

# ÄŒeslovas Venclovas

## List of Publications by Year in descending order

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Version: 2024-02-01

100  
papers

7,129  
citations

87723

38  
h-index

71532

76  
g-index

106  
all docs

106  
docs citations

106  
times ranked

6056  
citing authors

#	ARTICLE	IF	CITATIONS
1	NR5A1 c.991G>A splice site variant causes familial 46,XY partial gonadal dysgenesis with incomplete penetrance. <i>Clinical Endocrinology</i> , 2021, 94, 656-666.	1.2	9
2	Genome Replication of Bacterial and Archaeal Viruses. , 2021, , 429-438.		2
3	VoroCNN: deep convolutional neural network built on 3D Voronoi tessellation of protein structures. <i>Bioinformatics</i> , 2021, 37, 2332-2339.	1.8	27
4	VoroContacts: a tool for the analysis of interatomic contacts in macromolecular structures. <i>Bioinformatics</i> , 2021, 37, 4873-4875.	1.8	10
5	Modeling of protein complexes in <scp>CASP14</scp> with emphasis on the interaction interface prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1834-1843.	1.5	14
6	Modeling SARS-CoV-2 proteins in the CASP-commons experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1987-1996.	1.5	24
7	Prediction of protein assemblies, the next frontier: The <scp>CASP14&CAPRI</scp> experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1800-1823.	1.5	73
8	Transposon-associated TnpB is a programmable RNA-guided DNA endonuclease. <i>Nature</i> , 2021, 599, 692-696.	13.7	125
9	Template-based modeling of diverse protein interactions in CAPRI rounds 38&45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 939-947.	1.5	3
10	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020, 18, 67-83.	13.6	1,427
11	Diversity and evolution of B-family DNA polymerases. <i>Nucleic Acids Research</i> , 2020, 48, 10142-10156.	6.5	52
12	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antiviral defense. <i>Nucleic Acids Research</i> , 2020, 48, 8828-8847.	6.5	66
13	HEPN-MNT Toxin-Antitoxin System: The HEPN Ribonuclease Is Neutralized by OligoAMPylation. <i>Molecular Cell</i> , 2020, 80, 955-970.e7.	4.5	19
14	A catalogue of biochemically diverse CRISPR-Cas9 orthologs. <i>Nature Communications</i> , 2020, 11, 5512.	5.8	116
15	PAM recognition by miniature CRISPR-Cas12f nucleases triggers programmable double-stranded DNA target cleavage. <i>Nucleic Acids Research</i> , 2020, 48, 5016-5023.	6.5	175
16	Contact Area-Based Structural Analysis of Proteins and Their Complexes Using CAD-Score. <i>Methods in Molecular Biology</i> , 2020, 2112, 75-90.	0.4	6
17	Template-Based Modeling of Protein Complexes Using the PPI3D Web Server. <i>Methods in Molecular Biology</i> , 2020, 2165, 139-155.	0.4	6
18	Structural modeling of protein complexes: Current capabilities and challenges. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1222-1232.	1.5	12

