

# Dietmar Schomburg

## List of Publications by Year in descending order

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258  
papers

15,031  
citations

23567

58  
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23533

111  
g-index

286  
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286  
docs citations

286  
times ranked

18775  
citing authors

#	ARTICLE	IF	CITATIONS
1	QMEAN: A comprehensive scoring function for model quality assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 261-277.	2.6	888
2	BRENDA, the enzyme database: updates and major new developments. <i>Nucleic Acids Research</i> , 2004, 32, 431D-433.	14.5	679
3	BRENDA, enzyme data and metabolic information. <i>Nucleic Acids Research</i> , 2002, 30, 47-49.	14.5	606
4	GC-MS libraries for the rapid identification of metabolites in complex biological samples. <i>FEBS Letters</i> , 2005, 579, 1332-1337.	2.8	596
5	CUPSAT: prediction of protein stability upon point mutations. <i>Nucleic Acids Research</i> , 2006, 34, W239-W242.	14.5	572
6	MetaboliteDetector: Comprehensive Analysis Tool for Targeted and Nontargeted GC/MS Based Metabolome Analysis. <i>Analytical Chemistry</i> , 2009, 81, 3429-3439.	6.5	407
7	BRENDA, the enzyme information system in 2011. <i>Nucleic Acids Research</i> , 2011, 39, D670-D676.	14.5	382
8	BRENDA in 2013: integrated reactions, kinetic data, enzyme function data, improved disease classification: new options and contents in BRENDA. <i>Nucleic Acids Research</i> , 2012, 41, D764-D772.	14.5	358
9	BRENDA, the ELIXIR core data resource in 2021: new developments and updates. <i>Nucleic Acids Research</i> , 2021, 49, D498-D508.	14.5	347
10	BRENDA in 2019: a European ELIXIR core data resource. <i>Nucleic Acids Research</i> , 2019, 47, D542-D549.	14.5	335
11	BRENDA, AMENDA and FRENDA the enzyme information system: new content and tools in 2009. <i>Nucleic Acids Research</i> , 2009, 37, D588-D592.	14.5	331
12	Phylogenomics of <i>Rhodobacteraceae</i> reveals evolutionary adaptation to marine and non-marine habitats. <i>ISME Journal</i> , 2017, 11, 1483-1499.	9.8	283
13	The open conformation of a <i>Pseudomonas</i> lipase. <i>Structure</i> , 1997, 5, 187-202.	3.3	275
14	1.8 and 1.9 Å resolution structures of the <i>Penicillium amagasakiense</i> and <i>Aspergillus niger</i> glucose oxidases as a basis for modelling substrate complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 969-977.	2.5	264
15	BRENDA in 2017: new perspectives and new tools in BRENDA. <i>Nucleic Acids Research</i> , 2017, 45, D380-D388.	14.5	251
16	BRENDA in 2015: exciting developments in its 25th year of existence. <i>Nucleic Acids Research</i> , 2015, 43, D439-D446.	14.5	183
17	GTP plus water mimic ATP in the active site of protein kinase CK2. <i>Nature Structural Biology</i> , 1999, 6, 1100-1103.	9.7	176
18	BRENDA: a resource for enzyme data and metabolic information. <i>Trends in Biochemical Sciences</i> , 2002, 27, 54-56.	7.5	172

