

# Gilbert Deleage

## List of Publications by Year in descending order

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81  
papers

7,404  
citations

109137

35  
h-index

66788

78  
g-index

81  
all docs

81  
docs citations

81  
times ranked

9385  
citing authors

#	ARTICLE	IF	CITATIONS
1	NPS@: Network Protein Sequence Analysis. Trends in Biochemical Sciences, 2000, 25, 147-150.	3.7	1,468
2	Consensus proposals for a unified system of nomenclature of hepatitis C virus genotypes. Hepatology, 2005, 42, 962-973.	3.6	1,303
3	Geno3D: automatic comparative molecular modelling of protein. Bioinformatics, 2002, 18, 213-214.	1.8	378
4	Genetic capsid modifications allow efficient re-targeting of adeno-associated virus type 2. Nature Medicine, 1999, 5, 1052-1056.	15.2	337
5	An algorithm for protein secondary structure prediction based on class prediction. Protein Engineering, Design and Selection, 1987, 1, 289-294.	1.0	316
6	SOPM: a self-optimized method for protein secondary structure prediction. Protein Engineering, Design and Selection, 1994, 7, 157-164.	1.0	296
7	PDB_REDO: automated re-refinement of X-ray structure models in the PDB. Journal of Applied Crystallography, 2009, 42, 376-384.	1.9	204
8	HBVdb: a knowledge database for Hepatitis B Virus. Nucleic Acids Research, 2013, 41, D566-D570.	6.5	178
9	Conservation of the Conformation and Positive Charges of Hepatitis C Virus E2 Envelope Glycoprotein Hypervariable Region 1 Points to a Role in Cell Attachment. Journal of Virology, 2001, 75, 5703-5710.	1.5	167
10	A new bioinformatic approach to detect common 3D sites in protein structures. Proteins: Structure, Function and Bioinformatics, 2003, 52, 137-145.	1.5	154
11	Structure and organization of the Bombyx mori sericin 1 gene and of the sericins 1 deduced from the sequence of the Ser 1B cDNA. Insect Biochemistry and Molecular Biology, 1997, 27, 469-477.	1.2	129
12	ANTHEPROT: An integrated protein sequence analysis software with client/server capabilities. Computers in Biology and Medicine, 2001, 31, 259-267.	3.9	128
13	euHCVdb: the European hepatitis C virus database. Nucleic Acids Research, 2007, 35, D363-D366.	6.5	128
14	Modifications in the binding domain of avian retrovirus envelope protein to redirect the host range of retroviral vectors. Journal of Virology, 1994, 68, 4609-4619.	1.5	124
15	Prediction of amphipathic in-plane membrane anchors in monotopic proteins using a SVM classifier. BMC Bioinformatics, 2006, 7, 255.	1.2	121
16	Insights into Early Extracellular Matrix Evolution: Spongin Short Chain Collagen-Related Proteins Are Homologous to Basement Membrane Type IV Collagens and Form a Novel Family Widely Distributed in Invertebrates. Molecular Biology and Evolution, 2006, 23, 2288-2302.	3.5	106
17	A comprehensive system for consistent numbering of HCV sequences, proteins and epitopes. Hepatology, 2006, 44, 1355-1361.	3.6	105
18	Protein structure prediction. Implications for the biologist. Biochimie, 1997, 79, 681-686.	1.3	89

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19	A common mechanism for ATP hydrolysis in ABC transporter and helicase superfamilies. Trends in Biochemical Sciences, 2001, 26, 539-544.	3.7	86
20	The SuMo server: 3D search for protein functional sites. Bioinformatics, 2005, 21, 3929-3930.	1.8	79
21	Dimerization Kinetics of HIV-1 and HIV-2 Reverse Transcriptase: A Two Step Process. Journal of Molecular Biology, 1995, 245, 508-521.	2.0	72
22	Characterization of a bacterial gene encoding an autophosphorylating protein tyrosine kinase. Gene, 1997, 204, 259-265.	1.0	69
23	Cloning and sequence analysis of a polygalacturonase-encoding gene from the phytopathogenic fungus Sclerotinia sclerotiorum. Gene, 1994, 146, 233-237.	1.0	63
24	Recombinant N-terminal Nucleotide-binding Domain from Mouse P-glycoprotein. Journal of Biological Chemistry, 1996, 271, 11652-11658.	1.6	60
25	NMR Structure and Molecular Dynamics of the In-Plane Membrane Anchor of Nonstructural Protein 5A from Bovine Viral Diarrhea Virus,. Biochemistry, 2006, 45, 2221-2233.	1.2	53
26	Identification of related proteins with weak sequence identity using secondary structure information. Protein Science, 2001, 10, 788-797.	3.1	50
27	AF15q14, a novel partner gene fused to the MLL gene in an acute myeloid leukaemia with a t(11;15)(q23;q14). Oncogene, 2000, 19, 4446-4450.	2.6	49
28	ANTHEPROT 2.0: A three-dimensional module fully coupled with protein sequence analysis methods. Journal of Molecular Graphics, 1995, 13, 209-212.	1.7	47
29	ALIGNSEC: viewing protein secondary structure predictions within large multiple sequence alignments. Bioinformatics, 2017, 33, 3991-3992.	1.8	47
30	Antheprot: An interactive graphics software for analyzing protein structures from sequences. Journal of Molecular Graphics, 1991, 9, 188-190.	1.7	43
31	Identification of the idiosyncratic bacterial protein tyrosine kinase (BY-kinase) family signature. Bioinformatics, 2008, 24, 2427-2430.	1.8	42
32	Virus-neutralizing monoclonal antibody to a conserved epitope on the duck hepatitis B virus pre-S protein. Journal of Virology, 1990, 64, 1290-1297.	1.5	42
33	Three-dimensional structure of the DNA-binding domain of the fructose repressor from Escherichia coli by 1H and 15N NMR. Journal of Molecular Biology, 1997, 270, 496-510.	2.0	40
34	ViralORFeome: an integrated database to generate a versatile collection of viral ORFs. Nucleic Acids Research, 2010, 38, D371-D378.	6.5	38
35	Thyroglobulin Represents a Novel Molecular Architecture of Vertebrates. Journal of Biological Chemistry, 2016, 291, 16553-16566.	1.6	38
36	Duck hepatitis B virus can tolerate insertion, deletion, and partial frameshift mutation in the distal pre-S region. Journal of Virology, 1989, 63, 4965-4968.	1.5	37

