Heinrich Sticht

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/308073/publications.pdf Version: 2024-02-01

		25034	42399
305	12,693	57	92
papers	citations	h-index	g-index
202	222	202	20205
525	525	323	20595
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Range of genetic mutations associated with severe non-syndromic sporadic intellectual disability: an exome sequencing study. Lancet, The, 2012, 380, 1674-1682.	13.7	940
2	AMBER force-field parameters for phosphorylated amino acids in different protonation states: phosphoserine, phosphothreonine, phosphotyrosine, and phosphohistidine. Journal of Molecular Modeling, 2006, 12, 281-289.	1.8	337
3	Mutations in STRA6 Cause a Broad Spectrum of Malformations Including Anophthalmia, Congenital Heart Defects, Diaphragmatic Hernia, Alveolar Capillary Dysplasia, Lung Hypoplasia, and Mental Retardation. American Journal of Human Genetics, 2007, 80, 550-560.	6.2	316
4	The interleukin-10 family of cytokines. Trends in Immunology, 2002, 23, 89-96.	6.8	290
5	Structure of Amyloid A4-(1-40)-Peptide of Alzheimer's Disease. FEBS Journal, 1995, 233, 293-298.	0.2	273
6	Human TBX1 Missense Mutations Cause Gain of Function Resulting in the Same Phenotype as 22q11.2 Deletions. American Journal of Human Genetics, 2007, 80, 510-517.	6.2	195
7	Diagnostic Yield and Novel Candidate Genes by Exome Sequencing in 152 Consanguineous Families With Neurodevelopmental Disorders. JAMA Psychiatry, 2017, 74, 293.	11.0	186
8	Identification of a novel loss-of-function calcium channel gene mutation in short QT syndrome (SQTS6). European Heart Journal, 2011, 32, 1077-1088.	2.2	178
9	Mutations in MEF2C from the 5q14.3q15 microdeletion syndrome region are a frequent cause of severe mental retardation and diminish MECP2 and CDKL5 expression. Human Mutation, 2010, 31, 722-733.	2.5	163
10	Allergic Cross-reactivity Made Visible. Journal of Biological Chemistry, 2001, 276, 22756-22763.	3.4	151
11	De Novo Mutations in the Genome Organizer CTCF Cause Intellectual Disability. American Journal of Human Genetics, 2013, 93, 124-131.	6.2	151
12	B Cell Repertoire Analysis Identifies New Antigenic Domains on Glycoprotein B of Human Cytomegalovirus which Are Target of Neutralizing Antibodies. PLoS Pathogens, 2011, 7, e1002172.	4.7	136
13	Heterozygous NTF4 Mutations Impairing Neurotrophin-4 Signaling in Patients with Primary Open-Angle Glaucoma. American Journal of Human Genetics, 2009, 85, 447-456.	6.2	134
14	The structure of iron–sulfur proteins. Progress in Biophysics and Molecular Biology, 1998, 70, 95-136.	2.9	131
15	Structural Rearrangements of HIV-1 Tat-responsive RNA upon Binding of Neomycin B. Journal of Biological Chemistry, 2000, 275, 20660-20666.	3.4	131
16	The T-cell Lymphokine Interleukin-26 Targets Epithelial Cells through the Interleukin-20 Receptor 1 and Interleukin-10 Receptor 2 Chains. Journal of Biological Chemistry, 2004, 279, 33343-33351.	3.4	126
17	Severely Incapacitating Mutations in Patients with Extreme Short Stature Identify RNA-Processing Endoribonuclease RMRP as an Essential Cell Growth Regulator. American Journal of Human Genetics, 2005, 77, 795-806.	6.2	117
18	Structure determination of human and murine beta-defensins reveals structural conservation in the absence of significant sequence similarity. Protein Science, 2001, 10, 2470-2479.	7.6	115

#	Article	IF	CITATIONS
19	Synthetic Peptides as Protein Mimics. Frontiers in Bioengineering and Biotechnology, 2015, 3, 211.	4.1	113
20	Gene dosage-dependent rescue of HSP neurite defects in SPG4 patients' neurons. Human Molecular Genetics, 2014, 23, 2527-2541.	2.9	111
21	Estrogen and progesterone receptors: from molecular structures to clinical targets. Cellular and Molecular Life Sciences, 2009, 66, 2405-2426.	5.4	108
22	Structural Analysis of the Protein Phosphatase 1 Docking Motif: Molecular Description of Binding Specificities Identifies Interacting Proteins. Chemistry and Biology, 2006, 13, 49-59.	6.0	107
23	Oral Treatment with the <scp>d</scp> -Enantiomeric Peptide D3 Improves the Pathology and Behavior of Alzheimer's Disease Transgenic Mice. ACS Chemical Neuroscience, 2010, 1, 639-648.	3.5	107
24	A Peroxisomal Disorder of Severe Intellectual Disability, Epilepsy, and Cataracts Due to Fatty Acyl-CoA Reductase 1 Deficiency. American Journal of Human Genetics, 2014, 95, 602-610.	6.2	106
25	Clinical relevance of systematic phenotyping and exome sequencing in patients with short stature. Genetics in Medicine, 2018, 20, 630-638.	2.4	101
26	Responsiveness of B cells is regulated by the hinge region of IgD. Nature Immunology, 2015, 16, 534-543.	14.5	98
27	Protective capacity of neutralizing and non-neutralizing antibodies against glycoprotein B of cytomegalovirus. PLoS Pathogens, 2017, 13, e1006601.	4.7	91
28	Mutations in IL36RN in Patients with Generalized Pustular Psoriasis. Journal of Investigative Dermatology, 2013, 133, 2634-2637.	0.7	89
29	Further delineation of Pitt-Hopkins syndrome: phenotypic and genotypic description of 16 novel patients. Journal of Medical Genetics, 2008, 45, 738-744.	3.2	86
30	Novel Mode of Phosphorylation-triggered Reorganization of the Nuclear Lamina during Nuclear Egress of Human Cytomegalovirus. Journal of Biological Chemistry, 2010, 285, 13979-13989.	3.4	86
31	The CD83 Molecule – An Important Immune Checkpoint. Frontiers in Immunology, 2020, 11, 721.	4.8	86
32	Â-Helix nucleation by a calcium-binding peptide loop. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 903-908.	7.1	83
33	A mutation of the epithelial sodium channel associated with atypical cystic fibrosis increases channel open probability and reduces Na ⁺ self inhibition. Journal of Physiology, 2010, 588, 1211-1225.	2.9	83
34	A Specific A/T Polymorphism in Western Tyrosine Phosphorylation B-Motifs Regulates Helicobacter pylori CagA Epithelial Cell Interactions. PLoS Pathogens, 2015, 11, e1004621.	4.7	83
35	Disturbed Wnt Signalling due to a Mutation in CCDC88C Causes an Autosomal Recessive Non-Syndromic Hydrocephalus with Medial Diverticulum. Molecular Syndromology, 2010, 1, 99-112.	0.8	82
36	The genetic basis for most patients with pustular skin disease remains elusive. British Journal of Dermatology, 2018, 178, 740-748.	1.5	82

