

# Vladimir Potapov

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6075843/publications.pdf>

Version: 2024-02-01

22  
papers

1,465  
citations

567144

15  
h-index

642610

23  
g-index

26  
all docs

26  
docs citations

26  
times ranked

2599  
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing computational methods for predicting protein stability upon mutation: good on average but not in the details. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 553-560.	1.0	325
2	Examining Sources of Error in PCR by Single-Molecule Sequencing. <i>PLoS ONE</i> , 2017, 12, e0169774.	1.1	208
3	Comprehensive Profiling of Four Base Overhang Ligation Fidelity by T4 DNA Ligase and Application to DNA Assembly. <i>ACS Synthetic Biology</i> , 2018, 7, 2665-2674.	1.9	132
4	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	2.0	131
5	The Limit of Accuracy of Protein Modeling: Influence of Crystal Packing on Protein Structure. <i>Journal of Molecular Biology</i> , 2005, 351, 431-442.	2.0	117
6	SPACE: a suite of tools for protein structure prediction and analysis based on complementarity and environment. <i>Nucleic Acids Research</i> , 2005, 33, W39-W43.	6.5	105
7	Base modifications affecting RNA polymerase and reverse transcriptase fidelity. <i>Nucleic Acids Research</i> , 2018, 46, 5753-5763.	6.5	91
8	Enabling one-pot Golden Gate assemblies of unprecedented complexity using data-optimized assembly design. <i>PLoS ONE</i> , 2020, 15, e0238592.	1.1	48
9	Computational Redesign of a Protein-Protein Interface for High Affinity and Binding Specificity Using Modular Architecture and Naturally Occurring Template Fragments. <i>Journal of Molecular Biology</i> , 2008, 384, 109-119.	2.0	44
10	Data-Driven Prediction and Design of bZIP Coiled-Coil Interactions. <i>PLoS Computational Biology</i> , 2015, 11, e1004046.	1.5	38
11	A single-molecule sequencing assay for the comprehensive profiling of T4 DNA ligase fidelity and bias during DNA end-joining. <i>Nucleic Acids Research</i> , 2018, 46, e79-e79.	6.5	31
12	Four Distances between Pairs of Amino Acids Provide a Precise Description of their Interaction. <i>PLoS Computational Biology</i> , 2009, 5, e1000470.	1.5	29
13	Protein-Protein Recognition: Juxtaposition of Domain and Interface Cores in Immunoglobulins and Other Sandwich-like Proteins. <i>Journal of Molecular Biology</i> , 2004, 342, 665-679.	2.0	25
14	Protein structure modelling and evaluation based on a 4-distance description of side-chain interactions. <i>BMC Bioinformatics</i> , 2010, 11, 374.	1.2	24
15	Pol V-Mediated Translesion Synthesis Elicits Localized Untargeted Mutagenesis during Post-replicative Gap Repair. <i>Cell Reports</i> , 2018, 24, 1290-1300.	2.9	22
16	A Barcoding Strategy Enabling Higher-Throughput Library Screening by Microscopy. <i>ACS Synthetic Biology</i> , 2015, 4, 1205-1216.	1.9	17
17	Programmable cleavage of linear double-stranded DNA by combined action of Argonaute CbAgo from <i>Clostridium butyricum</i> and nuclease deficient RecBC helicase from <i>E. coli</i> . <i>Nucleic Acids Research</i> , 2022, 50, 4616-4629.	6.5	15
18	Mismatch discrimination and sequence bias during end-joining by DNA ligases. <i>Nucleic Acids Research</i> , 2022, 50, 4647-4658.	6.5	12

#	ARTICLE	IF	CITATIONS
19	Biochemical reconstitution and genetic characterization of the major oxidative damage base excision DNA repair pathway in <i>Thermococcus kodakarensis</i> . <i>DNA Repair</i> , 2020, 86, 102767.	1.3	11
20	Amino acid distribution rules predict protein fold. <i>Biochemical Society Transactions</i> , 2013, 41, 616-619.	1.6	9
21	About Factors Providing the Fast Protein-Protein Recognition in Processes of Complex Formation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2003, 21, 257-266.	2.0	6
22	Residueâ€“Residue Contacts: Application to Analysis of Secondary Structure Interactions. <i>Methods in Molecular Biology</i> , 2012, 932, 159-173.	0.4	1