

Andrey V Kajava

List of Publications by Year in descending order

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151
papers

10,277
citations

38742

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37204

96
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156
all docs

156
docs citations

156
times ranked

12678
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Aspartateâ€phobia of thermophiles as a reaction to deleterious chemical transformations. <i>BioEssays</i> , 2022, 44, e2100213. | 2.5 | 2 |
| 2 | The C-terminal segment of <i>Leishmania major</i> HslU: Toward potential inhibitors of LmHslVU activity. <i>Biorganic Chemistry</i> , 2022, 119, 105539. | 4.1 | 1 |
| 3 | TAPASS: Tool for annotation of protein amyloidogenicity in the context of other structural states. <i>Journal of Structural Biology</i> , 2022, 214, 107840. | 2.8 | 9 |
| 4 | Predicting Protein Conformational Disorder and Disordered Binding Sites. <i>Methods in Molecular Biology</i> , 2022, 2449, 95-147. | 0.9 | 4 |
| 5 | Seroreactivity of the Severe Acute Respiratory Syndrome Coronavirus 2 Recombinant S Protein, Receptor-Binding Domain, and Its Receptor-Binding Motif in COVID-19 Patients and Their Cross-Reactivity With Pre-COVID-19 Samples From Malaria-Endemic Areas. <i>Frontiers in Immunology</i> , 2022, 13, 856033. | 4.8 | 5 |
| 6 | A SARSâ€CoV-2 Spike Receptor Binding Motif Peptide Induces Anti-Spike Antibodies in Mice and Is Recognized by COVID-19 Patients. <i>Frontiers in Immunology</i> , 2022, 13, . | 4.8 | 2 |
| 7 | RepeatsDB in 2021: improved data and extended classification for protein tandem repeat structures. <i>Nucleic Acids Research</i> , 2021, 49, D452-D457. | 14.5 | 37 |
| 8 | Critical assessment of protein intrinsic disorder prediction. <i>Nature Methods</i> , 2021, 18, 472-481. | 19.0 | 187 |
| 9 | Immunoreactivity of Sera From Low to Moderate Malaria-Endemic Areas Against <i>Plasmodium vivax</i> rPvs48/45 Proteins Produced in <i>Escherichia coli</i> and Chinese Hamster Ovary Systems. <i>Frontiers in Immunology</i> , 2021, 12, 634738. | 4.8 | 7 |
| 10 | Identification of a Region in the Common Amino-terminal Domain of Hendra Virus P, V, and W Proteins Responsible for Phase Transition and Amyloid Formation. <i>Biomolecules</i> , 2021, 11, 1324. | 4.0 | 20 |
| 11 | Î² ^{133p53} isoform pro-invasive activity is regulated through an aggregation-dependent mechanism in cancer cells. <i>Nature Communications</i> , 2021, 12, 5463. | 12.8 | 17 |
| 12 | DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276. | 14.5 | 141 |
| 13 | Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472. | 6.5 | 70 |
| 14 | Modeling polymorphic ventricular tachycardia at rest using patient-specific induced pluripotent stem cell-derived cardiomyocytes. <i>EBioMedicine</i> , 2020, 60, 103024. | 6.1 | 19 |
| 15 | Trimeric SARS-CoV-2 Spike Proteins Produced from CHO Cells in Bioreactors Are High-Quality Antigens. <i>Processes</i> , 2020, 8, 1539. | 2.8 | 18 |
| 16 | Amyloidogenicity as a driving force for the formation of functional oligomers. <i>Journal of Structural Biology</i> , 2020, 212, 107604. | 2.8 | 3 |
| 17 | Multifunctional Amyloid Oligomeric Nanoparticles for Specific Cell Targeting and Drug Delivery. <i>Biomacromolecules</i> , 2020, 21, 4302-4312. | 5.4 | 10 |
| 18 | Point mutations affecting yeast prion propagation change the structure of its amyloid fibrils. <i>Journal of Molecular Liquids</i> , 2020, 314, 113618. | 4.9 | 4 |

