Sergey V Korolev

List of Publications by Year
in descending order

53	3,461	236925 25	182427 51
papers	citations	h-index	g-index

59	59	59	4150
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Major Domain Swiveling Revealed by the Crystal Structures of Complexes of E. coli Rep Helicase Bound to Single-Stranded DNA and ADP. Cell, 1997, 90, 635-647.	28.9	493
2	Mutations in Cohesin Complex Members SMC3 and SMC1A Cause a Mild Variant of Cornelia de Lange Syndrome with Predominant Mental Retardation. American Journal of Human Genetics, 2007, 80, 485-494.	6.2	445
3	Proliferating cell nuclear antigen (PCNA): ringmaster of the genome. International Journal of Radiation Biology, 2001, 77, 1007-1021.	1.8	287
4	Structure of the RPA trimerization core and its role in the multistep DNA-binding mechanism of RPA. EMBO Journal, 2002, 21, 1855-1863.	7.8	282
5	SSB Functions as a Sliding Platform that Migrates on DNA via Reptation. Cell, 2011, 146, 222-232.	28.9	180
6	Phospholipase iPLA2Î² averts ferroptosis by eliminating a redox lipid death signal. Nature Chemical Biology, 2021, 17, 465-476.	8.0	168
7	The crystal structure of spermidine synthase with a multisubstrate adduct inhibitor. Nature Structural Biology, 2002, 9, 27-31.	9.7	124
8	Structure of N-myristoyltransferase with bound myristoylCoA and peptide substrate analogs. Nature Structural Biology, 1998, 5, 1091-1097.	9.7	118
9	Comparisons between the structures of HCV and Rep helicases reveal structural similarities between SF1 and SF2 superâ€families of helicases. Protein Science, 1998, 7, 605-610.	7.6	105
10	Crystal structures of the Klenow fragment of Thermus aquaticus DNA polymerase I complexed with deoxyribonucleoside triphosphates. Protein Science, 1998, 7, 1116-1123.	7.6	102
11	Anchoring Notch Genetics and Biochemistry. Molecular Cell, 2004, 13, 619-626.	9.7	101
12	Crystal structure of enteropeptidase light chain complexed with an analog of the trypsinogen activation peptide 1 1Edited by R. Huber. Journal of Molecular Biology, 1999, 292, 361-373.	4.2	97
13	Mechanism of RecO recruitment to DNA by single-stranded DNA binding protein. Nucleic Acids Research, 2011, 39, 6305-6314.	14.5	95
14	The 2B domain of the Escherichia coli Rep protein is not required for DNA helicase activity. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16006-16011.	7.1	63
15	A Novel Structure of DNA Repair Protein RecO from Deinococcus radiodurans. Structure, 2004, 12, 1881-1889.	3.3	60
16	Rotations of the 2B Sub-domain of E. coli UvrD Helicase/Translocase Coupled to Nucleotide and DNA Binding. Journal of Molecular Biology, 2011, 411, 633-648.	4.2	57
17	The Role for Zinc in Replication Protein A. Journal of Biological Chemistry, 2000, 275, 27332-27338.	3.4	55
18	Structural conservation of RecF and Rad50: implications for DNA recognition and RecF function. EMBO Journal, 2007, 26, 867-877.	7.8	54

