Dietmar Schomburg

List of Publications by Year
in descending order

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258 papers	15,031 citations	23567 58 h-index	23533 111 g-index

286 all docs	286 docs citations	286 times ranked	18775 citing authors

#	Article	IF	Citations
1	Complex and flexible catabolism in Aromatoleum aromaticumâ€‰<scp>pCyN1</scp>. Environmental Microbiology, 2022, 24, 3195-3211.	3.8	4
2	The Metano Modeling Toolbox MMTB: An Intuitive, Web-Based Toolbox Introduced by Two Use Cases. Metabolites, 2021, 11, 113.	2.9	2
3	Influence of L-lactate and low glucose concentrations on the metabolism and the toxin formation of Clostridioides difficile. PLoS ONE, 2021, 16, e0244988.	2.5	13
4	BRENDA, the ELIXIR core data resource in 2021: new developments and updates. Nucleic Acids Research, 2021, 49, D498-D508.	14.5	347
5	Utilization of Phenol as Carbon Source by the Thermoacidophilic Archaeon Saccharolobus solfataricus P2 Is Limited by Oxygen Supply and the Cellular Stress Response. Frontiers in Microbiology, 2020, 11, 587032.	3.5	2
6	MetaboMAPS: Pathway sharing and multi-omics data visualization in metabolic context. F1000Research, 2020, 9, 288.	1.6	8
7	MetaboMAPS: Pathway sharing and multi-omics data visualization in metabolic context. F1000Research, 2020, 9, 288.	1.6	8
8	Amino Acid and Sugar Catabolism in the Marine Bacterium Phaeobacter inhibens DSM 17395 from an Energetic Viewpoint. Applied and Environmental Microbiology, 2019, 85, .	3.1	8
9	Metabolite profiling of the cold adaptation ofPseudomonas putidaKT2440 and coldâ€sensitive mutants. Environmental Microbiology Reports, 2019, 11, 777-783.	2.4	1
10	The Impact of Pyroglutamate:Sulfolobus acidocaldariusHas a Growth Advantage overSaccharolobus solfataricusin Glutamate-Containing Media. Archaea, 2019, 2019, 1-9.	2.3	3
11	BRENDA in 2019: a European ELIXIR core data resource. Nucleic Acids Research, 2019, 47, D542-D549.	14.5	335
12	DISBi: A Flexible Framework for Integrating Systems Biology Data. Lecture Notes in Computer Science, 2019, , 97-102.	1.3	0
13	STRENDA DB: enabling the validation and sharing of enzyme kinetics data. FEBS Journal, 2018, 285, 2193-2204.	4.7	38
14	The marine bacterium Phaeobacter inhibens secures external ammonium by rapid buildup of intracellular nitrogen stocks. FEMS Microbiology Ecology, 2018, 94, .	2.7	7
15	Dealing with salinity extremes and nitrogen limitation â€“ an unexpected strategy of the marine bacterium Dinoroseobacter shibae. Environmental Microbiology, 2017, 19, 894-908.	3.8	10
16	Phylogenomics of Rhodobacteraceae reveals evolutionary adaptation to marine and non-marine habitats. ISME Journal, 2017, 11, 1483-1499.	9.8	283
17	Clostridioides difficile 630Î”erm in silico and in vivo â€“ quantitative growth and extensive polysaccharide secretion. FEBS Open Bio, 2017, 7, 602-615.	2.3	64
18	Oxidative Stickland reactions in an obligate aerobic organism â€“ amino acid catabolism in the Crenarchaeon Sulfolobus solfataricus. FEBS Journal, 2017, 284, 2078-2095.	4.7	19

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19	Fixation of CO₂ using the ethylmalonylâ€CoA pathway in the photoheterotrophic marine bacterium Dinoroseobacter shibae. Environmental Microbiology, 2017, 19, 2645-2660.	3.8	29
20	The limits to growth â€“ energetic burden of the endogenous antibiotic tropodithietic acid in Phaeobacter inhibens DSM 17395. PLoS ONE, 2017, 12, e0177295.	2.5	18
21	Systems biology of the modified branched Entner-Doudoroff pathway in Sulfolobus solfataricus. PLoS ONE, 2017, 12, e0180331.	2.5	11
