

Andrey V Kajava

List of Publications by Year in descending order

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151
papers

10,277
citations

38742

50
h-index

37204

96
g-index

156
all docs

156
docs citations

156
times ranked

12678
citing authors

#	ARTICLE	IF	CITATIONS
1	The leucine-rich repeat as a protein recognition motif. <i>Current Opinion in Structural Biology</i> , 2001, 11, 725-732.	5.7	1,454
2	Structural diversity of leucine-rich repeat proteins 1 1Edited by F. Cohen. <i>Journal of Molecular Biology</i> , 1998, 277, 519-527.	4.2	489
3	Epithelial barrier function: assembly and structural features of the cornified cell envelope. <i>BioEssays</i> , 2002, 24, 789-800.	2.5	422
4	"Fluorescent Timer": Protein That Changes Color with Time. <i>Science</i> , 2000, 290, 1585-1588.	12.6	347
5	Tubulin Polyglutamylase Enzymes Are Members of the TTL Domain Protein Family. <i>Science</i> , 2005, 308, 1758-1762.	12.6	289
6	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
7	Functional architecture of the retromer cargo-recognition complex. <i>Nature</i> , 2007, 449, 1063-1067.	27.8	250
8	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	14.5	242
9	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
10	Modeling of the three-dimensional structure of proteins with the typical leucine-rich repeats. <i>Structure</i> , 1995, 3, 867-877.	3.3	226
11	Tandem repeats in proteins: From sequence to structure. <i>Journal of Structural Biology</i> , 2012, 179, 279-288.	2.8	188
12	Critical assessment of protein intrinsic disorder prediction. <i>Nature Methods</i> , 2021, 18, 472-481.	19.0	187
13	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
14	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
15	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
16	T-REKS: identification of Tandem REpeats in sequences with a K-meanS based algorithm. <i>Bioinformatics</i> , 2009, 25, 2632-2638.	4.1	162
17	De novo design of fibrils made of short β -helical coiled coil peptides. <i>Chemistry and Biology</i> , 2001, 8, 1025-1032.	6.0	151
18	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	14.5	141

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19	β^2 arcades: recurring motifs in naturally occurring and disease-related amyloid fibrils. FASEB Journal, 2010, 24, 1311-1319.	0.5	121
20	"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
21	A Model of the Three-dimensional Structure of Ice Nucleation Proteins. Journal of Molecular Biology, 1993, 232, 709-717.	4.2	119
22	β^2 -Rolls, β^2 -Helices, and Other β^2 -Solenoid Proteins. Advances in Protein Chemistry, 2006, 73, 55-96.	4.4	119
23	Protein tandem repeats – the more perfect, the less structured. FEBS Journal, 2010, 277, 2673-2682.	4.7	119
24	Review: Proteins with Repeated Sequence – Structural Prediction and Modeling. Journal of Structural Biology, 2001, 134, 132-144.	2.8	117
25	Assessment of the ability to model proteins with leucine-rich repeats in light of the latest structural information. Protein Science, 2002, 11, 1082-1090.	7.6	110
26	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
27	The Axial Channel of the 20S Proteasome Opens Upon Binding of the PA200 Activator. Journal of Molecular Biology, 2005, 346, 1221-1227.	4.2	102
28	Systematic FTIR Spectroscopy Study of the Secondary Structure Changes in Human Serum Albumin under Various Denaturation Conditions. Biomolecules, 2019, 9, 359.	4.0	99
29	The turn of the screw: Variations of the abundant β^2 -solenoid motif in passenger domains of Type V secretory proteins. Journal of Structural Biology, 2006, 155, 306-315.	2.8	90
30	Protein tandem repeats - the more perfect, the less structured. FEBS Journal, 2010, 277, 2673-2682.	4.7	85
31	Redesign of a Four-helix Bundle Protein by Phage Display Coupled with Proteolysis and Structural Characterization by NMR and X-ray Crystallography. Journal of Molecular Biology, 2002, 323, 253-262.	4.2	84
32	A structure-based approach to predict predisposition to amyloidosis. Alzheimer's and Dementia, 2015, 11, 681-690.	0.8	82
33	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
34	Evolution of Proteasome Regulators in Eukaryotes. Genome Biology and Evolution, 2015, 7, 1363-1379.	2.5	77
35	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
36	New HEAT-like repeat motifs in proteins regulating proteasome structure and function. Journal of Structural Biology, 2004, 146, 425-430.	2.8	75