| # | ARTICLE | IF | CITATIONS |
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| 19 | Census of halide-binding sites in protein structures. <i>Bioinformatics</i> , 2020, 36, 3064-3071. | 4.1 | 11 |
| 20 | Opposite Modulation of RAC1 by Mutations in TRIO Is Associated with Distinct, Domain-Specific Neurodevelopmental Disorders. <i>American Journal of Human Genetics</i> , 2020, 106, 338-355. | 6.2 | 58 |
| 21 | Tally-2.0: upgraded validator of tandem repeat detection in protein sequences. <i>Bioinformatics</i> , 2020, 36, 3260-3262. | 4.1 | 2 |
| 22 | FTIR Spectroscopy Study of the Secondary Structure Changes in Human Serum Albumin and Trypsin under Neutral Salts. <i>Biomolecules</i> , 2020, 10, 606. | 4.0 | 34 |
| 23 | Estimation of amyloid aggregate sizes with semi-denaturing detergent agarose gel electrophoresis and its limitations. <i>Prion</i> , 2020, 14, 118-128. | 1.8 | 11 |
| 24 | Systematic FTIR Spectroscopy Study of the Secondary Structure Changes in Human Serum Albumin under Various Denaturation Conditions. <i>Biomolecules</i> , 2019, 9, 359. | 4.0 | 99 |
| 25 | Tandem repeats lead to sequence assembly errors and impose multi-level challenges for genome and protein databases. <i>Nucleic Acids Research</i> , 2019, 47, 10994-11006. | 14.5 | 236 |
| 26 | Prion soft amyloid core driven self-assembly of globular proteins into bioactive nanofibrils. <i>Nanoscale</i> , 2019, 11, 12680-12694. | 5.6 | 16 |
| 27 | The HslV Protease from <i>Leishmania major</i> and Its Activation by C-terminal HslU Peptides. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1021. | 4.1 | 3 |
| 28 | Porins and Amyloids are Coded by Similar Sequence Motifs. <i>Proteomics</i> , 2019, 19, 1800075. | 2.2 | 5 |
| 29 | Design of a New [PSI ⁺]-No-More Mutation in SUP35 With Strong Inhibitory Effect on the [PSI ⁺] Prion Propagation. <i>Frontiers in Molecular Neuroscience</i> , 2019, 12, 274. | 2.9 | 10 |
| 30 | Editorial for special issue "Proteins with tandem repeats: sequences, structures and functions". <i>Journal of Structural Biology</i> , 2018, 201, 86-87. | 2.8 | 2 |
| 31 | BetaSerpentine: a bioinformatics tool for reconstruction of amyloid structures. <i>Bioinformatics</i> , 2018, 34, 599-608. | 4.1 | 15 |
| 32 | Classification of β^2 -hairpin repeat proteins. <i>Journal of Structural Biology</i> , 2018, 201, 130-138. | 2.8 | 25 |
| 33 | Post-Translational Modifications and Diastolic Calcium Leak Associated to the Novel RyR2-D3638A Mutation Lead to CPVT in Patient-Specific hiPSC-Derived Cardiomyocytes. <i>Journal of Clinical Medicine</i> , 2018, 7, 423. | 2.4 | 40 |
| 34 | Protein Co-Aggregation Related to Amyloids: Methods of Investigation, Diversity, and Classification. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2292. | 4.1 | 31 |
| 35 | Establishment of Constraints on Amyloid Formation Imposed by Steric Exclusion of Globular Domains. <i>Journal of Molecular Biology</i> , 2018, 430, 3835-3846. | 4.2 | 15 |
| 36 | DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227. | 14.5 | 242 |