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19	Estimation of model accuracy in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1361-1377.	1.5	78
20	Blind prediction of homoâ€ and heteroâ€ protein complexes: The CASP13â€CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	1.5	99
21	VoroMQA web server for assessing three-dimensional structures of proteins and protein complexes. <i>Nucleic Acids Research</i> , 2019, 47, W437-W442.	6.5	32
22	New insights into the structures and interactions of bacterial Y-family DNA polymerases. <i>Nucleic Acids Research</i> , 2019, 47, 4393-4405.	6.5	27
23	Comparative analysis of methods for evaluation of protein models against native structures. <i>Bioinformatics</i> , 2019, 35, 937-944.	1.8	34
24	The H-subunit of the restriction endonuclease CgII contains a prototype DEAD-Z1 helicase-like motor. <i>Nucleic Acids Research</i> , 2018, 46, 2560-2572.	6.5	1
25	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.	2.0	31
26	Modeling of protein complexes in CAPRI Round 37 using templateâ€based approach combined with model selection. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 292-301.	1.5	9
27	DnaQ exonucleaseâ€like domain of Cas2 promotes spacer integration in a type Iâ€ CRISPRâ€Cas system. <i>EMBO Reports</i> , 2018, 19, .	2.0	31
28	The PPI3D web server for searching, analyzing and modeling proteinâ€protein interactions in the context of 3D structures. <i>Bioinformatics</i> , 2017, 33, 935-937.	1.8	39
29	VoroMQA: Assessment of protein structure quality using interatomic contact areas. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1131-1145.	1.5	149
30	A structureâ€function analysis of the yeast Elg1 protein reveals the importance of PCNA unloading in genome stability maintenance. <i>Nucleic Acids Research</i> , 2017, 45, gkx1348.	6.5	34
31	Cover Image, Volume 85, Issue 6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C1.	1.5	0
32	A cyclic oligonucleotide signaling pathway in type III CRISPR-Cas systems. <i>Science</i> , 2017, 357, 605-609.	6.0	382
33	Type III CRISPR-Cas Immunity: Major Differences Brushed Aside. <i>Trends in Microbiology</i> , 2017, 25, 49-61.	3.5	133
34	Structure of Csm2 elucidates the relationship between small subunits of CRISPRâ€Cas effector complexes. <i>FEBS Letters</i> , 2016, 590, 1521-1529.	1.3	21
35	The logic of DNA replication in double-stranded DNA viruses: insights from global analysis of viral genomes. <i>Nucleic Acids Research</i> , 2016, 44, 4551-4564.	6.5	80
36	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.	4.5	224

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37	Viral DNA replication: new insights and discoveries from large scale computational analysis. BMC Bioinformatics, 2015, 16, .	1.2	3
38	Human HLTf mediates postreplication repair by its HIRAN domain-dependent replication fork remodelling. Nucleic Acids Research, 2015, 43, gkv896.	6.5	51
39	Functional mapping of the plant small RNA methyltransferase: HEN1 physically interacts with HYL1 and DICER-LIKE 1 proteins. Nucleic Acids Research, 2015, 43, 2802-2812.	6.5	67
40	The Cytolytic Activity of Vaginolysin Strictly Depends on Cholesterol and Is Potentiated by Human CD59. Toxins, 2015, 7, 110-128.	1.5	34
41	The use of interatomic contact areas to quantify discrepancies between RNA 3D models and reference structures. Nucleic Acids Research, 2014, 42, 5407-5415.	6.5	8
42	Voronota: A fast and reliable tool for computing the vertices of the Voronoi diagram of atomic balls. Journal of Computational Chemistry, 2014, 35, 672-681.	1.5	62
43	The CAD-score web server: contact area-based comparison of structures and interfaces of proteins, nucleic acids and their complexes. Nucleic Acids Research, 2014, 42, W259-W263.	6.5	15
44	Conformational Analysis of Processivity Clamps in Solution Demonstrates that Tertiary Structure Does Not Correlate with Protein Dynamics. Structure, 2014, 22, 572-581.	1.6	30
45	Herpesviral helicase-primase subunit UL8 is inactivated B-family polymerase. Bioinformatics, 2014, 30, 2093-2097.	1.8	11
46	Programmable RNA Shredding by the Type III-A CRISPR-Cas System of Streptococcus thermophilus. Molecular Cell, 2014, 56, 506-517.	4.5	278
47	Comprehensive analysis of DNA polymerase III Î± subunits and their homologs in bacterial genomes. Nucleic Acids Research, 2014, 42, 1393-1413.	6.5	59
48	CAD-score: A new contact area difference-based function for evaluation of protein structural models. Proteins: Structure, Function and Bioinformatics, 2013, 81, 149-162.	1.5	123
49	A vitamin B <sub>12</sub> transporter in Mycobacterium tuberculosis. Open Biology, 2013, 3, 120175.	1.5	83
50	Structural and functional analysis of rare missense mutations in human chorionic gonadotrophin Î²-subunit. Molecular Human Reproduction, 2012, 18, 379-390.	1.3	21
51	Two distinct SSB protein families in nucleo-cytoplasmic large DNA viruses. Bioinformatics, 2012, 28, 3186-3190.	1.8	15
52	A novel inducible mutagenesis system in Mycobacterium tuberculosis. FASEB Journal, 2012, 26, 222.1.	0.2	2
53	The N-terminal region of the bacterial DNA polymerase PolC features a pair of domains, both distantly related to domain Î± of the DNA polymerase III Î± subunit. FEBS Journal, 2011, 278, 3109-3118.	2.2	4
54	Methods for Sequence-Structure Alignment. Methods in Molecular Biology, 2011, 857, 55-82.	0.4	10