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19	The structure of iPLA2Î² reveals dimeric active sites and suggests mechanisms of regulation and localization. Nature Communications, 2018, 9, 765.	12.8	53
20	High Resolution Crystal Structure of Human Î²-Glucuronidase Reveals Structural Basis of Lysosome Targeting. PLoS ONE, 2013, 8, e79687.	2.5	52
21	Plasmodium falciparum SSB Tetramer Wraps Single-Stranded DNA with Similar Topology but Opposite Polarity to E. coli SSB. Journal of Molecular Biology, 2012, 420, 269-283.	4.2	36
22	Termination of translation in bacteria may be modulated via specific interaction between peptide chain release factor 2 and the last peptidyl-tRNASer/Phe. Nucleic Acids Research, 1993, 21, 2891-2897.	14.5	34
23	A dual role for mycobacterial RecO in RecA-dependent homologous recombination and RecA-independent single-strand annealing. Nucleic Acids Research, 2013, 41, 2284-2295.	14.5	34
24	Crystal Structure of a Novel Shikimate Dehydrogenase from Haemophilus influenzae. Journal of Biological Chemistry, 2005, 280, 17101-17108.	3.4	33
25	The crystal structure of a partial mouse Notch-1 ankyrin domain: Repeats 4 through 7 preserve an ankyrin fold. Protein Science, 2005, 14, 1274-1281.	7.6	27
26	RecR-mediated Modulation of RecF Dimer Specificity for Single- and Double-stranded DNA. Journal of Biological Chemistry, 2009, 284, 1425-1434.	3.4	26
27	Preliminary crystallographic study of the phenylalanyl-tRNA synthetase from Thermus thermophilus HB8. Journal of Molecular Biology, 1987, 198, 555-556.	4.2	22
28	5â€² Contexts ofEscherichia coliand human termination codons are similar. Nucleic Acids Research, 1995, 23, 4712-4716.	14.5	22
29	SCF E3-Mediated Autoubiquitination Negatively Regulates Activity of Cdc34 E2 but Plays a Nonessential Role in the Catalytic Cycle In Vitro and In Vivo. Molecular and Cellular Biology, 2007, 27, 5860-5870.	2.3	18
30	Advances in structural studies of recombination mediator proteins. Biophysical Chemistry, 2017, 225, 27-37.	2.8	18
31	Novel RNA and DNA strand exchange activity of the PALB2 DNA binding domain and its critical role for DNA repair in cells. ELife, 2019, 8, .	6.0	18
32	Phage P4 origin-binding domain structure reveals a mechanism for regulation of DNA-binding activity by homo- and heterodimerization of winged helix proteins. Molecular Microbiology, 2002, 43, 855-867.	2.5	16
33	Autotracing ofEscherichia coliacetate CoA-transferase Î±-subunit structure using 3.4â€…Ã… MAD and 1.9â€…Ã… native data. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2116-2121.	2.5	16
34	Structural Studies of SSB Interaction with RecO. Methods in Molecular Biology, 2012, 922, 123-131.	0.9	16
35	Crystal structure of glutamine amidotransferase fromThermotoga maritima. Proteins: Structure, Function and Bioinformatics, 2002, 49, 420-422.	2.6	14
36	RecO Protein Initiates DNA Recombination and Strand Annealing through Two Alternative DNA Binding Mechanisms. Journal of Biological Chemistry, 2014, 289, 28846-28855.	3.4	14

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37	DNA helicases, motors that move along nucleic acids: Lessons from the SF1 helicase superfamily. The Enzymes, 2003, , 303-VII.	1.7	12
38	Crystal structure ofBacillus subtilis YdaF protein: A putative ribosomalN-acetyltransferase. Proteins: Structure, Function and Bioinformatics, 2004, 57, 850-853.	2.6	10
39	The loop-less tmCdc34 E2 mutant defective in polyubiquitination in vitro and in vivo supports yeast growth in a manner dependent on Ubp14 and Cka2. Cell Division, 2011, 6, 7.	2.4	10
40	Using surface-bound rubidium ions for protein phasing. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1008-1012.	2.5	9
41	ATP Binding, ATP Hydrolysis, and Protein Dimerization Are Required for RecF to Catalyze an Early Step in the Processing and Recovery of Replication Forks Disrupted by DNA Damage. Journal of Molecular Biology, 2010, 401, 579-589.	4.2	9
42	A MUB E2 structure reveals E1 selectivity between cognate ubiquitin E2s in eukaryotes. Nature Communications, 2016, 7, 12580.	12.8	9
43	Rous Sarcoma Virus Synaptic Complex Capable of Concerted Integration Is Kinetically Trapped by Human Immunodeficiency Virus Integrase Strand Transfer Inhibitors. Journal of Biological Chemistry, 2014, 289, 19648-19658.	3.4	8
44	Artificial protein vaccines with predetermined tertiary structure: application to anti-HTV-1 vaccine design. Protein Engineering, Design and Selection, 1993, 6, 997-1001.	2.1	7
45	1.6 Ã... crystal structure of YteR protein from Bacillus subtilis, a predicted lyase. Proteins: Structure, Function and Bioinformatics, 2005, 60, 561-565.	2.6	7
46	Structural Insight into the Mechanism of PALB2 Interaction with MRG15. Genes, 2021, 12, 2002.	2.4	6
47	Retrovirus Integrase-DNA Structure Elucidates Concerted Integration Mechanisms. Viruses, 2010, 2, 1185-1189.	3.3	5
48	Structural dissection of sequence recognition and catalytic mechanism of human LINE-1 endonuclease. Nucleic Acids Research, 2021, 49, 11350-11366.	14.5	4
49	SSB Functions as a Sliding Platform that Migrates on DNA via Reptation. Cell, 2011, 146, 485.	28.9	3
50	Crystal structure of a predicted precorrin-8x methylmutase from Thermoplasma acidophilum. Proteins: Structure, Function and Bioinformatics, 2004, 58, 751-754.	2.6	2
51	ATP-Binding Cassette Properties of Recombination Mediator Protein RecF. , 0, , .		1
52	New evidence for dimerization of the short variant of PLA2g6, and regulation of its catalytic activity by Ca2+/calmodulin and Ca2+ influx factor.. FASEB Journal, 2013, 27, 1004.5.	0.5	0
53	Novel crystal structure of calcium independent phospholipase iPLA2Î²: mechanism of activity regulation and membrane localization. FASEB Journal, 2018, 32, 672.2.	0.5	0