

# Bengt Persson

## List of Publications by Year in descending order

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153  
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36303

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155  
docs citations

155  
times ranked

31315  
citing authors

#	ARTICLE	IF	CITATIONS
1	Baseline characteristics of 547 new onset heart failure patients in the PREFERS heart failure study. ESC Heart Failure, 2022, 9, 2125-2138.	3.1	3
2	ELIXIRâ€œEXCELERATE: establishing Europe's data infrastructure for the life science research of the future. EMBO Journal, 2021, 40, e107409.	7.8	18
3	Metabolomic Profile in HFpEF vs HFrEF Patients. Journal of Cardiac Failure, 2020, 26, 1050-1059.	1.7	46
4	Increased iron absorption in patients with chronic heart failure and iron deficiency. Journal of Cardiac Failure, 2020, 26, 440-443.	1.7	7
5	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. Bioinformatics, 2020, 36, 2636-2642.	4.1	47
6	The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164.	8.8	39
7	Novel non-classic CYP21A2 variants, including combined alleles, identified in patients with congenital adrenal hyperplasia. Clinical Biochemistry, 2019, 73, 50-56.	1.9	2
8	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
9	Transcriptomics of cardiac biopsies reveals differences in patients with or without diagnostic parameters for heart failure with preserved ejection fraction. Scientific Reports, 2019, 9, 3179.	3.3	35
10	Spatial detection of fetal marker genes expressed at low level in adult human heart tissue. Scientific Reports, 2017, 7, 12941.	3.3	62
11	Functional and Structural Consequences of Nine CYP21A2 Mutations Ranging from Very Mild to Severe Effects. International Journal of Endocrinology, 2016, 2016, 1-10.	1.5	8
12	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	5.3	8,670
13	Rationale and design of the PREFERS (Preserved and Reduced Ejection Fraction) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF Stockholm county of 2.1 million inhabitants. European Journal of Heart Failure, 2016, 18, 1287-1297.	7.1	17
14	Computational studies of human class V alcohol dehydrogenase - the odd sibling. BMC Biochemistry, 2016, 17, 16.	4.4	11
15	Mutations in SLC12A5 in epilepsy of infancy with migrating focal seizures. Nature Communications, 2015, 6, 8038.	12.8	160
16	In vitro functional studies of rare CYP21A2 mutations and establishment of an activity gradient for nonclassic mutations improve phenotype predictions in congenital adrenal hyperplasia. Clinical Endocrinology, 2015, 82, 37-44.	2.4	22
17	The mammalian alcohol dehydrogenase genome shows several gene duplications and gene losses resulting in a large set of different enzymes including pseudoenzymes. Chemico-Biological Interactions, 2015, 234, 80-84.	4.0	6
18	The ELIXIR channel in F1000Research. F1000Research, 2015, 4, 1471.	1.6	3

