

# Hui Lu

## List of Publications by Year in descending order

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135  
papers

9,102  
citations

71102

41  
h-index

43889

91  
g-index

140  
all docs

140  
docs citations

140  
times ranked

11504  
citing authors

#	ARTICLE	IF	CITATIONS
1	Template-based protein structure modeling using the RaptorX web server. Nature Protocols, 2012, 7, 1511-1522.	12.0	1,474
2	Mechanical unfolding intermediates in titin modules. Nature, 1999, 402, 100-103.	27.8	789
3	Unfolding of Titin Immunoglobulin Domains by Steered Molecular Dynamics Simulation. Biophysical Journal, 1998, 75, 662-671.	0.5	658
4	Reverse engineering of the giant muscle protein titin. Nature, 2002, 418, 998-1002.	27.8	487
5	The mechanical stability of ubiquitin is linkage dependent. Nature Structural and Molecular Biology, 2003, 10, 738-743.	8.2	436
6	Contour Length and Refolding Rate of a Small Protein Controlled by Engineered Disulfide Bonds. Biophysical Journal, 2007, 92, 225-233.	0.5	285
7	The Key Event in Force-Induced Unfolding of Titin's Immunoglobulin Domains. Biophysical Journal, 2000, 79, 51-65.	0.5	282
8	A distance-dependent atomic knowledge-based potential for improved protein structure selection. Proteins: Structure, Function and Bioinformatics, 2001, 44, 223-232.	2.6	282
9	A statistical framework for cross-tissue transcriptome-wide association analysis. Nature Genetics, 2019, 51, 568-576.	21.4	262
10	Steered molecular dynamics simulations of force-induced protein domain unfolding. Proteins: Structure, Function and Bioinformatics, 1999, 35, 453-463.	2.6	246
11	Steered Molecular Dynamics. Lecture Notes in Computational Science and Engineering, 1999, , 39-65.	0.3	240
12	MULTIPROSPECTOR: An algorithm for the prediction of protein-protein interactions by multimeric threading. Proteins: Structure, Function and Bioinformatics, 2002, 49, 350-364.	2.6	239
13	Correlation between gene expression profiles and protein-protein interactions within and across genomes. Bioinformatics, 2005, 21, 2730-2738.	4.1	160
14	Steered molecular dynamics simulation of conformational changes of immunoglobulin domain I27 interpret atomic force microscopy observations. Chemical Physics, 1999, 247, 141-153.	1.9	145
15	Kernel-based machine learning protocol for predicting DNA-binding proteins. Nucleic Acids Research, 2005, 33, 6486-6493.	14.5	142
16	Development of Unified Statistical Potentials Describing Protein-Protein Interactions. Biophysical Journal, 2003, 84, 1895-1901.	0.5	137
17	Cholesterol modulates cell signaling and protein networking by specifically interacting with PDZ domain-containing scaffold proteins. Nature Communications, 2012, 3, 1249.	12.8	129
18	Single-molecule force spectroscopy reveals a mechanically stable protein fold and the rational tuning of its mechanical stability. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9278-9283.	7.1	117

