-325. | 1.1 | 33 |
| 54 | Generating enzyme and radicalâ€”mediated bisubstrates as tools for investigating Gcn5â€”related <i>N</i> -acetyltransferases. FEBS Letters, 2017, 591, 2348-2361. | 1.3 | 5 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 55 | Insight into the 3D structure and substrate specificity of previously uncharacterized GNAT superfamily acetyltransferases from pathogenic bacteria. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 55-64. | 1.1 | 13 |
| 56 | Databases, Repositories, and Other Data Resources in Structural Biology. <i>Methods in Molecular Biology</i> , 2017, 1607, 643-665. | 0.4 | 6 |
| 57 | Sharing Big Data. <i>IUCr</i> , 2017, 4, 3-4. | 1.0 | 2 |
| 58 | <i>CheckMyMetal</i> : a macromolecular metal-binding validation tool. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 223-233. | 1.1 | 268 |
| 59 | The Integrated Resource for Reproducibility in Macromolecular Crystallography (IRRM). <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a218-a218. | 0.0 | 0 |
| 60 | What's hiding in the PDB? Reinvestigation of structural data for the biomedically important enzymes metallo- β -lactamases. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a281-a281. | 0.0 | 0 |
| 61 | A public database of macromolecular diffraction experiments. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C627-C627. | 0.0 | 1 |
| 62 | Crystallographic tools towards understanding of macromolecular structure–function relationships. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C35-C35. | 0.0 | 0 |
| 63 | Correcting the record of structural publications requires joint effort of the community and journal editors. <i>FEBS Journal</i> , 2016, 283, 4452-4457. | 2.2 | 31 |
| 64 | Protein purification and crystallization artifacts: The tale usually not told. <i>Protein Science</i> , 2016, 25, 720-733. | 3.1 | 46 |
| 65 | Recombinant production of enzymatically active male contraceptive drug target hTSSK2 - Localization of the TSKS domain phosphorylated by TSSK2. <i>Protein Expression and Purification</i> , 2016, 121, 88-96. | 0.6 | 12 |
| 66 | The impact of structural genomics: the first quinquennial. <i>Journal of Structural and Functional Genomics</i> , 2016, 17, 1-16. | 1.2 | 60 |
| 67 | Circulatory zinc transport is controlled by distinct interdomain sites on mammalian albumins. <i>Chemical Science</i> , 2016, 7, 6635-6648. | 3.7 | 67 |
| 68 | A public database of macromolecular diffraction experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1181-1193. | 1.1 | 103 |
| 69 | Dissecting the Structural Elements for the Activation of β -Ketoacyl-(Acyl Carrier Protein) Reductase from <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2016, 198, 463-476. | 1.0 | 14 |
| 70 | <i>Fitmunk</i> : improving protein structures by accurate, automatic modeling of side-chain conformations. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 266-280. | 1.1 | 25 |
| 71 | Crystal structure of equine serum albumin in complex with cetirizine reveals a novel drug binding site. <i>Molecular Immunology</i> , 2016, 71, 143-151. | 1.0 | 19 |
| 72 | Safeguarding Structural Data Repositories against Bad Apples. <i>Structure</i> , 2016, 24, 216-220. | 1.6 | 34 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 73 | The young person's guide to the PDB. <i>Postepy Biochemii</i> , 2016, 62, 242-249. | 0.5 | 2 |
| 74 | Magnesium-binding architectures in RNA crystal structures: validation, binding preferences, classification and motif detection. <i>Nucleic Acids Research</i> , 2015, 43, 3789-3801. | 6.5 | 89 |
| 75 | Data to knowledge: how to get meaning from your result. <i>IUCr</i> , 2015, 2, 45-58. | 1.0 | 12 |
| 76 | X-ray crystallography over the past decade for novel drug discovery – where are we heading next?. <i>Expert Opinion on Drug Discovery</i> , 2015, 10, 975-989. | 2.5 | 59 |
| 77 | Structural Analysis of Der p 1 Antibody Complexes and Comparison with Complexes of Proteins or Peptides with Monoclonal Antibodies. <i>Journal of Immunology</i> , 2015, 195, 307-316. | 0.4 | 23 |