#	Article	IF	CITATIONS
37	Cytomegaloviral proteins that associate with the nuclear lamina: components of a postulated nuclear egress complex. Journal of General Virology, 2009, 90, 579-590.	2.9	81
38	Proteomic Analysis of the Multimeric Nuclear Egress Complex of Human Cytomegalovirus. Molecular and Cellular Proteomics, 2014, 13, 2132-2146.	3.8	79
39	Palmoplantar Pustular Psoriasis Is Associated with Missense Variants in CARD14 , but Not with Loss-of-Function Mutations in IL36RN in European Patients. Journal of Investigative Dermatology, 2015, 135, 2538-2541.	0.7	78
40	Channel Estimation for Diffusive Molecular Communications. IEEE Transactions on Communications, 2016, , 1-1.	7.8	78
41	AMPA-receptor specific biogenesis complexes control synaptic transmission and intellectual ability. Nature Communications, 2017, 8, 15910.	12.8	77
42	Variants in ASB10 are associated with open-angle glaucoma. Human Molecular Genetics, 2012, 21, 1336-1349.	2.9	76
43	Amyloid-β dimers in the absence of plaque pathology impair learning and synaptic plasticity. Brain, 2016, 139, 509-525.	7.6	74
44	Antitermination in bacteriophage λ. FEBS Journal, 2000, 267, 2397-2408.	0.2	72
45	Structural Investigation of the Binding of a Herpesviral Protein to the SH3 Domain of Tyrosine Kinase Lckâ€,‡. Biochemistry, 2002, 41, 5120-5130.	2.5	72
46	Null Mutation in PGAP1 Impairing Gpi-Anchor Maturation in Patients with Intellectual Disability and Encephalopathy. PLoS Genetics, 2014, 10, e1004320.	3.5	72
47	The clinical significance of small copy number variants in neurodevelopmental disorders. Journal of Medical Genetics, 2014, 51, 677-688.	3.2	72
48	De novo missense mutations in the NAA10 gene cause severe non-syndromic developmental delay in males and females. European Journal of Human Genetics, 2015, 23, 602-609.	2.8	72
49	Crystal Structure of the Human Cytomegalovirus pUL50-pUL53 Core Nuclear Egress Complex Provides Insight into a Unique Assembly Scaffold for Virus-Host Protein Interactions. Journal of Biological Chemistry, 2015, 290, 27452-27458.	3.4	71
50	Identification of the variant Ala335Val of MED25 as responsible for CMT2B2: molecular data, functional studies of the SH3 recognition motif and correlation between wild-type MED25 and PMP22 RNA levels in CMT1A animal models. Neurogenetics, 2009, 10, 275-287.	1.4	68
51	Differential contribution of EFâ€hands to the Ca ²⁺ â€dependent activation in the plant twoâ€pore channel TPC1. Plant Journal, 2011, 68, 424-432.	5.7	68
52	Structure of Human Parathyroid Hormone 1–37 in Solution. Journal of Biological Chemistry, 1995, 270, 15194-15202.	3.4	66
53	CD and NMR Studies of Prion Protein (PrP) Helix 1. Journal of Biological Chemistry, 2003, 278, 50175-50181.	3.4	66
54	Confirmation of mutations in <i>PROSC</i> as a novel cause of vitamin B _₆ -dependent epilepsy. Journal of Medical Genetics, 2017, 54, 809-814.	3.2	66

#	Article	IF	CITATIONS
55	Conformational Stability of Fibrillar Amyloid-Beta Oligomers via Protofilament Pair Formation – A Systematic Computational Study. PLoS ONE, 2013, 8, e70521.	2.5	64
56	Mutations in CYP1B1 cause primary congenital glaucoma by reduction of either activity or abundance of the enzyme. Human Mutation, 2008, 29, 1147-1153.	2.5	62
57	Rational Design of β-Sheet Ligands Against Aβ ₄₂ -Induced Toxicity. Journal of the American Chemical Society, 2011, 133, 4348-4358.	13.7	61
58	Campylobacter jejuni enters gut epithelial cells and impairs intestinal barrier function through cleavage of occludin by serine protease HtrA. Gut Pathogens, 2019, 11, 4.	3.4	61
59	Casein kinase 2-dependent serine phosphorylation of MuSK regulates acetylcholine receptor aggregation at the neuromuscular junction. Genes and Development, 2006, 20, 1800-1816.	5.9	60
60	Crystal Structure of Cytomegalovirus IE1 Protein Reveals Targeting of TRIM Family Member PML via Coiled-Coil Interactions. PLoS Pathogens, 2014, 10, e1004512.	4.7	60
61	Haploinsufficiency of vascular endothelial growth factor related signaling genes is associated with tetralogy of Fallot. Genetics in Medicine, 2019, 21, 1001-1007.	2.4	58
62	Elucidation of the phenotypic spectrum and genetic landscape in primary and secondary microcephaly. Genetics in Medicine, 2019, 21, 2043-2058.	2.4	57
63	T4SS-dependent TLR5 activation by Helicobacter pylori infection. Nature Communications, 2019, 10, 5717.	12.8	56
64	A Dual Phenotype of Periventricular Nodular Heterotopia and Frontometaphyseal Dysplasia in One Patient Caused by a Single FLNA Mutation Leading to Two Functionally Different Aberrant Transcripts. American Journal of Human Genetics, 2004, 74, 731-737.	6.2	55
65	Analysis of the Structureâ^'Activity Relationship of Four Herpesviral UL97 Subfamily Protein Kinases Reveals Partial but not Full Functional Conservationâ€. Journal of Medicinal Chemistry, 2006, 49, 7044-7053.	6.4	55
66	Profiling of <i>WDR36</i> Missense Variants in German Patients with Glaucoma. , 2008, 49, 270.		55
67	Independent <i>NF1</i> and <i>PTPN11</i> mutations in a family with neurofibromatosisâ€Noonan syndrome. American Journal of Medical Genetics, Part A, 2009, 149A, 1263-1267.	1.2	55
68	Structure of the equine infectious anemia virus Tat protein. Science, 1994, 264, 1584-1587.	12.6	53
69	Genome-Wide Association Study of <scp>l</scp> -Arginine and Dimethylarginines Reveals Novel Metabolic Pathway for Symmetric Dimethylarginine. Circulation: Cardiovascular Genetics, 2014, 7, 864-872.	5.1	53
70	Genetic screening confirms heterozygous mutations in ACAN as a major cause of idiopathic short stature. Scientific Reports, 2017, 7, 12225.	3.3	53
71	Myeloperoxidase Modulates Inflammation in Generalized Pustular Psoriasis and Additional Rare Pustular Skin Diseases. American Journal of Human Genetics, 2020, 107, 527-538.	6.2	53
72	Solution structure of the glycosylated second type 2 module of fibronectin. Journal of Molecular Biology, 1998, 276, 177-187.	4.2	52