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| 37 | Usage of a dataset of NMR resolved protein structures to test aggregation versus solubility prediction algorithms. <i>Protein Science</i> , 2017, 26, 1864-1869. | 7.6 | 14 |
| 38 | RepeatsDB 2.0: improved annotation, classification, search and visualization of repeat protein structures. <i>Nucleic Acids Research</i> , 2017, 45, D308-D312. | 14.5 | 33 |
| 39 | Identification of the Autochaperone Domain in the Type Va Secretion System (T5aSS): Prevalent Feature of Autotransporters with a \hat{I}^2 -Helical Passenger. <i>Frontiers in Microbiology</i> , 2017, 8, 2607. | 3.5 | 17 |
| 40 | Functional assignment to positively selected sites in the core type <i>Ill</i> effector <i>RipG</i> 7 from <i>R</i> <i>alstonia solanacearum</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 553-564. | 4.2 | 39 |
| 41 | Global genetic diversity of the <i>Plasmodium vivax</i> transmission-blocking vaccine candidate Pvs48/45. <i>Malaria Journal</i> , 2016, 15, 202. | 2.3 | 16 |
| 42 | Tally: a scoring tool for boundary determination between repetitive and non-repetitive protein sequences. <i>Bioinformatics</i> , 2016, 32, 1952-1958. | 4.1 | 1 |
| 43 | \hat{I}^{\pm} -Synuclein Amyloid Fibrils with Two Entwined, Asymmetrically Associated Protofibrils. <i>Journal of Biological Chemistry</i> , 2016, 291, 2310-2318. | 3.4 | 48 |
| 44 | In search of the boundary between repetitive and non-repetitive protein sequences. <i>Biochemical Society Transactions</i> , 2015, 43, 807-811. | 3.4 | 6 |
| 45 | Restricted mobility of side chains on concave surfaces of solenoid proteins may impart heightened potential for intermolecular interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1654-1664. | 2.6 | 1 |
| 46 | Designs on a curve. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 103-105. | 8.2 | 6 |
| 47 | Structure-based view on [<i>PSI</i> ⁺] prion properties. <i>Prion</i> , 2015, 9, 190-199. | 1.8 | 17 |
| 48 | Evolution of Proteasome Regulators in Eukaryotes. <i>Genome Biology and Evolution</i> , 2015, 7, 1363-1379. | 2.5 | 77 |
| 49 | TAPO: A combined method for the identification of tandem repeats in protein structures. <i>FEBS Letters</i> , 2015, 589, 2611-2619. | 2.8 | 26 |
| 50 | Single substitution in bacteriophage T4 RNase H alters the ratio between its exo- and endonuclease activities. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015, 781, 49-57. | 1.0 | 1 |
| 51 | A structure-based approach to predict predisposition to amyloidosis. <i>Alzheimer's and Dementia</i> , 2015, 11, 681-690. | 0.8 | 82 |
| 52 | <i>Plasmodium vivax</i> Antigen Discovery Based on Alpha-Helical Coiled Coil Protein Motif. <i>PLoS ONE</i> , 2014, 9, e100440. | 2.5 | 10 |
| 53 | <i>Plasmodium falciparum</i> merozoite surface protein 2: epitope mapping and fine specificity of human antibody response against non-polymorphic domains. <i>Malaria Journal</i> , 2014, 13, 510. | 2.3 | 19 |
| 54 | RepeatsDB: a database of tandem repeat protein structures. <i>Nucleic Acids Research</i> , 2014, 42, D352-D357. | 14.5 | 53 |