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55	Computational analysis of DNA replicases in double-stranded DNA viruses: relationship with the genome size. <i>Nucleic Acids Research</i> , 2011, 39, 8291-8305.	6.5	17
56	Identification of new homologs of PD-(D/E)XK nucleases by support vector machines trained on data derived from profileâ€“profile alignments. <i>Nucleic Acids Research</i> , 2011, 39, 1187-1196.	6.5	34
57	Voroprot: an interactive tool for the analysis and visualization of complex geometric features of protein structure. <i>Bioinformatics</i> , 2011, 27, 723-724.	1.8	18
58	Detection of distant evolutionary relationships between protein families using theory of sequence profile-profile comparison. <i>BMC Bioinformatics</i> , 2010, 11, 89.	1.2	43
59	Thermodynamics of radical binding to human Hsp90 alpha and beta isoforms. <i>Biophysical Chemistry</i> , 2010, 152, 153-163.	1.5	23
60	Essential roles for <i>imuA</i> - and <i>imuB</i> -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, 13093-13098.	3.3	113
61	COMA server for protein distant homology search. <i>Bioinformatics</i> , 2010, 26, 1905-1906.	1.8	30
62	How Proteins Slide on DNA. <i>Biological and Medical Physics Series</i> , 2010, , 39-68.	0.3	4
63	The use of automatic tools and human expertise in templateâ€“based modeling of CASP8 target proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 81-88.	1.5	20
64	Re-searcher: a system for recurrent detection of homologous protein sequences. <i>BMC Bioinformatics</i> , 2008, 9, 296.	1.2	5
65	Molecular modeling-based analysis of interactions in the RFC-dependent clamp-loading process. <i>Protein Science</i> , 2008, 11, 2403-2416.	3.1	33
66	Distinct Double- and Single-Stranded DNA Binding of <i>E. coli</i> Replicative DNA Polymerase III Î± Subunit. <i>ACS Chemical Biology</i> , 2008, 3, 577-587.	1.6	32
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, 10358-10363.	3.3	38
68	Restriction endonuclease BpuI specific for the 5â€“CCCGT sequence is related to the archaeal Holliday junction resolvase family. <i>Nucleic Acids Research</i> , 2007, 35, 2377-2389.	6.5	9
69	Physical and functional interactions between MutY glycosylase homologue (MYH) and checkpoint proteins Rad9â€“Rad1â€“Hus1. <i>Biochemical Journal</i> , 2006, 400, 53-62.	1.7	83
70	DNA Sliding Clamps: Just the Right Twist to Load onto DNA. <i>Current Biology</i> , 2005, 15, R989-R992.	1.8	10
71	PSI-BLAST-ISS: an intermediate sequence search tool for estimation of the position-specific alignment reliability. <i>BMC Bioinformatics</i> , 2005, 6, 185.	1.2	32
72	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, 99-105.	1.5	66