#	Article	IF	CITATIONS
73	The role of recessive inheritance in early-onset epileptic encephalopathies: a combined whole-exome sequencing and copy number study. European Journal of Human Genetics, 2019, 27, 408-421.	2.8	52
74	Crystal Structure Analysis and Solution Studies of Human Lck-SH3; Zinc-induced Homodimerization Competes with the Binding of Proline-rich Motifs. Journal of Molecular Biology, 2007, 365, 1417-1428.	4.2	51
75	Amyloid-β42 Oligomer Structures from Fibrils: A Systematic Molecular Dynamics Study. Journal of Physical Chemistry B, 2010, 114, 2219-2226.	2.6	49
76	Missense Variants in RHOBTB2 Cause a Developmental and Epileptic Encephalopathy in Humans, and Altered Levels Cause Neurological Defects in Drosophila. American Journal of Human Genetics, 2018, 102, 44-57.	6.2	49
77	Structure ofSynechococcus elongatus[Fe2S2] Ferredoxin in Solutionâ€. Biochemistry, 1996, 35, 12831-12841.	2.5	48
78	De Novo Variants in the F-Box Protein FBXO11 in 20 Individuals with a Variable Neurodevelopmental Disorder. American Journal of Human Genetics, 2018, 103, 305-316.	6.2	48
79	CTCF variants in 39 individuals with a variable neurodevelopmental disorder broaden the mutational and clinical spectrum. Genetics in Medicine, 2019, 21, 2723-2733.	2.4	48
80	Rare Loss-of-Function Mutation in SERPINA3 in Generalized Pustular Psoriasis. Journal of Investigative Dermatology, 2020, 140, 1451-1455.e13.	0.7	48
81	Recognition of T-rich single-stranded DNA by the cold shock protein Bs-CspB in solution. Nucleic Acids Research, 2006, 34, 4561-4571.	14.5	47
82	Spatially clustering de novo variants in CYFIP2, encoding the cytoplasmic FMRP interacting protein 2, cause intellectual disability and seizures. European Journal of Human Genetics, 2019, 27, 747-759.	2.8	47
83	Solution structure of cytochrome c6 from the thermophilic cyanobacterium Synechococcus elongatus. EMBO Journal, 1998, 17, 27-36.	7.8	46
84	Structural Insight into the Giant Ca2+-Binding Adhesin SiiE: Implications for the Adhesion of Salmonella enterica to Polarized Epithelial Cells. Structure, 2013, 21, 741-752.	3.3	46
85	Autosomal-Recessive Mutations in the tRNA Splicing Endonuclease Subunit TSEN15 Cause Pontocerebellar Hypoplasia and Progressive Microcephaly. American Journal of Human Genetics, 2016, 99, 228-235.	6.2	44
86	De Novo Variants in MAPK8IP3 Cause Intellectual Disability with Variable Brain Anomalies. American Journal of Human Genetics, 2019, 104, 203-212.	6.2	44
87	Structural characterization of Lyn-SH3 domain in complex with a herpesviral protein reveals an extended recognition motif that enhances binding affinity. Protein Science, 2005, 14, 2487-2498.	7.6	43
88	Combining Independent Drug Classes into Superior, Synergistically Acting Hybrid Molecules. Angewandte Chemie - International Edition, 2010, 49, 8743-8746.	13.8	43
89	The Prolyl Isomerase Pin1 Promotes the Herpesvirus-Induced Phosphorylation-Dependent Disassembly of the Nuclear Lamina Required for Nucleocytoplasmic Egress. PLoS Pathogens, 2016, 12, e1005825.	4.7	43
90	Characterization of Recombinant Human Cytomegaloviruses Encoding IE1 Mutants L174P and 1-382 Reveals that Viral Targeting of PML Bodies Perturbs both Intrinsic and Innate Immune Responses. Journal of Virology, 2016, 90, 1190-1205.	3.4	42

#	Article	IF	CITATIONS
91	Further corroboration of distinct functional features in SCN2A variants causing intellectual disability or epileptic phenotypes. Molecular Medicine, 2019, 25, 6.	4.4	42
92	Relevance of conserved lysine and arginine residues in transmembrane helices for the transport activity of organic anion transporting polypeptide 1B3. British Journal of Pharmacology, 2010, 159, 698-708.	5.4	41
93	Structural Basis for the Recognition of Human Cytomegalovirus Glycoprotein B by a Neutralizing Human Antibody. PLoS Pathogens, 2014, 10, e1004377.	4.7	41
94	Insights into amprenavir resistance in E35D HIV-1 protease mutation from molecular dynamics and binding free-energy calculations. Journal of Molecular Modeling, 2007, 13, 297-304.	1.8	40
95	Synthetic Protein Scaffolds Based on Peptide Motifs and Cognate Adaptor Domains for Improving Metabolic Productivity. Frontiers in Bioengineering and Biotechnology, 2015, 3, 191.	4.1	40
96	Mutations in DCPS and EDC3 in autosomal recessive intellectual disability indicate a crucial role for mRNA decapping in neurodevelopment. Human Molecular Genetics, 2015, 24, 3172-3180.	2.9	40
97	Overexpression, Purification, and Biochemical Characterization of the Extracellular Human CD83 Domain and Generation of Monoclonal Antibodies. Protein Expression and Purification, 2002, 24, 445-452.	1.3	39
98	Hybrid Compounds. BioDrugs, 2012, 26, 21-31.	4.6	39
99	The cytomegalovirus egress proteins pUL50 and pUL53 are translocated to the nuclear envelope through two distinct modes of nuclear import. Journal of General Virology, 2013, 94, 2056-2069.	2.9	39
100	The human cytomegalovirus nuclear egress complex unites multiple functions: Recruitment of effectors, nuclear envelope rearrangement, and docking to nuclear capsids. Reviews in Medical Virology, 2017, 27, e1934.	8.3	39
101	Group I Metabotropic Glutamate Receptors Bind to Protein Phosphatase 1C. Journal of Biological Chemistry, 2003, 278, 50682-50690.	3.4	38
102	CD83 is a dimer: Comparative analysis of monomeric and dimeric isoforms. Biochemical and Biophysical Research Communications, 2005, 329, 132-139.	2.1	37
103	Characterization of two mutations in the SPTLC1 subunit of serine palmitoyltransferase associated with hereditary sensory and autonomic neuropathy type I. Human Mutation, 2011, 32, E2211-E2225.	2.5	37
104	The chemical class of quinazoline compounds provides a core structure for the design of anticytomegaloviral kinase inhibitors. Antiviral Research, 2016, 134, 130-143.	4.1	37
105	A computational strategy for the prediction of functional linear peptide motifs in proteins. Bioinformatics, 2007, 23, 3297-3303.	4.1	36
106	Conformational Switch upon Phosphorylation: Human CDK Inhibitor p19 ^{INK4d} between the Native and Partially Folded State. ACS Chemical Biology, 2009, 4, 53-63.	3.4	36
107	Oxidative stress-induced posttranslational modifications of human hemoglobin in erythrocytes. Archives of Biochemistry and Biophysics, 2013, 529, 34-44.	3.0	36
108	Toll-like Receptor 5 Activation by the CagY Repeat Domains of Helicobacter pylori. Cell Reports, 2020, 32, 108159.	6.4	36