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19	Multimeric Threading-Based Prediction of Protein-Protein Interactions on a Genomic Scale: Application to the <i>Saccharomyces cerevisiae</i> Proteome. <i>Genome Research</i> , 2003, 13, 1146-1154.	5.5	102
20	Quantum dynamics of the femtosecond photoisomerization of retinal in bacteriorhodopsin. <i>Faraday Discussions</i> , 1998, 110, 447-462.	3.2	83
21	Differential Roles of Phosphatidylserine, PtdIns(4,5)P2, and PtdIns(3,4,5)P3 in Plasma Membrane Targeting of C2 Domains. <i>Journal of Biological Chemistry</i> , 2008, 283, 26047-26058.	3.4	75
22	Solvent molecules bridge the mechanical unfolding transition state of a protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3185-3190.	7.1	73
23	Acetylproteomic Analysis Reveals Functional Implications of Lysine Acetylation in Human Spermatozoa (sperm). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1009-1023.	3.8	70
24	NAPS: a residue-level nucleic acid-binding prediction server. <i>Nucleic Acids Research</i> , 2010, 38, W431-W435.	14.5	66
25	Argonaute integrated single-tube PCR system enables supersensitive detection of rare mutations. <i>Nucleic Acids Research</i> , 2021, 49, e75-e75.	14.5	66
26	Probing static disorder in Arrhenius kinetics by single-molecule force spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11336-11340.	7.1	65
27	Genome-wide Functional Annotation of Dual-Specificity Protein- and Lipid-Binding Modules that Regulate Protein Interactions. <i>Molecular Cell</i> , 2012, 46, 226-237.	9.7	62
28	Intrinsically disordered protein-specific force field <scp>CHARMM</scp>36<scp>IDPSFF</scp>. <i>Chemical Biology and Drug Design</i> , 2018, 92, 1722-1735.	3.2	62
29	Three Electronic State Model of the Primary Phototransformation of Bacteriorhodopsin. <i>Biophysical Journal</i> , 1998, 75, 1689-1699.	0.5	61
30	Unfolding of titin domains studied by molecular dynamics simulations. <i>Journal of Muscle Research and Cell Motility</i> , 2002, 23, 513-521.	2.0	61
31	Residue-level prediction of DNA-binding sites and its application on DNA-binding protein predictions. <i>FEBS Letters</i> , 2007, 581, 1058-1066.	2.8	61
32	Mechanically Untying a Protein Slipknot: Multiple Pathways Revealed by Force Spectroscopy and Steered Molecular Dynamics Simulations. <i>Journal of the American Chemical Society</i> , 2012, 134, 10428-10435.	13.7	60
33	Molecular Basis of the Potent Membrane-remodeling Activity of the Epsin 1 N-terminal Homology Domain. <i>Journal of Biological Chemistry</i> , 2010, 285, 531-540.	3.4	59
34	Structural Bioinformatics Prediction of Membrane-binding Proteins. <i>Journal of Molecular Biology</i> , 2006, 359, 486-495.	4.2	58
35	Finding new structural and sequence attributes to predict possible disease association of single amino acid polymorphism (SAP). <i>Bioinformatics</i> , 2007, 23, 1444-1450.	4.1	55
36	Chemistry on a Single Protein, Vascular Cell Adhesion Molecule-1, during Forced Unfolding. <i>Journal of Biological Chemistry</i> , 2004, 279, 45865-45874.	3.4	53

