Vladimir Potapov

List of Publications by Year
in descending order

22	1,465	567144 15	642610 23
papers	citations	h-index	g-index

26	26	26	2599
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Programmable cleavage of linear double-stranded DNA by combined action of Argonaute CbAgo from Clostridium butyricum and nuclease deficient RecBC helicase from E. coli. Nucleic Acids Research, 2022, 50, 4616-4629.	6.5	15
2	Mismatch discrimination and sequence bias during end-joining by DNA ligases. Nucleic Acids Research, 2022, 50, 4647-4658.	6.5	12
3	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
4	Enabling one-pot Golden Gate assemblies of unprecedented complexity using data-optimized assembly design. PLoS ONE, 2020, 15, e0238592.	1.1	48
5	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
6	Pol V-Mediated Translesion Synthesis Elicits Localized Untargeted Mutagenesis during Post-replicative Gap Repair. Cell Reports, 2018, 24, 1290-1300.	2.9	22
7	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
8	Base modifications affecting RNA polymerase and reverse transcriptase fidelity. Nucleic Acids Research, 2018, 46, 5753-5763.	6.5	91
9	Examining Sources of Error in PCR by Single-Molecule Sequencing. PLoS ONE, 2017, 12, e0169774.	1.1	208
10	Data-Driven Prediction and Design of bZIP Coiled-Coil Interactions. PLoS Computational Biology, 2015, 11, e1004046.	1.5	38
11	A Barcoding Strategy Enabling Higher-Throughput Library Screening by Microscopy. ACS Synthetic Biology, 2015, 4, 1205-1216.	1.9	17
12	Amino acid distribution rules predict protein fold. Biochemical Society Transactions, 2013, 41, 616-619.	1.6	9
13	Residueâ€“Residue Contacts: Application to Analysis of Secondary Structure Interactions. Methods in Molecular Biology, 2012, 932, 159-173.	0.4	1
14	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	2.0	131
15	Protein structure modelling and evaluation based on a 4-distance description of side-chain interactions. BMC Bioinformatics, 2010, 11, 374.	1.2	24
16	Four Distances between Pairs of Amino Acids Provide a Precise Description of their Interaction. PLoS Computational Biology, 2009, 5, e1000470.	1.5	29
17	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
18	Computational Redesign of a Proteinâ€“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

#	Article	IF	Citations
19	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
20	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
21	Proteinâ€“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
22	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