| 78 | 100 Years later: Celebrating the contributions of x-ray crystallography to allergy and clinical immunology. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 29-37.e10. | 1.5 | 33 |
| 79 | Sperm Lysozyme-Like Protein 1 (SLLP1), an intra-acrosomal oolemmal-binding sperm protein, reveals filamentous organization in protein crystal form. <i>Andrology</i> , 2015, 3, 756-771. | 1.9 | 9 |
| 80 | Crystallography and chemistry should always go together: a cautionary tale of protein complexes with cisplatin and carboplatin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1965-1979. | 2.5 | 52 |
| 81 | Structural characterization of the putative ABC-type 2 transporter from <i>Thermotoga maritima</i> MSB8. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 215-222. | 1.2 | 1 |
| 82 | The future of crystallography in drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2014, 9, 125-137. | 2.5 | 70 |
| 83 | Edc3 Function in Yeast and Mammals Is Modulated by Interaction with NAD-Related Compounds. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 613-622. | 0.8 | 10 |
| 84 | The major cockroach allergen Bla g 4 binds tyramine and octopamine. <i>Molecular Immunology</i> , 2014, 60, 86-94. | 1.0 | 22 |
| 85 | Double trouble – Buffer selection and isotope tag presence may be responsible for nonreproducibility of biomedical experiments. <i>Protein Science</i> , 2014, 23, 1359-1368. | 3.1 | 83 |
| 86 | The crystal structure of pyrimidine/thiamin biosynthesis precursor-like domain-containing protein CAE31940 from proteobacterium <i>Bordetella bronchiseptica</i> RB50, and evolutionary insight into the NMT1/THI5 family. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 73-81. | 1.2 | 0 |
| 87 | Antigenic Determinants On Der p 1 Identified By Mutagenesis Analysis Based On The Structure Of Allergen-Antibody Complexes. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, AB164. | 1.5 | 1 |
| 88 | Validation of metal-binding sites in macromolecular structures with the CheckMyMetal web server. <i>Nature Protocols</i> , 2014, 9, 156-170. | 5.5 | 254 |
| 89 | Factors correlating with significant differences between X-ray structures of myoglobin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 481-491. | 2.5 | 13 |
| 90 | Check your metal - not every density blob is a water molecule. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C1483-C1483. | 0.0 | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 91 | Transforming biomedical and structural data into information and knowledge. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C492-C492. | 0.0 | 0 |
| 92 | Data Management in the Modern Structural Biology and Biomedical Research Environment. Methods in Molecular Biology, 2014, 1140, 1-25. | 0.4 | 34 |
| 93 | The Quality and Validation of Structures from Structural Genomics. Methods in Molecular Biology, 2014, 1091, 297-314. | 0.4 | 23 |
| 94 | Avoidable errors in deposited macromolecular structures: an impediment to efficient data mining. IUCr, 2014, 1, 179-193. | 1.0 | 58 |
| 95 | Structural analysis of GNAT acetyltransferases and protein acetylation. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C299-C299. | 0.0 | 0 |
| 96 | Structural Biology Knowledgebase: An Integrated Resource for Modern Biologists. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C493-C493. | 0.0 | 0 |
| 97 | Protein crystallography for aspiring crystallographers or how to avoid pitfalls and traps in macromolecular structure determination. FEBS Journal, 2013, 280, 5705-5736. | 2.2 | 95 |
| 98 | Broad substrate screen as a tool to identify substrates for bacterial Gcn5-related N-acetyltransferases with unknown substrate specificity. Protein Science, 2013, 22, 222-230. | 3.1 | 45 |
| 99 | Structural Analysis Reveals Molecular Basis for Interactions of Group 1 Allergens with Species Specific and Cross-Reactive Antibodies. Journal of Allergy and Clinical Immunology, 2013, 131, AB15. | 1.5 | 1 |
| 100 | Structural, Functional, and Inhibition Studies of a Gcn5-related N-Acetyltransferase (GNAT) Superfamily Protein PA4794. Journal of Biological Chemistry, 2013, 288, 30223-30235. | 1.6 | 37 |