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37	Boosting the prediction and understanding of DNA-binding domains from sequence. <i>Nucleic Acids Research</i> , 2010, 38, 3149-3158.	14.5	50
38	Predicting essential genes for identifying potential drug targets in <i>Aspergillus fumigatus</i> . <i>Computational Biology and Chemistry</i> , 2014, 50, 29-40.	2.3	50
39	Simulated Refolding of Stretched Titin Immunoglobulin Domains. <i>Biophysical Journal</i> , 2001, 81, 2268-2277.	0.5	48
40	Multi-omics facilitated variable selection in Cox-regression model for cancer prognosis prediction. <i>Methods</i> , 2017, 124, 100-107.	3.8	45
41	The PDZ2 domain of zonula occludens-1 and -2 is a phosphoinositide binding domain. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 3951-3966.	5.4	44
42	Ab initio protein structure prediction on a genomic scale: Application to the <i>Mycoplasma genitalium</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5993-5998.	7.1	41
43	Application of statistical potentials to protein structure refinement from low resolution ab initio models. <i>Biopolymers</i> , 2003, 70, 575-584.	2.4	40
44	A Single-Molecule Perspective on the Role of Solvent Hydrogen Bonds in Protein Folding and Chemical Reactions. <i>ChemPhysChem</i> , 2008, 9, 2836-2847.	2.1	39
45	Residue-Specific Force Field Improving the Sample of Intrinsically Disordered Proteins and Folded Proteins. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4793-4805.	5.4	39
46	Assessment of tumor mutation burden calculation from gene panel sequencing data. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 3401-3409.	2.0	38
47	The molecular basis of ceramide-1-phosphate recognition by C2 domains. <i>Journal of Lipid Research</i> , 2013, 54, 636-648.	4.2	34
48	A New Exhaustive Method and Strategy for Finding Motifs in ChIP-Enriched Regions. <i>PLoS ONE</i> , 2014, 9, e86044.	2.5	34
49	Stabilization Provided by Neighboring Strands Is Critical for the Mechanical Stability of Proteins. <i>Biophysical Journal</i> , 2008, 95, 3935-3942.	0.5	33
50	Meta-analysis of sex differences in gene expression in schizophrenia. <i>BMC Systems Biology</i> , 2016, 10, 9.	3.0	31
51	Nuclear Segmentation in Histopathological Images Using Two-Stage Stacked U-Nets With Attention Mechanism. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 573866.	4.1	31
52	A three-gene panel that distinguishes benign from malignant thyroid nodules. <i>International Journal of Cancer</i> , 2015, 136, 1646-1654.	5.1	30
53	A disease similarity matrix based on the uniqueness of shared genes. <i>BMC Medical Genomics</i> , 2017, 10, 26.	1.5	28
54	Mechanical Signaling on the Single Protein Level Studied Using Steered Molecular Dynamics. <i>Cell Biochemistry and Biophysics</i> , 2009, 55, 141-152.	1.8	27

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55	Comparison of SARS and NL63 Papain-Like Protease Binding Sites and Binding Site Dynamics: Inhibitor Design Implications. <i>Journal of Molecular Biology</i> , 2011, 414, 272-288.	4.2	23
56	More Overweight Adolescents Think They Are Just Fine. <i>American Journal of Preventive Medicine</i> , 2015, 49, 670-677.	3.0	22
57	MeTaDoR: a comprehensive resource for membrane targeting domains and their host proteins. <i>Bioinformatics</i> , 2007, 23, 3110-3112.	4.1	21
58	Analysis of Combinatorial Regulation: Scaling of Partnerships between Regulators with the Number of Governed Targets. <i>PLoS Computational Biology</i> , 2010, 6, e1000755.	3.2	21
59	Network-based prediction and knowledge mining of disease genes. <i>BMC Medical Genomics</i> , 2015, 8, S9.	1.5	20
60	High-dimensional omics data analysis using a variable screening protocol with prior knowledge integration (SKI). <i>BMC Systems Biology</i> , 2016, 10, 118.	3.0	19
61	Transcription Factors Contribute to Differential Expression in Cellular Pathways in Lung Adenocarcinoma and Lung Squamous Cell Carcinoma. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 836-847.	3.6	19
62	Computer Modeling of Force-Induced Titin Domain Unfolding. <i>Advances in Experimental Medicine and Biology</i> , 2000, 481, 143-162.	1.6	18
63	Evaluation Framework for Successful Artificial Intelligence-Enabled Clinical Decision Support Systems: Mixed Methods Study. <i>Journal of Medical Internet Research</i> , 2021, 23, e25929.	4.3	17
64	Learning to Translate Sequence and Structure to Function: Identifying DNA Binding and Membrane Binding Proteins. <i>Annals of Biomedical Engineering</i> , 2007, 35, 1043-1052.	2.5	16
65	Multiclass classification of sarcomas using pathway based feature selection method. <i>Journal of Theoretical Biology</i> , 2014, 362, 3-8.	1.7	16
66	Genome-wide sequence-based prediction of peripheral proteins using a novel semi-supervised learning technique. <i>BMC Bioinformatics</i> , 2010, 11, S6.	2.6	15
67	Texture Synthesis Based Thyroid Nodule Detection From Medical Ultrasound Images: Interpreting and Suppressing the Adversarial Effect of In-place Manual Annotation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 599.	4.1	15
68	DNA Damage Response and Repair Gene Alterations Increase Tumor Mutational Burden and Promote Poor Prognosis of Advanced Lung Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 708294.	2.8	15
69	Structure Based Prediction of Binding Residues on DNA-binding Proteins. , 2005, 2005, 2611-4.		14
70	Hemodynamic Phenotypes of Hypertension Based on Cardiac Output and Systemic Vascular Resistance. <i>American Journal of Medicine</i> , 2020, 133, e127-e139.	1.5	14
71	Probing osmolyte participation in the unfolding transition state of a protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9759-9764.	7.1	13
72	On the Improvement of Free-Energy Calculation from Steered Molecular Dynamics Simulations Using Adaptive Stochastic Perturbation Protocols. <i>PLoS ONE</i> , 2014, 9, e101810.	2.5	13