22	The fate of lysine: Non-targeted stable isotope analysis reveals parallel ways for lysine catabolization in Phaeobacter inhibens. PLoS ONE, 2017, 12, e0186395.	2.5	7
23	BRENDA in 2017: new perspectives and new tools in BRENDA. Nucleic Acids Research, 2017, 45, D380-D388.	14.5	251
24	Manual curation and reannotation of the genomes of Clostridium difficile 630Î”erm and C. difficile 630. Journal of Medical Microbiology, 2017, 66, 286-293.	1.8	117
25	BrEPS 2.0: Optimization of sequence pattern prediction for enzyme annotation. PLoS ONE, 2017, 12, e0182216.	2.5	7
26	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
27	A systems biology approach reveals major metabolic changes in the thermoacidophilic archaeon S ulfolobus solfataricus in response to the carbon source L â€fucose versus D â€glucose. Molecular Microbiology, 2016, 102, 882-908.	2.5	69
28	Time-resolved amino acid uptake of Clostridium difficile 630Î”erm and concomitant fermentation product and toxin formation. BMC Microbiology, 2015, 15, 281.	3.3	132
29	A transferable plasticity region in <scp>C</scp>ampylobacter coli allows isolates of an otherwise nonâ€glycolytic foodâ€borne pathogen to catabolize glucose. Molecular Microbiology, 2015, 98, 809-830.	2.5	26
30	BRENDA in 2015: exciting developments in its 25th year of existence. Nucleic Acids Research, 2015, 43, D439-D446.	14.5	183
31	Comprehensive molecular, genomic and phenotypic analysis of a major clone of Enterococcus faecalis MLST ST40. BMC Genomics, 2015, 16, 175.	2.8	33
32	High-Throughput Screening of a Corynebacterium glutamicum Mutant Library on Genomic and Metabolic Level. PLoS ONE, 2014, 9, e86799.	2.5	17
33	'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
34	Pathways and substrateâ€specific regulation of amino acid degradation in <scp>P</scp>haeobacter inhibensâ€¦<scp>DSM</scp> 17395 (archetype of the marine <scp>R</scp>oseobacter clade). Environmental Microbiology, 2014, 16, 218-238.	3.8	28
35	Utilization of hostâ€derived cysteineâ€containing peptides overcomes the restricted sulphur metabolism of <scp>C</scp>ampylobacter jejuni. Molecular Microbiology, 2014, 93, 1224-1245.	2.5	33
36	Gene Regulatory and Metabolic Adaptation Processes of Dinoroseobacter shibae DFL12T during Oxygen Depletion. Journal of Biological Chemistry, 2014, 289, 13219-13231.	3.4	25

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37	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
38	Standardization in enzymologyâ€"Data integration in the world×³s enzyme information system BRENDA. Perspectives in Science, 2014, 1, 15-23.	0.6	21
39	Standards for Reporting Enzyme Data: The STRENDA Consortium: What it aims to do and why it should be helpful. Perspectives in Science, 2014, 1, 131-137.	0.6	65
40	Common Abbreviations (Other abbreviations are defined in the text). , 2013, , 399-399.		0
41	Software LS-MIDA for efficient mass isotopomer distribution analysis in metabolic modelling. BMC Bioinformatics, 2013, 14, 218.	2.6	21
42	A metabolite-centric view on flux distributions in genome-scale metabolic models. BMC Systems Biology, 2013, 7, 33.	3.0	17
43	Adaptation of <scp>P</scp>haeobacter inhibens<scp>DSM</scp> 17395 to growth with complex nutrients. Proteomics, 2013, 13, 2851-2868.	2.2	45
44	Intraclonal diversity of the Pseudomonas aeruginosa cystic fibrosis airway isolates TBCF10839 and TBCF121838: distinct signatures of transcriptome, proteome, metabolome, adherence and pathogenicity despite an almost identical genome sequence. Environmental Microbiology, 2013, 15, 191-210.	3.8	66
45	Dynamics of amino acid utilization in <scp>P</scp>haeobacter inhibens<scp>DSM</scp> 17395. Proteomics, 2013, 13, 2869-2885.	2.2	22