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| 55 | TRDistiller: A rapid filter for enrichment of sequence datasets with proteins containing tandem repeats. <i>Journal of Structural Biology</i> , 2014, 186, 386-391. | 2.8 | 11 |
| 56 | Drosophila Spag Is the Homolog of RNA Polymerase II-associated Protein 3 (RPAP3) and Recruits the Heat Shock Proteins 70 and 90 (Hsp70 and Hsp90) during the Assembly of Cellular Machineries. <i>Journal of Biological Chemistry</i> , 2014, 289, 6236-6247. | 3.4 | 41 |
| 57 | Conformational Switching in PolyGln Amyloid Fibrils Resulting from a Single Amino Acid Insertion. <i>Biophysical Journal</i> , 2014, 106, 2134-2142. | 0.5 | 3 |
| 58 | Evolutionary link between metazoan RHIM motif and prion-forming domain of fungal heterokaryon incompatibility factor HET-s/HET-s. <i>Scientific Reports</i> , 2014, 4, 7436. | 3.3 | 47 |
| 59 | Breaking the amyloidogenicity code: Methods to predict amyloids from amino acid sequence. <i>FEBS Letters</i> , 2013, 587, 1089-1095. | 2.8 | 62 |
| 60 | Effect of Charged Residues in the N-domain of Sup35 Protein on Prion [PSI ⁺] Stability and Propagation. <i>Journal of Biological Chemistry</i> , 2013, 288, 28503-28513. | 3.4 | 21 |
| 61 | Antigenicity and immunogenicity of a novel chimeric peptide antigen based on the <i>P. vivax</i> circumsporozoite protein. <i>Vaccine</i> , 2013, 31, 4923-4930. | 3.8 | 19 |
| 62 | EpCAM Controls Actomyosin Contractility and Cell Adhesion by Direct Inhibition of PKC. <i>Developmental Cell</i> , 2013, 27, 263-277. | 7.0 | 50 |
| 63 | Repeat or not repeat? Statistical validation of tandem repeat prediction in genomic sequences. <i>Nucleic Acids Research</i> , 2012, 40, 10005-10017. | 14.5 | 47 |
| 64 | Malaria Vaccine Development Using Synthetic Peptides as a Technical Platform. <i>Advances in Immunology</i> , 2012, 114, 107-149. | 2.2 | 14 |
| 65 | Cell Biological Characterization of the Malaria Vaccine Candidate Trophozoite Exported Protein 1. <i>PLoS ONE</i> , 2012, 7, e46112. | 2.5 | 23 |
| 66 | <sc>PRDB</sc>: <sc>P</sc>rotein <sc>R</sc>peat <sc>D</sc>ata<sc>B</sc>ase. <i>Proteomics</i> , 2012, 12, 1333-1336. | 2.2 | 12 |
| 67 | Tandem repeats in proteins: From sequence to structure. <i>Journal of Structural Biology</i> , 2012, 179, 279-288. | 2.8 | 188 |
| 68 | Malaria vaccine candidate: Design of a multivalent subunit $\hat{\pm}$ -helical coiled coil poly-epitope. <i>Vaccine</i> , 2011, 29, 7090-7099. | 3.8 | 26 |
| 69 | Identification of Residues within Tropomodulin-1 Responsible for Its Localization at the Pointed Ends of the Actin Filaments in Cardiac Myocytes. <i>Journal of Biological Chemistry</i> , 2011, 286, 2194-2204. | 3.4 | 36 |
| 70 | Protein tandem repeats "the more perfect, the less structured. <i>FEBS Journal</i> , 2010, 277, 2673-2682. | 4.7 | 119 |
| 71 | A Network of Hydrogen Bonds on the Surface of TLR2 Controls Ligand Positioning and Cell Signaling. <i>Journal of Biological Chemistry</i> , 2010, 285, 6227-6234. | 3.4 | 19 |
| 72 | Structural basis for the wobbler mouse neurodegenerative disorder caused by mutation in the Vps54 subunit of the GARP complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12860-12865. | 7.1 | 67 |

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| 73 | Long Synthetic Peptides for the Production of Vaccines and Drugs: A Technological Platform Coming of Age. <i>Science Translational Medicine</i> , 2010, 2, 50rv3. | 12.4 | 20 |
| 74 | Protein Homorepeats. <i>Advances in Protein Chemistry and Structural Biology</i> , 2010, 79, 59-88. | 2.3 | 62 |
| 75 | Î² arcades: recurring motifs in naturally occurring and disease-related amyloid fibrils. <i>FASEB Journal</i> , 2010, 24, 1311-1319. | 0.5 | 121 |
| 76 | Malaria vaccine: why is it taking so long?. <i>Expert Review of Vaccines</i> , 2010, 9, 111-114. | 4.4 | 4 |
| 77 | Protein tandem repeats - the more perfect, the less structured. <i>FEBS Journal</i> , 2010, 277, 2673-2682. | 4.7 | 85 |
| 78 | T-REKS: identification of Tandem REpeats in sequences with a K-meanS based algorithm. <i>Bioinformatics</i> , 2009, 25, 2632-2638. | 4.1 | 162 |
| 79 | Vaccine Potentials of an Intrinsically Unstructured Fragment Derived from the Blood Stage-Associated <i>Plasmodium falciparum</i> Protein PFF0165c. <i>Infection and Immunity</i> , 2009, 77, 5701-5709. | 2.2 | 50 |
| 80 | The C-terminal domain of <i>Plasmodium falciparum</i> merozoite surface protein 3 self-assembles into Î±-helical coiled coil tetramer. <i>Molecular and Biochemical Parasitology</i> , 2009, 165, 153-161. | 1.1 | 20 |
| 81 | EtpB Is a Pore-Forming Outer Membrane Protein Showing TpsB Protein Features Involved in the Two-Partner Secretion System. <i>Journal of Membrane Biology</i> , 2009, 230, 143-154. | 2.1 | 4 |
| 82 | Sequence Conservation in <i>Plasmodium falciparum</i> Î±-Helical Coiled Coil Domains Proposed for Vaccine Development. <i>PLoS ONE</i> , 2009, 4, e5419. | 2.5 | 20 |
| 83 | Longitudinal analyses of immune responses to <i>Plasmodium falciparum</i> derived peptides corresponding to novel blood stage antigens in coastal Kenya. <i>Vaccine</i> , 2008, 26, 1963-1971. | 3.8 | 18 |
| 84 | Three-Dimensional Structure of Canine Adenovirus Serotype 2 Capsid. <i>Journal of Virology</i> , 2008, 82, 3192-3203. | 3.4 | 64 |
| 85 | Origin and Evolution of GALA-LRR, a New Member of the CC-LRR Subfamily: From Plants to Bacteria?. <i>PLoS ONE</i> , 2008, 3, e1694. | 2.5 | 46 |
| 86 | Protein Structure Based Strategies for Antigen Discovery and Vaccine Development Against Malaria and Other Pathogens. <i>Endocrine, Metabolic and Immune Disorders - Drug Targets</i> , 2007, 7, 259-265. | 1.2 | 50 |
| 87 | Molecular Determinant for Specific Ca/Ba Selectivity Profiles of Low and High Threshold Ca ²⁺ Channels. <i>Journal of General Physiology</i> , 2007, 130, 415-425. | 1.9 | 22 |
| 88 | Functional architecture of the retromer cargo-recognition complex. <i>Nature</i> , 2007, 449, 1063-1067. | 27.8 | 250 |
| 89 | Rapid Identification of Malaria Vaccine Candidates Based on Î±-Helical Coiled Coil Protein Motif. <i>PLoS ONE</i> , 2007, 2, e645. | 2.5 | 71 |
| 90 | Î²-Sheet Structures in Fibrous Proteins. <i>Advances in Protein Chemistry</i> , 2006, 73, 1-15. | 4.4 | 50 |