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19	IntEnz, the integrated relational enzyme database. <i>Nucleic Acids Research</i> , 2004, 32, 434D-437.	14.5	160
20	The BRENDA Tissue Ontology (BTO): the first all-integrating ontology of all organisms for enzyme sources. <i>Nucleic Acids Research</i> , 2011, 39, D507-D513.	14.5	153
21	BRENDA, AMENDA and FRENDA: the enzyme information system in 2007. <i>Nucleic Acids Research</i> , 2007, 35, D511-D514.	14.5	140
22	How <i>Pseudomonas aeruginosa</i> adapts to various environments: a metabolomic approach. <i>Environmental Microbiology</i> , 2010, 12, 1734-1747.	3.8	139
23	The substrate specificity-determining amino acid code of 4-coumarate:CoA ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8601-8606.	7.1	137
24	Atomic Resolution Structures of R-specific Alcohol Dehydrogenase from <i>Lactobacillus brevis</i> Provide the Structural Bases of its Substrate and Cosubstrate Specificity. <i>Journal of Molecular Biology</i> , 2005, 349, 801-813.	4.2	135
25	Crystal Structure of a Bacterial Lipase from <i>Chromobacterium viscosum</i> ATCC 6918 Refined at 1.6 Å Resolution. <i>Journal of Molecular Biology</i> , 1996, 259, 704-717.	4.2	133
26	The Structure of an Inverting GH43 $\beta$ -Xylosidase from <i>Geobacillus stearothermophilus</i> with its Substrate Reveals the Role of the Three Catalytic Residues. <i>Journal of Molecular Biology</i> , 2006, 359, 97-109.	4.2	132
27	Time-resolved amino acid uptake of <i>Clostridium difficile</i> 630 <sup>Herm</sup> and concomitant fermentation product and toxin formation. <i>BMC Microbiology</i> , 2015, 15, 281.	3.3	132
28	Growth phase-dependent global protein and metabolite profiles of <i>Phaeobacter gallaeciensis</i> strain DSM 17395, a member of the marine <i>Roseobacter</i> clade. <i>Proteomics</i> , 2009, 9, 3677-3697.	2.2	128
29	Crystal structure and snapshots along the reaction pathway of a family 51 $\beta$ -L-arabinofuranosidase. <i>EMBO Journal</i> , 2003, 22, 4922-4932.	7.8	127
30	The Crystal Structure of R-specific Alcohol Dehydrogenase from <i>Lactobacillus brevis</i> Suggests the Structural Basis of its Metal Dependency. <i>Journal of Molecular Biology</i> , 2003, 327, 317-328.	4.2	121
31	The metabolic response of <i>P. putida</i> KT2442 producing high levels of polyhydroxyalkanoate under single- and multiple-nutrient-limited growth: Highlights from a multi-level omics approach. <i>Microbial Cell Factories</i> , 2012, 11, 34.	4.0	117
32	Manual curation and reannotation of the genomes of <i>Clostridium difficile</i> 630 <sup>Herm</sup> and <i>C. difficile</i> 630. <i>Journal of Medical Microbiology</i> , 2017, 66, 286-293.	1.8	117
33	Metabolic pathway analysis web service (Pathway Hunter Tool at CUBIC). <i>Bioinformatics</i> , 2005, 21, 1189-1193.	4.1	115
34	Comprehensive analysis of metabolites in <i>Corynebacterium glutamicum</i> by gas chromatography/mass spectrometry. <i>Biological Chemistry</i> , 2004, 385, 853-861.	2.5	114
35	Prediction of Protein Three-dimensional Structures in Insertion and Deletion Regions: A Procedure for Searching Data Bases of Representative Protein Fragments Using Geometric Scoring Criteria. <i>Journal of Molecular Biology</i> , 1995, 253, 114-131.	4.2	111
36	Antibiotics from Gliding Bacteria, LIV. Isolation and Structure Elucidation of Soraphen A1 $\pm$ , a Novel Antifungal Macrolide from <i>Sorangium cellulosum</i> . <i>Liebigs Annalen Der Chemie</i> , 1993, 1993, 1017-1021.	0.8	106