| 101 | Structure and Function of the Peanut Panallergen Ara h 8. Journal of Allergy and Clinical Immunology, 2013, 131, AB19. | 1.5 | 0 |
| 102 | De Novo Creation of an Antibody Binding Epitope On Group 1 Mite Allergens. Journal of Allergy and Clinical Immunology, 2013, 131, AB16. | 1.5 | 0 |
| 103 | Structure of isochorismate synthase Dhbc from Bacillus anthracis. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 956-961. | 0.7 | 2 |
| 104 | Structural and bioinformatic analysis of the kiwifruit allergen Act d 11, a member of the family of ripening-related proteins. Molecular Immunology, 2013, 56, 794-803. | 1.0 | 43 |
| 105 | Serum albumins' Unusual allergens. Biochimica Et Biophysica Acta - General Subjects, 2013, 1830, 5375-5381. | 1.1 | 89 |
| 106 | Biophysical analysis of the putative acetyltransferase SACOL2570 from methicillin-resistant Staphylococcus aureus. Journal of Structural and Functional Genomics, 2013, 14, 97-108. | 1.2 | 9 |
| 107 | Ultratight crystal packing of a 10 kDa protein. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 464-470. | 2.5 | 9 |
| 108 | Structural and functional insight into the universal stress protein family. Evolutionary Applications, 2013, 6, 434-449. | 1.5 | 94 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 109 | Abstract 2747: EWS-FLI1 reduces RNA Helicase A activity.. , 2013, , . | | 0 |
| 110 | Molecular basis for phosphospecific recognition of histone H3 tails by Survivin paralogues at inner centromeres. <i>Molecular Biology of the Cell</i> , 2012, 23, 1457-1466. | 0.9 | 53 |
| 111 | Identification of Unknown Protein Function Using Metabolite Cocktail Screening. <i>Structure</i> , 2012, 20, 1715-1725. | 1.6 | 45 |
| 112 | Structure of anabolic ornithine carbamoyltransferase from <i>Campylobacter jejuni</i> at 2.7 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1018-1024. | 0.7 | 4 |
| 113 | Assessing the accuracy of template-based structure prediction metaservers by comparison with structural genomics structures. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 213-225. | 1.2 | 10 |
| 114 | Substrate Specificity of Mammalian N-Terminal $\hat{\pm}$ -Amino Methyltransferase NRMT. <i>Biochemistry</i> , 2012, 51, 5942-5950. | 1.2 | 51 |
| 115 | Molecular Determinants for Antibody Binding on Group 1 House Dust Mite Allergens. <i>Journal of Biological Chemistry</i> , 2012, 287, 7388-7398. | 1.6 | 75 |
| 116 | Structure of <i>Escherichia coli</i> RutC, a member of the YjgF family and putative aminoacrylate peracid reductase of the <i>rut</i> operon. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1294-1299. | 0.7 | 15 |
| 117 | <i>Alternaria alternata</i> allergen Alt a 1: A unique $\hat{\pm}$ -barrel protein dimer found exclusively in fungi. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 130, 241-247.e9. | 1.5 | 99 |
| 118 | Mechanism of N ¹⁰ -formyltetrahydrofolate synthetase derived from complexes with intermediates and inhibitors. <i>Protein Science</i> , 2012, 21, 219-228. | 3.1 | 21 |
| 119 | A multi-faceted analysis of RutD reveals a novel family of $\hat{\pm}$ / $\hat{2}$ hydrolases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2359-2368. | 1.5 | 7 |
| 120 | Crystal structure of a putative isochorismatase hydrolase from <i>Oleispira antarctica</i> . <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 27-36. | 1.2 | 22 |
| 121 | Crystal structures of putative phosphoglycerate kinases from <i>B. anthracis</i> and <i>C. jejuni</i> . <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 15-26. | 1.2 | 7 |
| 122 | Asymmetric synthesis and evaluation of a hydroxyphenylamide voltage-gated sodium channel blocker in human prostate cancer xenografts. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 2180-2188. | 1.4 | 20 |
| 123 | Structural characterization of <i>Helicobacter pylori</i> dethiobiotin synthetase reveals differences between family members. <i>FEBS Journal</i> , 2012, 279, 1093-1105. | 2.2 | 15 |
| 124 | Structural and immunologic characterization of bovine, horse, and rabbit serum albumins. <i>Molecular Immunology</i> , 2012, 52, 174-182. | 1.0 | 756 |