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| 91 | β -Rolls, β -Helices, and Other β -Solenoid Proteins. <i>Advances in Protein Chemistry</i> , 2006, 73, 55-96. | 4.4 | 119 |
| 92 | Standard Conformations of β -Arches in β -Solenoid Proteins. <i>Journal of Molecular Biology</i> , 2006, 358, 1094-1105. | 4.2 | 69 |
| 93 | The turn of the screw: Variations of the abundant β -solenoid motif in passenger domains of Type V secretory proteins. <i>Journal of Structural Biology</i> , 2006, 155, 306-315. | 2.8 | 90 |
| 94 | Synthetic RGD-containing β -helical coiled coil peptides promote integrin-dependent cell adhesion. <i>Journal of Peptide Science</i> , 2006, 12, 206-212. | 1.4 | 47 |
| 95 | Structure, Function, and Amyloidogenesis of Fungal Prions: Filament Polymorphism and Prion Variants. <i>Advances in Protein Chemistry</i> , 2006, 73, 125-180. | 4.4 | 59 |
| 96 | Interactions of Bax and tBid with Lipid Monolayers. <i>Journal of Membrane Biology</i> , 2005, 207, 1-9. | 2.1 | 19 |
| 97 | The Axial Channel of the 20S Proteasome Opens Upon Binding of the PA200 Activator. <i>Journal of Molecular Biology</i> , 2005, 346, 1221-1227. | 4.2 | 102 |
| 98 | The Parallel Superpleated Beta-structure as a Model for Amyloid Fibrils of Human Amylin. <i>Journal of Molecular Biology</i> , 2005, 348, 247-252. | 4.2 | 180 |
| 99 | Tubulin Polyglutamylase Enzymes Are Members of the TTL Domain Protein Family. <i>Science</i> , 2005, 308, 1758-1762. | 12.6 | 289 |
| 100 | Organization of designed nanofibrils assembled from β -helical peptides as determined by electron microscopy. <i>Journal of Peptide Science</i> , 2004, 10, 291-297. | 1.4 | 26 |
| 101 | A model for Ure2p prion filaments and other amyloids: The parallel superpleated β -structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7885-7890. | 7.1 | 167 |
| 102 | Interactions of the Human Calcitonin Fragment 9 β -32 with Phospholipids: A Monolayer Study. <i>Biophysical Journal</i> , 2004, 87, 386-395. | 0.5 | 30 |
| 103 | LRR8 extracellular domain is composed of 17 leucine-rich repeats. <i>Molecular Immunology</i> , 2004, 41, 561-562. | 2.2 | 17 |
| 104 | New HEAT-like repeat motifs in proteins regulating proteasome structure and function. <i>Journal of Structural Biology</i> , 2004, 146, 425-430. | 2.8 | 75 |
| 105 | NMR Solution Structure of Mob1, a Mitotic Exit Network Protein and its Interaction with an NDR Kinase Peptide. <i>Journal of Molecular Biology</i> , 2004, 337, 167-182. | 4.2 | 34 |
| 106 | In Vivo Homodimerisation of HTLV-1 Gag and MA Gives Clues to the Retroviral Capsid and TM Envelope Protein Arrangement. <i>Journal of Molecular Biology</i> , 2004, 343, 903-916. | 4.2 | 14 |
| 107 | Shift of fibril-forming ability of the designed β -helical coiled-coil peptides into the physiological pH region. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 1125-1130. | 2.1 | 25 |
| 108 | The Carboxy Terminus of Prospero Regulates Its Subcellular Localization. <i>Molecular and Cellular Biology</i> , 2003, 23, 1014-1024. | 2.3 | 17 |

