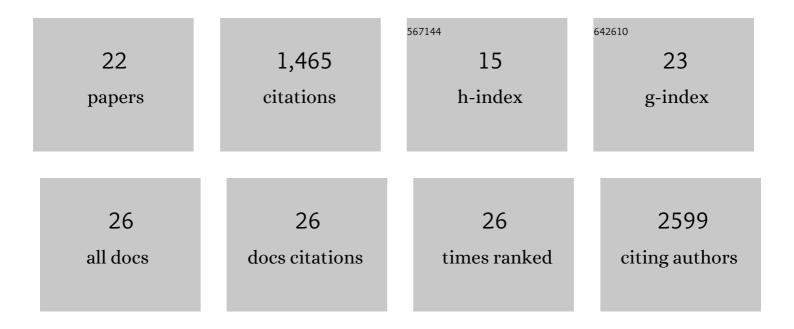
Vladimir Potapov

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Assessing computational methods for predicting protein stability upon mutation: good on average but not in the details. Protein Engineering, Design and Selection, 2009, 22, 553-560.	1.0	325
2	Examining Sources of Error in PCR by Single-Molecule Sequencing. PLoS ONE, 2017, 12, e0169774.	1.1	208
3	Comprehensive Profiling of Four Base Overhang Ligation Fidelity by T4 DNA Ligase and Application to DNA Assembly. ACS Synthetic Biology, 2018, 7, 2665-2674.	1.9	132
4	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	2.0	131
5	The Limit of Accuracy of Protein Modeling: Influence of Crystal Packing on Protein Structure. Journal of Molecular Biology, 2005, 351, 431-442.	2.0	117
6	SPACE: a suite of tools for protein structure prediction and analysis based on complementarity and environment. Nucleic Acids Research, 2005, 33, W39-W43.	6.5	105
7	Base modifications affecting RNA polymerase and reverse transcriptase fidelity. Nucleic Acids Research, 2018, 46, 5753-5763.	6.5	91
8	Enabling one-pot Golden Gate assemblies of unprecedented complexity using data-optimized assembly design. PLoS ONE, 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. Journal of Molecular Biology, 2008, 384, 109-119.	2.0	44
10	Data-Driven Prediction and Design of bZIP Coiled-Coil Interactions. PLoS Computational Biology, 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. Nucleic Acids Research, 2018, 46, e79-e79.	6.5	31
12	Four Distances between Pairs of Amino Acids Provide a Precise Description of their Interaction. PLoS Computational Biology, 2009, 5, e1000470.	1.5	29
13	Protein–Protein Recognition: Juxtaposition of Domain and Interface Cores in Immunoglobulins and Other Sandwich-like Proteins. Journal of Molecular Biology, 2004, 342, 665-679.	2.0	25
14	Protein structure modelling and evaluation based on a 4-distance description of side-chain interactions. BMC Bioinformatics, 2010, 11, 374.	1.2	24
15	Pol V-Mediated Translesion Synthesis Elicits Localized Untargeted Mutagenesis during Post-replicative Gap Repair. Cell Reports, 2018, 24, 1290-1300.	2.9	22
16	A Barcoding Strategy Enabling Higher-Throughput Library Screening by Microscopy. ACS Synthetic Biology, 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> . Nucleic Acids Research, 2022, 50, 4616-4629.	6.5	15
18	Mismatch discrimination and sequence bias during end-joining by DNA ligases. Nucleic Acids Research, 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 Thermococcus kodakarensis. DNA Repair, 2020, 86, 102767.	1.3	11
20	Amino acid distribution rules predict protein fold. Biochemical Society Transactions, 2013, 41, 616-619.	1.6	9
21	About Factors Providing the Fast Protein-Protein Recognition in Processes of Complex Formation. Journal of Biomolecular Structure and Dynamics, 2003, 21, 257-266.	2.0	6
22	Residue–Residue Contacts: Application to Analysis of Secondary Structure Interactions. Methods in Molecular Biology, 2012, 932, 159-173.	0.4	1