| 125 | Structure of a short-chain dehydrogenase/reductase from <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 632-637. | 0.7 | 3 |
| 126 | Single Enantiomer of YK-4-279 Demonstrates Specificity in Targeting the Oncogene EWS-FLI1. <i>Oncotarget</i> , 2012, 3, 172-182. | 0.8 | 83 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 127 | Structural Biology Knowledgebase: a biologists resource for protein structure and sample information. <i>FASEB Journal</i> , 2012, 26, lb194. | 0.2 | 0 |
| 128 | The Enzyme Function Initiative. <i>Biochemistry</i> , 2011, 50, 9950-9962. | 1.2 | 169 |
| 129 | The Structural Biology Knowledgebase - search Online for Protein Sequences, Structures, Functions, Methods and More. <i>Biophysical Journal</i> , 2011, 100, 319a. | 0.2 | 0 |
| 130 | X-ray crystallography: assessment and validation of proteinâ€‘small molecule complexes for drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2011, 6, 771-782. | 2.5 | 53 |
| 131 | Structural Analysis of a Putative Aminoglycoside N-Acetyltransferase from <i>Bacillus anthracis</i> . <i>Journal of Molecular Biology</i> , 2011, 410, 411-423. | 2.0 | 17 |
| 132 | The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 45-54. | 1.2 | 65 |
| 133 | Crystal structure of a putative transcriptional regulator SCO0520 from <i>Streptomyces coelicolor</i> A3(2) reveals an unusual dimer among TetR family proteins. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 149-157. | 1.2 | 6 |
| 134 | The HP1a Disordered C Terminus and Chromo Shadow Domain Cooperate to Select Target Peptide Partners. <i>ChemBioChem</i> , 2011, 12, 1084-1096. | 1.3 | 49 |
| 135 | Structural and Immunologic Characterization of Ara h 1, a Major Peanut Allergen. <i>Journal of Biological Chemistry</i> , 2011, 286, 39318-39327. | 1.6 | 89 |
| 136 | Structural and immunologic characterization of Ara h 1, a major peanut allergen.. <i>Journal of Biological Chemistry</i> , 2011, 286, 44294. | 1.6 | 1 |
| 137 | To automate or not to automate: this is the question. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 211-221. | 1.2 | 23 |
| 138 | Unmet challenges of structural genomics. <i>Current Opinion in Structural Biology</i> , 2010, 20, 587-597. | 2.6 | 49 |
| 139 | An experimental charge density of HEPES. <i>Acta Crystallographica Section B: Structural Science</i> , 2010, 66, 482-492. | 1.8 | 17 |
| 140 | Diffraction data analysis in the presence of radiation damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 426-436. | 2.5 | 57 |
| 141 | Is too `creative' language acceptable in crystallography?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1041-1042. | 2.5 | 2 |
| 142 | New surface contacts formed upon reductive lysine methylation: Improving the probability of protein crystallization. <i>Protein Science</i> , 2010, 19, 1395-1404. | 3.1 | 35 |
| 143 | NRMT is an Î±-N-methyltransferase that methylates RCC1 and retinoblastoma protein. <i>Nature</i> , 2010, 466, 1125-1128. | 13.7 | 109 |
| 144 | How to use the PSI Structural Genomics Knowledgebase to Enable Research. <i>Biophysical Journal</i> , 2010, 98, 250a. | 0.2 | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 145 | Macromolecular Crystals. <i>Crystal Growth and Design</i> , 2010, 10, 580-586. | 1.4 | 8 |
| 146 | Crystal structure and molecular modeling study of N-carbamoylsarcosine amidase Ta0454 from <i>Thermoplasma acidophilum</i> . <i>Journal of Structural Biology</i> , 2010, 169, 304-311. | 1.3 | 13 |
| 147 | 2,4-Dichlorobenzaldehyde. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2010, 66, o243-o243. | 0.2 | 1 |
| 148 | HOW TO USE THE PSI STRUCTURAL GENOMICS KNOWLEDGEBASE TO ENABLE RESEARCH. <i>FASEB Journal</i> , 2010, 24, 902.2. | 0.2 | 0 |
| 149 | X-Ray Diffraction Experiment. <i>Advances in Protein Chemistry and Structural Biology</i> , 2009, 77, 23-40. | 1.0 | 10 |
| 150 | Structural and Functional Characterizations of SsgB, a Conserved Activator of Developmental Cell Division in Morphologically Complex Actinomycetes. <i>Journal of Biological Chemistry</i> , 2009, 284, 25268-25279. | 1.6 | 23 |