#	Article	IF	CITATIONS
109	Specific Residues of a Conserved Domain in the N Terminus of the Human Cytomegalovirus pUL50 Protein Determine Its Intranuclear Interaction with pUL53. Journal of Biological Chemistry, 2012, 287, 24004-24016.	3.4	35
110	Characterization of a Discontinuous Neutralizing Epitope on Glycoprotein B of Human Cytomegalovirus. Journal of Virology, 2013, 87, 8927-8939.	3.4	35
111	<i>NDST1</i> missense mutations in autosomal recessive intellectual disability. American Journal of Medical Genetics, Part A, 2014, 164, 2753-2763.	1.2	34
112	Genotype-phenotype evaluation of MED13L defects in the light of a novel truncating and a recurrent missense mutation. European Journal of Medical Genetics, 2017, 60, 451-464.	1.3	34
113	Solution Structure of the Human CC Chemokine 2:Â A Monomeric Representative of the CC Chemokine Subtypeâ€,‡. Biochemistry, 1999, 38, 5995-6002.	2.5	33
114	Two isoforms of the protein kinase pUL97 of human cytomegalovirus are differentially regulated in their nuclear translocation. Journal of General Virology, 2011, 92, 638-649.	2.9	33
115	Alanine-glyoxylate aminotransferase 2 (AGXT2) Polymorphisms Have Considerable Impact on Methylarginine and β-aminoisobutyrate Metabolism in Healthy Volunteers. PLoS ONE, 2014, 9, e88544.	2.5	33
116	The pH-dependent Client Release from the Collagen-specific Chaperone HSP47 Is Triggered by a Tandem Histidine Pair. Journal of Biological Chemistry, 2016, 291, 12612-12626.	3.4	33
117	N ⁸ â€acetylspermidine as a potential plasma biomarker for Snyderâ€Robinson syndrome identified by clinical metabolomics. Journal of Inherited Metabolic Disease, 2016, 39, 131-137.	3.6	33
118	Systematic Analysis of Phosphotyrosine Antibodies Recognizing Single Phosphorylated EPIYA-Motifs in CagA of Western-Type Helicobacter pylori Strains. PLoS ONE, 2014, 9, e96488.	2.5	33
119	New insights into the clinical and molecular spectrum of the novel CYFIP2-related neurodevelopmental disorder and impairment of the WRC-mediated actin dynamics. Genetics in Medicine, 2021, 23, 543-554.	2.4	32
120	Selection and Characterization of Tau Binding á´Enantiomeric Peptides with Potential for Therapy of Alzheimer Disease. PLoS ONE, 2016, 11, e0167432.	2.5	32
121	A Two-α-Helix Extra Domain Mediates the Halophilic Character of a Plant-Type Ferredoxin from Halophilic Archaeaâ€,‡. Biochemistry, 2005, 44, 29-39.	2.5	31
122	Dual Selection Pressure by Drugs and HLA Class I-Restricted Immune Responses on Human Immunodeficiency Virus Type 1 Protease. Journal of Virology, 2007, 81, 2887-2898.	3.4	31
123	The polynucleotide kinase 3′-phosphatase gene (PNKP) is involved in Charcot-Marie-Tooth disease (CMT2B2) previously related to MED25. Neurogenetics, 2018, 19, 215-225.	1.4	31
124	Pathogenic WDFY3 variants cause neurodevelopmental disorders and opposing effects on brain size. Brain, 2019, 142, 2617-2630.	7.6	31
125	A Survey of Biological Building Blocks for Synthetic Molecular Communication Systems. IEEE Communications Surveys and Tutorials, 2020, 22, 2765-2800.	39.4	31
126	Role of the N-terminus for the stability of an amyloid-β fibril with three-fold symmetry. PLoS ONE, 2017, 12. e0186347.	2.5	31

#	Article	IF	CITATIONS
127	Molecular Dynamics Simulations of HIV-1 Protease Suggest Different Mechanisms Contributing to Drug Resistance. Journal of Chemical Theory and Computation, 2005, 1, 315-324.	5.3	30
128	Effect of pathogenic mutations on the structure and dynamics of Alzheimer's Aβ42-amyloid oligomers. Journal of Molecular Modeling, 2010, 16, 1011-1020.	1.8	30
129	Infantile Epileptic Encephalopathy, Transient Choreoathetotic Movements, and Hypersomnia due to a De Novo Missense Mutation in the SCN2A Gene. Neuropediatrics, 2014, 45, 261-264.	0.6	30
130	Variants in CPLX1 in two families with autosomal-recessive severe infantile myoclonic epilepsy and ID. European Journal of Human Genetics, 2017, 25, 889-893.	2.8	30
131	SUMO E3 ligases are expressed in the retina and regulate SUMOylation of the metabotropic glutamate receptor 8b. Biochemical Journal, 2011, 435, 365-371.	3.7	29
132	Expanding the clinical and mutational spectrum of Kaufman oculocerebrofacial syndrome with biallelic UBE3B mutations. Human Genetics, 2014, 133, 939-949.	3.8	29
133	Systematic analysis of phosphotyrosine antibodies recognizing single phosphorylated EPIYA-motifs in CagA of East Asian-type Helicobacter pylori strains. BMC Microbiology, 2016, 16, 201.	3.3	29
134	Amino-Terminal Processing of Helicobacter pylori Serine Protease HtrA: Role in Oligomerization and Activity Regulation. Frontiers in Microbiology, 2018, 9, 642.	3.5	29
135	De novo variants in PAK1 lead to intellectual disability with macrocephaly and seizures. Brain, 2019, 142, 3351-3359.	7.6	29
136	Viroporins: Structure, function, and their role in the life cycle of SARS-CoV-2. International Journal of Biochemistry and Cell Biology, 2022, 145, 106185.	2.8	29
137	Secondary Structure and Tertiary Fold of the Birch Pollen Allergen Bet v 1 in Solution. Journal of Biological Chemistry, 1996, 271, 19243-19250.	3.4	28
138	Two novel mutations in the insulin binding subunit of the insulin receptor gene without insulin binding impairment in a patient with Rabson–Mendenhall syndrome. Molecular Genetics and Metabolism, 2008, 94, 356-362.	1.1	28
139	Validation of the reliability of computational O-GlcNAc prediction. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 416-421.	2.3	28
140	DYNC2LI1 mutations broaden the clinical spectrum of dynein-2 defects. Scientific Reports, 2015, 5, 11649.	3.3	28
141	Mutations in the B.1.1.7 SARS-CoV-2 Spike Protein Reduce Receptor-Binding Affinity and Induce a Flexible Link to the Fusion Peptide. Biomedicines, 2021, 9, 525.	3.2	28
142	Inhibition of SARS CoV Envelope Protein by Flavonoids and Classical Viroporin Inhibitors. Frontiers in Microbiology, 2021, 12, 692423.	3.5	28
143	High-resolution crystal structures of two prototypical β- and γ-herpesviral nuclear egress complexes unravel the determinants of subfamily specificity. Journal of Biological Chemistry, 2020, 295, 3189-3201.	3.4	28
144	A new redox-dependent mechanism of MMP-1 activity control comprising reduced low-molecular-weight thiols and oxidizing radicals. Journal of Molecular Medicine, 2009, 87, 261-272.	3.9	27