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| 109 | Analysis of DsRed Mutants. <i>Journal of Biological Chemistry</i> , 2002, 277, 7633-7636. | 3.4 | 66 |
| 110 | What Curves α -Solenoids?. <i>Journal of Biological Chemistry</i> , 2002, 277, 49791-49798. | 3.4 | 73 |
| 111 | Processing of <i>Escherichia coli</i> Alkaline Phosphatase. <i>Journal of Biological Chemistry</i> , 2002, 277, 50396-50402. | 3.4 | 8 |
| 112 | Redesign of a Four-helix Bundle Protein by Phage Display Coupled with Proteolysis and Structural Characterization by NMR and X-ray Crystallography. <i>Journal of Molecular Biology</i> , 2002, 323, 253-262. | 4.2 | 84 |
| 113 | A novel potential surface protein in <i>Trichomonas vaginalis</i> contains a leucine-rich repeat shared by micro-organisms from all three domains of life. <i>Molecular and Biochemical Parasitology</i> , 2002, 125, 195-199. | 1.1 | 31 |
| 114 | Epithelial barrier function: assembly and structural features of the cornified cell envelope. <i>BioEssays</i> , 2002, 24, 789-800. | 2.5 | 422 |
| 115 | Assessment of the ability to model proteins with leucine-rich repeats in light of the latest structural information. <i>Protein Science</i> , 2002, 11, 1082-1090. | 7.6 | 110 |
| 116 | Analysis of Etoposide Binding to Subdomains of Human DNA Topoisomerase II α in the Absence of DNA. <i>Biochemistry</i> , 2001, 40, 1624-1634. | 2.5 | 52 |
| 117 | Review: Proteins with Repeated Sequence—Structural Prediction and Modeling. <i>Journal of Structural Biology</i> , 2001, 134, 132-144. | 2.8 | 117 |
| 118 | Structure—function analysis of <i>Yersinia pestis</i> YopM's interaction with α -thrombin to rule on its significance in systemic plague and to model YopM's mechanism of binding host proteins. <i>Microbial Pathogenesis</i> , 2001, 30, 193-209. | 2.9 | 35 |
| 119 | Beta-helix model for the filamentous haemagglutinin adhesin of <i>Bordetella pertussis</i> and related bacterial secretory proteins. <i>Molecular Microbiology</i> , 2001, 42, 279-292. | 2.5 | 163 |
| 120 | De novo design of fibrils made of short α -helical coiled coil peptides. <i>Chemistry and Biology</i> , 2001, 8, 1025-1032. | 6.0 | 151 |
| 121 | The leucine-rich repeat as a protein recognition motif. <i>Current Opinion in Structural Biology</i> , 2001, 11, 725-732. | 5.7 | 1,454 |
| 122 | Structure of an IgE-Binding Peptide from Fungal Enolases. <i>International Archives of Allergy and Immunology</i> , 2001, 124, 93-94. | 2.1 | 3 |
| 123 | Suramin blocks nucleotide triphosphate binding to ribosomal protein L3 from <i>Trypanoplasma borreli</i> . <i>FEBS Journal</i> , 2000, 267, 1723-1731. | 0.2 | 6 |
| 124 | When protein folding is simplified to protein coiling: the continuum of solenoid protein structures. <i>Trends in Biochemical Sciences</i> , 2000, 25, 509-515. | 7.5 | 254 |
| 125 | The Net Charge of the First 18 Residues of the Mature Sequence Affects Protein Translocation across the Cytoplasmic Membrane of Gram-Negative Bacteria. <i>Journal of Bacteriology</i> , 2000, 182, 2163-2169. | 2.2 | 56 |
| 126 | Heart-specific splice-variant of a human mitochondrial ribosomal protein (mRNA processing; tissue) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 2.2 | 22 |