| 151 | Benefits of Structural Genomics for Drug Discovery Research. <i>Infectious Disorders - Drug Targets</i> , 2009, 9, 459-474. | 0.4 | 26 |
| 152 | The protein structure initiative structural genomics knowledgebase. <i>Nucleic Acids Research</i> , 2009, 37, D365-D368. | 6.5 | 94 |
| 153 | The crystal structure of the AF2331 protein from <i>Archaeoglobus fulgidus</i> DSM 4304 forms an unusual interdigitated dimer with a new type of $\alpha + \beta^2$ fold. <i>Protein Science</i> , 2009, 18, 2410-2419. | 3.1 | 11 |
| 154 | The structure of pyogenecin immunity protein, a novel bacteriocin-like immunity protein from <i>Streptococcus pyogenes</i> . <i>BMC Structural Biology</i> , 2009, 9, 75. | 2.3 | 6 |
| 155 | Crystal Structures of Mite Allergens Der f 1 and Der p 1 Reveal Differences in Surface-Exposed Residues that May Influence Antibody Binding. <i>Journal of Molecular Biology</i> , 2009, 386, 520-530. | 2.0 | 79 |
| 156 | The Protein Structure Initiative Structural Genomics Knowledgebase. <i>FASEB Journal</i> , 2009, 23, 858.10. | 0.2 | 0 |
| 157 | Data mining of metal ion environments present in protein structures. <i>Journal of Inorganic Biochemistry</i> , 2008, 102, 1765-1776. | 1.5 | 273 |
| 158 | Targeting a Uniquely Nonspecific Prenyl Synthase with Bisphosphonates to Combat Cryptosporidiosis. <i>Chemistry and Biology</i> , 2008, 15, 1296-1306. | 6.2 | 39 |
| 159 | Analysis of solvent content and oligomeric states in protein crystals—does symmetry matter?. <i>Protein Science</i> , 2008, 17, 623-632. | 3.1 | 54 |
| 160 | Protein crystallography for non-crystallographers, or how to get the best (but not more) from published macromolecular structures. <i>FEBS Journal</i> , 2008, 275, 1-21. | 2.2 | 231 |
| 161 | Determination of Protein Structures—A Series of Fortunate Events. <i>Biophysical Journal</i> , 2008, 95, 1-9. | 0.2 | 128 |
| 162 | Synthesis and Solid-State Study of Supramolecular Host-Guest Assemblies: Bis[6-O,6-O-(1,2:3,4-diisopropylidene- β -D-galactopyranosyl)thiophosphoryl] Dichalcogenides. <i>Journal of Organic Chemistry</i> , 2008, 73, 4388-4397. | 1.7 | 11 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 163 | Structural Insight into the Mechanism of Substrate Specificity and Catalytic Activity of an HD-Domain Phosphohydrolase: The 5'-Deoxyribonucleotidase YfbR from Escherichia coli. <i>Journal of Molecular Biology</i> , 2008, 378, 215-226. | 2.0 | 62 |
| 164 | Crystal Structure of the MACPF Domain of Human Complement Protein C8 α in Complex with the C8 β Subunit. <i>Journal of Molecular Biology</i> , 2008, 379, 331-342. | 2.0 | 70 |
| 165 | Asymmetric Synthesis of 2,3-Dihydro-2-arylquinazolin-4-ones: Methodology and Application to a Potent Fluorescent Tubulin Inhibitor with Anticancer Activity. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 4620-4631. | 2.9 | 184 |
| 166 | Function-Biased Choice of Additives for Optimization of Protein Crystallization: The Case of the Putative Thioesterase PA5185 from <i>Pseudomonas aeruginosa</i> PAO1. <i>Crystal Growth and Design</i> , 2008, 8, 4054-4061. | 1.4 | 5 |
| 167 | A Novel Family of Sequence-specific Endoribonucleases Associated with the Clustered Regularly Interspaced Short Palindromic Repeats. <i>Journal of Biological Chemistry</i> , 2008, 283, 20361-20371. | 1.6 | 177 |
| 168 | Biochemical and Structural Characterization of Apolipoprotein A-I Binding Protein, a Novel Phosphoprotein with a Potential Role in Sperm Capacitation. <i>Endocrinology</i> , 2008, 149, 2108-2120. | 1.4 | 42 |
| 169 | 2,3-Difluorobenzoic acid. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2008, 64, o466-o466. | 0.2 | 3 |
| 170 | Phosphorylation Regulates SIRT1 Function. <i>PLoS ONE</i> , 2008, 3, e4020. | 1.1 | 244 |
| 171 | Crystal structure of a transcriptional regulator TM1030 from <i>Thermotoga maritima</i> solved by an unusual MAD experiment. <i>Journal of Structural Biology</i> , 2007, 159, 424-432. | 1.3 | 9 |
| 172 | Stacks of DMANH ⁺ scaffolding for ribbon shaped Cl ⁻ bridged oxonium ions. <i>CrystEngComm</i> , 2007, 9, 152-157. | 1.3 | 6 |