#	Article	IF	CITATIONS
145	Molecular Engineering of a Secreted, Highly Homogeneous, and Neurotoxic AÎ ² Dimer. ACS Chemical Neuroscience, 2011, 2, 242-248.	3.5	27
146	A Multiple Piccolino-RIBEYE Interaction Supports Plate-Shaped Synaptic Ribbons in Retinal Neurons. Journal of Neuroscience, 2019, 39, 2606-2619.	3.6	27
147	Expanding the clinical spectrum of COL1A1 mutations in different forms of glaucoma. Orphanet Journal of Rare Diseases, 2016, 11, 108.	2.7	26
148	Hypomorphic Pathogenic Variants in TAF13 Are Associated with Autosomal-Recessive Intellectual Disability and Microcephaly. American Journal of Human Genetics, 2017, 100, 555-561.	6.2	26
149	Human Cytomegalovirus Nuclear Capsids Associate with the Core Nuclear Egress Complex and the Viral Protein Kinase pUL97. Viruses, 2018, 10, 35.	3.3	26
150	The Structure of the Coliphage HK022 Nun Protein-λ-phage boxB RNA Complex. Journal of Biological Chemistry, 2001, 276, 32064-32070.	3.4	25
151	A mutation in the β-subunit of ENaC identified in a patient with cystic fibrosis-like symptoms has a gain-of-function effect. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2013, 304, L43-L55.	2.9	25
152	Equine infectious anemia virus Tat is a predominantly helical protein. FEBS Journal, 1993, 218, 973-976.	0.2	24
153	Trifluoroethanol Stabilizes a Helix-Turn-Helix Motif in Equine Infectious-Anemia-Virus Trans -Activator Protein. FEBS Journal, 1994, 225, 855-861.	0.2	24
154	NMR spectroscopy reveals common structural features of the birch pollen allergen Bet v 1 and the cherry allergen Pru a 1. Applied Magnetic Resonance, 1999, 17, 449-464.	1.2	24
155	Characterization of Lck-Binding Elements in the Herpesviral Regulatory Tip Proteinâ€. Biochemistry, 2004, 43, 14932-14939.	2.5	24
156	Functional and Structural Relevance of Conserved Positively Charged Lysine Residues in Organic Anion Transporting Polypeptide 1B3. Molecular Pharmacology, 2011, 80, 400-406.	2.3	24
157	Identification of a Neutralizing Epitope within Antigenic Domain 5 of Glycoprotein B of Human Cytomegalovirus. Journal of Virology, 2015, 89, 361-372.	3.4	24
158	Analysis of naturally occurring mutations in the human uptake transporter NaCT important for bone and brain development and energy metabolism. Scientific Reports, 2018, 8, 11330.	3.3	24
159	Loss-of-function and missense variants in NSD2 cause decreased methylation activity and are associated with a distinct developmental phenotype. Genetics in Medicine, 2021, 23, 1474-1483.	2.4	24
160	A pair of noncompeting neutralizing human monoclonal antibodies protecting from disease in a SARSâ€CoVâ€⊋ infection model. European Journal of Immunology, 2022, 52, 770-783.	2.9	24
161	Binding, Domain Orientation, and Dynamics of the Lck SH3â ^{~,} SH2 Domain Pair and Comparison with Other Src-Family Kinases. Biochemistry, 2005, 44, 13043-13050.	2.5	23
162	The transcription regulator RbsR represents a novel interaction partner of the phosphoprotein HPr-Ser46-P in Bacillus subtilis. FEBS Journal, 2006, 273, 1251-1261.	4.7	23

#	Article	IF	CITATIONS
163	Loss of function of SVBP leads to autosomal recessive intellectual disability, microcephaly, ataxia, and hypotonia. Genetics in Medicine, 2019, 21, 1790-1796.	2.4	23
164	Nuclear Egress Complexes of HCMV and Other Herpesviruses: Solving the Puzzle of Sequence Coevolution, Conserved Structures and Subfamily-Spanning Binding Properties. Viruses, 2020, 12, 683.	3.3	23
165	Eukaryotically Encoded and Chloroplast-located Rubredoxin Is Associated with Photosystem II. Journal of Biological Chemistry, 2000, 275, 30058-30063.	3.4	22
166	Mimicking titration experiments with MD simulations: A protocol for the investigation of pH-dependent effects on proteins. Scientific Reports, 2016, 6, 22523.	3.3	22
167	Campylobacter jejuni Serine Protease HtrA Cleaves the Tight Junction Component Claudin-8. Frontiers in Cellular and Infection Microbiology, 2020, 10, 590186.	3.9	22
168	An NMR-Derived Model for the Solution Structure of Oxidized Thermotoga maritima 1[Fe4-S4] Ferredoxin. FEBS Journal, 1996, 237, 726-735.	0.2	21
169	Nuclear import of isoforms of the cytomegalovirus kinase pUL97 is mediated by differential activity of NLS1 and NLS2 both acting through classical importin-α binding. Journal of General Virology, 2012, 93, 1756-1768.	2.9	21
170	The Cyclin-Dependent Kinase Ortholog pUL97 of Human Cytomegalovirus Interacts with Cyclins. Viruses, 2013, 5, 3213-3230.	3.3	21
171	The Conformational Stability of Nonfibrillar Amyloid-β Peptide Oligomers Critically Depends on the C-Terminal Peptide Length. ACS Chemical Neuroscience, 2014, 5, 161-167.	3.5	21
172	A severe congenital myasthenic syndrome with "dropped head―caused by novel <i>MUSK</i> mutations. Muscle and Nerve, 2015, 52, 668-673.	2.2	21
173	MAP4-Dependent Regulation of Microtubule Formation Affects Centrosome, Cilia, and Golgi Architecture as a Central Mechanism in Growth Regulation. Human Mutation, 2015, 36, 87-97.	2.5	21
174	Probing the potential of CnaB-type domains for the design of tag/catcher systems. PLoS ONE, 2017, 12, e0179740.	2.5	21
175	Structure Predictions and Interaction Studies Indicate Homology of Separase N-Terminal Regulatory Domains and Drosophila THR. Cell Cycle, 2004, 3, 177-183.	2.6	20
176	Impact of the Câ€ŧerminal Disulfide Bond on the Folding and Stability of Onconase. ChemBioChem, 2010, 11, 978-986.	2.6	20
177	Small ubiquitin-related modifier (SUMO) pathway-mediated enhancement of human cytomegalovirus replication correlates with a recruitment of SUMO-1/3 proteins to viral replication compartments. Journal of General Virology, 2013, 94, 1373-1384.	2.9	20
178	DAPK-HSF1 interaction as a new positive feedback loop for TNF-induced apoptosis in colorectal cancer cells. Journal of Cell Science, 2014, 127, 5273-87.	2.0	20
179	Evidence for genetic overlap between adult onset Still's disease and hereditary periodic fever syndromes. Rheumatology International, 2018, 38, 111-120.	3.0	20
180	De novo variants in SNAP25 cause an early-onset developmental and epileptic encephalopathy. Genetics in Medicine, 2021, 23, 653-660.	2.4	20