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37	Observing local and global properties of metabolic pathways: "load points"™ and "choke points"™ in the metabolic networks. <i>Bioinformatics</i> , 2006, 22, 1767-1774.	4.1	102
38	BRAGI: A comprehensive protein modeling program system. <i>Journal of Molecular Graphics</i> , 1988, 6, 161-165.	1.1	101
39	Hydrogen Bonding and Molecular Surface Shape Complementarity as a Basis for Protein Docking. <i>Journal of Molecular Biology</i> , 1996, 264, 199-210.	4.2	101
40	Closely related <i>Campylobacter jejuni</i> strains from different sources reveal a generalist rather than a specialist lifestyle. <i>BMC Genomics</i> , 2011, 12, 584.	2.8	101
41	Effects of carbohydrate depletion on the structure, stability and activity of glucose oxidase from <i>Aspergillus niger</i> . <i>BBA - Proteins and Proteomics</i> , 1991, 1080, 138-142.	2.1	98
42	Biochemical Characterization and Identification of the Catalytic Residues of a Family 43 $\beta$ -D-Xylosidase from <i>Geobacillus stearothermophilus</i> . <i>Biochemistry</i> , 2005, 44, 387-397.	2.5	93
43	Investigation of the solution structure of the human parathyroid hormone fragment (1-34) by proton NMR spectroscopy, distance geometry, and molecular dynamics calculations. <i>Biochemistry</i> , 1991, 30, 6936-6942.	2.5	91
44	X-ray Structure of a Dihydropyrimidinase from <i>Thermus</i> sp. at 1.3Å... Resolution. <i>Journal of Molecular Biology</i> , 2002, 320, 143-156.	4.2	87
45	Crystal Structure of $\beta$ -Hydantoinase from <i>Bacillus stearothermophilus</i> : Insight into the Stereochemistry of Enantioselectivity. <i>Biochemistry</i> , 2002, 41, 9410-9417.	2.5	87
46	Crystallization and preliminary X-ray diffraction studies of a deglycosylated glucose oxidase from <i>Aspergillus niger</i> . <i>Journal of Molecular Biology</i> , 1990, 213, 207-209.	4.2	74
47	The Structure of a Bacterial L-Amino Acid Oxidase from <i>Rhodococcus opacus</i> Gives New Evidence for the Hydride Mechanism for Dehydrogenation. <i>Journal of Molecular Biology</i> , 2007, 367, 234-248.	4.2	71
48	A systems biology approach reveals major metabolic changes in the thermoacidophilic archaeon <i>Sulfolobus solfataricus</i> in response to the carbon source L-xylose versus D-glucose. <i>Molecular Microbiology</i> , 2016, 102, 882-908.	2.5	69
49	The Crucial Role of Trehalose and Structurally Related Oligosaccharides in the Biosynthesis and Transfer of Mycolic Acids in <i>Corynebacterineae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 26573-26585.	3.4	67
50	Crp Induces Switching of the CsrB and CsrC RNAs in <i>Yersinia pseudotuberculosis</i> and Links Nutritional Status to Virulence. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 158.	3.9	67
51	Similarities between protein 3-D structures. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 1175-1187.	2.1	66
52	Intraclonal diversity of the <i>Pseudomonas aeruginosa</i> cystic fibrosis airway isolates TBCF10839 and TBCF121838: distinct signatures of transcriptome, proteome, metabolome, adherence and pathogenicity despite an almost identical genome sequence. <i>Environmental Microbiology</i> , 2013, 15, 191-210.	3.8	66
53	Standards for Reporting Enzyme Data: The STRENDA Consortium: What it aims to do and why it should be helpful. <i>Perspectives in Science</i> , 2014, 1, 131-137.	0.6	65
54	Molecular Analysis of Laminin N-terminal Domains Mediating Self-interactions. <i>Journal of Biological Chemistry</i> , 2004, 279, 44504-44512.	3.4	64