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19	On an Early Gene for Membrane-Integral Inorganic Pyrophosphatase in the Genome of an Apparently Pre-LUCA Extremophile, the Archaeon <i>Candidatus Korarchaeum cryptofilum</i> . <i>Journal of Molecular Evolution</i> , 2014, 78, 140-147.	1.8	7
20	A mutation interfering with 5-lipoxygenase domain interaction leads to increased enzyme activity. <i>Archives of Biochemistry and Biophysics</i> , 2014, 545, 179-185.	3.0	17
21	Analysis of mammalian alcohol dehydrogenase 5 (ADH5): Characterisation of rat ADH5 with comparisons to the corresponding human variant. <i>Chemico-Biological Interactions</i> , 2013, 202, 97-103.	4.0	10
22	Novel candidate genes for 46,XY gonadal dysgenesis identified by a customized 1ÅM array-CGH platform. <i>European Journal of Medical Genetics</i> , 2013, 56, 661-668.	1.3	17
23	Origin and evolution of medium chain alcohol dehydrogenases. <i>Chemico-Biological Interactions</i> , 2013, 202, 91-96.	4.0	30
24	Classification and nomenclature of the superfamily of short-chain dehydrogenases/reductases (SDRs). <i>Chemico-Biological Interactions</i> , 2013, 202, 111-115.	4.0	123
25	Unbiased Approach for Virus Detection in Skin Lesions. <i>PLoS ONE</i> , 2013, 8, e65953.	2.5	55
26	Phylogenetically diverse TT virus viremia among pregnant women. <i>Virology</i> , 2012, 432, 427-434.	2.4	26
27	The Plant Short-Chain Dehydrogenase (SDR) superfamily: genome-wide inventory and diversification patterns. <i>BMC Plant Biology</i> , 2012, 12, 219.	3.6	115
28	Characterization of the Viral Microbiome in Patients with Severe Lower Respiratory Tract Infections, Using Metagenomic Sequencing. <i>PLoS ONE</i> , 2012, 7, e30875.	2.5	154
29	Evolutionary Conservation of the Ribosomal Biogenesis Factor <i>Rbm19/Mrd1</i> : Implications for Function. <i>PLoS ONE</i> , 2012, 7, e43786.	2.5	10
30	Investigating Protein Variants Using Structural Calculation Techniques. <i>Methods in Molecular Biology</i> , 2011, 857, 313-330.	0.9	0
31	An efficient simulator of 454 data using configurable statistical models. <i>BMC Research Notes</i> , 2011, 4, 449.	1.4	27
32	Characterization of new medium-chain alcohol dehydrogenases adds resolution to duplications of the class I/III and the sub-class I genes. <i>Chemico-Biological Interactions</i> , 2011, 191, 8-13.	4.0	4
33	FAAST: Flow-space Assisted Alignment Search Tool. <i>BMC Bioinformatics</i> , 2011, 12, 293.	2.6	8
34	RSpred, a set of Hidden Markov Models to detect and classify the RIFIN and STEVOR proteins of <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2011, 12, 119.	2.8	9
35	An unbiased metagenomic search for infectious agents using monozygotic twins discordant for chronic fatigue. <i>BMC Microbiology</i> , 2011, 11, 2.	3.3	21
36	The insulin receptor substrate-4 (IRS-4) gene and schizophrenia: no evidence for a main genetic factor, however one report of a single schizophrenia patient with a mutation. <i>Neuroendocrinology Letters</i> , 2011, 32, 52-8.	0.2	2

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37	Association between body mass index and insulin receptor substrate-4 (IRS-4) gene polymorphisms in patients with schizophrenia. <i>Neuroendocrinology Letters</i> , 2011, 32, 634-40.	0.2	3
38	Enrichment of ligands with molecular dockings and subsequent characterization for human alcohol dehydrogenase 3. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 3005-3015.	5.4	7
39	Model of the complex of Parathyroid hormone-2 receptor and Tuberoinsfundibular peptide of 39 residues. <i>BMC Research Notes</i> , 2010, 3, 270.	1.4	3
40	Classification of the short-chain dehydrogenase/reductase superfamily using hidden Markov models. <i>FEBS Journal</i> , 2010, 277, 2375-2386.	4.7	148
41	Subdivision of the MDR superfamily of medium-chain dehydrogenases/reductases through iterative hidden Markov model refinement. <i>BMC Bioinformatics</i> , 2010, 11, 534.	2.6	35
42	Functionally Important Amino Acids in the <i>Arabidopsis</i> Thylakoid Phosphate Transporter: Homology Modeling and Site-Directed Mutagenesis. <i>Biochemistry</i> , 2010, 49, 6430-6439.	2.5	13
43	Superfamilies SDR and MDR: From early ancestry to present forms. Emergence of three lines, a Zn-metalloenzyme, and distinct variabilities. <i>Biochemical and Biophysical Research Communications</i> , 2010, 396, 125-130.	2.1	68
44	Quasispecies dynamics and molecular evolution of human norovirus capsid P region during chronic infection. <i>Journal of General Virology</i> , 2009, 90, 432-441.	2.9	26
45	BRICHOS - a superfamily of multidomain proteins with diverse functions. <i>BMC Research Notes</i> , 2009, 2, 180.	1.4	79
46	The SDR (short-chain dehydrogenase/reductase and related enzymes) nomenclature initiative. <i>Chemico-Biological Interactions</i> , 2009, 178, 94-98.	4.0	329
47	Autoimmune T cell responses to antigenic peptides presented by bronchoalveolar lavage cell HLA-DR molecules in sarcoidosis. <i>Clinical Immunology</i> , 2009, 133, 353-363.	3.2	63
48	Investigation and prediction of the severity of p53 mutants using parameters from structural calculations. <i>FEBS Journal</i> , 2009, 276, 4142-4155.	4.7	12
49	Prediction of partial membrane protein topologies using a consensus approach. <i>Protein Science</i> , 2009, 11, 2974-2980.	7.6	35
50	Short-chain dehydrogenase/reductase (SDR) relationships: A large family with eight clusters common to human, animal, and plant genomes. <i>Protein Science</i> , 2009, 11, 636-641.	7.6	200
51	Molecular dynamics studies of $\alpha$ -helix stability in fibril-forming peptides. <i>Journal of Computer-Aided Molecular Design</i> , 2008, 22, 53-58.	2.9	14
52	Medium- and short-chain dehydrogenase/reductase gene and protein families. <i>Cellular and Molecular Life Sciences</i> , 2008, 65, 3879-94.	5.4	163
53	Medium- and short-chain dehydrogenase/reductase gene and protein families. <i>Cellular and Molecular Life Sciences</i> , 2008, 65, 3895-906.	5.4	738
54	Quantitative membrane proteomics applying narrow range peptide isoelectric focusing for studies of small cell lung cancer resistance mechanisms. <i>Proteomics</i> , 2008, 8, 3008-3018.	2.2	72