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37	What Curves $\hat{1}$ -Solenoids?. Journal of Biological Chemistry, 2002, 277, 49791-49798.	3.4	73
38	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
39	Rapid Identification of Malaria Vaccine Candidates Based on $\hat{1}$ -Helical Coiled Coil Protein Motif. PLoS ONE, 2007, 2, e645.	2.5	71
40	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	6.5	70
41	Standard Conformations of $\hat{2}$ -Arches in $\hat{2}$ -Solenoid Proteins. Journal of Molecular Biology, 2006, 358, 1094-1105.	4.2	69
42	Structural basis for the wobbler mouse neurodegenerative disorder caused by mutation in the Vps54 subunit of the GARP complex. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12860-12865.	7.1	67
43	Analysis of DsRed Mutants. Journal of Biological Chemistry, 2002, 277, 7633-7636.	3.4	66
44	Three-Dimensional Structure of Canine Adenovirus Serotype 2 Capsid. Journal of Virology, 2008, 82, 3192-3203.	3.4	64
45	Protein Homorepeats. Advances in Protein Chemistry and Structural Biology, 2010, 79, 59-88.	2.3	62
46	Breaking the amyloidogenicity code: Methods to predict amyloids from amino acid sequence. FEBS Letters, 2013, 587, 1089-1095.	2.8	62
47	Positively charged lysine at the N-terminus of the signal peptide of the <i>Escherichia coli</i> alkaline phosphatase provides the secretion efficiency and is involved in the interaction with anionic phospholipids. FEBS Letters, 1997, 403, 203-207.	2.8	61
48	Structure, Function, and Amyloidogenesis of Fungal Prions: Filament Polymorphism and Prion Variants. Advances in Protein Chemistry, 2006, 73, 125-180.	4.4	59
49	Opposite Modulation of RAC1 by Mutations in TRIO Is Associated with Distinct, Domain-Specific Neurodevelopmental Disorders. American Journal of Human Genetics, 2020, 106, 338-355.	6.2	58
50	The Net Charge of the First 18 Residues of the Mature Sequence Affects Protein Translocation across the Cytoplasmic Membrane of Gram-Negative Bacteria. Journal of Bacteriology, 2000, 182, 2163-2169.	2.2	56
51	RepeatsDB: a database of tandem repeat protein structures. Nucleic Acids Research, 2014, 42, D352-D357.	14.5	53
52	Analysis of Etoposide Binding to Subdomains of Human DNA Topoisomerase II in the Absence of DNA. Biochemistry, 2001, 40, 1624-1634.	2.5	52
53	$\hat{2}$ -Structures in Fibrous Proteins. Advances in Protein Chemistry, 2006, 73, 1-15.	4.4	50
54	Protein Structure Based Strategies for Antigen Discovery and Vaccine Development Against Malaria and Other Pathogens. Endocrine, Metabolic and Immune Disorders - Drug Targets, 2007, 7, 259-265.	1.2	50

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55	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
56	EpCAM Controls Actomyosin Contractility and Cell Adhesion by Direct Inhibition of PKC. <i>Developmental Cell</i> , 2013, 27, 263-277.	7.0	50
57	β -Synuclein Amyloid Fibrils with Two Entwined, Asymmetrically Associated Protofibrils. <i>Journal of Biological Chemistry</i> , 2016, 291, 2310-2318.	3.4	48
58	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
59	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
60	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
61	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
62	The Open Reading Frame III Product of Cauliflower Mosaic Virus Forms a Tetramer through a N-terminal Coiled-coil. <i>Journal of Biological Chemistry</i> , 1998, 273, 29015-29021.	3.4	43
63	<i>Drosophila</i> 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
64	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
65	Functional assignment to positively selected sites in the core type III effector <i>RipC</i> from <i>Ralstonia solanacearum</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 553-564.	4.2	39
66	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
67	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
68	Structure-function analysis of <i>Yersinia pestis</i> YopM's interaction with β -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
69	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
70	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
71	Structure-Function Relationships of Two Loss-of-Function Mutations of the Thyrotropin Receptor Gene. <i>Thyroid</i> , 1999, 9, 995-1000.	4.5	33
72	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