| 173 | 3-(1-Pyridinio)propanesulfonate and 3-(benzyltrimethylammonio)propanesulfonate monohydrate. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2007, 63, o114-o116. | 0.4 | 3 |
| 174 | An extremely SAD case: structure of a putative redox-enzyme maturation protein from <i>Archaeoglobus fulgidus</i> at 3.4 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 348-354. | 2.5 | 23 |
| 175 | The many faces of radiation-induced changes. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 24-33. | 1.0 | 48 |
| 176 | 3-(1-Methylpiperidinio)-1-propanesulfonate. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2007, 63, o282-o283. | 0.2 | 1 |
| 177 | N,N,N',N'-Tetrakis(carboxymethyl)-2,2'-(ethylenedioxy)dianilinium dichloride dihydrate. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2007, 63, o754-o756. | 0.2 | 1 |
| 178 | 2-(Biphenyl-4-yl)-2,3-dihydroquinazolin-4(1H)-one. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2007, 63, o891-o893. | 0.2 | 0 |
| 179 | 3-Iodo-L-tyrosine hemihydrate. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2007, 63, o1557-o1559. | 0.2 | 0 |
| 180 | 2-Amino-4-(4-chloro-3-methylphenyl)-5-propyl-1,3-thiazolium iodide. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2007, 63, o1598-o1600. | 0.2 | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 181 | trans-1-Hydroxycyclopentan-2-aminium chloride. Acta Crystallographica Section E: Structure Reports Online, 2007, 63, o2697-o2698. | 0.2 | 0 |
| 182 | Dexamethasone at 119 K. Acta Crystallographica Section E: Structure Reports Online, 2007, 63, o2791-o2793. | 0.2 | 13 |
| 183 | Absolute configuration from a redetermination of (+)-5-bromo-1-[(2R,4S,5R)-4-hydroxy-5-(hydroxymethyl)oxolan-2-yl]pyrimidine-2,4-dione at 118â€¦(2) K. Acta Crystallographica Section E: Structure Reports Online, 2007, 63, o4159-o4160. | 0.2 | 0 |
| 184 | In situ proteolysis for protein crystallization and structure determination. Nature Methods, 2007, 4, 1019-1021. | 9.0 | 197 |
| 185 | Structural genomics: keeping up with expanding knowledge of the protein universe. Current Opinion in Structural Biology, 2007, 17, 347-353. | 2.6 | 42 |
| 186 | Crystal Structure of RNase T, an Exoribonuclease Involved in tRNA Maturation and End Turnover. Structure, 2007, 15, 417-428. | 1.6 | 37 |
| 187 | Crystal structures of TM0549 and NE1324-two orthologs ofE. coliHAS isozyme III small regulatory subunit. Protein Science, 2007, 16, 1360-1367. | 3.1 | 17 |
| 188 | Kinetic, Spectroscopic, and Structural Investigations of the Soybean Lipoxygenase-1 First-Coordination Sphere Mutant, Asn694Glyâ€¦. Biochemistry, 2006, 45, 10233-10242. | 1.2 | 17 |
| 189 | Crystal Structure of Pseudomonas aeruginosa SPM-1 Provides Insights into Variable Zinc Affinity of Metallo-Î²-lactamases. Journal of Molecular Biology, 2006, 357, 890-903. | 2.0 | 88 |
| 190 | Crystal structure of 6-(4-difluoromethoxy-3-methoxyphenyl)-3(2H)- pyridazinone, C12H10F2N2O3. Zeitschrift Fur Kristallographie - New Crystal Structures, 2006, 221, 359-360. | 0.1 | 0 |
| 191 | Crystal structure of 2,6-dichlorobenzaldehyde, C7H4Cl2O. Zeitschrift Fur Kristallographie - New Crystal Structures, 2006, 221, 545-546. | 0.1 | 0 |
| 192 | HKL-3000: the integration of data reduction and structure solution " from diffraction images to an initial model in minutes. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 859-866. | 2.5 | 1,822 |
| 193 | Disodium 4-nitrophenylphosphate hexahydrate. Acta Crystallographica Section E: Structure Reports Online, 2006, 62, m884-m886. | 0.2 | 0 |
| 194 | 3-(Ethylidimethylammonio)propanesulfonate. Acta Crystallographica Section E: Structure Reports Online, 2006, 62, o5757-o5759. | 0.2 | 2 |
| 195 | The tetramer structure of the Neryv homology two domain, NHR2, is critical for AML1/ETO's activity. Cancer Cell, 2006, 9, 249-260. | 7.7 | 121 |
| 196 | Continua of Interactions between Pairs of Atoms in Molecular Crystals. Chemistry - A European Journal, 2006, 12, 1941-1949. | 1.7 | 73 |
| 197 | Map2mod-a server for evaluation of crystallographic models and their agreement with electron density maps. Bioinformatics, 2006, 22, 1660-1661. | 1.8 | 4 |