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55	Solution structure of the hydrophilic region of HIV-1 encoded virus protein U (Vpu) by CD and <sup>1</sup> H NMR spectroscopy. International Journal of Peptide and Protein Research, 1995, 45, 35-43.	0.1	64
56	<i>Clostridioides difficile</i> 6301 <sup>erm</sup> in silico and in vivo quantitative growth and extensive polysaccharide secretion. FEBS Open Bio, 2017, 7, 602-615.	2.3	64
57	Structural analysis and prediction of protein mutant stability using distance and torsion potentials: Role of secondary structure and solvent accessibility. Proteins: Structure, Function and Bioinformatics, 2006, 66, 41-52.	2.6	61
58	A method for enzyme quenching in microbial metabolome analysis successfully applied to gram-positive and gram-negative bacteria and yeast. Analytical Biochemistry, 2009, 394, 192-201.	2.4	61
59	The Structure of l-Hydantoinase from <i>Arthobacter aurescens</i> Leads to an Understanding of Dihydropyrimidinase Substrate and Enantio Specificity. Biochemistry, 2002, 41, 8589-8597.	2.5	59
60	Crystal structure of a ternary complex of d-2-hydroxyisocaproate dehydrogenase from <i>Lactobacillus casei</i> , NAD <sup>+</sup> and 2-oxoisocaproate at 1.9 Å... resolution 1.1 Edited by R. Huber. Journal of Molecular Biology, 1997, 267, 640-660.	4.2	58
61	Solution structure of the cytoplasmic domain of the human immunodeficiency virus type 1 encoded virus protein U (Vpu). International Journal of Peptide and Protein Research, 1996, 47, 297-310.	0.1	57
62	BKM-react, an integrated biochemical reaction database. BMC Biochemistry, 2011, 12, 42.	4.4	56
63	Phosphorus derivatives of anthracene and their dimers. Chemische Berichte, 1992, 125, 2187-2197.	0.2	55
64	Hot standards for the thermoacidophilic archaeon <i>Sulfolobus solfataricus</i> . Extremophiles, 2010, 14, 119-142.	2.3	55
65	Amino acid similarity coefficients for protein modeling and sequence alignment derived from main-chain folding angles. Journal of Molecular Biology, 1991, 219, 481-497.	4.2	53
66	Glycosynthase Activity of <i>Geobacillus stearothermophilus</i> GH52 Xylosidase: Efficient Synthesis of Xylooligosaccharides from D-Xylopyranosyl Fluoride through a Conjugated Reaction. ChemBioChem, 2007, 8, 2145-2151.	2.6	52
67	Aspects of the mechanism of catalysis of glucose oxidase: a docking, molecular mechanics and quantum chemical study. Journal of Computer-Aided Molecular Design, 1998, 12, 425-440.	2.9	51
68	SYSTEMONAS -- an integrated database for systems biology analysis of <i>Pseudomonas</i> . Nucleic Acids Research, 2007, 35, D533-D537.	14.5	50
69	EnzymeDetector: an integrated enzyme function prediction tool and database. BMC Bioinformatics, 2011, 12, 376.	2.6	50
70	Prediction of protein thermostability with a direction- and distance-dependent knowledge-based potential. Protein Science, 2005, 14, 2682-2692.	7.6	49
71	Human Embryonic Stem Cells and Embryonal Carcinoma Cells Have Overlapping and Distinct Metabolic Signatures. PLoS ONE, 2012, 7, e39896.	2.5	45
72	Adaptation of <i>Haemobacter inhibens</i> DSM 17395 to growth with complex nutrients. Proteomics, 2013, 13, 2851-2868.	2.2	45