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73	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
74	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
75	Interactions of the Human Calcitonin Fragment 9â€“32 with Phospholipids: A Monolayer Study. <i>Biophysical Journal</i> , 2004, 87, 386-395.	0.5	30
76	Structural classification of $\hat{1}\pm\hat{1}^2\hat{1}^2$ and $\hat{1}^2\hat{1}^2\hat{1}\pm$ supersecondary structure units in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 30, 193-212.	2.6	26
77	Organization of designed nanofibrils assembled from $\hat{1}\pm$ -helical peptides as determined by electron microscopy. <i>Journal of Peptide Science</i> , 2004, 10, 291-297.	1.4	26
78	Malaria vaccine candidate: Design of a multivalent subunit $\hat{1}\pm$ -helical coiled coil poly-epitope. <i>Vaccine</i> , 2011, 29, 7090-7099.	3.8	26
79	TAPO: A combined method for the identification of tandem repeats in protein structures. <i>FEBS Letters</i> , 2015, 589, 2611-2619.	2.8	26
80	Shift of fibril-forming ability of the designed $\hat{1}\pm$ -helical coiled-coil peptides into the physiological pH region. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 1125-1130.	2.1	25
81	Classification of $\hat{1}^2$ -hairpin repeat proteins. <i>Journal of Structural Biology</i> , 2018, 201, 130-138.	2.8	25
82	Cell Biological Characterization of the Malaria Vaccine Candidate Trophozoite Exported Protein 1. <i>PLoS ONE</i> , 2012, 7, e46112.	2.5	23
83	Heart-specific splice-variant of a human mitochondrial ribosomal protein (mRNA processing; tissue) Tj ETQq1 1 0.784314 rgBJ/Overl	2.2	22
84	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
85	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
86	Thermodynamic Studies of the Collagen-like Region of Human Subcomponent C1q. <i>Journal of Molecular Biology</i> , 1993, 234, 654-660.	4.2	20
87	The C-terminal domain of <i>Plasmodium falciparum</i> merozoite surface protein 3 self-assembles into $\hat{1}\pm$ -helical coiled coil tetramer. <i>Molecular and Biochemical Parasitology</i> , 2009, 165, 153-161.	1.1	20
88	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
89	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
90	Sequence Conservation in <i>Plasmodium falciparum</i> $\hat{1}\pm$ -Helical Coiled Coil Domains Proposed for Vaccine Development. <i>PLoS ONE</i> , 2009, 4, e5419.	2.5	20

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91	Interactions of Bax and tBid with Lipid Monolayers. <i>Journal of Membrane Biology</i> , 2005, 207, 1-9.	2.1	19
92	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
93	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
94	<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
95	Modeling polymorphic ventricular tachycardia at rest using patient-specific induced pluripotent stem cell-derived cardiomyocytes. <i>EBioMedicine</i> , 2020, 60, 103024.	6.1	19
96	Modeling of a five-stranded coiled coil structure for the assembly domain of the cartilage oligomeric matrix protein. , 1996, 24, 218-226.		18
97	Dimorphism of polyglycine I: structural models for crystal modifications. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 436-442.	2.5	18
98	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
99	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
100	The Carboxy Terminus of Prospero Regulates Its Subcellular Localization. <i>Molecular and Cellular Biology</i> , 2003, 23, 1014-1024.	2.3	17
101	LRR8 extracellular domain is composed of 17 leucine-rich repeats. <i>Molecular Immunology</i> , 2004, 41, 561-562.	2.2	17
102	Structure-based view on [<i>PSI</i> ⁺] prion properties. <i>Prion</i> , 2015, 9, 190-199.	1.8	17
103	Identification of the Autochaperone Domain in the Type Va Secretion System (T5aSS): Prevalent Feature of Autotransporters with a $\hat{1}^2$ -Helical Passenger. <i>Frontiers in Microbiology</i> , 2017, 8, 2607.	3.5	17
104	$\hat{1}^{133p53}\hat{1}^2$ isoform pro-invasive activity is regulated through an aggregation-dependent mechanism in cancer cells. <i>Nature Communications</i> , 2021, 12, 5463.	12.8	17
105	Molecular packing in type I collagen fibrils. <i>Journal of Molecular Biology</i> , 1991, 218, 815-823.	4.2	16
106	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
107	Prion soft amyloid core driven self-assembly of globular proteins into bioactive nanofibrils. <i>Nanoscale</i> , 2019, 11, 12680-12694.	5.6	16
108	Left-handed topology of super-secondary structure formed by aligned $\hat{1}^{\pm}$ -helix and $\hat{1}^2$ -hairpin. <i>FEBS Letters</i> , 1992, 302, 8-10.	2.8	15

