Anton V Zavialov

List of Publications by Year
in descending order

40	3,269	279798 23	315739 38
papers	citations	h-index	g-index

40	40	40	4073
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Early-Onset Stroke and Vasculopathy Associated with Mutations in ADA2. New England Journal of Medicine, 2014, 370, 911-920.	27.0	687
2	Receptor binding studies disclose a novel class of highâ€affinity inhibitors of the Escherichia coli FimH adhesin. Molecular Microbiology, 2005, 55, 441-455.	2.5	372
3	Metacaspases. Cell Death and Differentiation, 2011, 18, 1279-1288.	11.2	292
4	Structure and Biogenesis of the Capsular F1 Antigen from Yersinia pestis. Cell, 2003, 113, 587-596.	28.9	238
5	Tudor staphylococcal nuclease is an evolutionarily conserved component of the programmed cell death degradome. Nature Cell Biology, 2009, 11, 1347-1354.	10.3	192
6	Human adenosine deaminase 2 induces differentiation of monocytes into macrophages and stimulates proliferation of T helper cells and macrophages. Journal of Leukocyte Biology, 2010, 88, 279-290.	3.3	192
7	A Posttermination Ribosomal Complex Is the Guanine Nucleotide Exchange Factor for Peptide Release Factor RF3. Cell, 2001, 107, 115-124.	28.9	186
8	The affinity of the FimH fimbrial adhesin is receptor-driven and quasi-independent of Escherichia coli pathotypes. Molecular Microbiology, 2006, 61, 1556-1568.	2.5	139
9	Structural basis for Acinetobacter baumannii biofilm formation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5558-5563.	7.1	122
10	Structural Basis for the Growth Factor Activity of Human Adenosine Deaminase ADA2. Journal of Biological Chemistry, 2010, 285, 12367-12377.	3.4	99
11	Resolving the energy paradox of chaperone/usher-mediated fibre assembly. Biochemical Journal, 2005, 389, 685-694.	3.7	90
12	Adhesive organelles of Gram-negative pathogens assembled with the classical chaperone/usher machinery: structure and function from a clinical standpoint. FEMS Microbiology Reviews, 2010, 34, 317-378.	8.6	84
13	Donor strand complementation mechanism in the biogenesis of nonâ€pilus systems. Molecular Microbiology, 2002, 45, 983-995.	2.5	65
14	FGL chaperone-assembled fimbrial polyadhesins: anti-immune armament of Gram-negative bacterial pathogens. FEMS Microbiology Reviews, 2007, 31, 478-514.	8.6	65
15	The effect of the intersubunit disulfide bond on the structural and functional properties of the small heat shock protein Hsp25. International Journal of Biological Macromolecules, 1998, 22, 163-173.	7.5	55
16	Influence of the conserved disulphide bond, exposed to the putative binding pocket, on the structure and function of the immunoglobulin-like molecular chaperone Caf1M of Yersinia pestis. Biochemical Journal, 1997, 324, 571-578.	3.7	44
17	Structural Insight into Host Recognition by Aggregative Adherence Fimbriae of Enteroaggregative Escherichia coli. PLoS Pathogens, 2014, 10, e1004404.	4.7	38
18	Structural Insight into Archaic and Alternative Chaperone-Usher Pathways Reveals a Novel Mechanism of Pilus Biogenesis. PLoS Pathogens, 2015, 11, e1005269.	4.7	32