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73	Polysulfonyleamine. XL Darstellung von Silber(I)-disulfonyleamid-Acetonitril-Komplexen. Röntgenstrukturanalytische und thermochemische Charakterisierung von Tetraacetonitrilsilber(I)-bis(dimethylamido)argentat(I) und von (1,1,3,3-Tetraoxo-1,3,2-benzodithiazolido)acetonitrilsilber(I). Zeitschrift Fur Anorganische Und Allgemeine Chemie, 1993, 619, 912-922.	1.2	44
74	Genome-Scale Reconstruction and Analysis of the Metabolic Network in the Hyperthermophilic Archaeon Sulfolobus Solfataricus. PLoS ONE, 2012, 7, e43401.	2.5	44
75	Preparation and Structure of a Diphosphorus Compound with Positive Charges on the Two Directly Bonded Phosphorus Atoms. Angewandte Chemie International Edition in English, 1985, 24, 975-976.	4.4	43
76	Isolation and structure elucidation of hymatoxins B - E and other phytotoxins from Hypoxylon mammatum fungal pathogen of leuce poplars. Tetrahedron, 1991, 47, 8351-8360.	1.9	40
77	Enzyme data and metabolic information: BRENDA, a resource for research in biology, biochemistry, and medicine. Gene Function & Disease, 2000, 1, 109-118.	0.3	40
78	A combination of metabolome and transcriptome analyses reveals new targets of the Corynebacterium glutamicum nitrogen regulator AmtR. Journal of Biotechnology, 2009, 140, 68-74.	3.8	39
79	Unexpected Active-Site Flexibility in the Structure of Human Neutrophil Elastase in Complex with a New Dihydropyrimidone Inhibitor. Journal of Molecular Biology, 2011, 409, 681-691.	4.2	39
80	A high-throughput method for microbial metabolome analysis using gas chromatography/mass spectrometry. Analytical Biochemistry, 2007, 367, 143-151.	2.4	38
81	STRENDAB: enabling the validation and sharing of enzyme kinetics data. FEBS Journal, 2018, 285, 2193-2204.	4.7	38
82	Conserved arginine-516 of Penicillium amagasakiense glucose oxidase is essential for the efficient binding of D-glucose. Biochemical Journal, 2000, 347, 553.	3.7	36
83	Regulatory and Metabolic Networks for the Adaptation of Pseudomonas aeruginosa Biofilms to Urinary Tract-Like Conditions. PLoS ONE, 2013, 8, e71845.	2.5	36
84	Carbohydrate Catabolism in Phaeobacter inhibens DSM 17395, a Member of the Marine Roseobacter Clade. Applied and Environmental Microbiology, 2014, 80, 4725-4737.	3.1	35
85	Cyclophanes-XXV. Tetrahedron, 1986, 42, 1655-1663.	1.9	34
86	Computational modeling of protein mutant stability: analysis and optimization of statistical potentials and structural features reveal insights into prediction model development. BMC Structural Biology, 2007, 7, 54.	2.3	34
87	Native plasmids restrict growth of Phaeobacter inhibens DSM 17395: Energetic costs of plasmids assessed by quantitative physiological analyses. Environmental Microbiology, 2016, 18, 4817-4829.	3.8	34
88	[P4Aryl6][Me3SnF2]2 (Aryl = 2,6-(MeO)2C6H3): An Unusual Ion Pair Consisting of a Planar 2,4-Diphospho-1,3-diphosphoniacyclobutane Dication and the Difluorotrimethylstannate Anion. Angewandte Chemie International Edition in English, 1989, 28, 1507-1509.	4.4	33
89	Crystal Structure of Full Length Topoisomerase I from Thermotoga maritima. Journal of Molecular Biology, 2006, 358, 1328-1340.	4.2	33
90	Contribution of Amino Acid Catabolism to the Tissue Specific Persistence of Campylobacter jejuni in a Murine Colonization Model. PLoS ONE, 2012, 7, e50699.	2.5	33