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109	Use of transcription reporters with novel p53 binding sites to target tumour cells expressing endogenous or virally transduced p53 mutants with altered sequence-specificity. <i>Oncogene</i> , 1998, 16, 685-690.	5.9	15
110	BetaSerpentine: a bioinformatics tool for reconstruction of amyloid structures. <i>Bioinformatics</i> , 2018, 34, 599-608.	4.1	15
111	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
112	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
113	Malaria Vaccine Development Using Synthetic Peptides as a Technical Platform. <i>Advances in Immunology</i> , 2012, 114, 107-149.	2.2	14
114	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
115	<scp>PRDB</scp>: <scp>P</scp>rotein <scp>R</scp>peat <scp>D</scp>ata<scp>B</scp>ase. <i>Proteomics</i> , 2012, 12, 1333-1336.	2.2	12
116	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
117	Census of halide-binding sites in protein structures. <i>Bioinformatics</i> , 2020, 36, 3064-3071.	4.1	11
118	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
119	Stereochemical Analysis of Interaction of Signal Peptide with Phospholipids at the Initiation of Protein Translocation Across the Membrane. <i>Journal of Biomolecular Structure and Dynamics</i> , 1991, 9, 143-157.	3.5	10
120	Molecular modelling of the 3-D structure of RNA tetraloops with different nucleotide sequences. <i>Nucleic Acids Research</i> , 1993, 21, 4556-4562.	14.5	10
121	Plasmodium vivax Antigen Discovery Based on Alpha-Helical Coiled Coil Protein Motif. <i>PLoS ONE</i> , 2014, 9, e100440.	2.5	10
122	Multifunctional Amyloid Oligomeric Nanoparticles for Specific Cell Targeting and Drug Delivery. <i>Biomacromolecules</i> , 2020, 21, 4302-4312.	5.4	10
123	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
124	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
125	Î±-Helical solenoid model for the human involucrin. <i>FEBS Letters</i> , 2000, 473, 127-131.	2.8	8
126	Processing of Escherichia coli Alkaline Phosphatase. <i>Journal of Biological Chemistry</i> , 2002, 277, 50396-50402.	3.4	8

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127	Immunoreactivity of Sera From Low to Moderate Malaria-Endemic Areas Against Plasmodium vivax rPvs48/45 Proteins Produced in Escherichia coli and Chinese Hamster Ovary Systems. <i>Frontiers in Immunology</i> , 2021, 12, 634738.	4.8	7
128	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
129	In search of the boundary between repetitive and non-repetitive protein sequences. <i>Biochemical Society Transactions</i> , 2015, 43, 807-811.	3.4	6
130	Designs on a curve. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 103-105.	8.2	6
131	Porins and Amyloids are Coded by Similar Sequence Motifs. <i>Proteomics</i> , 2019, 19, 1800075.	2.2	5
132	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
133	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
134	Malaria vaccine: why is it taking so long?. <i>Expert Review of Vaccines</i> , 2010, 9, 111-114.	4.4	4
135	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
136	Predicting Protein Conformational Disorder and Disordered Binding Sites. <i>Methods in Molecular Biology</i> , 2022, 2449, 95-147.	0.9	4
137	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. <i>International Journal of Peptide Research and Therapeutics</i> , 1997, 4, 297-304.	0.1	3
138	Structure of an IgE-Binding Peptide from Fungal Enolases. <i>International Archives of Allergy and Immunology</i> , 2001, 124, 93-94.	2.1	3
139	Conformational Switching in PolyGln Amyloid Fibrils Resulting from a Single Amino Acid Insertion. <i>Biophysical Journal</i> , 2014, 106, 2134-2142.	0.5	3
140	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
141	Amyloidogenicity as a driving force for the formation of functional oligomers. <i>Journal of Structural Biology</i> , 2020, 212, 107604.	2.8	3
142	Structural classification of $\beta\alpha\beta$ and $\beta\alpha\beta\alpha$ supersecondary structure units in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 30, 193-212.	2.6	3
143	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
144	Tally-2.0: upgraded validator of tandem repeat detection in protein sequences. <i>Bioinformatics</i> , 2020, 36, 3260-3262.	4.1	2

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145	Aspartateâ€phobia of thermophiles as a reaction to deleterious chemical transformations. <i>BioEssays</i> , 2022, 44, e2100213.	2.5	2
146	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
147	Title is missing!. <i>International Journal of Peptide Research and Therapeutics</i> , 1997, 4, 297-304.	0.1	1
148	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
149	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
150	Tally: a scoring tool for boundary determination between repetitive and non-repetitive protein sequences. <i>Bioinformatics</i> , 2016, 32, 1952-1958.	4.1	1
151	The C-terminal segment of <i>Leishmania major</i> HslU: Toward potential inhibitors of LmHslU activity. <i>Bioorganic Chemistry</i> , 2022, 119, 105539.	4.1	1