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37	Hepatitis C databases, principles and utility to researchers. <i>Hepatology</i> , 2006, 43, 1157-1165.	3.6	36
38	Definition of a consensus DNA-binding site for the Escherichia coli pleiotropic regulatory protein, FruR. <i>Molecular Microbiology</i> , 1996, 21, 257-266.	1.2	35
39	Conserved Determinants for Membrane Association of Nonstructural Protein 5A from Hepatitis C Virus and Related Viruses. <i>Journal of Virology</i> , 2007, 81, 2745-2757.	1.5	35
40	HCVDB. <i>Applied Bioinformatics</i> , 2004, 3, 237-240.	1.7	32
41	Structural Analysis of the Heparin-Binding Site of the NC1 Domain of Collagen XIV by CD and NMR. <i>Biochemistry</i> , 1999, 38, 6479-6488.	1.2	31
42	Detection of unrelated proteins in sequences multiple alignments by using predicted secondary structures. <i>Bioinformatics</i> , 2003, 19, 506-512.	1.8	31
43	BYKdb: the Bacterial protein tyrosine Kinase database. <i>Nucleic Acids Research</i> , 2012, 40, D321-D324.	6.5	30
44	Low Resolution Structure Determination Shows Procollagen C-Proteinase Enhancer to be an Elongated Multidomain Glycoprotein. <i>Journal of Biological Chemistry</i> , 2003, 278, 7199-7205.	1.6	29
45	Integrated databanks access and sequence/structure analysis services at the PBIL. <i>Nucleic Acids Research</i> , 2003, 31, 3393-3399.	6.5	28
46	Common topology within a non-collagenous domain of several different collagen types. <i>Matrix Biology</i> , 1994, 14, 233-239.	1.5	26
47	Mutation in the melanocortin 1 receptor is associated with amber colour in the Norwegian Forest Cat. <i>Animal Genetics</i> , 2009, 40, 547-552.	0.6	26
48	Efficient reconstitution of mitochondrial energy-transfer reactions from depleted membranes and F1-ATPase as a function of the amount of bound oligomycin sensitivity-conferring protein (OSCP). <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1986, 852, 55-67.	0.5	25
49	Secondary structure of P-glycoprotein investigated by circular dichroism and amino acid sequence analysis. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1998, 1371, 317-334.	1.4	25
50	Intrinsic tryptophan fluorescence of Schizosaccharomyces pombe mitochondrial F1-ATPase. A powerful probe for phosphate and nucleotide interactions. <i>Biochemistry</i> , 1991, 30, 3256-3262.	1.2	23
51	Identification and characterization of a heparin binding site within the NC1 domain of chicken collagen XIV. <i>Matrix Biology</i> , 1998, 17, 145-149.	1.5	23
52	Correlations between ATP hydrolysis, ATP synthesis, generation and utilization of $\hat{p}H$ in mitochondrial ATPase-ATP synthase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1983, 725, 464-471.	0.5	22
53	A computerized version of the Chou and Fasman method for predicting the secondary structure of proteins. <i>Analytical Biochemistry</i> , 1987, 163, 292-297.	1.1	21
54	Identification of Antigenic Regions of Duck Hepatitis B Virus Core Protein with Antibodies Elicited by DNA Immunization and Chronic Infection. <i>Journal of Virology</i> , 2004, 78, 1945-1953.	1.5	20

