

Gilbert Deleage

List of Publications by Year in Descending Order

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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 | Construction of atomic models of full hepatitis B vaccine particles at different stages of maturation. <i>Journal of Molecular Graphics and Modelling</i> , 2020 , 98, 107610 | 2.8 | 3 |
| 80 | ALIGNSEC: viewing protein secondary structure predictions within large multiple sequence alignments. <i>Bioinformatics</i> , 2017 , 33, 3991-3992 | 7.2 | 26 |
| 79 | Thyroglobulin Represents a Novel Molecular Architecture of Vertebrates. <i>Journal of Biological Chemistry</i> , 2016 , 291, 16553-66 | 5.4 | 25 |
| 78 | 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, 574-82 | 6.6 | 7 |
| 77 | BCL2DB: database of BCL-2 family members and BH3-only proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014, bau013 | 5 | 12 |
| 76 | HBVdb: a knowledge database for Hepatitis B Virus. <i>Nucleic Acids Research</i> , 2013 , 41, D566-70 | 20.1 | 125 |
| 75 | SuMo: A Tool for Protein Function Inference Based on 3D Structures Comparisons. <i>Focus on Structural Biology</i> , 2013 , 1-23 | | |
| 74 | BYKdb: the Bacterial protein tyrosine Kinase database. <i>Nucleic Acids Research</i> , 2012 , 40, D321-4 | 20.1 | 25 |
| 73 | ViralORFeome: an integrated database to generate a versatile collection of viral ORFs. <i>Nucleic Acids Research</i> , 2010 , 38, D371-8 | 20.1 | 35 |
| 72 | 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, 127-35 | 4.7 | 8 |
| 71 | PDB_REDO: automated re-refinement of X-ray structure models in the PDB. <i>Journal of Applied Crystallography</i> , 2009 , 42, 376-384 | 3.8 | 157 |
| 70 | Mutation in the melanocortin 1 receptor is associated with amber colour in the Norwegian Forest Cat. <i>Animal Genetics</i> , 2009 , 40, 547-52 | 2.5 | 22 |
| 69 | MSX-3D: a tool to validate 3D protein models using mass spectrometry. <i>Bioinformatics</i> , 2008 , 24, 2782-3 | 7.2 | 15 |
| 68 | Identification of the idiosyncratic bacterial protein tyrosine kinase (BY-kinase) family signature. <i>Bioinformatics</i> , 2008 , 24, 2427-30 | 7.2 | 37 |
| 67 | Blast sampling for structural and functional analyses. <i>BMC Bioinformatics</i> , 2007 , 8, 62 | 3.6 | 5 |
| 66 | euHCVdb: the European hepatitis C virus database. <i>Nucleic Acids Research</i> , 2007 , 35, D363-6 | 20.1 | 116 |
| 65 | Conserved determinants for membrane association of nonstructural protein 5A from hepatitis C virus and related viruses. <i>Journal of Virology</i> , 2007 , 81, 2745-57 | 6.6 | 30 |

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| 64 | Prediction of amphipathic in-plane membrane anchors in monotopic proteins using a SVM classifier. <i>BMC Bioinformatics</i> , 2006 , 7, 255 | 3.6 | 102 |
| 63 | Hepatitis C databases, principles and utility to researchers. <i>Hepatology</i> , 2006 , 43, 1157-65 | 11.2 | 33 |
| 62 | A comprehensive system for consistent numbering of HCV sequences, proteins and epitopes. <i>Hepatology</i> , 2006 , 44, 1355-61 | 11.2 | 93 |
| 61 | Characterization of prostate-specific antigen binding peptides selected by phage display technology. <i>Journal of Molecular Recognition</i> , 2006 , 19, 10-20 | 2.6 | 10 |
| 60 | 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> , 2006 , 23, 2288-302 | 8.3 | 85 |
| 59 | Grid Deployment of Legacy Bioinformatics Applications with Transparent Data Access 2006 , | | 6 |
| 58 | NMR structure and molecular dynamics of the in-plane membrane anchor of nonstructural protein 5A from bovine viral diarrhea virus. <i>Biochemistry</i> , 2006 , 45, 2221-33 | 3.2 | 44 |
| 57 | Web Services Interface to Run Protein Sequence Tools on Grid, Testcase of Protein Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2006 , 240-249 | 0.9 | 1 |
| 56 | MAGOS: multiple alignment and modelling server. <i>Bioinformatics</i> , 2006 , 22, 2164-5 | 7.2 | 2 |
| 55 | The SuMo server: 3D search for protein functional sites. <i>Bioinformatics</i> , 2005 , 21, 3929-30 | 7.2 | 71 |
| 54 | GeneFarm, structural and functional annotation of Arabidopsis gene and protein families by a network of experts. <i>Nucleic Acids Research</i> , 2005 , 33, D641-6 | 20.1 | 15 |
| 53 | Consensus proposals for a unified system of nomenclature of hepatitis C virus genotypes. <i>Hepatology</i> , 2005 , 42, 962-73 | 11.2 | 1136 |
| 52 | Selective recognition of enzymatically active prostate-specific antigen (PSA) by anti-PSA monoclonal antibodies. <i>Journal of Molecular Recognition</i> , 2005 , 18, 225-35 | 2.6 | 16 |
| 51 | 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, 1945-53 | 6.6 | 19 |
| 50 | Characterization of mimotopes mimicking an immunodominant conformational epitope on the hepatitis C virus NS3 helicase. <i>Journal of Medical Virology</i> , 2004 , 72, 385-95 | 19.7 | 13 |
| 49 | HCVDB: hepatitis C virus sequences database. <i>Applied Bioinformatics</i> , 2004 , 3, 237-40 | | 28 |
| 48 | Integrated databanks access and sequence/structure analysis services at the PBIL. <i>Nucleic Acids Research</i> , 2003 , 31, 3393-9 | 20.1 | 25 |
| 47 | Conservation of amino acids into multiple alignments involved in pairwise interactions in three-dimensional protein structures. <i>Journal of Bioinformatics and Computational Biology</i> , 2003 , 1, 505-520 | | 1 |