| 198 | DENZO and SCALEPACK. , 2006, , 226-235. | | 29 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 199 | Structure of human thymidylate synthase under low-salt conditions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 622-627. | 2.5 | 25 |
| 200 | 3-(Morpholinium-1-yl)propanesulfonate. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2005, 61, o3190-o3191. | 0.2 | 2 |
| 201 | Double chromodomains cooperate to recognize the methylated histone H3 tail. <i>Nature</i> , 2005, 438, 1181-1185. | 13.7 | 484 |
| 202 | The structural genomics experimental pipeline: Insights from global target lists. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 201-210. | 1.5 | 36 |
| 203 | L-Methioninium chloride and L-selenomethioninium chloride at 103 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2004, 60, o868-o871. | 0.4 | 3 |
| 204 | Harvesting the high-hanging fruit: the structure of the YdeN gene product from <i>Bacillus subtilis</i> at 1.8 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1101-1107. | 2.5 | 23 |
| 205 | Expression, Purification and the 1.8 Å Resolution Crystal Structure of Human Neuron Specific Enolase. <i>Journal of Molecular Biology</i> , 2004, 341, 1015-1021. | 2.0 | 53 |
| 206 | Structural and Functional Characterization of the NHR2 and Runt Domains of AML1/ETO. <i>Blood</i> , 2004, 104, 482-482. | 0.6 | 1 |
| 207 | Multiparametric scaling of diffraction intensities. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2003, 59, 228-234. | 0.3 | 623 |
| 208 | Measurement errors and their consequences in protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2031-2038. | 2.5 | 59 |
| 209 | Crystal Structure of Human Complement Protein C8 β at 1.2 Å Resolution Reveals a Lipocalin Fold and a Distinct Ligand Binding Site. <i>Biochemistry</i> , 2002, 41, 7030-7037. | 1.2 | 41 |
| 210 | Structure of <i>Bacillus subtilis</i> YXKOA member of the UPF0031 family and a putative kinase. <i>Journal of Structural Biology</i> , 2002, 139, 161-170. | 1.3 | 19 |
| 211 | Structural and Functional Characterization of Second-Coordination Sphere Mutants of Soybean Lipoxygenase-1. <i>Biochemistry</i> , 2001, 40, 7509-7517. | 1.2 | 120 |
| 212 | Human Thymidylate Synthase Is in the Closed Conformation When Complexed with dUMP and Raltitrexed, an Antifolate Drug. <i>Biochemistry</i> , 2001, 40, 1897-1902. | 1.2 | 100 |
| 213 | Using surface-bound rubidium ions for protein phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1008-1012. | 2.5 | 9 |
| 214 | Structure of Human Thymidylate Synthase Suggests Advantages of Chemotherapy with Noncompetitive Inhibitors. <i>Journal of Biological Chemistry</i> , 2001, 276, 14170-14177. | 1.6 | 67 |
| 215 | Strategies for macromolecular synchrotron crystallography. <i>Structure</i> , 2000, 8, R105-R110. | 1.6 | 73 |
| 216 | The Crystal Structure of N10-Formyltetrahydrofolate Synthetase from <i>Moorella thermoacetica</i> . <i>Biochemistry</i> , 2000, 39, 3920-3926. | 1.2 | 27 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 217 | Cation Binding and Thermostability of FTHFS Monovalent Cation Binding Sites and Thermostability of N10-Formyltetrahydrofolate Synthetase from <i>Moorella thermoacetica</i> ., <i>Biochemistry</i> , 2000, 39, 14481-14486. | 1.2 | 16 |
| 218 | Catalytic Cysteine of Thymidylate Synthase Is Activated upon Substrate Binding. <i>Biochemistry</i> , 2000, 39, 6969-6978. | 1.2 | 20 |
| 219 | Structure of a microbial homologue of mammalian platelet-activating factor acetylhydrolases: <i>Streptomyces exfoliatus</i> lipase at 1.9 Å resolution. <i>Structure</i> , 1998, 6, 511-519. | 1.6 | 107 |
| 220 | Uncovering a Calcium-Regulated Membrane-Binding Mechanism for Soybean Lipoxygenase-1. <i>Biochemistry</i> , 1998, 37, 15481-15490. | 1.2 | 53 |
| 221 | Mechanism of Enolase: The Crystal Structure of Asymmetric Dimer Enolase ² -Phospho-d-glycerate/Enolase ² -Phosphoenolpyruvate at 2.0 Å... Resolution. <i>Biochemistry</i> , 1997, 36, 12526-12534. | 1.2 | 115 |
