

Ceslovas Venclovas

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

101 papers	4,582 citations	34 h-index	66 g-index
105 ext. papers	5,905 ext. citations	9.4 avg, IF	5.78 L-index

#	Paper	IF	Citations
101	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020 , 18, 67-83	22.2	545
100	A modified definition of Sov, a segment-based measure for protein secondary structure prediction assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 34, 220-3	4.2	257
99	Structure-based predictions of Rad1, Rad9, Hus1 and Rad17 participation in sliding clamp and clamp-loading complexes. <i>Nucleic Acids Research</i> , 2000 , 28, 2481-93	20.1	234
98	A cyclic oligonucleotide signaling pathway in type III CRISPR-Cas systems. <i>Science</i> , 2017 , 357, 605-609	33.3	226
97	Programmable RNA shredding by the type III-A CRISPR-Cas system of <i>Streptococcus thermophilus</i> . <i>Molecular Cell</i> , 2014 , 56, 506-17	17.6	195
96	Processing and analysis of CASP3 protein structure predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 22-29	4.2	193
95	Progress over the first decade of CASP experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61 Suppl 7, 225-36	4.2	160
94	Spatiotemporal Control of Type III-A CRISPR-Cas Immunity: Coupling DNA Degradation with the Target RNA Recognition. <i>Molecular Cell</i> , 2016 , 62, 295-306	17.6	149
93	A sliding clamp model for the Rad1 family of cell cycle checkpoint proteins. <i>Cell</i> , 1999 , 96, 769-70	56.2	138
92	Processing and analysis of CASP3 protein structure predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , Suppl 3, 22-9	4.2	122
91	Processing and evaluation of predictions in CASP4. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , Suppl 5, 13-21	4.2	114
90	Assessment of progress over the CASP experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 585-95	4.2	101
89	CAD-score: a new contact area difference-based function for evaluation of protein structural models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 149-62	4.2	90
88	Type III CRISPR-Cas Immunity: Major Differences Brushed Aside. <i>Trends in Microbiology</i> , 2017 , 25, 49-61	12.4	88
87	Essential roles for imuAQ and imuB-encoded accessory factors in DnaE2-dependent mutagenesis in <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 13093-8	11.5	84
86	VoroMQA: Assessment of protein structure quality using interatomic contact areas. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, 1131-1145	4.2	82
85	Physical and functional interactions between MutY glycosylase homologue (MYH) and checkpoint proteins Rad9-Rad1-Hus1. <i>Biochemical Journal</i> , 2006 , 400, 53-62	3.8	76