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73	A Lesion-Based Response Prediction Model Using Pretherapy PET/CT Image Features for Y90 Radioembolization to Hepatic Malignancies. <i>Technology in Cancer Research and Treatment</i> , 2017, 16, 620-629.	1.9	13
74	Identification of human circadian genes based on time course gene expression profiles by using a deep learning method. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2274-2283.	3.8	13
75	Efforts to reduce the disparity between permanent residents and temporary migrants: Stop TB experiences in Shanghai, China. <i>Tropical Medicine and International Health</i> , 2015, 20, 1033-1040.	2.3	12
76	A novel joint analysis framework improves identification of differentially expressed genes in cross disease transcriptomic analysis. <i>BioData Mining</i> , 2018, 11, 3.	4.0	12
77	VCFâ€Server: A webâ€based visualization tool for highâ€throughput variant data mining and management. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e00641.	1.2	12
78	Improving the Diagnosis of Phenylketonuria by Using a Machine Learningâ€Based Screening Model of Neonatal MRM Data. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 115.	3.5	12
79	Computational Methods for the Prediction of Microbial Essential Genes. <i>Current Bioinformatics</i> , 2014, 9, 89-101.	1.5	12
80	CO-EXPRESSION AMONG CONSTITUENTS OF A MOTIF IN THE PROTEINâ€PROTEIN INTERACTION NETWORK. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 1-17.	0.8	11
81	Calcium Induced Regulation of Skeletal Troponin â€” Computational Insights from Molecular Dynamics Simulations. <i>PLoS ONE</i> , 2013, 8, e58313.	2.5	11
82	Classification of Benign and Malignant Thyroid Nodules Using a Combined Clinical Information and Gene Expression Signatures. <i>PLoS ONE</i> , 2016, 11, e0164570.	2.5	11
83	RNA-seq Based Transcription Characterization of Fusion Breakpoints as a Potential Estimator for Its Oncogenic Potential. <i>BioMed Research International</i> , 2017, 2017, 1-8.	1.9	11
84	Analysis of economic burden and its associated factors of twenty-three rare diseases in Shanghai. <i>Orphanet Journal of Rare Diseases</i> , 2019, 14, 233.	2.7	11
85	Association of HIV infection and cognitive impairment in older adults: A meta-analysis. <i>Ageing Research Reviews</i> , 2021, 68, 101310.	10.9	11
86	Current inversions induced by resonant coupling to surface waves in a nanosized water pump. <i>Physical Review E</i> , 2015, 92, 053017.	2.1	10
87	A new method to measure the semantic similarity from query phenotypic abnormalities to diseases based on the human phenotype ontology. <i>BMC Bioinformatics</i> , 2018, 19, 162.	2.6	10
88	Closing Human Reference Genome Gaps: Identifying and Characterizing Gap-Closing Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2801-2809.	1.8	10
89	Lymphocyte activation gene-3 is associated with programmed death-ligand 1 and programmed cell death protein 1 in small cell lung cancer. <i>Annals of Translational Medicine</i> , 2021, 9, 1468-1468.	1.7	10
90	Do transportation subsidies and living allowances improve tuberculosis control outcomes among internal migrants in urban Shanghai, China?. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2013, 4, 19-24.	0.6	10