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91	Utilization of host-derived cysteine-containing peptides overcomes the restricted sulphur metabolism of <i>Campylobacter jejuni</i> . <i>Molecular Microbiology</i> , 2014, 93, 1224-1245.	2.5	33
92	Comprehensive molecular, genomic and phenotypic analysis of a major clone of <i>Enterococcus faecalis</i> MLST ST40. <i>BMC Genomics</i> , 2015, 16, 175.	2.8	33
93	Preparation of ortho-substituted aryldifluorophosphines, 2- $\text{XC}_6\text{H}_4\text{PF}_2$ (X = MeO or Me <sub>2</sub> N), and some of their derivatives. X-ray crystal structure determination of (2-MeOC <sub>6</sub> H <sub>4</sub> P) <sub>4</sub> and of the platinum complex, Cl <sub>2</sub> Pt(2-MeOC <sub>6</sub> H <sub>4</sub> PF <sub>2</sub> ) <sub>2</sub> . <i>Polyhedron</i> , 1987, 6, 1295-1307.	2.2	31
94	Stereoselective microbial reduction of racemic acetyl(t-butyl)methylphenylsilane by <i>Trigonopsis variabilis</i> (DSM 70714) and <i>Cornebacterium dioxydans</i> (ATCC 2176). <i>Journal of Organometallic Chemistry</i> , 1991, 403, 29-41.	1.8	31
95	Structural base of the interaction of a monoclonal antibody against p24 of HIV-1 with its peptide epitope. <i>Molecular Immunology</i> , 1993, 30, 1213-1221.	2.2	31
96	NMR Spectroscopic Evidence That Helodermin, unlike Other Members of the Secretin/VIP Family of Peptides, Is Substantially Structured in Water. <i>Biochemistry</i> , 1996, 35, 5955-5962.	2.5	30
97	Antibiotika aus Gleitenden Bakterien, XXXVII. Sorangicin A, ein hochwirksames Antibiotikum mit neuartiger Makrolid-Polyether-Struktur aus <i>Sorangium cellulosum</i> , So ce12: Spektroskopische Strukturaufklärung, Kristall- und Lösungsstruktur. <i>Liebigs Annalen Der Chemie</i> , 1989, 1989, 111-119.	0.8	29
98	Fixation of CO <sub>2</sub> using the ethylmalonyl-CoA pathway in the photoheterotrophic marine bacterium <i>Dinoroseobacter shibae</i> . <i>Environmental Microbiology</i> , 2017, 19, 2645-2660.	3.8	29
99	Importance of anchor group positioning in protein loop prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 56-64.	2.6	28
100	Investigation of the influence of charge derivatization on the fragmentation of multiply protonated peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 47-58.	2.8	28
101	Expression, purification, and aggregation studies of His-tagged thermoalkalophilic lipase from <i>Bacillus thermocatenuatus</i> . <i>Protein Expression and Purification</i> , 2004, 34, 103-110.	1.3	28
102	Pathways and substrate-specific regulation of amino acid degradation in <i>Proteobacterium</i> <i>inhibens</i> (DSM 17395 (archetype of the marine <i>Roseobacter</i> clade). <i>Environmental Microbiology</i> , 2014, 16, 218-238.	3.8	28
103	Ansa-Steroids. <i>Tetrahedron Letters</i> , 1985, 26, 1705-1706.	1.4	27
104	Automatic Assignment of EC Numbers. <i>PLoS Computational Biology</i> , 2010, 6, e1000661.	3.2	27
105	A transferable plasticity region in <i>Campylobacter coli</i> allows isolates of an otherwise non-glycolytic foodborne pathogen to catabolize glucose. <i>Molecular Microbiology</i> , 2015, 98, 809-830.	2.5	26
106	Antibiotika aus Gleitenden Bakterien, XXVII. Angiolam A – ein neues Antibiotikum aus <i>Angiococcus disciformis</i> (Myxobacterales). <i>Liebigs Annalen Der Chemie</i> , 1985, 1985, 2088-2097.	0.8	25
107	The synthesis and the crystal and molecular structure of the fungicide bis(4-fluorophenyl)-methyl(1H-1,2,4-triazol-1-yl-methyl)silane (flusilazole, DPX H 6573). <i>Applied Organometallic Chemistry</i> , 1989, 3, 133-139.	3.5	25
108	Inhibition of <i>Streptomyces griseus</i> aminopeptidase and effects of calcium ions on catalysis and binding. Comparisons with the homologous enzyme <i>Aeromonas proteolytica</i> aminopeptidase. <i>FEBS Journal</i> , 1998, 258, 313-319.	0.2	25