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| 46 | Detection of unrelated proteins in sequences multiple alignments by using predicted secondary structures. <i>Bioinformatics</i> , 2003 , 19, 506-12 | 7.2 | 24 |
| 45 | A new bioinformatic approach to detect common 3D sites in protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 137-45 | 4.2 | 134 |
| 44 | Low resolution structure determination shows procollagen C-proteinase enhancer to be an elongated multidomain glycoprotein. <i>Journal of Biological Chemistry</i> , 2003 , 278, 7199-205 | 5.4 | 26 |
| 43 | Geno3D: automatic comparative molecular modelling of protein. <i>Bioinformatics</i> , 2002 , 18, 213-4 | 7.2 | 347 |
| 42 | 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, 213-21 | 3.8 | 9 |
| 41 | HCVDB : base de données de séquences du virus de l'hépatite C et outils bio-informatiques d'analyse. <i>Medecine/Sciences</i> , 2002 , 18, 639-639 | | |
| 40 | Involvement of the C-terminal end of the prostrate-specific antigen in a conformational epitope: characterization by proteolytic degradation of monoclonal antibody-bound antigen and mass spectrometry. <i>Journal of Molecular Recognition</i> , 2001 , 14, 406-13 | 2.6 | 2 |
| 39 | Identification of related proteins with weak sequence identity using secondary structure information. <i>Protein Science</i> , 2001 , 10, 788-97 | 6.3 | 46 |
| 38 | ANTHEPROT: an integrated protein sequence analysis software with client/server capabilities. <i>Computers in Biology and Medicine</i> , 2001 , 31, 259-67 | 7 | 118 |
| 37 | A common mechanism for ATP hydrolysis in ABC transporter and helicase superfamilies. <i>Trends in Biochemical Sciences</i> , 2001 , 26, 539-44 | 10.3 | 80 |
| 36 | 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> , 2001 , 75, 5703-10 | 6.6 | 151 |
| 35 | Analysis of prostate specific antigen and alpha1-antichymotrypsin interaction using anti-peptide monoclonal antibodies. <i>Journal of Urology</i> , 2001 , 165, 301-6 | 2.5 | 3 |
| 34 | Evidence for distinct complement regulatory and measles virus binding sites on CD46 SCR2. <i>European Journal of Immunology</i> , 2000 , 30, 3457-62 | 6.1 | 8 |
| 33 | 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> , 2000 , 19, 4446-50 | 9.2 | 40 |
| 32 | NPS@: network protein sequence analysis. <i>Trends in Biochemical Sciences</i> , 2000 , 25, 147-50 | 10.3 | 1250 |
| 31 | Des protéines en 3D. <i>Biofutur</i> , 2000 , 2000, 64-65 | | 3 |
| 30 | Genetic capsid modifications allow efficient re-targeting of adeno-associated virus type 2. <i>Nature Medicine</i> , 1999 , 5, 1052-6 | 50.5 | 273 |
| 29 | Structural analysis of the heparin-binding site of the NC1 domain of collagen XIV by CD and NMR. <i>Biochemistry</i> , 1999 , 38, 6479-88 | 3.2 | 30 |