| 222 | [20] Processing of X-ray diffraction data collected in oscillation mode. <i>Methods in Enzymology</i> , 1997, 276, 307-326. | 0.4 | 30,205 |
| 223 | Crystal structure of RhoA-GDP and its functional implications. <i>Nature Structural Biology</i> , 1997, 4, 699-703. | 9.7 | 158 |
| 224 | Crystal Structure of Soybean Lipoxygenase L-1 at 1.4 Å... Resolution. <i>Biochemistry</i> , 1996, 35, 10687-10701. | 1.2 | 416 |
| 225 | Crystallization and preliminary X-ray analysis of the cytoplasmic domain of human erythrocyte band 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 293-297. | 1.5 | 9 |
| 226 | Crystallization and preliminary X-ray investigation of lipoxygenase-3 from soybeans. <i>Protein Science</i> , 1995, 4, 1233-1235. | 3.1 | 2 |
| 227 | Crystallization at low salt concentration and alkaline pH and preliminary crystallographic data for a monoclinic form of yeast enolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994, 50, 335-336. | 2.5 | 1 |
| 228 | Crystallographic determination of the active site iron and its ligands in soybean lipoxygenase L-1. <i>Biochemistry</i> , 1993, 32, 6320-6323. | 1.2 | 162 |
| 229 | The structure determination of Sindbis virus core protein using isomorphous replacement and molecular replacement averaging between two crystal forms. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1992, 48, 430-442. | 0.3 | 17 |
| 230 | Removal of salt from a salt-induced protein crystal without cross-linking. Preliminary examination of "desalted" crystals of phosphoglucomutase by x-ray crystallography at low temperature. <i>Biochemistry</i> , 1991, 30, 6866-6875. | 1.2 | 19 |
| 231 | Structure of Sindbis virus core protein reveals a chymotrypsin-like serine proteinase and the organization of the virion. <i>Nature</i> , 1991, 354, 37-43. | 13.7 | 329 |
| 232 | Crystallization and preliminary structure analysis of an insect virus with T=4 quasi-symmetry: <i>Nudaurelia capensis</i> virus. <i>Acta Crystallographica Section B: Structural Science</i> , 1991, 47, 23-29. | 1.8 | 22 |
| 233 | Antiferromagnetic states in $\text{CoMg}_{1-x}\text{PO}$ (abstract). <i>Journal of Applied Physics</i> , 1990, 67, 5990-5990. | 1.1 | 0 |
| 234 | Phason velocities in TaS_2 by x-ray diffuse scattering. <i>Physical Review B</i> , 1989, 39, 1360-1362. | 1.1 | 7 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 235 | STUDIES OF FCC HEISENBERG ANTIFERROMAGNETS BY MONTE CARLO SIMULATION ON LARGE SPIN ARRAYS. Journal De Physique Colloque, 1988, 49, C8-1551-C8-1552. | 0.2 | 12 |
| 236 | Crystallization of Fe-Si-B metallic glasses studied by X-ray synchrotron radiation. Journal of Materials Science, 1987, 22, 4144-4152. | 1.7 | 16 |
| 237 | High temperature behaviour of spin waves in Fe _{3-x} MnxSi. Solid State Communications, 1986, 57, 47-51. | 0.9 | 5 |
| 238 | Neutron scattering studies of Cd _{1-x} MnxTe (invited). Journal of Applied Physics, 1984, 55, 2305-2309. | 1.1 | 39 |
| 239 | Spin waves in Fe _{1-x} Al _x Si system. Solid State Communications, 1983, 46, 217-219. | 0.9 | 10 |
| 240 | Neutron Scattering Studies of the "Antiferromagnetic Phase" of Cd _{1-x} MnxTe. Physica Scripta, 1982, 25, 731-734. | 1.2 | 6 |
| 241 | A phenomenological description of the paramagnet-antiferromagnet transition in Cd _{1-x} MnxTe. Journal of Magnetism and Magnetic Materials, 1982, 30, 215-222. | 1.0 | 11 |
| 242 | Spin waves in Fe _{3-x} MnxSi ordered alloys. Solid State Communications, 1981, 38, 773-775. | 0.9 | 3 |
| 243 | Secondary extinction in rotating single-crystal slabs. The Acta Crystallographica Section A, Crystal Physics, Diffractionoretical and General Crystallography, 1979, 35, 861-870. | 0.6 | 0 |
| 244 | A simple method of orientating single crystals on time-of-flight neutron spectrometers. Nuclear Instruments & Methods, 1974, 119, 141-144. | 1.2 | 0 |
| 245 | Explanation of neutron diffraction phenomena observed in vibrating piezoelectric crystals. Physica Status Solidi A, 1972, 9, 423-433. | 1.7 | 12 |
| 246 | Spinning single crystal tof method for structure analysis. Nuclear Instruments & Methods, 1970, 77, 13-20. | 1.2 | 6 |