46	Enzyme-substrate complexes of the quinate/shikimate dehydrogenase from Corynebacterium glutamicum enable new insights in substrate and cofactor binding, specificity, and discrimination. Biological Chemistry, 2013, 394, 1505-1516.	2.5	8
47	Unraveling the function of the two Entnerâ€"Doudoroff branches in the thermoacidophilic CrenarchaeonSulfolobusÂsolfataricusP2. FEBS Journal, 2013, 280, 1126-1138.	4.7	18
48	Swimming in Light: A Large-Scale Computational Analysis of the Metabolism of Dinoroseobacter shibae. PLoS Computational Biology, 2013, 9, e1003224.	3.2	12
49	Regulatory and Metabolic Networks for the Adaptation of Pseudomonas aeruginosa Biofilms to Urinary Tract-Like Conditions. PLoS ONE, 2013, 8, e71845.	2.5	36
50	Analysis of in vivo Function of Predicted Isoenzymesâ€"A Metabolomic Approach. OMICS A Journal of Integrative Biology, 2012, 16, 668-680.	2.0	4
51	BRENDA in 2013: integrated reactions, kinetic data, enzyme function data, improved disease classification: new options and contents in BRENDA. Nucleic Acids Research, 2012, 41, D764-D772.	14.5	358
52	Human Embryonic Stem Cells and Embryonal Carcinoma Cells Have Overlapping and Distinct Metabolic Signatures. PLoS ONE, 2012, 7, e39896.	2.5	45
53	Genome-Scale Reconstruction and Analysis of the Metabolic Network in the Hyperthermophilic Archaeon Sulfolobus Solfataricus. PLoS ONE, 2012, 7, e43401.	2.5	44
54	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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55	Crp Induces Switching of the CsrB and CsrC RNAs in Yersinia pseudotuberculosis and Links Nutritional Status to Virulence. Frontiers in Cellular and Infection Microbiology, 2012, 2, 158.	3.9	67
56	The metabolic response of P. putida KT2442 producing high levels of polyhydroxyalkanoate under single- and multiple-nutrient-limited growth: Highlights from a multi-level omics approach. Microbial Cell Factories, 2012, 11, 34.	4.0	117
57	The BRENDA Tissue Ontology (BTO): the first all-integrating ontology of all organisms for enzyme sources. Nucleic Acids Research, 2011, 39, D507-D513.	14.5	153
58	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
59	Closely related Campylobacter jejuni strains from different sources reveal a generalist rather than a specialist lifestyle. BMC Genomics, 2011, 12, 584.	2.8	101
60	Functional curation of the Sulfolobus solfataricus P2 and S. acidocaldarius 98-3 complete genome sequences. Extremophiles, 2011, 15, 711-712.	2.3	20
61	BKM-react, an integrated biochemical reaction database. BMC Biochemistry, 2011, 12, 42.	4.4	56
62	Development of a classification scheme for disease-related enzyme information. BMC Bioinformatics, 2011, 12, 329.	2.6	19
63	EnzymeDetector: an integrated enzyme function prediction tool and database. BMC Bioinformatics, 2011, 12, 376.	2.6	50
64	BRENDA, the enzyme information system in 2011. Nucleic Acids Research, 2011, 39, D670-D676.	14.5	382
65	â€œHot standardsâ€•for the thermoacidophilic archaeon Sulfolobus solfataricus. Extremophiles, 2010, 14, 119-142.	2.3	55
66	KID - an algorithm for fast and efficient text mining used to automatically generate a database containing kinetic information of enzymes. BMC Bioinformatics, 2010, 11, 375.	2.6	12
67	Impact of adenylyltransferase GlnE on nitrogen starvation response in Corynebacterium glutamicum. Journal of Biotechnology, 2010, 145, 244-252.	3.8	11
68	A large-scale protein-function database. Nature Chemical Biology, 2010, 6, 785-785.	8.0	22