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91	Healthcare seeking behaviour among Chinese elderly. International Journal of Health Care Quality Assurance, 2017, 30, 248-259.	0.9	9
92	Comprehensive Analysis of Ubiquitously Expressed Genes in Humans from A Data-driven Perspective. Genomics, Proteomics and Bioinformatics, 2023, 21, 164-176.	6.9	9
93	Loosely-packed dynamical structures with partially-melted surface being the key for thermophilic argonaute proteins achieving high DNA-cleavage activity. Nucleic Acids Research, 2022, 50, 7529-7544.	14.5	9
94	Improved protein fold assignment using support vector machines. International Journal of Bioinformatics Research and Applications, 2005, 1, 319.	0.2	8
95	Intelligible machine learning with malibu. , 2008, 2008, 3795-8.		8
96	Quantum-Dot-Based Aptamer Beacons for $\{m K\}^{+}$ Detection. IEEE Sensors Journal, 2013, 13, 1549-1553.	4.7	8
97	A Herpes Simplex Virus Thymidine Kinase-Induced Mouse Model of Hepatocellular Carcinoma Associated with Up-Regulated Immune-Inflammatory-Related Signals. Genes, 2018, 9, 380.	2.4	8
98	Genomic analysis of a spinal muscular atrophy (SMA) discordant family identifies a novel mutation in TLL2, an activator of growth differentiation factor 8 (myostatin): a case report. BMC Medical Genetics, 2019, 20, 204.	2.1	8
99	Steered molecular dynamics simulations of force-induced protein domain unfolding. Proteins: Structure, Function and Bioinformatics, 1999, 35, 453-463.	2.6	8
100	Mining knowledge for the methylation status of CpG islands using alternating decision trees. , 2008, 2008, 3787-90.		7
101	A novel essential domain perspective for exploring gene essentiality. Bioinformatics, 2015, 31, 2921-2929.	4.1	7
102	Integrative Analysis of Membrane Proteome and MicroRNA Reveals Novel Lung Cancer Metastasis Biomarkers. Frontiers in Genetics, 2020, 11, 1023.	2.3	7
103	Relationship of Age With the Hemodynamic Parameters in Individuals With Elevated Blood Pressure. Journal of the American Geriatrics Society, 2020, 68, 1520-1528.	2.6	7
104	Machine Learning for Protein Structure and Function Prediction. Annual Reports in Computational Chemistry, 2008, , 41-66.	1.7	6
105	Identification of cancer-related genes and motifs in the human gene regulatory network. IET Systems Biology, 2015, 9, 128-134.	1.5	6
106	Improving accuracy of estimating glomerular filtration rate using artificial neural network: model development and validation. Journal of Translational Medicine, 2020, 18, 120.	4.4	6
107	Improved protein fold assignment using support vector machines. International Journal of Bioinformatics Research and Applications, 2006, 1, 319.	0.2	6
108	Molecular dynamics provides new insights into the mechanism of calcium signal transduction and interdomain interactions in cardiac troponin. FEBS Open Bio, 2021, 11, 1841-1853.	2.3	5