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|-----|---|------|-----------|
| 127 | Î±-Helical solenoid model for the human involucrin. FEBS Letters, 2000, 473, 127-131. | 2.8 | 8 |
| 128 | "Fluorescent Timer": Protein That Changes Color with Time. Science, 2000, 290, 1585-1588. | 12.6 | 347 |
| 129 | IgE-binding epitopes of enolases, a class of highly conserved fungal allergens. Journal of Allergy and Clinical Immunology, 2000, 106, 887-895. | 2.9 | 109 |
| 130 | Structure-Function Relationships of Two Loss-of-Function Mutations of the Thyrotropin Receptor Gene. Thyroid, 1999, 9, 995-1000. | 4.5 | 33 |
| 131 | Dimorphism of polyglycine I: structural models for crystal modifications. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 436-442. | 2.5 | 18 |
| 132 | Use of transcription reporters with novel p53 binding sites to target tumour cells expressing endogenous or virally transduced p53 mutants with altered sequence-specificity. Oncogene, 1998, 16, 685-690. | 5.9 | 15 |
| 133 | Structural classification of Î±Î² and Î²Î± supersecondary structure units in proteins. Proteins: Structure, Function and Bioinformatics, 1998, 30, 193-212. | 2.6 | 26 |
| 134 | Processing of Escherichia coli alkaline phosphatase: role of the primary structure of the signal peptide cleavage region 1 Edited by A. R. Fersht. Journal of Molecular Biology, 1998, 277, 859-870. | 4.2 | 75 |
| 135 | Structural diversity of leucine-rich repeat proteins 1 Edited by F. Cohen. Journal of Molecular Biology, 1998, 277, 519-527. | 4.2 | 489 |
| 136 | A model of Cdc25 phosphatase catalytic domain and Cdk-interaction surface based on the presence of a rhodanese homology domain. Journal of Molecular Biology, 1998, 282, 195-208. | 4.2 | 81 |
| 137 | Denaturation of Type I Collagen Fibrils Is an Endothermic Process Accompanied by a Noticeable Change in the Partial Heat Capacity. Biochemistry, 1998, 37, 8147-8152. | 2.5 | 72 |
| 138 | The Open Reading Frame III Product of Cauliflower Mosaic Virus Forms a Tetramer through a N-terminal Coiled-coil. Journal of Biological Chemistry, 1998, 273, 29015-29021. | 3.4 | 43 |
| 139 | Structural classification of Î±Î² and Î²Î± supersecondary structure units in proteins. Proteins: Structure, Function and Bioinformatics, 1998, 30, 193-212. | 2.6 | 3 |
| 140 | "Peptabody": A new type of high avidity binding protein. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 1663-1668. | 7.1 | 120 |
| 141 | Positively charged lysine at the N-terminus of the signal peptide of the Escherichia coli alkaline phosphatase provides the secretion efficiency and is involved in the interaction with anionic phospholipids. FEBS Letters, 1997, 403, 203-207. | 2.8 | 61 |
| 142 | Title is missing!. International Journal of Peptide Research and Therapeutics, 1997, 4, 297-304. | 0.1 | 1 |
| 143 | Mutation Gln54Leu of the conserved polar residue in the interfacial coiled coil position (d) results in significant stabilization of the original structure of the COMP pentamerization domain. International Journal of Peptide Research and Therapeutics, 1997, 4, 297-304. | 0.1 | 3 |
| 144 | Modeling of a five-stranded coiled coil structure for the assembly domain of the cartilage oligomeric matrix protein. , 1996, 24, 218-226. | | 18 |

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