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55	Carbamazepine protects against neuronal hyperplasia and abnormal gene expression in the megecephaly mouse. <i>Neurobiology of Disease</i> , 2008, 32, 364-376.	4.4	10
56	The Fellowship of the RING: The RINGâ€™B-Box Linker Region Interacts with the RING in TRIM21/Ro52, Contains a Native Autoantigenic Epitope in Sjögren Syndrome, and is an Integral and Conserved Region in TRIM Proteins. <i>Journal of Molecular Biology</i> , 2008, 377, 431-449.	4.2	23
57	Epstein-Barr Virus Encodes Three Bona Fide Ubiquitin-Specific Proteases. <i>Journal of Virology</i> , 2008, 82, 10477-10486.	3.4	36
58	Disruption of the GDNF Binding Site in NCAM Dissociates Ligand Binding and Homophilic Cell Adhesion. <i>Journal of Biological Chemistry</i> , 2007, 282, 12734-12740.	3.4	28
59	Characterization of oligopeptide patterns in large protein sets. <i>BMC Genomics</i> , 2007, 8, 346.	2.8	11
60	A new polymorphism in the coding region of exon four in HSD17B2 in relation to risk of sporadic and hereditary breast cancer. <i>Breast Cancer Research and Treatment</i> , 2007, 106, 57-64.	2.5	12
61	Identification of HLA-DRâ€™bound peptides presented by human bronchoalveolar lavage cells in sarcoidosis. <i>Journal of Clinical Investigation</i> , 2007, 117, 3576-3582.	8.2	112
62	Ontology Annotation Treebrowser. <i>Applied Bioinformatics</i> , 2006, 5, 225-236.	1.6	12
63	A promiscuous glutathione transferase transformed into a selective thiolester hydrolase. <i>Organic and Biomolecular Chemistry</i> , 2006, 4, 90-97.	2.8	3
64	Molecular Model of Human CYP21 Based on Mammalian CYP2C5: Structural Features Correlate with Clinical Severity of Mutations Causing Congenital Adrenal Hyperplasia. <i>Molecular Endocrinology</i> , 2006, 20, 2946-2964.	3.7	77
65	Prediction of coenzyme specificity in dehydrogenases/ reductases. A hidden Markov model-based method and its application on complete genomes. <i>FEBS Journal</i> , 2006, 273, 1177-1184.	4.7	50
66	Analysis of ancient sequence motifs in the H <sup>+</sup> -PPase family. <i>FEBS Journal</i> , 2006, 273, 5183-5193.	4.7	15
67	Mutation analysis of the human 5-lipoxygenase C-terminus: Support for a stabilizing C-terminal loop. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1749, 123-131.	2.3	10
68	Bioinformatic and enzymatic characterization of the MAPEG superfamily. <i>FEBS Journal</i> , 2005, 272, 1688-1703.	4.7	134
69	Comparative analysis of amino acid distributions in integral membrane proteins from 107 genomes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 606-616.	2.6	108
70	Folding into a Î²-Hairpin Can Prevent Amyloid Fibril Formationâ€™. <i>Biochemistry</i> , 2004, 43, 4655-4661.	2.5	25
71	Unfolding a Folding Disease: Folding, Misfolding and Aggregation of the Marble Brain Syndrome-associated Mutant H107Y of Human Carbonic Anhydrase II. <i>Journal of Molecular Biology</i> , 2004, 342, 619-633.	4.2	51
72	Short-chain dehydrogenases/reductases (SDR): the 2002 update. <i>Chemico-Biological Interactions</i> , 2003, 143-144, 247-253.	4.0	546