69	How Pseudomonas aeruginosa adapts to various environments: a metabolomic approach. Environmental Microbiology, 2010, 12, 1734-1747.	3.8	139
70	Automatic Assignment of EC Numbers. PLoS Computational Biology, 2010, 6, e1000661.	3.2	27
71	Enzyme Databases. Methods in Molecular Biology, 2010, 609, 113-128.	0.9	15
72	An Emergent Self-Organizing Map Based Analysis Pipeline for Comparative Metabolome Studies. In Silico Biology, 2009, 9, 163-178.	0.9	16

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73	Automatic assignment of reaction operators to enzymatic reactions. Bioinformatics, 2009, 25, 3135-3142.	4.1	19
74	mSpecs: a software tool for the administration and editing of mass spectral libraries in the field of metabolomics. BMC Bioinformatics, 2009, 10, 229.	2.6	5
75	Growth phaseâ€dependent global protein and metabolite profiles of Phaeobacter gallaeciensis strain DSM 17395, a member of the marine Roseobacterâ€clade. Proteomics, 2009, 9, 3677-3697.	2.2	128
76	A metabolic network described in absolute terms. Nature Chemical Biology, 2009, 5, 535-536.	8.0	7
77	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
78	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
79	MetaboliteDetector: Comprehensive Analysis Tool for Targeted and Nontargeted GC/MS Based Metabolome Analysis. Analytical Chemistry, 2009, 81, 3429-3439.	6.5	407
80	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
81	BRENDA, AMENDA and FRENDA the enzyme information system: new content and tools in 2009. Nucleic Acids Research, 2009, 37, D588-D592.	14.5	331
82	An emergent self-organizing map based analysis pipeline for comparative metabolome studies. In Silico Biology, 2009, 9, 163-78.	0.9	3
83	Efficient comprehensive scoring of docked protein complexes using probabilistic support vector machines. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1367-1378.	2.6	23
84	1.6 Ã... structure of an NAD+-dependent quinate dehydrogenase fromCorynebacterium glutamicum. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 803-809.	2.5	7
85	QMEAN: A comprehensive scoring function for model quality assessment. Proteins: Structure, Function and Bioinformatics, 2008, 71, 261-277.	2.6	888
86	Crystal structure and stereochemical studies of KD(P)G aldolase from Thermoproteus tenax. Proteins: Structure, Function and Bioinformatics, 2008, 72, 35-43.	2.6	14
87	Stable carbon isotope discrimination by human 3-hydroxy-3-methylglutaryl-coenzyme A reductase. Journal of Lipid Research, 2008, 49, 2620-2626.	4.2	2
88	SYSTOMONAS -- an integrated database for systems biology analysis of Pseudomonas. Nucleic Acids Research, 2007, 35, D533-D537.	14.5	50
89	BRENDA, AMENDA and FRENDA: the enzyme information system in 2007. Nucleic Acids Research, 2007, 35, D511-D514.	14.5	140
90	In vivo labeling with stable isotopes as a tool for the identification of unidentified peaks in the metabolome analysis of Corynebacterium glutamicum by GC/MS. Biological Chemistry, 2007, 388, 865-71.	2.5	4

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91	The Structure of a Bacterial l-Amino Acid Oxidase from Rhodococcus opacus Gives New Evidence for the Hydride Mechanism for Dehydrogenation. Journal of Molecular Biology, 2007, 367, 234-248.	4.2	71
92	Glycosynthase Activity of Geobacillus stearothermophilus GH52 Î²â€Xylosidase: Efficient Synthesis of Xylooligosaccharides from Î±â€<scp>D</scp>â€Xylopyranosyl Fluoride through a Conjugated Reaction. ChemBioChem, 2007, 8, 2145-2151.	2.6	52
93	A high-throughput method for microbial metabolome analysis using gas chromatography/mass spectrometry. Analytical Biochemistry, 2007, 367, 143-151.	2.4	38