#	Article	IF	CITATIONS
181	Identification and characterization of a eukaryotically encoded rubredoxin in a cryptomonad alga1. FEBS Letters, 2000, 471, 191-196.	2.8	19
182	Functional Null Mutations in the Gonosomal Homologue Gene TBL1Y are Associated with Non-Syndromic Coarctation of the Aorta. Current Molecular Medicine, 2012, 12, 199-205.	1.3	19
183	Noncanonical NF-κB Activation by the Oncoprotein Tio Occurs Through a Nonconserved TRAF3-Binding Motif. Science Signaling, 2013, 6, ra27.	3.6	19
184	Proteomic Interaction Patterns between Human Cyclins, the Cyclin-Dependent Kinase Ortholog pUL97 and Additional Cytomegalovirus Proteins. Viruses, 2016, 8, 219.	3.3	19
185	SPATA5 mutations cause a distinct autosomal recessive phenotype of intellectual disability, hypotonia and hearing loss. Orphanet Journal of Rare Diseases, 2016, 11, 130.	2.7	19
186	Cyclins B1, T1, and H differ in their molecular mode of interaction with cytomegalovirus protein kinase pUL97. Journal of Biological Chemistry, 2019, 294, 6188-6203.	3.4	19
187	HIV-1 Fusion Is Blocked through Binding of GB Virus C E2D Peptides to the HIV-1 gp41 Disulfide Loop. PLoS ONE, 2013, 8, e54452.	2.5	18
188	Inhibition of RAS Activation Due to a Homozygous Ezrin Variant in Patients with Profound Intellectual Disability. Human Mutation, 2015, 36, 270-278.	2.5	18
189	CD83 and GRASP55 interact in human dendritic cells. Biochemical and Biophysical Research Communications, 2015, 459, 42-48.	2.1	18
190	Structural and functional dissection reveals distinct roles of Ca2+-binding sites in the giant adhesin SiiE of Salmonella enterica. PLoS Pathogens, 2017, 13, e1006418.	4.7	18
191	The Interaction between Cyclin B1 and Cytomegalovirus Protein Kinase pUL97 is Determined by an Active Kinase Domain. Viruses, 2015, 7, 4582-4601.	3.3	17
192	A Metadynamics-Based Protocol for the Determination of GPCR-Ligand Binding Modes. International Journal of Molecular Sciences, 2019, 20, 1970.	4.1	17
193	Computational decomposition reveals reshaping of the SARSâ€CoVâ€⊋–ACE2 interface among viral variants expressing the N501Y mutation. Journal of Cellular Biochemistry, 2021, 122, 1863-1872.	2.6	17
194	Multiple Modes of Interaction between Lck and CD28. Journal of Immunology, 2005, 174, 3839-3840.	0.8	16
195	PNUTS forms a trimeric protein complex with GABAC receptors and protein phosphatase 1. Molecular and Cellular Neurosciences, 2008, 37, 808-819.	2.2	16
196	Structural Model of the HIV-1 Tat(46–58)-TAR Complex. Journal of Biomolecular Structure and Dynamics, 1998, 16, 683-692.	3.5	15
197	Synthesis and characterization of the human CC chemokineHCC-2. Chemical Biology and Drug Design, 1999, 54, 505-513.	1.1	15
198	Identification of a Ninein (NIN) mutation in a family with spondyloepimetaphyseal dysplasia with joint laxity (leptodactylic type)-like phenotype. Matrix Biology, 2013, 32, 387-392.	3.6	15

#	Article	IF	CITATIONS
199	Solution structure of the autophagy-related protein LC3C reveals a polyproline II motif on a mobile tether with phosphorylation site. Scientific Reports, 2019, 9, 14167.	3.3	15
200	Genotype–epigenotype–phenotype correlations in females with frontometaphyseal dysplasia. American Journal of Medical Genetics, Part A, 2006, 140A, 1069-1073.	1.2	14
201	DNA binding by Corynebacterium glutamicum TetR-type transcription regulator AmtR. BMC Molecular Biology, 2009, 10, 73.	3.0	14
202	Expanding the genotypic and phenotypic spectrum of severe serine biosynthesis disorders. Human Mutation, 2020, 41, 1615-1628.	2.5	14
203	Potent Tau Aggregation Inhibitor Dâ€Peptides Selected against Tauâ€Repeat 2 Using Mirror Image Phage Display. ChemBioChem, 2021, 22, 3049-3059.	2.6	14
204	A proline to glycine mutation in the Lck SH3-domain affects conformational sampling and increases ligand binding affinity. FEBS Letters, 2007, 581, 1555-1560.	2.8	13
205	Functional analysis of chemically synthesized derivatives of the human CC chemokine CCL15/HCC-2, a high affinity CCR1 ligand. Chemical Biology and Drug Design, 2008, 63, 36-47.	1.1	13
206	Binding properties of SUMO-interacting motifs (SIMs) in yeast. Journal of Molecular Modeling, 2015, 21, 50.	1.8	13
207	Modulation of Recombinant Human α1 Glycine Receptors by Mono- and Disaccharides: A Kinetic Study. ACS Chemical Neuroscience, 2016, 7, 1077-1087.	3.5	13
208	Pontocerebellar hypoplasia due to bi-allelic variants in MINPP1. European Journal of Human Genetics, 2021, 29, 411-421.	2.8	13
209	Properties of Oligomeric Interaction of the Cytomegalovirus Core Nuclear Egress Complex (NEC) and Its Sensitivity to an NEC Inhibitory Small Molecule. Viruses, 2021, 13, 462.	3.3	13
210	Rare Large Scale Subdomain Motions in Prion Protein can Initiate Aggregation. Journal of Biomolecular Structure and Dynamics, 2006, 23, 581-590.	3.5	12
211	Effects of the V82A and I54V mutations on the dynamics and ligand binding properties of HIV-1 protease. Journal of Molecular Modeling, 2010, 16, 1577-1583.	1.8	12
212	Phenotypic Variability in a Large Czech Family with a Dynamin 2–Associated Charcot-Marie-Tooth Neuropathy. Journal of Neurogenetics, 2011, 25, 182-188.	1.4	12
213	Structural characterization of intracellular C-terminal domains of group III metabotropic glutamate receptors. FEBS Letters, 2011, 585, 511-516.	2.8	12
214	Premature Osteoarthritis as Presenting Sign of Type II Collagenopathy: A Case Report and Literature Review. Seminars in Arthritis and Rheumatism, 2013, 42, 355-360.	3.4	12
215	IFN-γ-response mediator GBP-1 represses human cell proliferation by inhibiting the Hippo signaling transcription factor TEAD. Biochemical Journal, 2018, 475, 2955-2967.	3.7	12
216	Improving the efficiency of the Gaussian conformational database potential for the refinement of protein and nucleic acid structures. Journal of Biomolecular NMR, 2001, 21, 373-375.	2.8	11

#	Article	IF	CITATIONS
217	Crystal Structure of the Extracellular Domain of the Human Dendritic Cell Surface Marker CD83. Journal of Molecular Biology, 2017, 429, 1227-1243.	4.2	11
218	Evolutionary conserved networks of human height identify multiple Mendelian causes of short stature. European Journal of Human Genetics, 2019, 27, 1061-1071.	2.8	11
219	Bi-allelic variants in SPATA5L1 lead to intellectual disability, spastic-dystonic cerebral palsy, epilepsy, and hearing loss. American Journal of Human Genetics, 2021, 108, 2006-2016.	6.2	11
220	N-Terminus to Arginine Side-Chain Cyclization of Linear Peptidic Neuropeptide Y Y ₄ Receptor Ligands Results in Picomolar Binding Constants. Journal of Medicinal Chemistry, 2021, 64, 16746-16769.	6.4	11
221	De novo variants in ATP2B1 lead to neurodevelopmental delay. American Journal of Human Genetics, 2022, 109, 944-952.	6.2	11
222	Molecular Dynamics Simulation of Equine Infectious Anemia Virus Tat Protein in Water and in 40% Trifluoroethanol. Journal of Biomolecular Structure and Dynamics, 1994, 12, 19-36.	3.5	10
223	Solution structure of a zinc substituted eukaryotic rubredoxin from the cryptomonad alga <i>Guillardia theta</i> . Protein Science, 2000, 9, 1474-1486.	7.6	10
224	A common structural mechanism underlying GCMB mutations that cause hypoparathyroidism. Medical Hypotheses, 2006, 67, 482-487.	1.5	10
225	A protein-specifically adapted scoring function for the reranking of docking solutions. Proteins: Structure, Function and Bioinformatics, 2007, 67, 98-111.	2.6	10
226	Insight into the Phosphoryl Transfer of the Escherichia coli Glucose Phosphotransferase System from QM/MM Simulations. Journal of Physical Chemistry B, 2008, 112, 13391-13400.	2.6	10
227	pHâ€dependent molecular dynamics of vesicular stomatitis virus glycoprotein G. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2601-2613.	2.6	10
228	Whole exome sequencing reveals a novel de novo FOXC1 mutation in a patient with unrecognized Axenfeld–Rieger syndrome and glaucoma. Gene, 2015, 568, 76-80.	2.2	10
229	Interaction of Glycolipids with the Macrophage Surface Receptor Mincle – a Systematic Molecular Dynamics Study. Scientific Reports, 2018, 8, 5374.	3.3	10
230	Agonist Binding and G Protein Coupling in Histamine H2 Receptor: A Molecular Dynamics Study. International Journal of Molecular Sciences, 2020, 21, 6693.	4.1	10
231	A Molecular Model for the Differential Activation of STAT3 and STAT6 by the Herpesviral Oncoprotein Tip. PLoS ONE, 2012, 7, e34306.	2.5	10
232	A novel D-amino acid peptide with therapeutic potential (ISAD1) inhibits aggregation of neurotoxic disease-relevant mutant Tau and prevents Tau toxicity in vitro. Alzheimer's Research and Therapy, 2022, 14, 15.	6.2	10
233	Smaller, Stronger, More Stable: Peptide Variants of a SARS-CoV-2 Neutralizing Miniprotein. International Journal of Molecular Sciences, 2022, 23, 6309.	4.1	10
234	Effect of HPr phosphorylation on structure, dynamics, and interactions in the course of transcriptional control. Journal of Molecular Modeling, 2007, 13, 431-444.	1.8	9

