

ÄŒeslovas Venclovas

List of Publications by Year in descending order

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101
papers

7,129
citations

87886

38
h-index

71682

76
g-index

106
all docs

106
docs citations

106
times ranked

6056
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020, 18, 67-83.	28.6	1,427
2	A cyclic oligonucleotide signaling pathway in type III CRISPR-Cas systems. <i>Science</i> , 2017, 357, 605-609.	12.6	382
3	A modified definition of Sov, a segment-based measure for protein secondary structure prediction assessment. , 1999, 34, 220-223.		323
4	Programmable RNA Shredding by the Type III-A CRISPR-Cas System of <i>Streptococcus thermophilus</i> . <i>Molecular Cell</i> , 2014, 56, 506-517.	9.7	278
5	Structure-based predictions of Rad1, Rad9, Hus1 and Rad17 participation in sliding clamp and clamp-loading complexes. <i>Nucleic Acids Research</i> , 2000, 28, 2481-2493.	14.5	247
6	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.	9.7	224
7	Processing and analysis of CASP3 protein structure predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 22-29.	2.6	206
8	PAM recognition by miniature CRISPR-Cas12f nucleases triggers programmable double-stranded DNA target cleavage. <i>Nucleic Acids Research</i> , 2020, 48, 5016-5023.	14.5	175
9	Progress over the first decade of CASP experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 225-236.	2.6	172
10	VoroMQA: Assessment of protein structure quality using interatomic contact areas. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1131-1145.	2.6	149
11	A Sliding Clamp Model for the Rad1 Family of Cell Cycle Checkpoint Proteins. <i>Cell</i> , 1999, 96, 769-770.	28.9	143
12	Processing and analysis of CASP3 protein structure predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 22-29.	2.6	142
13	Type III CRISPR-Cas Immunity: Major Differences Brushed Aside. <i>Trends in Microbiology</i> , 2017, 25, 49-61.	7.7	133
14	Processing and evaluation of predictions in CASP4. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 13-21.	2.6	131
15	Transposon-associated TnpB is a programmable RNA-guided DNA endonuclease. <i>Nature</i> , 2021, 599, 692-696.	27.8	125
16	CAD-score: A new contact area difference-based function for evaluation of protein structural models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 149-162.	2.6	123
17	A catalogue of biochemically diverse CRISPR-Cas9 orthologs. <i>Nature Communications</i> , 2020, 11, 5512.	12.8	116
18	Essential roles for <i>imuA</i> ² - 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.	7.1	113

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19	Assessment of progress over the CASP experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 585-595.	2.6	110
20	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	2.6	99
21	Physical and functional interactions between MutY glycosylase homologue (MYH) and checkpoint proteins Rad9-Rad1-Hus1. <i>Biochemical Journal</i> , 2006, 400, 53-62.	3.7	83
22	A vitamin B ₁₂ transporter in <i>Mycobacterium tuberculosis</i> . <i>Open Biology</i> , 2013, 3, 120175.	3.6	83
23	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.	14.5	80
24	Estimation of model accuracy in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1361-1377.	2.6	78
25	Prediction of protein assemblies, the next frontier: The CASP14-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1800-1823.	2.6	73
26	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, 2802-2812.	14.5	67
27	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.	2.6	66
28	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antiviral defense. <i>Nucleic Acids Research</i> , 2020, 48, 8828-8847.	14.5	66
29	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, 2627-2637.	14.5	64
30	Five-stranded β -sheet sandwiched with two α -helices: A structural link between restriction endonucleases EcoRI and EcoRV. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 20, 279-282.	2.6	64
31	Comparison of performance in successive CASP experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 163-170.	2.6	62
32	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, 672-681.	3.3	62
33	Comprehensive analysis of DNA polymerase III subunits and their homologs in bacterial genomes. <i>Nucleic Acids Research</i> , 2014, 42, 1393-1413.	14.5	59
34	Comparative modeling in CASP5: Progress is evident, but alignment errors remain a significant hindrance. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 380-388.	2.6	52
35	Diversity and evolution of B-family DNA polymerases. <i>Nucleic Acids Research</i> , 2020, 48, 10142-10156.	14.5	52
36	Human HLTF mediates postreplication repair by its HIRAN domain-dependent replication fork remodelling. <i>Nucleic Acids Research</i> , 2015, 43, gkv896.	14.5	51