94	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
95	Combination of scoring schemes for protein docking. BMC Bioinformatics, 2007, 8, 279.	2.6	7
96	An Irreversible and Kinetically Controlled Process: Thermal Induced Denaturation of L-2-Hydroxyisocaproate Dehydrogenase from Lactobacillus confusus. Protein Journal, 2007, 26, 143-151.	1.6	9
97	A Likelihood Ratio Test for Differential Metabolic Profiles in Multiple Intensity Measurements. Lecture Notes in Computer Science, 2007, , 485-492.	1.3	0
98	The Structure of an Inverting GH43 Î²-Xylosidase from Geobacillus stearothermophilus with its Substrate Reveals the Role of the Three Catalytic Residues. Journal of Molecular Biology, 2006, 359, 97-109.	4.2	132
99	Crystal Structure of Full Length Topoisomerase I from Thermotoga maritima. Journal of Molecular Biology, 2006, 358, 1328-1340.	4.2	33
100	Crystallization and preliminary X-ray analysis of a bacterialL-amino-acid oxidase fromRhodococcus opacus. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 279-281.	0.7	5
101	Cloning, expression, purification and preliminary crystallographic characterization of a shikimate dehydrogenase fromCorynebacterium glutamicum. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 635-637.	0.7	3
102	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
103	Optimised amino acid specific weighting factors for unbound protein docking. BMC Bioinformatics, 2006, 7, 344.	2.6	3
104	CUPSAT: prediction of protein stability upon point mutations. Nucleic Acids Research, 2006, 34, W239-W242.	14.5	572
105	Observing local and global properties of metabolic pathways: â€˜load pointsâ€™ and â€˜choke pointsâ€™ in the metabolic networks. Bioinformatics, 2006, 22, 1767-1774.	4.1	102
106	The importance of uniformity in reporting protein-function data. Trends in Biochemical Sciences, 2005, 30, 11-12.	7.5	22
107	Metabolic Network Analysis: Implication And Application. BMC Bioinformatics, 2005, 6, S12.	2.6	1
108	Crystallization and preliminary crystallographic analysis of a flavoprotein NADH oxidase fromLactobacillus brevis. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 528-530.	0.7	5

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109	Crystallization and preliminary crystallographic analysis of a family 43 Î²-D-xylosidase fromGeobacillus stearothermophilusT-6. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 1054-1057.	0.7	4
110	Refinement of unbound protein docking studies using biological knowledge. Proteins: Structure, Function and Bioinformatics, 2005, 61, 1059-1067.	2.6	8
111	Concept-based annotation of enzyme classes. Bioinformatics, 2005, 21, 2059-2066.	4.1	12
112	The Crucial Role of Trehalose and Structurally Related Oligosaccharides in the Biosynthesis and Transfer of Mycolic Acids in Corynebacterineae. Journal of Biological Chemistry, 2005, 280, 26573-26585.	3.4	67
113	Metabolic pathway analysis web service (Pathway Hunter Tool at CUBIC). Bioinformatics, 2005, 21, 1189-1193.	4.1	115
114	BRAGI: linking and visualization of database information in a 3D viewer and modeling tool. Bioinformatics, 2005, 21, 1291-1293.	4.1	9
115	Biochemical Characterization and Identification of the Catalytic Residues of a Family 43 Î²-d-Xylosidase fromGeobacillus stearothermophilusT-6â€. Biochemistry, 2005, 44, 387-397.	2.5	93
116	Atomic Resolution Structures of R-specific Alcohol Dehydrogenase from Lactobacillus brevis Provide the Structural Bases of its Substrate and Cosubstrate Specificity. Journal of Molecular Biology, 2005, 349, 801-813.	4.2	135
117	GCâ€“MS libraries for the rapid identification of metabolites in complex biological samples. FEBS Letters, 2005, 579, 1332-1337.	2.8	596