#	Article	IF	Citations
19	Structural and Functional Significance of the FGL Sequence of the Periplasmic Chaperone Caf1M of Yersinia pestis. Journal of Bacteriology, 1999, 181, 2422-2429.	2.2	30
20	Thiol/disulfide exchange between small heat shock protein 25 and glutathione. BBA - Proteins and Proteomics, 1998, 1388, 123-132.	2.1	28
21	Crystal structure of enterotoxigenic <scp>E</scp>scherichia coli colonization factor <scp>CS</scp>6 reveals a novel type of functional assembly. Molecular Microbiology, 2012, 86, 1100-1115.	2.5	28
22	Allosteric Mechanism Controls Traffic in the Chaperone/Usher Pathway. Structure, 2012, 20, 1861-1871.	3.3	27
23	Large Is Fast, Small Is Tight: Determinants of Speed and Affinity in Subunit Capture by a Periplasmic Chaperone. Journal of Molecular Biology, 2012, 417, 294-308.	4.2	25
24	A novel self-capping mechanism controls aggregation of periplasmic chaperone Caf1M. Molecular Microbiology, 2007, 64, 153-164.	2.5	20
25	Secretion of Recombinant Proteins via the Chaperone/Usher Pathway in Escherichia coli. Applied and Environmental Microbiology, 2001, 67, 1805-1814.	3.1	17
26	Caf1A usher possesses a Caf1 subunit-like domain that is crucial for Caf1 fibre secretion. Biochemical Journal, 2009, 418, 541-551.	3.7	15
27	A new human challenge model for testing heat-stable toxin-based vaccine candidates for enterotoxigenic Escherichia coli diarrhea â€“ dose optimization, clinical outcomes, and CD4+ T cell responses. PLoS Neglected Tropical Diseases, 2019, 13, e0007823.	3.0	15
28	Structural basis for Myf and Psa fimbriaeâ€mediated tropism of pathogenic strains of Yersinia for host tissues. Molecular Microbiology, 2016, 102, 593-610.	2.5	14
29	Heterologous Complementation Studies With the YscX and YscY Protein Families Reveals a Specificity for Yersinia pseudotuberculosis Type III Secretion. Frontiers in Cellular and Infection Microbiology, 2018, 8, 80.	3.9	12
30	Overexpression, purification, crystallization and preliminary X-ray diffraction analysis of the F1 antigen Caf1Mâ€“Caf1 chaperoneâ€“subunit pre-assembly complex fromYersinia pestis. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 359-362.	2.5	10
31	Novel fusion proteins in the analysis of diabetes-associated autoantibodies to GAD65 and IA-2. Journal of Immunological Methods, 2000, 246, 91-96.	1.4	7
32	Crystallization and preliminary X-ray diffraction analysis of the Csu pili CsuCâ€“CsuA/B chaperoneâ€“major subunit pre-assembly complex fromAcinetobacter baumannii. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 770-774.	0.8	7
33	Methylation, crystallization and SAD phasing of the Csu pilus CsuCâ€“CsuE chaperoneâ€“adhesin subunit pre-assembly complex from Acinetobacter baumannii. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 450-454.	0.8	6
34	Archaic and alternative chaperones preserve pilin folding energy by providing incomplete structural information. Journal of Biological Chemistry, 2018, 293, 17070-17080.	3.4	5
35	Glycosphingolipids Recognized by Acinetobacter baumannii. Microorganisms, 2020, 8, 612.	3.6	5
36	Secreted bacterial adenosine deaminase is an evolutionary precursor of adenosine deaminase growth factor. Molecular Biology and Evolution, 2018, 35, 2851-2861.	8.9	3

#	Article	IF	Citations
37	Crystallization and sulfur SAD phasing of AggA, the major subunit of aggregative adherence fimbriae type I from theEscherichia colistrain that caused an outbreak of haemolytic-uraemic syndrome in Germany. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1389-1392.	0.7	2
38	Comparison of kinetic and enzymatic properties of intracellular phosphoserine aminotransferases from alkaliphilic and neutralophilic bacteria. Open Chemistry, 2020, 18, 149-164.	1.9	1
39	Mutagenesis Elucidates The Assembly Pathway and Structure of Yersinia pestis F1 Polymer. Advances in Experimental Medicine and Biology, 2004, 529, 113-116.	1.6	0
40	A novel self-capping mechanism controls aggregation of periplasmic chaperone Caf1M. Molecular Microbiology, 2007, 64, 872-872.	2.5	0