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109	RePhine: An Integrative Method for Identification of Drug Response-related Transcriptional Regulators. Genomics, Proteomics and Bioinformatics, 2021, 19, 534-548.	6.9	5
110	Visual Presentation as a Welcome Alternative to Textual Presentation of Gene Annotation Information. Advances in Experimental Medicine and Biology, 2010, 680, 709-715.	1.6	5
111	Weight spectrum and executive function in adolescents: the moderating role of negative emotions. Child and Adolescent Psychiatry and Mental Health, 2022, 16, 34.	2.5	5
112	Prediction of Specific Protein-DNA Recognition by Knowledge-based Two-body and Three-body Interaction Potentials. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 5017-20.	0.5	4
113	An improved machine learning protocol for the identification of correct Sequest search results. BMC Bioinformatics, 2010, 11, 591.	2.6	4
114	Efficient free-energy-profile reconstruction using adaptive stochastic perturbation protocols. Physical Review E, 2011, 84, 056705.	2.1	4
115	A structure-based protocol for learning the family-specific mechanisms of membrane-binding domains. Bioinformatics, 2012, 28, i431-i437.	4.1	4
116	Gut microbiota community adaption during young children fecal microbiota transplantation by 16s rDNA sequencing. Neurocomputing, 2016, 206, 66-72.	5.9	4
117	16S rDNA Gene Sequencing Analysis in Functional Dyspepsia Treated With Fecal Microbiota Transplantation. Journal of Pediatric Gastroenterology and Nutrition, 2017, 64, e80-e82.	1.8	4
118	Demographics, in-hospital analysis, and prevalence of 33 rare diseases with effective treatment in Shanghai. Orphanet Journal of Rare Diseases, 2021, 16, 262.	2.7	4
119	Pittâ€“Hopkins syndrome: phenotypic and genotypic description of four unrelated patients and structural analysis of corresponding missense mutations. Neurogenetics, 2021, 22, 161-169.	1.4	4
120	Computer simulation of I27 translocation through ClpY reveals a critical role of protein mechanical strength and local stability. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 1213-6.	0.5	3
121	CellSim: a novel software to calculate cell similarity and identify their co-regulation networks. BMC Bioinformatics, 2019, 20, 111.	2.6	3
122	Development of a Grid-based Statistical Potential for Protein Structure Prediction. , 2005, 2005, 6064-7.		2
123	Knowledgeâ€“based threeâ€“body potential for transcription factor binding site prediction. IET Systems Biology, 2016, 10, 23-29.	1.5	2
124	Machine-Learning Prediction of Drug-Induced Cardiac Arrhythmia: Analysis of Gene Expression and Clustering. Critical Reviews in Biomedical Engineering, 2018, 46, 245-275.	0.9	2
125	A Novel Joint Gene Set Analysis Framework Improves Identification of Enriched Pathways in Cross Disease Transcriptomic Analysis. Frontiers in Genetics, 2019, 10, 293.	2.3	2
126	Structural feature extraction protocol for classifying reversible membrane binding protein domains. , 2009, 2009, 6735-8.		1



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127	Identifying and characterizing the effects of calendar and environmental conditions on pediatric admissions in Shanghai. Journal of Big Data, 2019, 6, .	11.0	1
128	Functional Site Discovery From Incomplete Training Data: A Case Study With Nucleic Acidâ€™Binding Proteins. Frontiers in Genetics, 2019, 10, 729.	2.3	1
129	Correlations Between Phenotypes and Biological Process Ontologies in Monogenic Human Diseases. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 547-554.	3.6	1
130	Improving glomerular filtration rate estimation by semi-supervised learning: a development and external validation study. International Urology and Nephrology, 2021, 53, 1649-1658.	1.4	1
131	Steered molecular dynamics simulations of force-induced protein domain unfolding. , 1999, 35, 453.		1
132	Discovering Essential Domains in Essential Genes. Methods in Molecular Biology, 2015, 1279, 235-245.	0.9	1
133	Unfolding of titin domains studied by molecular dynamics simulations. , 2003, , 513-521.		1
134	Inferring Time-Lagged Causality Using the Derivative of Single-Cell Expression. International Journal of Molecular Sciences, 2022, 23, 3348.	4.1	1
135	Association of serum chemokine ligand 21 levels with asthma control in adults. Clinics, 2021, 76, e1713.	1.5	0