118	High level expression and single-step purification of hexahistidine-tagged l-2-hydroxyisocaproate dehydrogenase making use of a versatile expression vector set. Protein Expression and Purification, 2005, 39, 137-143.	1.3	19
119	Prediction of protein thermostability with a direction- and distance-dependent knowledge-based potential. Protein Science, 2005, 14, 2682-2692.	7.6	49
120	IntEnz, the integrated relational enzyme database. Nucleic Acids Research, 2004, 32, 434D-437.	14.5	160
121	BRENDA, the enzyme database: updates and major new developments. Nucleic Acids Research, 2004, 32, 431D-433.	14.5	679
122	Molecular Analysis of Laminin N-terminal Domains Mediating Self-interactions. Journal of Biological Chemistry, 2004, 279, 44504-44512.	3.4	64
123	Efficient methods for filtering and ranking fragments for the prediction of structurally variable regions in proteins. Proteins: Structure, Function and Bioinformatics, 2004, 54, 583-595.	2.6	13
124	Expression, purification, and aggregation studies of His-tagged thermoalkalophilic lipase from Bacillus thermocatenulatus. Protein Expression and Purification, 2004, 34, 103-110.	1.3	28
125	Comprehensive analysis of metabolites in Corynebacterium glutamicum by gas chromatography/mass spectrometry. Biological Chemistry, 2004, 385, 853-861.	2.5	114
126	Crystal structure and snapshots along the reaction pathway of a family 51 Â-L-arabinofuranosidase. EMBO Journal, 2003, 22, 4922-4932.	7.8	127

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127	Crystallization and preliminary X-ray analysis of a family 51 glycoside hydrolase, the Î±-L-arabinofuranosidase fromGeobacillus stearothermophilusT-6. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 913-915.	2.5	12
128	The Crystal Structure of R-specific Alcohol Dehydrogenase from Lactobacillus brevis Suggests the Structural Basis of its Metal Dependency. Journal of Molecular Biology, 2003, 327, 317-328.	4.2	121
129	Crystal Structure of Creatininase from Pseudomonas putida: A Novel Fold and a Case of Convergent Evolution. Journal of Molecular Biology, 2003, 332, 287-301.	4.2	18
130	The substrate specificity-determining amino acid code of 4-coumarate:CoA ligase. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8601-8606.	7.1	137
131	BRENDA, enzyme data and metabolic information. Nucleic Acids Research, 2002, 30, 47-49.	14.5	606
132	The Structure of l-Hydantoinase from Arthobacter aurescens Leads to an Understanding of Dihydropyrimidinase Substrate and Enantio Specificity,. Biochemistry, 2002, 41, 8589-8597.	2.5	59
133	X-ray Structure of a Dihydropyrimidinase from Thermus sp. at 1.3Ã... Resolution. Journal of Molecular Biology, 2002, 320, 143-156.	4.2	87
134	Crystal Structure ofd-Hydantoinase fromBacillus stearothermophilus:Â Insight into the Stereochemistry of Enantioselectivityâ€,â€¡. Biochemistry, 2002, 41, 9410-9417.	2.5	87
135	BRENDA: a resource for enzyme data and metabolic information. Trends in Biochemical Sciences, 2002, 27, 54-56.	7.5	172
136	Investigation of the influence of charge derivatization on the fragmentation of multiply protonated peptides. Journal of the American Society for Mass Spectrometry, 2002, 13, 47-58.	2.8	28
137	Crystallization and preliminary crystallographic analysis of creatininase from Pseudomonas putida. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1356-1358.	2.5	3
138	Positioning of anchor groups in protein loop prediction: The importance of solvent accessibility and secondary structure elements. Proteins: Structure, Function and Bioinformatics, 2002, 47, 370-378.	2.6	11