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| 28 | Identification and characterization of a heparin binding site within the NC1 domain of chicken collagen XIV. <i>Matrix Biology</i> , 1998 , 17, 145-9 | 11.4 | 21 |
| 27 | Secondary structure of P-glycoprotein investigated by circular dichroism and amino acid sequence analysis. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1998 , 1371, 317-34 | 3.8 | 19 |
| 26 | Three-dimensional structure of the DNA-binding domain of the fructose repressor from Escherichia coli by 1H and 15N NMR. <i>Journal of Molecular Biology</i> , 1997 , 270, 496-510 | 6.5 | 34 |
| 25 | 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> , 1997 , 27, 469-77 | 4.5 | 106 |
| 24 | Protein structure prediction. Implications for the biologist. <i>Biochimie</i> , 1997 , 79, 681-6 | 4.6 | 84 |
| 23 | Characterization of a bacterial gene encoding an autophosphorylating protein tyrosine kinase. <i>Gene</i> , 1997 , 204, 259-65 | 3.8 | 61 |
| 22 | Recombinant N-terminal nucleotide-binding domain from mouse P-glycoprotein. Overexpression, purification, and role of cysteine 430. <i>Journal of Biological Chemistry</i> , 1996 , 271, 11652-8 | 5.4 | 60 |
| 21 | Definition of a consensus DNA-binding site for the Escherichia coli pleiotropic regulatory protein, FruR. <i>Molecular Microbiology</i> , 1996 , 21, 257-66 | 4.1 | 33 |
| 20 | Isolation and characterization of Urbain, a 20-hydroxyecdysone-inducible gene expressed during morphogenesis of Bombyx mori wing imaginal discs. <i>Roux's Archives of Developmental Biology</i> , 1996 , 205, 333-343 | | 15 |
| 19 | ANTHEPROT 2.0: a three-dimensional module fully coupled with protein sequence analysis methods. <i>Journal of Molecular Graphics</i> , 1995 , 13, 209-12, 199-200 | | 40 |
| 18 | Dimerization kinetics of HIV-1 and HIV-2 reverse transcriptase: a two step process. <i>Journal of Molecular Biology</i> , 1995 , 245, 508-21 | 6.5 | 65 |
| 17 | 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 | | 13 |
| 16 | Common topology within a non-collagenous domain of several different collagen types. <i>Matrix Biology</i> , 1994 , 14, 233-9 | 11.4 | 26 |
| 15 | Cloning and sequence analysis of a polygalacturonase-encoding gene from the phytopathogenic fungus Sclerotinia sclerotiorum. <i>Gene</i> , 1994 , 146, 233-7 | 3.8 | 55 |
| 14 | SOPM: a self-optimized method for protein secondary structure prediction. <i>Protein Engineering, Design and Selection</i> , 1994 , 7, 157-64 | 1.9 | 254 |
| 13 | Modifications in the binding domain of avian retrovirus envelope protein to redirect the host range of retroviral vectors. <i>Journal of Virology</i> , 1994 , 68, 4609-19 | 6.6 | 99 |
| 12 | ANTHEPROT: an interactive graphics software for analyzing protein structures from sequences. <i>Journal of Molecular Graphics</i> , 1991 , 9, 188-90, 167 | | 36 |
| 11 | Intrinsic tryptophan fluorescence of Schizosaccharomyces pombe mitochondrial F1-ATPase. A powerful probe for phosphate and nucleotide interactions. <i>Biochemistry</i> , 1991 , 30, 3256-62 | 3.2 | 23 |

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|----|--|-----|-----|
| 10 | 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, 9358-64 | 3.2 | 17 |
| 9 | Virus-neutralizing monoclonal antibody to a conserved epitope on the duck hepatitis B virus pre-S protein. <i>Journal of Virology</i> , 1990 , 64, 1290-7 | 6.6 | 33 |
| 8 | Epitope of OSCP oligomycin sensitivity conferring protein exposed at the surface of the mitochondrial ATPase-ATP synthase complex. <i>Biochimie</i> , 1989 , 71, 917-29 | 4.6 | 1 |
| 7 | Duck hepatitis B virus can tolerate insertion, deletion, and partial frameshift mutation in the distal pre-S region. <i>Journal of Virology</i> , 1989 , 63, 4965-8 | 6.6 | 27 |
| 6 | An algorithm for protein secondary structure prediction based on class prediction. <i>Protein Engineering, Design and Selection</i> , 1987 , 1, 289-94 | 1.9 | 261 |
| 5 | A computerized version of the Chou and Fasman method for predicting the secondary structure of proteins. <i>Analytical Biochemistry</i> , 1987 , 163, 292-7 | 3.1 | 17 |
| 4 | 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 | 4.6 | 21 |
| 3 | 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> , 1986 , 25, 2854-8 | 3.2 | 5 |
| 2 | Preparation of a highly coupled H(+)-transporting ATP synthase from pig heart mitochondria. <i>Methods in Enzymology</i> , 1986 , 126, 417-27 | 1.7 | 3 |
| 1 | Correlations between ATP hydrolysis, ATP synthesis, generation and utilization of delta pH in mitochondrial ATPase-ATP synthase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1983 , 725, 464-71 | 4.6 | 19 |