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73	Progress over the first decade of CASP experiments. Proteins: Structure, Function and Bioinformatics, 2005, 61, 225-236.	1.5	172
74	HhaI DNA Methyltransferase Uses the Protruding Gln237 for Active Flipping of Its Target Cytosine. Structure, 2004, 12, 1047-1055.	1.6	36
75	Sequence-structure mapping errors in the PDB: OB-fold domains. Protein Science, 2004, 13, 1594-1602.	3.1	15
76	Assessment of progress over the CASP experiments. Proteins: Structure, Function and Bioinformatics, 2003, 53, 585-595.	1.5	110
77	Comparative modeling in CASP5: Progress is evident, but alignment errors remain a significant hindrance. Proteins: Structure, Function and Bioinformatics, 2003, 53, 380-388.	1.5	52
78	Selection and characterization of anti-MUC-1 scFvs intended for targeted therapy. Clinical Cancer Research, 2003, 9, 3845S-53S.	3.2	8
79	Comparative modeling of CASP4 target proteins: Combining results of sequence search with three-dimensional structure assessment. Proteins: Structure, Function and Bioinformatics, 2001, 45, 47-54.	1.5	40
80	Processing and evaluation of predictions in CASP4. Proteins: Structure, Function and Bioinformatics, 2001, 45, 13-21.	1.5	131
81	Comparison of performance in successive CASP experiments. Proteins: Structure, Function and Bioinformatics, 2001, 45, 163-170.	1.5	62
82	Structure-based predictions of Rad1, Rad9, Hus1 and Rad17 participation in sliding clamp and clamp-loading complexes. Nucleic Acids Research, 2000, 28, 2481-2493.	6.5	247
83	Structure-based sequence alignment for the Î²-trefoil subdomain of the clostridial neurotoxin family provides residue level information about the putative ganglioside binding site. FEBS Letters, 2000, 482, 119-124.	1.3	39
84	Processing and analysis of CASP3 protein structure predictions. Proteins: Structure, Function and Bioinformatics, 1999, 37, 22-29.	1.5	206
85	Some measures of comparative performance in the three CASPs. Proteins: Structure, Function and Bioinformatics, 1999, 37, 231-237.	1.5	39
86	Addressing the issue of sequence-to-structure alignments in comparative modeling of CASP3 target proteins. Proteins: Structure, Function and Bioinformatics, 1999, 37, 73-80.	1.5	21
87	A modified definition of Sov, a segment-based measure for protein secondary structure prediction assessment. , 1999, 34, 220-223.		323
88	A Sliding Clamp Model for the Rad1 Family of Cell Cycle Checkpoint Proteins. Cell, 1999, 96, 769-770.	13.5	143
89	Processing and analysis of CASP3 protein structure predictions. Proteins: Structure, Function and Bioinformatics, 1999, Suppl 3, 22-9.	1.5	142
90	Some measures of comparative performance in the three CASPs. Proteins: Structure, Function and Bioinformatics, 1999, Suppl 3, 231-7.	1.5	4

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91	Numerical criteria for the evaluation of ab initio predictions of protein structure. Proteins: Structure, Function and Bioinformatics, 1997, 29, 140-150.	1.5	21
92	Criteria for evaluating protein structures derived from comparative modeling. Proteins: Structure, Function and Bioinformatics, 1997, 29, 7-13.	1.5	28
93	Numerical criteria for the evaluation of ab initio predictions of protein structure. Proteins: Structure, Function and Bioinformatics, 1997, 29, 140-150.	1.5	2
94	Numerical criteria for the evaluation of ab initio predictions of protein structure. Proteins: Structure, Function and Bioinformatics, 1997, Suppl 1, 140-50.	1.5	12
95	Criteria for evaluating protein structures derived from comparative modeling. Proteins: Structure, Function and Bioinformatics, 1997, Suppl 1, 7-13.	1.5	4
96	Different enzymes with similar structures involved in Mg <sup>2+</sup> -mediated polynucleotidyl transfer. Nature Structural Biology, 1995, 2, 838-841.	9.7	29
97	Five-stranded $\beta^2$ -sheet sandwiched with two $\alpha$ -helices: A structural link between restriction endonucleases EcoRI and EcoRV. Proteins: Structure, Function and Bioinformatics, 1994, 20, 279-282.	1.5	64
98	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. Nucleic Acids Research, 1992, 20, 2627-2637.	6.5	64
99	The path of a protein chain can be approximated by the conformation dictated by interpeptide ionic bridges. FEBS Letters, 1992, 302, 57-60.	1.3	0
100	Codon-anticodon pairing A model for interacting codon-anticodon duplexes located at the ribosomal A- and P-sites. FEBS Letters, 1992, 313, 133-137.	1.3	24