139	Strongly Connected Components can Predict Protein Structure. Electronic Notes in Discrete Mathematics, 2001, 8, 10-13.	0.4	1
140	Conserved arginine-516 of Penicillium amagasakiense glucose oxidase is essential for the efficient binding of Î²-d-glucose. Biochemical Journal, 2000, 347, 553.	3.7	36
141	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
142	Crystallization, preliminary X-ray analysis of a native and selenomethionineD-hydantoinase fromThermussp.. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1166-1169.	2.5	4
143	Crystallization and preliminary characterization of crystals ofR-alcohol dehydrogenase fromLactobacillus brevis. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1696-1698.	2.5	11
144	Identification of Residues Important Both for Primary Receptor Binding and Specificity in Fibroblast Growth Factor-7. Journal of Biological Chemistry, 2000, 275, 34881-34886.	3.4	17

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145	Purification of a d-hydantoinase using a laboratory-scale Streamline phenyl column as the initial step. Biomedical Applications, 2000, 737, 187-194.	1.7	10
146	Mutations Uncouple Human Fibroblast Growth Factor (FGF)-7 Biological Activity and Receptor Binding and Support Broad Specificity in the Secondary Receptor Binding Site of FGFs. Journal of Biological Chemistry, 1999, 274, 35016-35022.	3.4	16
147	1.8 and 1.9â€…Ã… resolution structures of thePenicillium amagasakienseandAspergillus nigerglucose oxidases as a basis for modelling substrate complexes. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 969-977.	2.5	264
148	GTP plus water mimic ATP in the active site of protein kinase CK2. Nature Structural Biology, 1999, 6, 1100-1103.	9.7	176
149	Importance of anchor group positioning in protein loop prediction. Proteins: Structure, Function and Bioinformatics, 1999, 37, 56-64.	2.6	28
150	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
151	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
152	Inhibition of Streptomyces griseus aminopeptidase and effects of calcium ions on catalysis and binding . Comparisons with the homologous enzyme Aeromonas proteolytica aminopeptidase. FEBS Journal, 1998, 258, 313-319.	0.2	25
153	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
154	Crystal structure of a ternary complex of d -2-hydroxyisocaproate dehydrogenase from Lactobacillus casei , NAD + and 2-oxoisocaproate at 1.9 Ã… resolution 1 1Edited by R. Huber. Journal of Molecular Biology, 1997, 267, 640-660.	4.2	58
155	Birch pollen profilin: structural organization and interaction with poly-(l-proline) peptides as revealed by NMR. FEBS Letters, 1997, 411, 291-295.	2.8	19
156	The open conformation of a Pseudomonas lipase. Structure, 1997, 5, 187-202.	3.3	275
157	NMR Spectroscopic Evidence That Helodermin, unlike Other Members of the Secretin/VIP Family of Peptides, Is Substantially Structured in Water. Biochemistry, 1996, 35, 5955-5962.	2.5	30
158	Crystal Structure of a Bacterial Lipase fromChromobacterium viscosumATCC 6918 Refined at 1.6 Ã… Resolution. Journal of Molecular Biology, 1996, 259, 704-717.	4.2	133
159	Hydrogen Bonding and Molecular Surface Shape Complementarity as a Basis for Protein Docking. Journal of Molecular Biology, 1996, 264, 199-210.	4.2	101
160	Computer-aided modeling of structure stabilizing disulfide bonds in recombinant human interferon-Î³. Pharmaceutica Acta Helvetiae, 1996, 71, 37-44.	1.2	0
161	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
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