84	PAM recognition by miniature CRISPR-Cas12f nucleases triggers programmable double-stranded DNA target cleavage. <i>Nucleic Acids Research</i> , 2020 , 48, 5016-5023	20.1	72
83	A vitamin B12 transporter in Mycobacterium tuberculosis. <i>Open Biology</i> , 2013 , 3, 120175	7	63
82	Five-stranded beta-sheet sandwiched with two alpha-helices: a structural link between restriction endonucleases EcoRI and EcoRV. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 20, 279-82	4.2	60
81	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1200-1221	4.2	58
80	How are tRNAs and mRNA arranged in the ribosome? An attempt to correlate the stereochemistry of the tRNA-mRNA interaction with constraints imposed by the ribosomal topography. <i>Nucleic Acids Research</i> , 1992 , 20, 2627-37	20.1	58
79	Comparison of performance in successive CASP experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , Suppl 5, 163-70	4.2	56
78	Comparative modeling in CASP6 using consensus approach to template selection, sequence-structure alignment, and structure assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61 Suppl 7, 99-105	4.2	53
77	Comparative modeling in CASP5: progress is evident, but alignment errors remain a significant hindrance. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 380-8	4.2	50
76	Comprehensive analysis of DNA polymerase III β subunits and their homologs in bacterial genomes. <i>Nucleic Acids Research</i> , 2014 , 42, 1393-413	20.1	48
75	The logic of DNA replication in double-stranded DNA viruses: insights from global analysis of viral genomes. <i>Nucleic Acids Research</i> , 2016 , 44, 4551-64	20.1	47
74	Functional mapping of the plant small RNA methyltransferase: HEN1 physically interacts with HYL1 and DICER-LIKE 1 proteins. <i>Nucleic Acids Research</i> , 2015 , 43, 2802-12	20.1	43
73	Human HLTF mediates postreplication repair by its HIRAN domain-dependent replication fork remodelling. <i>Nucleic Acids Research</i> , 2015 , 43, 10277-91	20.1	42
72	A catalogue of biochemically diverse CRISPR-Cas9 orthologs. <i>Nature Communications</i> , 2020 , 11, 5512	17.4	41
71	Voronota: A fast and reliable tool for computing the vertices of the Voronoi diagram of atomic balls. <i>Journal of Computational Chemistry</i> , 2014 , 35, 672-81	3.5	40
70	Estimation of model accuracy in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1361-1377	4.3	39
69	Detection of distant evolutionary relationships between protein families using theory of sequence profile-profile comparison. <i>BMC Bioinformatics</i> , 2010 , 11, 89	3.6	39
68	Structure-based sequence alignment for the beta-trefoil subdomain of the clostridial neurotoxin family provides residue level information about the putative ganglioside binding site. <i>FEBS Letters</i> , 2000 , 482, 119-24	3.8	36
67	Generation of DNA cleavage specificities of type II restriction endonucleases by reassortment of target recognition domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 10358-63	11.5	32

66	Comparative modeling of CASP4 target proteins: combining results of sequence search with three-dimensional structure assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , Suppl 5, 47-54	4.2	32
65	HhaI DNA methyltransferase uses the protruding Gln237 for active flipping of its target cytosine. <i>Structure</i> , 2004 , 12, 1047-55	5.2	31
64	Molecular modeling-based analysis of interactions in the RFC-dependent clamp-loading process. <i>Protein Science</i> , 2002 , 11, 2403-16	6.3	29
63	The cytolytic activity of vaginolysin strictly depends on cholesterol and is potentiated by human CD59. <i>Toxins</i> , 2015 , 7, 110-28	4.9	28
62	COMA server for protein distant homology search. <i>Bioinformatics</i> , 2010 , 26, 1905-6	7.2	28
61	Criteria for evaluating protein structures derived from comparative modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 7-13	4.2	28
60	PSI-BLAST-ISS: an intermediate sequence search tool for estimation of the position-specific alignment reliability. <i>BMC Bioinformatics</i> , 2005 , 6, 185	3.6	28
59	Some measures of comparative performance in the three CASPs. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 231-237	4.2	27
58	Different enzymes with similar structures involved in Mg(2+)-mediated polynucleotidyl transfer. <i>Nature Structural Biology</i> , 1995 , 2, 838-41		27
57	Identification of new homologs of PD-(D/E)XK nucleases by support vector machines trained on data derived from profile-profile alignments. <i>Nucleic Acids Research</i> , 2011 , 39, 1187-96	20.1	26
56	Distinct double- and single-stranded DNA binding of E. coli replicative DNA polymerase III alpha subunit. <i>ACS Chemical Biology</i> , 2008 , 3, 577-87	4.9	26
55	Novel Families of Archaeo-Eukaryotic Primases Associated with Mobile Genetic Elements of Bacteria and Archaea. <i>Journal of Molecular Biology</i> , 2018 , 430, 737-750	6.5	22
54	Codon-anticodon pairing. A model for interacting codon-anticodon duplexes located at the ribosomal A- and P-sites. <i>FEBS Letters</i> , 1992 , 313, 133-7	3.8	22
53	DnaQ exonuclease-like domain of Cas2 promotes spacer integration in a type I-E CRISPR-Cas system. <i>EMBO Reports</i> , 2018 , 19,	6.5	21
52	Conformational analysis of processivity clamps in solution demonstrates that tertiary structure does not correlate with protein dynamics. <i>Structure</i> , 2014 , 22, 572-581	5.2	21
51	Numerical criteria for the evaluation of ab initio predictions of protein structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 140-150	4.2	21
50	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antiviral defense. <i>Nucleic Acids Research</i> , 2020 , 48, 8828-8847	20.1	21
49	Comparative analysis of methods for evaluation of protein models against native structures. <i>Bioinformatics</i> , 2019 , 35, 937-944	7.2	21