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73	Coenzyme-based functional assignments of short-chain dehydrogenases/reductases (SDRs). <i>Chemico-Biological Interactions</i> , 2003, 143-144, 271-278.	4.0	183
74	Multiplicity of eukaryotic ADH and other MDR forms. <i>Chemico-Biological Interactions</i> , 2003, 143-144, 255-261.	4.0	18
75	Catalytic Activities of Human Alpha Class Glutathione Transferases toward Carcinogenic Dibenzo[ <i>a,l</i> ]pyrene Diol Epoxides. <i>Chemical Research in Toxicology</i> , 2002, 15, 825-831.	3.3	29
76	Medium-chain dehydrogenases/reductases (MDR). <i>FEBS Journal</i> , 2002, 269, 4267-4276.	0.2	140
77	Short-chain dehydrogenases/reductases (SDRs). <i>FEBS Journal</i> , 2002, 269, 4409-4417.	0.2	355
78	Human type 10 17 $\beta$ -hydroxysteroid dehydrogenase: molecular modelling and substrate docking. <i>Journal of Molecular Graphics and Modelling</i> , 2001, 19, 514-520.	2.4	12
79	Variations and constant patterns in eukaryotic MDR enzymes. <i>Chemico-Biological Interactions</i> , 2001, 130-132, 491-498.	4.0	11
80	Prediction of Amyloid Fibril-forming Proteins. <i>Journal of Biological Chemistry</i> , 2001, 276, 12945-12950.	3.4	274
81	Biochemical Defects in 11-cis-Retinol Dehydrogenase Mutants Associated with Fundus Albipunctatus. <i>Journal of Biological Chemistry</i> , 2001, 276, 49251-49257.	3.4	31
82	Cloning of a Novel Growth Hormone-Regulated Rat Complementary Deoxyribonucleic Acid with Homology to the Human $\beta$ 1B-Glycoprotein, Characterizing a New Protein Family*. <i>Endocrinology</i> , 2001, 142, 2695-2701.	2.8	11
83	Tetra- and Nonapeptidyl Motifs in the Origin and Evolution of Photosynthetic Bioenergy Conversion. , 2001, , 173-178.		3
84	Cloning of a Novel Growth Hormone-Regulated Rat Complementary Deoxyribonucleic Acid with Homology to the Human $\beta$ 1B-Glycoprotein, Characterizing a New Protein Family. <i>Endocrinology</i> , 2001, 142, 2695-2701.	2.8	6
85	Pharmacogenetics of the Alcohol Dehydrogenase System. <i>Pharmacology</i> , 2000, 61, 184-191.	2.2	52
86	The N-terminal Domain of 5-Lipoxygenase Binds Calcium and Mediates Calcium Stimulation of Enzyme Activity. <i>Journal of Biological Chemistry</i> , 2000, 275, 38787-38793.	3.4	151
87	Molecular Basis for Differential Substrate Specificity in Class IV Alcohol Dehydrogenases. <i>Journal of Biological Chemistry</i> , 2000, 275, 25180-25187.	3.4	35
88	Consensus predictions of membrane protein topology. <i>FEBS Letters</i> , 2000, 486, 267-269.	2.8	91
89	Membrane-associated Proteins in Eicosanoid and Glutathione Metabolism (MAPEG). <i>American Journal of Respiratory and Critical Care Medicine</i> , 2000, 161, S20-S24.	5.6	138
90	Human liver class I alcohol dehydrogenase $\beta$ isozyme: the sole cytosolic $\beta$ -hydroxysteroid dehydrogenase of iso bile acids. <i>Hepatology</i> , 2000, 31, 990-996.	7.3	26