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55	Interaction between .delta. and .epsilon. subunits of F1-ATPase from pig heart mitochondria. Circular dichroism and intrinsic fluorescence of purified and reconstituted .delta..epsilon. complex. <i>Biochemistry</i> , 1990, 29, 9358-9364.	1.2	18
56	Isolation and characterization of Urbain, a 20-hydroxyecdysone-inducible gene expressed during morphogenesis of <i>Bombyx mori</i> wing imaginal discs. <i>Roux's Archives of Developmental Biology</i> , 1996, 205, 333-343.	1.2	17
57	MSX-3D: a tool to validate 3D protein models using mass spectrometry. <i>Bioinformatics</i> , 2008, 24, 2782-2783.	1.8	17
58	BCL2DB: database of BCL-2 family members and BH3-only proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau013-bau013.	1.4	17
59	GeneFarm, structural and functional annotation of Arabidopsis gene and protein families by a network of experts. <i>Nucleic Acids Research</i> , 2004, 33, D641-D646.	6.5	16
60	Selective recognition of enzymatically active prostate-specific antigen (PSA) by anti-PSA monoclonal antibodies. <i>Journal of Molecular Recognition</i> , 2005, 18, 225-235.	1.1	16
61	Characterization of Two Genes Coding for a Similar Four-Cysteine Motif of the Amino-Terminal Propeptide of a Sea Urchin Fibrillar Collagen. <i>FEBS Journal</i> , 1995, 234, 59-65.	0.2	13
62	Characterization of mimotopes mimicking an immunodominant conformational epitope on the hepatitis C virus NS3 helicase. <i>Journal of Medical Virology</i> , 2004, 72, 385-395.	2.5	13
63	Grid Deployment of Legacy Bioinformatics Applications with Transparent Data Access. , 2006, , .		11
64	Characterization of prostate-specific antigen binding peptides selected by phage display technology. <i>Journal of Molecular Recognition</i> , 2006, 19, 10-20.	1.1	11
65	Evidence for crucial electrostatic interactions between Bcl-2 homology domains BH3 and BH4 in the anti-apoptotic Nr-13 protein. <i>Biochemical Journal</i> , 2002, 368, 213-221.	1.7	10
66	Ultradeep Pyrosequencing and Molecular Modeling Identify Key Structural Features of Hepatitis B Virus RNase H, a Putative Target for Antiviral Intervention. <i>Journal of Virology</i> , 2014, 88, 574-582.	1.5	10
67	Evidence for distinct complement regulatory and measles virus binding sites on CD46 SCR2. <i>European Journal of Immunology</i> , 2000, 30, 3457-3462.	1.6	9
68	SM2PH-db: an interactive system for the integrated analysis of phenotypic consequences of missense mutations in proteins involved in human genetic diseases. <i>Human Mutation</i> , 2010, 31, 127-135.	1.1	9
69	Blast sampling for structural and functional analyses. <i>BMC Bioinformatics</i> , 2007, 8, 62.	1.2	6
70	Structural aspects and orientation mechanism of mitochondrial F1-adenosine triphosphatase. Evidence for a negative electric birefringence due to a permanent moment perpendicular to the long axes of the particle. <i>Biochemistry</i> , 1986, 25, 2854-2858.	1.2	5
71	[39] Preparation of a highly coupled H <sup>+</sup> -transporting ATP synthase from pig heart mitochondria. <i>Methods in Enzymology</i> , 1986, 126, 417-427.	0.4	4
72	ANALYSIS OF PROSTATE SPECIFIC ANTIGEN AND Î±1-ANTICHYMOTRYPSIN INTERACTION USING ANTIPEPTIDE MONOCLONAL ANTIBODIES. <i>Journal of Urology</i> , 2001, 165, 301-306.	0.2	4

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73	Des protéines en 3D. Biofutur, 2000, 2000, 64-65.	0.0	3
74	Involvement of the C-terminal end of the prostate-specific antigen in a conformational epitope: characterization by proteolytic degradation of monoclonal antibody-bound antigen and mass spectrometry. Journal of Molecular Recognition, 2001, 14, 406-413.	1.1	3
75	Construction of atomic models of full hepatitis B vaccine particles at different stages of maturation. Journal of Molecular Graphics and Modelling, 2020, 98, 107610.	1.3	3
76	MAGOS: multiple alignment and modelling server. Bioinformatics, 2006, 22, 2164-2165.	1.8	2
77	Epitope of OSCP oligomycin sensitivity conferring protein exposed at the surface of the mitochondrial ATPase-ATP synthase complex. Biochimie, 1989, 71, 917-929.	1.3	1
78	Conservation of Amino Acids into Multiple Alignments Involved in Pairwise Interactions in Three-Dimensional Protein Structures. Journal of Bioinformatics and Computational Biology, 2003, 01, 505-520.	0.3	1
79	Web Services Interface to Run Protein Sequence Tools on Grid, Testcase of Protein Sequence Alignment. Lecture Notes in Computer Science, 2006, , 240-249.	1.0	1
80	HCVDB : base de données de séquences du virus de l'hépatite C et outils bio-informatiques d'analyse. Médecine/Sciences, 2002, 18, 639-639.	0.0	0
81	SuMo: A Tool for Protein Function Inference Based on 3D Structures Comparisons. Focus on Structural Biology, 2013, , 1-23.	0.1	0