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37	Detection of distant evolutionary relationships between protein families using theory of sequence profile-profile comparison. <i>BMC Bioinformatics</i> , 2010, 11, 89.	2.6	43
38	Comparative modeling of CASP4 target proteins: Combining results of sequence search with three-dimensional structure assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 47-54.	2.6	40
39	Some measures of comparative performance in the three CASPs. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 231-237.	2.6	39
40	Structure-based sequence alignment for the β -trefoil subdomain of the clostridial neurotoxin family provides residue level information about the putative ganglioside binding site. <i>FEBS Letters</i> , 2000, 482, 119-124.	2.8	39
41	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.	4.1	39
42	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.	7.1	38
43	HhaI DNA Methyltransferase Uses the Protruding Gln237 for Active Flipping of Its Target Cytosine. <i>Structure</i> , 2004, 12, 1047-1055.	3.3	36
44	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.	14.5	34
45	The Cytolytic Activity of Vaginolysin Strictly Depends on Cholesterol and Is Potentiated by Human CD59. <i>Toxins</i> , 2015, 7, 110-128.	3.4	34
46	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, gkw1348.	14.5	34
47	Comparative analysis of methods for evaluation of protein models against native structures. <i>Bioinformatics</i> , 2019, 35, 937-944.	4.1	34
48	Molecular modeling-based analysis of interactions in the RFC-dependent clamp-loading process. <i>Protein Science</i> , 2008, 11, 2403-2416.	7.6	33
49	PSI-BLAST-ISS: an intermediate sequence search tool for estimation of the position-specific alignment reliability. <i>BMC Bioinformatics</i> , 2005, 6, 185.	2.6	32
50	Distinct Double- and Single-Stranded DNA Binding of <i>E. coli</i> Replicative DNA Polymerase III β Subunit. <i>ACS Chemical Biology</i> , 2008, 3, 577-587.	3.4	32
51	VoroMQA web server for assessing three-dimensional structures of proteins and protein complexes. <i>Nucleic Acids Research</i> , 2019, 47, W437-W442.	14.5	32
52	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.	4.2	31
53	DnaQ exonucleaseâ€“like domain of Cas2 promotes spacer integration in a type Iâ€“CRISPRâ€“Cas system. <i>EMBO Reports</i> , 2018, 19, .	4.5	31
54	COMA server for protein distant homology search. <i>Bioinformatics</i> , 2010, 26, 1905-1906.	4.1	30

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55	Conformational Analysis of Processivity Clamps in Solution Demonstrates that Tertiary Structure Does Not Correlate with Protein Dynamics. <i>Structure</i> , 2014, 22, 572-581.	3.3	30
56	Different enzymes with similar structures involved in Mg ²⁺ -mediated polynucleotidyl transfer. <i>Nature Structural Biology</i> , 1995, 2, 838-841.	9.7	29
57	Criteria for evaluating protein structures derived from comparative modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 7-13.	2.6	28
58	New insights into the structures and interactions of bacterial Y-family DNA polymerases. <i>Nucleic Acids Research</i> , 2019, 47, 4393-4405.	14.5	27
59	VoroCNN: deep convolutional neural network built on 3D Voronoi tessellation of protein structures. <i>Bioinformatics</i> , 2021, 37, 2332-2339.	4.1	27
60	Codon-anticodon pairing A model for interacting codon-anticodon duplexes located at the ribosomal A- and P-sites. <i>FEBS Letters</i> , 1992, 313, 133-137.	2.8	24
61	Modeling SARSâ€CoVâ€2 proteins in the CASPâ€commons experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1987-1996.	2.6	24
62	Thermodynamics of radicicol binding to human Hsp90 alpha and beta isoforms. <i>Biophysical Chemistry</i> , 2010, 152, 153-163.	2.8	23
63	Numerical criteria for the evaluation of ab initio predictions of protein structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 140-150.	2.6	21
64	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.	2.6	21
65	Structural and functional analysis of rare missense mutations in human chorionic gonadotrophin Î²-subunit. <i>Molecular Human Reproduction</i> , 2012, 18, 379-390.	2.8	21
66	Structure of Csm2 elucidates the relationship between small subunits of CRISPRâ€Cas effector complexes. <i>FEBS Letters</i> , 2016, 590, 1521-1529.	2.8	21
67	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.	2.6	20
68	HEPN-MNT Toxin-Antitoxin System: The HEPN Ribonuclease Is Neutralized by OligoAMPylation. <i>Molecular Cell</i> , 2020, 80, 955-970.e7.	9.7	19
69	Voroprot: an interactive tool for the analysis and visualization of complex geometric features of protein structure. <i>Bioinformatics</i> , 2011, 27, 723-724.	4.1	18
70	Computational analysis of DNA replicases in double-stranded DNA viruses: relationship with the genome size. <i>Nucleic Acids Research</i> , 2011, 39, 8291-8305.	14.5	17
71	Sequence-structure mapping errors in the PDB: OB-fold domains. <i>Protein Science</i> , 2004, 13, 1594-1602.	7.6	15
72	Two distinct SSB protein families in nucleo-cytoplasmic large DNA viruses. <i>Bioinformatics</i> , 2012, 28, 3186-3190.	4.1	15