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91	Bioinformatics in protein analysis. , 2000, 88, 215-231.		56
92	Structural and Enzymatic Properties of a Gastric NADP(H)- dependent and Retinal-active Alcohol Dehydrogenase. Journal of Biological Chemistry, 1999, 274, 26021-26026.	3.4	31
93	Elapid venom toxins: multiple recruitments of ancient scaffolds. FEBS Journal, 1999, 259, 225-234.	0.2	46
94	T-cell-epitope mapping of the idiotypic monoclonal IgG heavy and light chains in multiple myeloma. , 1999, 80, 671-680.		43
95	Immunocytochemical detection and mapping of a cytokeratin 18 neo-epitope exposed during early apoptosis. Journal of Pathology, 1999, 187, 567-572.	4.5	564
96	SDR and MDR: completed genome sequences show these protein families to be large, of old origin, and of complex nature. FEBS Letters, 1999, 445, 261-264.	2.8	174
97	Structure and Chromosomal Assignment of the Sterol 12 $\beta$ -Hydroxylase Gene (CYP8B1) in Human and Mouse: Eukaryotic Cytochrome P-450 Gene Devoid of Introns. Genomics, 1999, 56, 184-196.	2.9	65
98	Common structural features of mepgâ€”a widespread superfamily of membrane associated proteins with highly divergent functions in eicosanoid and glutathione metabolism. Protein Science, 1999, 8, 689-692.	7.6	291
99	Bioinformatics in Studies of SDR and MDR Enzymes. Advances in Experimental Medicine and Biology, 1999, 463, 373-377.	1.6	7
100	Structure-Function Relationships of 3 $\alpha$ -Hydroxysteroid Dehydrogenases Involved in Bile Acid Metabolism. Advances in Experimental Medicine and Biology, 1999, 463, 389-394.	1.6	2
101	A Highly Active Microsomal Glutathione Transferase from Frog ( <i>Xenopus laevis</i> ) Liver That Is Not Activated by N-Ethylmaleimide. Biochemical and Biophysical Research Communications, 1998, 246, 466-469.	2.1	6
102	Sorbitol Dehydrogenase of <i>Drosophila</i> . Journal of Biological Chemistry, 1998, 273, 34293-34301.	3.4	19
103	Cellular UDP-Glucose Deficiency Caused by a Single Point Mutation in the UDP-Glucose Pyrophosphorylase Gene. Journal of Biological Chemistry, 1997, 272, 23784-23791.	3.4	77
104	Guinea Pig and Bovine $\alpha$ -Crystallins Have Distinct Functional Characteristics Highlighting Replacements in Otherwise Similar Structuresâ€”â€”. Biochemistry, 1997, 36, 5353-5362.	2.5	34
105	Active Site Directed Mutagenesis of 3 $\alpha$ /17 $\beta$ -Hydroxysteroid Dehydrogenase Establishes Differential Effects on Short-Chain Dehydrogenase/Reductase Reactions. Biochemistry, 1997, 36, 34-40.	2.5	148
106	Mycotoxin-Dependent Formaldehyde Dehydrogenase, A Prokaryotic Medium-Chain Dehydrogenase/Reductase, Phylogenetically Links Different Eukaryotic Alcohol Dehydrogenases Primary Structure, Conformational Modelling and Functional Correlations. FEBS Journal, 1997, 248, 282-289.	0.2	47
107	The 11 $\beta$ -Hydroxysteroid Dehydrogenase System, A Determinant of Glucocorticoid and Mineralocorticoid Action. Function, Gene Organization and Protein Structures of 11 $\beta$ -Hydroxysteroid Dehydrogenase Isoforms. FEBS Journal, 1997, 249, 355-360.	0.2	72
108	Prediction of membrane protein topology utilizing multiple sequence alignments. The Protein Journal, 1997, 16, 453-457.	1.1	106