#	Article	IF	CITATIONS
235	Application of information theory to feature selection in protein docking. Journal of Molecular Modeling, 2012, 18, 1285-1297.	1.8	9
236	Biallelic <i>SEMA3A</i> defects cause a novel type of syndromic short stature. American Journal of Medical Genetics, Part A, 2013, 161, 2880-2889.	1.2	9
237	Binding of histamine to the H1 receptor—a molecular dynamics study. Journal of Molecular Modeling, 2018, 24, 346.	1.8	9
238	Conformational Dynamics of Herpesviral NEC Proteins in Different Oligomerization States. International Journal of Molecular Sciences, 2018, 19, 2908.	4.1	9
239	The C-terminal coiled-coil domain of Corynebacterium diphtheriae DIP0733 is crucial for interaction with epithelial cells and pathogenicity in invertebrate animal model systems. BMC Microbiology, 2018, 18, 106.	3.3	9
240	Matricellular Protein SPARCL1 Regulates Blood Vessel Integrity and Antagonizes Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2021, 27, 1491-1502.	1.9	9
241	The peptidyl-prolyl cis/trans isomerase Pin1 interacts with three early regulatory proteins of human cytomegalovirus. Virus Research, 2020, 285, 198023.	2.2	9
242	Equine infectious anemia virus transactivator is a homeodomain-type protein 1 1Edited by J. Karn. Journal of Molecular Biology, 1998, 277, 749-755.	4.2	8
243	Effects of Histidine Protonation and Phosphorylation on Histidine-Containing Phosphocarrier Protein Structure, Dynamics, and Physicochemical Properties. Biochemistry, 2007, 46, 12314-12326.	2.5	8
244	Mouse ApoM Displays an Unprecedented Seven-Stranded Lipocalin Fold: Folding Decoy or Alternative Native Fold?. Journal of Molecular Biology, 2010, 404, 363-371.	4.2	8
245	A comparative study of HIV-1 and HTLV-I protease structure and dynamics reveals a conserved residue interaction network. Journal of Molecular Modeling, 2011, 17, 2693-2705.	1.8	8
246	An Inhibitory Peptide Derived from the a-subunit of the Epithelial Sodium Channel (ENaC) Shows a Helical Conformation. Cellular Physiology and Biochemistry, 2012, 29, 761-774.	1.6	8
247	Identification of the Structural Features that Mediate Binding Specificity in the Recognition of STAT Proteins by Dual-Specificity Phosphatases. Journal of Biomolecular Structure and Dynamics, 2012, 29, 777-792.	3.5	8
248	Single Expressed Glycine Receptor Domains Reconstitute Functional Ion Channels without Subunit-specific Desensitization Behavior. Journal of Biological Chemistry, 2014, 289, 29135-29147.	3.4	8
249	Mutations in herpes simplex virus gD protein affect receptor binding by different molecular mechanisms. Journal of Molecular Modeling, 2014, 20, 2192.	1.8	8
250	Channel estimation techniques for diffusion-based molecular communications. , 2016, , .		8
251	The degenerin region of the human bile acid-sensitive ion channel (BASIC) is involved in channel inhibition by calcium and activation by bile acids. Pflugers Archiv European Journal of Physiology, 2018, 470, 1087-1102.	2.8	8
252	Probing the role of intercalating protein sidechains for kink formation in DNA. PLoS ONE, 2018, 13, e0192605.	2.5	8

#	Article	IF	CITATIONS
253	Transfer of HTLV-1 p8 and Gag to target T-cells depends on VASP, a novel interaction partner of p8. PLoS Pathogens, 2020, 16, e1008879.	4.7	8
254	A Novel Strain-Specific Neutralizing Epitope on Glycoprotein H of Human Cytomegalovirus. Journal of Virology, 2021, 95, e0065721.	3.4	8
255	Dynamic regulatory interaction between cytomegalovirus major tegument protein pp65 and protein kinase pUL97 in intracellular compartments, dense bodies and virions. Journal of General Virology, 2017, 98, 2850-2863.	2.9	8
256	The crystal structure of the varicella-zoster Orf24-Orf27 nuclear egress complex spotlights multiple determinants of herpesvirus subfamily specificity. Journal of Biological Chemistry, 2022, 298, 101625.	3.4	8
257	Merging bioresponsive release of insulin-like growth factor I with 3D printable thermogelling hydrogels. Journal of Controlled Release, 2022, 347, 115-126.	9.9	8
258	Episodic psychosis, ataxia, motor neuropathy with pyramidal signs (PAMP syndrome)Âcaused by a novel mutation in ADPRHL2 (AHR3). Neurological Sciences, 2021, 42, 3871-3878.	1.9	7
259	Functional Relevance of the Interaction between Human Cyclins and the Cytomegalovirus-Encoded CDK-Like Protein Kinase pUL97. Viruses, 2021, 13, 1248.	3.3	7
260	<i>De novo</i> missense variants in FBXO11 alter its protein expression and subcellular localization. Human Molecular Genetics, 2022, 31, 440-454.	2.9	7
261	Structure and Activity of a Chimeric Interleukin-8-Melanoma-Growth-Stimulatory-Activity Protein. FEBS Journal, 1996, 235, 26-35.	0.2	6
262	Molecular modeling of the interleukin-19 receptor complex. Journal of Molecular Modeling, 2004, 10, 290-6.	1.8	6
263	Structural Basis for Species Selectivity in the HIV-1 gp120-CD4 Interaction: Restoring Affinity to gp120 in Murine CD4 Mimetic Peptides. Advances in Bioinformatics, 2011, 2011, 1-12.	5.7	6
264	Peptides presenting the binding site of human CD4 for the HIV-1 envelope glycoprotein gp120. Beilstein Journal of Organic Chemistry, 2012, 8, 1858-1866.	2.2	6
265	Characterization of a Single-Chain Variable Fragment Recognizing a Linear Epitope of Aβ: A Biotechnical Tool for Studies on Alzheimer's Disease?. PLoS ONE, 2013, 8, e59820.	2.5	6
266	A Homozygous Mutation in GPT2 Associated with Nonsyndromic Intellectual Disability in a Consanguineous Family from Costa Rica. JIMD Reports, 2017, 36, 59-66.	1.5	6
267	Sequence-specific 1H, 13C and 15N resonance assignments of the major cherry allergen Pru a 1. Journal of Biomolecular NMR, 2000, 18, 71-72.	2.8	5
268	Sequence-specific 1H, 13C and 15N resonance assignments and secondary structure of [2Fe-2S] ferredoxin from Halobacterium salinarum. Journal of Biomolecular NMR, 2000, 16, 347-348.	2.8	5
269	An information-theoretic classification of amino acids for the assessment of interfaces in protein–protein docking. Journal of Molecular Modeling, 2013, 19, 3901-3910.	1.8	5
270	Expression, Purification, and Structural Analysis of Intracellular C-Termini from Metabotropic Glutamate Receptors. Methods in Enzymology, 2013, 520, 257-279.	1.0	5