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73	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-W263.	14.5	15
74	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.	2.6	14
75	Structural modeling of protein complexes: Current capabilities and challenges. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1222-1232.	2.6	12
76	Numerical criteria for the evaluation of ab initio predictions of protein structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 140-150.	2.6	12
77	Herpesviral helicase-primase subunit UL8 is inactivated B-family polymerase. <i>Bioinformatics</i> , 2014, 30, 2093-2097.	4.1	11
78	DNA Sliding Clamps: Just the Right Twist to Load onto DNA. <i>Current Biology</i> , 2005, 15, R989-R992.	3.9	10
79	Methods for Sequenceâ€“Structure Alignment. <i>Methods in Molecular Biology</i> , 2011, 857, 55-82.	0.9	10
80	VoroContacts: a tool for the analysis of interatomic contacts in macromolecular structures. <i>Bioinformatics</i> , 2021, 37, 4873-4875.	4.1	10
81	Restriction endonuclease BpuII specific for the 5â€²-CCCGT sequence is related to the archaeal Holliday junction resolvase family. <i>Nucleic Acids Research</i> , 2007, 35, 2377-2389.	14.5	9
82	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.	2.6	9
83	NR5A1 c.991â€¦ spliceâ€“site variant causes familial 46,XY partial gonadal dysgenesis with incomplete penetrance. <i>Clinical Endocrinology</i> , 2021, 94, 656-666.	2.4	9
84	The use of interatomic contact areas to quantify discrepancies between RNA 3D models and reference structures. <i>Nucleic Acids Research</i> , 2014, 42, 5407-5415.	14.5	8
85	Selection and characterization of anti-MUC-1 scFvs intended for targeted therapy. <i>Clinical Cancer Research</i> , 2003, 9, 3845S-53S.	7.0	8
86	Contact Area-Based Structural Analysis of Proteins and Their Complexes Using CAD-Score. <i>Methods in Molecular Biology</i> , 2020, 2112, 75-90.	0.9	6
87	Template-Based Modeling of Protein Complexes Using the PPI3D Web Server. <i>Methods in Molecular Biology</i> , 2020, 2165, 139-155.	0.9	6
88	Re-searcher: a system for recurrent detection of homologous protein sequences. <i>BMC Bioinformatics</i> , 2008, 9, 296.	2.6	5
89	The Nâ€“terminal region of the bacterial DNA polymerase PolC features a pair of domains, both distantly related to domainâ€“v of the DNA polymerase III Î¼, subunit. <i>FEBS Journal</i> , 2011, 278, 3109-3118.	4.7	4
90	How Proteins Slide on DNA. <i>Biological and Medical Physics Series</i> , 2010, , 39-68.	0.4	4

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91	Some measures of comparative performance in the three CASPs. Proteins: Structure, Function and Bioinformatics, 1999, 37, 231-237.	2.6	4
92	Criteria for evaluating protein structures derived from comparative modeling. Proteins: Structure, Function and Bioinformatics, 1997, 29, 7-13.	2.6	4
93	Viral DNA replication: new insights and discoveries from large scale computational analysis. BMC Bioinformatics, 2015, 16, .	2.6	3
94	Template-based modeling of diverse protein interactions in CAPRI rounds 38-45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 939-947.	2.6	3
95	Genome Replication of Bacterial and Archaeal Viruses. , 2021, , 429-438.		2
96	Numerical criteria for the evaluation of ab initio predictions of protein structure. Proteins: Structure, Function and Bioinformatics, 1997, 29, 140-150.	2.6	2
97	A novel inducible mutagenesis system in Mycobacterium tuberculosis. FASEB Journal, 2012, 26, 222.1.	0.5	2
98	The H-subunit of the restriction endonuclease CgII contains a prototype DEAD-Z1 helicase-like motor. Nucleic Acids Research, 2018, 46, 2560-2572.	14.5	1
99	The path of a protein chain can be approximated by the conformation dictated by interpeptide ionic bridges. FEBS Letters, 1992, 302, 57-60.	2.8	0
100	Cover Image, Volume 85, Issue 6. Proteins: Structure, Function and Bioinformatics, 2017, 85, C1.	2.6	0
101	Addressing the issue of sequence-to-structure alignments in comparative modeling of CASP3 target proteins. Proteins: Structure, Function and Bioinformatics, 1999, 37, 73-80.	2.6	0