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109	Molecular modelling of human gastric alcohol dehydrogenase (class IV) and substrate docking: differences towards the classical liver enzyme (class I). FEBS Letters, 1996, 395, 99-102.	2.8	21
110	Primary structure and homology. FEBS Letters, 1996, 380, 301-301.	2.8	0
111	Arabidopsis Formaldehyde Dehydrogenase. Molecular Properties of Plant Class III Alcohol Dehydrogenase Provide Further Insights into the Origins, Structure and Function of Plant Class P and Liver Class I Alcohol Dehydrogenases. FEBS Journal, 1996, 241, 849-857.	0.2	81
112	Topology prediction of membrane proteins. Protein Science, 1996, 5, 363-371.	7.6	118
113	Alcohol Dehydrogenase Variability. Advances in Experimental Medicine and Biology, 1996, , 281-289.	1.6	8
114	Structure-Function Relationships of SDR Hydroxysteroid Dehydrogenases. Advances in Experimental Medicine and Biology, 1996, 414, 403-415.	1.6	29
115	TMAP: a new email and WWW service for membrane-protein structural predictions. Trends in Biochemical Sciences, 1995, 20, 204-205.	7.5	52
116	Ethanol utilization regulatory protein: Profile alignments give no evidence of origin through aldehyde and alcohol dehydrogenase gene fusion. Protein Science, 1995, 4, 2621-2624.	7.6	4
117	Short-chain dehydrogenases/reductases (SDR). Biochemistry, 1995, 34, 6003-6013.	2.5	1,230
118	Protein Structure Prediction: Recognition of Primary, Secondary, and Tertiary Structural Features from Amino Acid Sequence. Critical Reviews in Biochemistry and Molecular Biology, 1995, 30, 1-94.	5.2	132
119	The Alcohol Dehydrogenase System. Advances in Experimental Medicine and Biology, 1995, 372, 281-294.	1.6	47
120	Short-Chain Dehydrogenases/Reductases. Advances in Experimental Medicine and Biology, 1995, 372, 383-395.	1.6	24
121	MPSA short communications. The Protein Journal, 1994, 13, 431-512.	1.1	0
122	Prediction of Transmembrane Segments in Proteins Utilising Multiple Sequence Alignments. Journal of Molecular Biology, 1994, 237, 182-192.	4.2	452
123	A Super-Family of Medium-Chain Dehydrogenases/Reductases (MDR). FEBS Journal, 1994, 226, 15-22.	0.2	15
124	A Super-Family of Medium-Chain Dehydrogenases/Reductases (MDR). Sub-Lines including zeta-Crystallin, Alcohol and Polyol Dehydrogenases, Quinone Oxidoreductases, Enoyl Reductases, VAT-1 and other Proteins. FEBS Journal, 1994, 226, 15-22.	0.2	147
125	Glucose-6-phosphate dehydrogenase. Structure-function relationships and the Pichia jadinii enzyme structure. FEBS Journal, 1993, 212, 41-49.	0.2	26
126	Basic features of class-I alcohol dehydrogenase: variable and constant segments coordinated by inter-class and intra-class variability. Conclusions from characterization of the alligator enzyme. FEBS Journal, 1993, 216, 49-56.	0.2	33

