

# Gilbert Deleage

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

81  
papers

6,340  
citations

33  
h-index

79  
g-index

81  
ext. papers

6,850  
ext. citations

7.2  
avg, IF

5.13  
L-index

#	Paper	IF	Citations
81	NPS@: network protein sequence analysis. <i>Trends in Biochemical Sciences</i> , <b>2000</b> , 25, 147-50	10.3	1250
80	Consensus proposals for a unified system of nomenclature of hepatitis C virus genotypes. <i>Hepatology</i> , <b>2005</b> , 42, 962-73	11.2	1136
79	Geno3D: automatic comparative molecular modelling of protein. <i>Bioinformatics</i> , <b>2002</b> , 18, 213-4	7.2	347
78	Genetic capsid modifications allow efficient re-targeting of adeno-associated virus type 2. <i>Nature Medicine</i> , <b>1999</b> , 5, 1052-6	50.5	273
77	An algorithm for protein secondary structure prediction based on class prediction. <i>Protein Engineering, Design and Selection</i> , <b>1987</b> , 1, 289-94	1.9	261
76	SOPM: a self-optimized method for protein secondary structure prediction. <i>Protein Engineering, Design and Selection</i> , <b>1994</b> , 7, 157-64	1.9	254
75	PDB_REDO: automated re-refinement of X-ray structure models in the PDB. <i>Journal of Applied Crystallography</i> , <b>2009</b> , 42, 376-384	3.8	157
74	Conservation of the conformation and positive charges of hepatitis C virus E2 envelope glycoprotein hypervariable region 1 points to a role in cell attachment. <i>Journal of Virology</i> , <b>2001</b> , 75, 5703-10	6.6	151
73	A new bioinformatic approach to detect common 3D sites in protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 52, 137-45	4.2	134
72	HBVdb: a knowledge database for Hepatitis B Virus. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D566-70	20.1	125
71	ANTHEPROT: an integrated protein sequence analysis software with client/server capabilities. <i>Computers in Biology and Medicine</i> , <b>2001</b> , 31, 259-67	7	118
70	euHCVdb: the European hepatitis C virus database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D363-6	20.1	116
69	Structure and organization of the Bombyx mori sericin 1 gene and of the sericins 1 deduced from the sequence of the Ser 1B cDNA. <i>Insect Biochemistry and Molecular Biology</i> , <b>1997</b> , 27, 469-77	4.5	106
68	Prediction of amphipathic in-plane membrane anchors in monotopic proteins using a SVM classifier. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 255	3.6	102
67	Modifications in the binding domain of avian retrovirus envelope protein to redirect the host range of retroviral vectors. <i>Journal of Virology</i> , <b>1994</b> , 68, 4609-19	6.6	99
66	A comprehensive system for consistent numbering of HCV sequences, proteins and epitopes. <i>Hepatology</i> , <b>2006</b> , 44, 1355-61	11.2	93
65	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. <i>Molecular Biology and Evolution</i> , <b>2006</b> , 23, 2288-302	8.3	85