48	Structural and functional analysis of rare missense mutations in human chorionic gonadotrophin β -subunit. <i>Molecular Human Reproduction</i> , 2012 , 18, 379-90	4.4	19
47	A structure-function analysis of the yeast Elg1 protein reveals the importance of PCNA unloading in genome stability maintenance. <i>Nucleic Acids Research</i> , 2017 , 45, 3189-3203	20.1	18
46	The use of automatic tools and human expertise in template-based modeling of CASP8 target proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77 Suppl 9, 81-8	4.2	18
45	Addressing the issue of sequence-to-structure alignments in comparative modeling of CASP3 target proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 73-80	4.2	18
44	Voroprot: an interactive tool for the analysis and visualization of complex geometric features of protein structure. <i>Bioinformatics</i> , 2011 , 27, 723-4	7.2	17
43	Thermodynamics of radicicol binding to human Hsp90 alpha and beta isoforms. <i>Biophysical Chemistry</i> , 2010 , 152, 153-63	3.5	17
42	Prediction of protein assemblies, the next frontier: The CASP14-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1800-1823	4.2	17
41	VoroMQA web server for assessing three-dimensional structures of proteins and protein complexes. <i>Nucleic Acids Research</i> , 2019 , 47, W437-W442	20.1	16
40	Diversity and evolution of B-family DNA polymerases. <i>Nucleic Acids Research</i> , 2020 , 48, 10142-10156	20.1	15
39	Sequence-structure mapping errors in the PDB: OB-fold domains. <i>Protein Science</i> , 2004 , 13, 1594-602	6.3	14
38	Structure of Csm2 elucidates the relationship between small subunits of CRISPR-Cas effector complexes. <i>FEBS Letters</i> , 2016 , 590, 1521-9	3.8	14
37	Computational analysis of DNA replicases in double-stranded DNA viruses: relationship with the genome size. <i>Nucleic Acids Research</i> , 2011 , 39, 8291-305	20.1	13
36	Transposon-associated TnpB is a programmable RNA-guided DNA endonuclease. <i>Nature</i> , 2021 , 599, 692-696	30.4	13
35	The PPI3D web server for searching, analyzing and modeling protein-protein interactions in the context of 3D structures. <i>Bioinformatics</i> , 2017 , 33, 935-937	7.2	13
34	The CAD-score web server: contact area-based comparison of structures and interfaces of proteins, nucleic acids and their complexes. <i>Nucleic Acids Research</i> , 2014 , 42, W259-63	20.1	12
33	Two distinct SSB protein families in nucleo-cytoplasmic large DNA viruses. <i>Bioinformatics</i> , 2012 , 28, 3186-90	7.2	12
32	New insights into the structures and interactions of bacterial Y-family DNA polymerases. <i>Nucleic Acids Research</i> , 2019 , 47, 4393-4405	20.1	10
31	DNA sliding clamps: just the right twist to load onto DNA. <i>Current Biology</i> , 2005 , 15, R989-92	6.3	10