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127	Variability patterns of dehydrogenases versus peptide hormones and proteases/antiproteases. FEBS Letters, 1993, 335, 69-72.	2.8	5
128	Dual relationships of xylitol and alcohol dehydrogenases in families of two protein types. FEBS Letters, 1993, 324, 9-14.	2.8	40
129	Îŕ-Crystallin versus other members of the alcohol dehydrogenase super-family Variability as a functional characteristic. FEBS Letters, 1993, 322, 240-244.	2.8	21
130	Alcohol Dehydrogenases: Patterns of Protein Evolution. , 1993, , 275-282.		2
131	Characterization of two platelet aggregation inhibitor-like polypeptides from viper venom. Peptides, 1992, 13, 1033-1037.	2.4	6
132	Characterization of 4-hydroxyphenylpyruvate dioxygenase. Primary structure of the Pseudomonas enzyme. FEBS Journal, 1992, 205, 459-466.	0.2	51
133	Different segment similarities in long-chain dehydrogenases. Biochemical and Biophysical Research Communications, 1991, 177, 218-223.	2.1	19
134	Lipoprotein lipases and vitellogenins in relation to the known three-dimensional structure of pancreatic lipase. FEBS Letters, 1991, 288, 33-36.	2.8	19
135	Proton-translocating transhydrogenase from photosynthetic bacteria. Biochemical Society Transactions, 1991, 19, 573-575.	3.4	6
136	Functionally important regions of glucose-6-phosphate dehydrogenase defined by the Saccharomyces cerevisiae enzyme and its differences from the mammalian and insect forms. FEBS Journal, 1991, 198, 485-491.	0.2	18
137	Characteristics of short-chain alcohol dehydrogenases and related enzymes. FEBS Journal, 1991, 200, 537-543.	0.2	432
138	A Fragment of Triosephosphate Isomerase Competes with the Vasoactive Intestinal Polypeptide (VIP) for Binding to the VIP Receptor.. Acta Chemica Scandinavica, 1991, 45, 63-67.	0.7	0
139	Alcohol dehydrogenases. Biochemical Society Transactions, 1990, 18, 169-171.	3.4	14
140	Sea snake (Microcephalophis gracilis) hemoglobin: Primary structure and relationships to other forms. The Protein Journal, 1990, 9, 533-541.	1.1	13
141	Fast atom bombardment mass spectrometry and chemical analysis in determinations of acyl-blocked protein structures. FEBS Letters, 1990, 269, 194-196.	2.8	10
142	Primary structure of the hemoglobin ?-chain of Rose-ringed Parakeet (Psittacula krameri). The Protein Journal, 1989, 8, 481-486.	1.1	3
143	Structural features of lipoprotein lipase. Lipase family relationships, binding interactions, non-equivalence of lipase cofactors, vitellogenin similarities and functional subdivision of lipoprotein lipase. FEBS Journal, 1989, 179, 39-45.	0.2	129
144	Human insulin-like growth-factor-binding protein. Low-molecular-mass form: protein sequence and cDNA cloning. FEBS Journal, 1989, 180, 259-265.	0.2	49

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145	Eye lens .zeta.-crystallin relationships to the family of "long-chain" alcohol/polyol dehydrogenases. Protein trimming and conservation of stable parts. <i>Biochemistry</i> , 1989, 28, 6133-6139.	2.5	100
146	Isolation and characterization of porcine diazepam-binding inhibitor, a polypeptide not only of cerebral occurrence but also common in intestinal tissues and with effects on regulation of insulin release. <i>FEBS Journal</i> , 1988, 174, 239-244.	0.2	127
147	Primary structure of the hemoglobin $\gamma$ -chain of rose-ringed parakeet ( <i>Psittacula krameri</i> ). <i>The Protein Journal</i> , 1988, 7, 561-569.	1.1	13
148	Alcohol dehydrogenases and aldehyde dehydrogenases. <i>Biochemical Society Transactions</i> , 1988, 16, 223-227.	3.4	12
149	Novel N-terminal fragments of pro- $\beta$ -melanocyte-stimulating hormone isolated from pig pituitary. <i>Regulatory Peptides</i> , 1987, 19, 325-333.	1.9	0
150	Characteristics of alcohol/polyol dehydrogenases. The zinc-containing long-chain alcohol dehydrogenases. <i>FEBS Journal</i> , 1987, 167, 195-201.	0.2	272
151	Sequence determinants of cytosolic N-terminal protein processing. <i>FEBS Journal</i> , 1986, 154, 193-196.	0.2	297
152	Structures of N-terminally acetylated proteins. <i>FEBS Journal</i> , 1985, 152, 523-527.	0.2	184
153	Amino acid sequence restriction in relation to proteolysis. <i>Bioscience Reports</i> , 1983, 3, 225-232.	2.4	16