64	Protein structure prediction. Implications for the biologist. <i>Biochimie</i> , <b>1997</b> , 79, 681-6	4.6	84
63	A common mechanism for ATP hydrolysis in ABC transporter and helicase superfamilies. <i>Trends in Biochemical Sciences</i> , <b>2001</b> , 26, 539-44	10.3	80
62	The SuMo server: 3D search for protein functional sites. <i>Bioinformatics</i> , <b>2005</b> , 21, 3929-30	7.2	71
61	Dimerization kinetics of HIV-1 and HIV-2 reverse transcriptase: a two step process. <i>Journal of Molecular Biology</i> , <b>1995</b> , 245, 508-21	6.5	65
60	Characterization of a bacterial gene encoding an autophosphorylating protein tyrosine kinase. <i>Gene</i> , <b>1997</b> , 204, 259-65	3.8	61
59	Recombinant N-terminal nucleotide-binding domain from mouse P-glycoprotein. Overexpression, purification, and role of cysteine 430. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 11652-8	5.4	60
58	Cloning and sequence analysis of a polygalacturonase-encoding gene from the phytopathogenic fungus <i>Sclerotinia sclerotiorum</i> . <i>Gene</i> , <b>1994</b> , 146, 233-7	3.8	55
57	Identification of related proteins with weak sequence identity using secondary structure information. <i>Protein Science</i> , <b>2001</b> , 10, 788-97	6.3	46
56	NMR structure and molecular dynamics of the in-plane membrane anchor of nonstructural protein 5A from bovine viral diarrhea virus. <i>Biochemistry</i> , <b>2006</b> , 45, 2221-33	3.2	44
55	AF15q14, a novel partner gene fused to the MLL gene in an acute myeloid leukaemia with a t(11;15)(q23;q14). <i>Oncogene</i> , <b>2000</b> , 19, 4446-50	9.2	40
54	ANTHEPROT 2.0: a three-dimensional module fully coupled with protein sequence analysis methods. <i>Journal of Molecular Graphics</i> , <b>1995</b> , 13, 209-12, 199-200		40
53	Identification of the idiosyncratic bacterial protein tyrosine kinase (BY-kinase) family signature. <i>Bioinformatics</i> , <b>2008</b> , 24, 2427-30	7.2	37
52	ANTHEPROT: an interactive graphics software for analyzing protein structures from sequences. <i>Journal of Molecular Graphics</i> , <b>1991</b> , 9, 188-90, 167		36
51	ViralORFeome: an integrated database to generate a versatile collection of viral ORFs. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D371-8	20.1	35
50	Three-dimensional structure of the DNA-binding domain of the fructose repressor from <i>Escherichia coli</i> by 1H and 15N NMR. <i>Journal of Molecular Biology</i> , <b>1997</b> , 270, 496-510	6.5	34
49	Hepatitis C databases, principles and utility to researchers. <i>Hepatology</i> , <b>2006</b> , 43, 1157-65	11.2	33
48	Definition of a consensus DNA-binding site for the <i>Escherichia coli</i> pleiotropic regulatory protein, FruR. <i>Molecular Microbiology</i> , <b>1996</b> , 21, 257-66	4.1	33
47	Virus-neutralizing monoclonal antibody to a conserved epitope on the duck hepatitis B virus pre-S protein. <i>Journal of Virology</i> , <b>1990</b> , 64, 1290-7	6.6	33

46	Conserved determinants for membrane association of nonstructural protein 5A from hepatitis C virus and related viruses. <i>Journal of Virology</i> , <b>2007</b> , 81, 2745-57	6.6	30
45	Structural analysis of the heparin-binding site of the NC1 domain of collagen XIV by CD and NMR. <i>Biochemistry</i> , <b>1999</b> , 38, 6479-88	3.2	30
44	HCVDB: hepatitis C virus sequences database. <i>Applied Bioinformatics</i> , <b>2004</b> , 3, 237-40		28
43	Duck hepatitis B virus can tolerate insertion, deletion, and partial frameshift mutation in the distal pre-S region. <i>Journal of Virology</i> , <b>1989</b> , 63, 4965-8	6.6	27
42	ALIGNSEC: viewing protein secondary structure predictions within large multiple sequence alignments. <i>Bioinformatics</i> , <b>2017</b> , 33, 3991-3992	7.2	26
41	Low resolution structure determination shows procollagen C-proteinase enhancer to be an elongated multidomain glycoprotein. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 7199-205	5.4	26
40	Common topology within a non-collagenous domain of several different collagen types. <i>Matrix Biology</i> , <b>1994</b> , 14, 233-9	11.4	26
39	BYKdb: the Bacterial protein tyrosine Kinase database. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D321-4	20.1	25
38	Integrated databanks access and sequence/structure analysis services at the PBIL. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3393-9	20.1	25
37	Thyroglobulin Represents a Novel Molecular Architecture of Vertebrates. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 16553-66	5.4	25
36	Detection of unrelated proteins in sequences multiple alignments by using predicted secondary structures. <i>Bioinformatics</i> , <b>2003</b> , 19, 506-12	7.2	24
35	Intrinsic tryptophan fluorescence of <i>Schizosaccharomyces pombe</i> mitochondrial F1-ATPase. A powerful probe for phosphate and nucleotide interactions. <i>Biochemistry</i> , <b>1991</b> , 30, 3256-62	3.2	23
34	Mutation in the melanocortin 1 receptor is associated with amber colour in the Norwegian Forest Cat. <i>Animal Genetics</i> , <b>2009</b> , 40, 547-52	2.5	22
33	Identification and characterization of a heparin binding site within the NC1 domain of chicken collagen XIV. <i>Matrix Biology</i> , <b>1998</b> , 17, 145-9	11.4	21
32	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> , <b>1986</b> , 852, 55-67	4.6	21
31	Secondary structure of P-glycoprotein investigated by circular dichroism and amino acid sequence analysis. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>1998</b> , 1371, 317-34	3.8	19
30	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> , <b>2004</b> , 78, 1945-53	6.6	19
29	Correlations between ATP hydrolysis, ATP synthesis, generation and utilization of delta pH in mitochondrial ATPase-ATP synthase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , <b>1983</b> , 725, 464-71	4.6	19