30	PAM recognition by miniature CRISPR nucleases triggers programmable double-stranded DNA target cleavage		9
29	Modeling of protein complexes in CAPRI Round 37 using template-based approach combined with model selection. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018 , 86 Suppl 1, 292-301	4.2	8
28	Structural modeling of protein complexes: Current capabilities and challenges. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1222-1232	4.2	8
27	Herpesviral helicase-primase subunit UL8 is inactivated B-family polymerase. <i>Bioinformatics</i> , 2014 , 30, 2093-7	7.2	8
26	Restriction endonuclease BpuJI specific for the 5QCCCGT sequence is related to the archaeal Holliday junction resolvase family. <i>Nucleic Acids Research</i> , 2007 , 35, 2377-89	20.1	8
25	VoroCNN: Deep convolutional neural network built on 3D Voronoi tessellation of protein structures. <i>Bioinformatics</i> , 2021 ,	7.2	8
24	Modeling SARS-CoV-2 proteins in the CASP-commons experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1987-1996	4.2	8
23	Selection and characterization of anti-MUC-1 scFvs intended for targeted therapy. <i>Clinical Cancer Research</i> , 2003 , 9, 3845S-53S	12.9	8
22	VoroCNN: Deep convolutional neural network built on 3D Voronoi tessellation of protein structures		6
21	HEPN-MNT Toxin-Antitoxin System: The HEPN Ribonuclease Is Neutralized by OligoAMPylation. <i>Molecular Cell</i> , 2020 , 80, 955-970.e7	17.6	5
20	Methods for sequence-structure alignment. <i>Methods in Molecular Biology</i> , 2012 , 857, 55-82	1.4	5
19	Numerical criteria for the evaluation of ab initio predictions of protein structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , Suppl 1, 140-50	4.2	5
18	The use of interatomic contact areas to quantify discrepancies between RNA 3D models and reference structures. <i>Nucleic Acids Research</i> , 2014 , 42, 5407-15	20.1	4
17	The N-terminal region of the bacterial DNA polymerase PolC features a pair of domains, both distantly related to domain V of the DNA polymerase III β subunit. <i>FEBS Journal</i> , 2011 , 278, 3109-18	5.7	4
16	Re-searcher: a system for recurrent detection of homologous protein sequences. <i>BMC Bioinformatics</i> , 2008 , 9, 296	3.6	4
15	Some measures of comparative performance in the three CASPs. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , Suppl 3, 231-7	4.2	4
14	Template-based modeling of diverse protein interactions in CAPRI rounds 38-45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 939-947	4.2	3
13	How Proteins Slide on DNA 2010 , 39-68		3

12	Biochemically diverse CRISPR-Cas9 orthologs		2
11	A novel inducible mutagenesis system in <i>Mycobacterium tuberculosis</i> . <i>FASEB Journal</i> , 2012 , 26, 222.1	0.9	2
10	NR5A1 c.991-1G>T splice-site variant causes familial 46,XY partial gonadal dysgenesis with incomplete penetrance. <i>Clinical Endocrinology</i> , 2021 , 94, 656-666	3.4	2
9	Modeling of protein complexes in CASP14 with emphasis on the interaction interface prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1834-1843	4.2	2
8	Contact Area-Based Structural Analysis of Proteins and Their Complexes Using CAD-Score. <i>Methods in Molecular Biology</i> , 2020 , 2112, 75-90	1.4	2
7	Template-Based Modeling of Protein Complexes Using the PPI3D Web Server. <i>Methods in Molecular Biology</i> , 2020 , 2165, 139-155	1.4	2
6	Criteria for evaluating protein structures derived from comparative modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , Suppl 1, 7-13	4.2	2
5	The H-subunit of the restriction endonuclease CglI contains a prototype DEAD-Z1 helicase-like motor. <i>Nucleic Acids Research</i> , 2018 , 46, 2560-2572	20.1	1
4	Numerical criteria for the evaluation of ab initio predictions of protein structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 140-150	4.2	1
3	Genome Replication of Bacterial and Archaeal Viruses 2021 , 429-438		0
2	Cover Image, Volume 85, Issue 6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, C1-C1	4.2	
1	The path of a protein chain can be approximated by the conformation dictated by interpeptide ionic bridges. <i>FEBS Letters</i> , 1992 , 302, 57-60	3.8	