#	Article	IF	CITATIONS
271	The Oligomeric Assemblies of Cytomegalovirus Core Nuclear Egress Proteins Are Associated with Host Kinases and Show Sensitivity to Antiviral Kinase Inhibitors. Viruses, 2022, 14, 1021.	3.3	5
272	Further characterization of <scp>Borjesonâ€Forssmanâ€Lehmann</scp> syndrome in females due to de novo variants in <scp><i>PHF6</i></scp> . Clinical Genetics, 2022, 102, 182-190.	2.0	5
273	Homology Modeling of Adenylosuccinate Synthetase fromSaccharomyces CerevisiaeReveals a Possible Binding Region for Single-Stranded ARS Sequences. Journal of Biomolecular Structure and Dynamics, 1997, 14, 667-675.	3.5	4
274	Thymosin β4 and Tissue Transglutaminase. Molecular Characterization of Cyclic Thymosin β4. Protein Journal, 2013, 32, 484-492.	1.6	4
275	Analysis of amino acid residues in the predicted transmembrane pore influencing transport kinetics of the hepatic drug transporter organic anion transporting polypeptide 1B1 (OATP1B1). Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 2894-2902.	2.6	4
276	Probing the Structure of the Escherichia coli Periplasmic Proteins HdeA and YmgD by Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2016, 120, 11845-11855.	2.6	4
277	Structure-based functional analysis of effector protein SifA in living cells reveals motifs important for Salmonella intracellular proliferation. International Journal of Medical Microbiology, 2018, 308, 84-96.	3.6	4
278	A proline-rich motif in the large intracellular loop of the glycine receptor α1 subunit interacts with the Pleckstrin homology domain of collybistin. Journal of Advanced Research, 2021, 29, 95-106.	9.5	4
279	Specific Engineered G Protein Coupling to Histamine Receptors Revealed from Cellular Assay Experiments and Accelerated Molecular Dynamics Simulations. International Journal of Molecular Sciences, 2021, 22, 10047.	4.1	4
280	De novo variants in the PABP domain of PABPC1 lead to developmental delay. Genetics in Medicine, 2022, , .	2.4	4
281	Structural Studies of the Equine Infectious Anemia Virus <i>trans</i> â€Activator Protein. FEBS Journal, 1996, 240, 45-52.	0.2	3
282	Effect of the SH3-SH2 domain linker sequence on the structure of Hck kinase. Journal of Molecular Modeling, 2011, 17, 1927-1934.	1.8	3
283	Confidence intervals for the mutual information. International Journal of Machine Intelligence and Sensory Signal Processing, 2014, 1, 201.	0.2	3
284	Investigation of the dynamics of the viral immediate-early protein 1 in different conformations and oligomerization states. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1029-1041.	3.5	3
285	Loss of PHF6 leads to aberrant development of human neuron-like cells. Scientific Reports, 2020, 10, 19030.	3.3	3
286	The recurrent missense mutation p.(Arg367Trp) in YARS1 causes a distinct neurodevelopmental phenotype. Journal of Molecular Medicine, 2021, 99, 1755-1768.	3.9	3
287	Effect of lons and Sequence Variants on the Antagonist Binding Properties of the Histamine H1 Receptor. International Journal of Molecular Sciences, 2022, 23, 1420.	4.1	3
288	Bi-allelic variants in <i>CHKA</i> cause a neurodevelopmental disorder with epilepsy and microcephaly. Brain, 2022, 145, 1916-1923.	7.6	3

#	Article	IF	CITATIONS
289	Sequence-specific 1H, 13C and 15N resonance assignments of the SH3-SH2 domain pair from the human tyrosine kinase Lck. Journal of Biomolecular NMR, 2003, 27, 405-406.	2.8	2
290	Motif-Mediated Protein Interactions and their Role in Disease. , 2010, , 272-294.		2
291	A tight lower bound on the mutual information of a binary and an arbitrary finite random variable as a function of the variational distance. , 2014, , .		2
292	Fine-Tuning of Neuronal Ion Channels–Mapping of Residues Involved in Glucose Sensitivity of Recombinant Human Glycine Receptors. ACS Chemical Neuroscience, 2020, 11, 3474-3483.	3.5	2
293	Clinical and molecular delineation of spondylocostal dysostosis type 3. Clinical Genetics, 2021, 99, 851-852.	2.0	2
294	Is there a sodium effect in fibrillar amyloid- \hat{l}^2 oligomers?. Journal of Cheminformatics, 2014, 6, .	6.1	1
295	Molecular mechanism of HIV-1 gp120 mutations that reduce CD4 binding affinity. Journal of Biomolecular Structure and Dynamics, 2014, 32, 52-64.	3.5	1
296	Identification of mutations in DYNC2LI1, a member of the mammalian cytoplasmic dynein 2 complex, expands the clinical spectrum of Jeune/ATD ciliopathies. Cilia, 2015, 4, .	1.8	1
297	Modulation of recombinant human alpha 1 glycine receptor by flavonoids and gingerols. Biological Chemistry, 2021, 402, 825-838.	2.5	1
298	Homodimerization of a proximal region within the C-terminus of the orphan G-protein coupled receptor GPR179. Neurochemistry International, 2021, 149, 105150.	3.8	1
299	A modeling strategy for G-protein coupled receptors. AIMS Biophysics, 2016, 3, 211-231.	0.6	1
300	Application of Methods from Information Theory in Protein-Interaction Analysis. Lecture Notes in Bioengineering, 2018, , 293-313.	0.4	0
301	Rare slow channel congenital myasthenic syndromes without repetitive compound muscle action potential and dramatic response to low dose fluoxetine. Acta Neurologica Belgica, 2021, 121, 1755-1760.	1.1	0
302	Molecular Simulations and Alzheimer× ³ s Disease. , 2021, , 54-70.		0
303	The Structure of Lentiviral Tat Proteins in Solution. , 1996, , 287-303.		Ο
304	A Computational Study of the Structure and Dynamics of the E. coli Transcription Factor RfaH. Current Biotechnology, 2015, 4, 26-38.	0.4	0
305	Characterizing the Interaction between the HTLV-1 Transactivator Tax-1 with Transcription Elongation Factor ELL2 and Its Impact on Viral Transactivation. International Journal of Molecular Sciences, 2021, 22, 13597.	4.1	0