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109	SulfoSYS (Sulfolobus Systems Biology): towards a silicon cell model for the central carbohydrate metabolism of the archaeon Sulfolobus solfataricus under temperature variation. Biochemical Society Transactions, 2009, 37, 58-64.	3.4	25
110	Gene Regulatory and Metabolic Adaptation Processes of Dinoroseobacter shibae DFL12T during Oxygen Depletion. Journal of Biological Chemistry, 2014, 289, 13219-13231.	3.4	25
111	Synthesis and Crystal Structure Determination of a $\lambda^3\text{P}^5$ P-Phosphorane of a Novel Type. Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences, 1983, 38, 702-704.	0.7	24
112	Dienes as chiral templates. Tetrahedron Letters, 1986, 27, 5833-5834.	1.4	24
113	MOLEKÜLSTRUKTUR EINES STABILEN PENTAOXY-SPIROPHOSPHORANS MIT PHOSPHOR ALS BRÜCKENKOPFATOM ZWISCHEN EINEM SECHSGLIEDRIGEN UND EINEM FÜNFGLIEDRIGEN RING. Phosphorous and Sulfur and the Related Elements, 1988, 35, 241-246.	0.2	24
114	'Isotopo' a database application for facile analysis and management of mass isotopomer data. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau077-bau077.	3.0	24
115	Efficient comprehensive scoring of docked protein complexes using probabilistic support vector machines. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1367-1378.	2.6	23
116	Notizen: Molekülstruktur von Bis[tris(diäthylamido)-titano]-ferrocen / Molecular Structure of Bis[tris(diethylamido)-titano]-ferrocene. Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences, 1975, 30, 636-636.	0.7	22
117	Cyclophanes, XXXV. DNMR, molecular mechanics, and crystal structures of 2,11-ärdithia[3.3]orthometacyclophane and 2,11-ärdithia[3.3]orthoparacyclophane. Chemische Berichte, 1990, 123, 2381-2386.	0.2	22
118	Large-scale production, purification and refolding of the full-length cellular prion protein from Syrian golden hamster in Escherichia coli using the glutathione S-transferase-fusion system. FEBS Journal, 1998, 251, 462-471.	0.2	22
119	Expression, purification and crystallization of the catalytic subunit of protein kinase CK2 from Zea mays. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 143-145.	2.5	22
120	The importance of uniformity in reporting protein-function data. Trends in Biochemical Sciences, 2005, 30, 11-12.	7.5	22
121	A large-scale protein-function database. Nature Chemical Biology, 2010, 6, 785-785.	8.0	22
122	Dynamics of amino acid utilization in <i>Halobacter salinarum</i> DSM 17395. Proteomics, 2013, 13, 2869-2885.	2.2	22
123	<i>Pentacoordiniertes Silicium: Intramolekulare Koordination bei O-Fluorsilylderivaten von N,N-disubstituierten Aminoethanolen bzw. N-fluorsilylsubstituierten Derivaten des Trimethylethylendiamins/Penta-co-ordinate Silicon: Intramolecular Coordination of O-Fluorosilyl Derivatives of N,N-Disubstituted Aminoethanols and of N-Fluorosilyl Substituted Derivatives of Trimethylethylendiamine. Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences</i>	0.7	21
124	Über die Umsetzung von N- bzw. O-trimethylsilylierten Derivaten des Ethanolamins mit Phosphor(III)-Halogen-Verbindungen: Intramolekulare Donator-Akzeptor-Wechselwirkungen in den Verbindungen $\text{CH}_3\text{OCH}_2\text{CH}_2\text{N}(\text{CH}_3)\text{PCl}_2$ , $(\text{CH}_3)_2\text{NCH}_2\text{CH}_2\text{OPCl}_2$ , $(\text{CH}_3)_2\text{NCH}_2\text{CH}_2\text{N}(\text{CH}_3)\text{P}(\text{C}_6\text{H}_5)_2$ , $(\text{CH}_3)_2\text{NCH}_2\text{CH}_2\text{N}(\text{CH}_3)\text{P}(\text{C}_6\text{H}_5)\text{Cl}$ und $(\text{CH}_3)_2\text{NCH}_2\text{CH}_2\text{N}(\text{CH}_3)\text{PCl}_2$ . Phosphorous and Sulfur and the Related Elements, 1986, 28, 327-336.	0.2	21
125	A flexible hydroazulene synthesis. Tetrahedron, 1988, 44, 4371-4388.	1.9	21
126	Antibiotics from Gliding Bacteria, LII. Thiangazole, a New Tris(thiazoline) Derivative From <i>Polyangium speciosum</i> : Absolute Configuration. Liebigs Annalen Der Chemie, 1993, 1993, 701-704.	0.8	21



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