28	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> , <b>1990</b> , 29, 9358-64	3.2	17
27	A computerized version of the Chou and Fasman method for predicting the secondary structure of proteins. <i>Analytical Biochemistry</i> , <b>1987</b> , 163, 292-7	3.1	17
26	Selective recognition of enzymatically active prostate-specific antigen (PSA) by anti-PSA monoclonal antibodies. <i>Journal of Molecular Recognition</i> , <b>2005</b> , 18, 225-35	2.6	16
25	MSX-3D: a tool to validate 3D protein models using mass spectrometry. <i>Bioinformatics</i> , <b>2008</b> , 24, 2782-3	7.2	15
24	GeneFarm, structural and functional annotation of Arabidopsis gene and protein families by a network of experts. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D641-6	20.1	15
23	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> , <b>1996</b> , 205, 333-343		15
22	Characterization of mimotopes mimicking an immunodominant conformational epitope on the hepatitis C virus NS3 helicase. <i>Journal of Medical Virology</i> , <b>2004</b> , 72, 385-95	19.7	13
21	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> , <b>1995</b> , 234, 59-65		13
20	BCL2DB: database of BCL-2 family members and BH3-only proteins. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2014</b> , 2014, bau013	5	12
19	Characterization of prostate-specific antigen binding peptides selected by phage display technology. <i>Journal of Molecular Recognition</i> , <b>2006</b> , 19, 10-20	2.6	10
18	Evidence for crucial electrostatic interactions between Bcl-2 homology domains BH3 and BH4 in the anti-apoptotic Nr-13 protein. <i>Biochemical Journal</i> , <b>2002</b> , 368, 213-21	3.8	9
17	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> , <b>2010</b> , 31, 127-35	4.7	8
16	Evidence for distinct complement regulatory and measles virus binding sites on CD46 SCR2. <i>European Journal of Immunology</i> , <b>2000</b> , 30, 3457-62	6.1	8
15	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> , <b>2014</b> , 88, 574-82	6.6	7
14	Grid Deployment of Legacy Bioinformatics Applications with Transparent Data Access <b>2006</b> ,		6
13	Blast sampling for structural and functional analyses. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 62	3.6	5
12	Structural aspects and orientation mechanism of mitochondrial F1 adenosinetriphosphatase. Evidence for a negative electric birefringence due to a permanent moment perpendicular to the long axes of the particle. <i>Biochemistry</i> , <b>1986</b> , 25, 2854-8	3.2	5
11	Construction of atomic models of full hepatitis B vaccine particles at different stages of maturation. <i>Journal of Molecular Graphics and Modelling</i> , <b>2020</b> , 98, 107610	2.8	3

10	Des protéines en 3D. <i>Biofutur</i> , <b>2000</b> , 2000, 64-65		3
9	Analysis of prostate specific antigen and alpha1-antichymotrypsin interaction using antipeptide monoclonal antibodies. <i>Journal of Urology</i> , <b>2001</b> , 165, 301-6	2.5	3
8	Preparation of a highly coupled H(+)-transporting ATP synthase from pig heart mitochondria. <i>Methods in Enzymology</i> , <b>1986</b> , 126, 417-27	1.7	3
7	MAGOS: multiple alignment and modelling server. <i>Bioinformatics</i> , <b>2006</b> , 22, 2164-5	7.2	2
6	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. <i>Journal of Molecular Recognition</i> , <b>2001</b> , 14, 406-13	2.6	2
5	Web Services Interface to Run Protein Sequence Tools on Grid, Testcase of Protein Sequence Alignment. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 240-249	0.9	1
4	Conservation of amino acids into multiple alignments involved in pairwise interactions in three-dimensional protein structures. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2003</b> , 1, 505-520	1	1
3	Epitope of OSCP oligomycin sensitivity conferring protein exposed at the surface of the mitochondrial ATPase-ATP synthase complex. <i>Biochimie</i> , <b>1989</b> , 71, 917-29	4.6	1
2	HCVDB : base de données de séquences du virus de l'hépatite C et outils bio-informatiques d'analyse. <i>Medecine/Sciences</i> , <b>2002</b> , 18, 639-639		
1	SuMo: A Tool for Protein Function Inference Based on 3D Structures Comparisons. <i>Focus on Structural Biology</i> , <b>2013</b> , 1-23		