Menachem Shoham

List of Publications by Year
in descending order

32 papers	1,687 citations	394421 19 h-index	454955 30 g-index
35 all docs	35 docs citations	35 times ranked	2239 citing authors

#	Article	IF	Citations
1	DAF in diabetic patients is subject to glycation/inactivation at its active site residues. Molecular Immunology, 2018, 93, 246-252.	2.2	3
2	Small-molecule AgrA inhibitors F12 and F19 act as antivirulence agents against Gram-positive pathogens. Scientific Reports, 2018, 8, 14578.	3.3	32
3	Biofilm inhibitors targeting the outer membrane protein A of Pasteurella multocida in swine. Biofouling, 2017, 33, 14-23.	2.2	5
4	Preventing the spread of infectious diseases: antivirulents versus antibiotics. Future Microbiology, 2017, 12, 365-368.	2.0	7
5	Novel Quorum-Quenching Agents Promote Methicillin-Resistant Staphylococcus aureus (MRSA) Wound Healing and Sensitize MRSA to Î²-Lactam Antibiotics. Antimicrobial Agents and Chemotherapy, 2015, 59, 1512-1518.	3.2	42
6	Combinatorial Synthesis and in Vitro Evaluation of a Biaryl Hydroxyketone Library as Antivirulence Agents against MRSA. ACS Combinatorial Science, 2014, 16, 85-91.	3.8	23
7	Discovery of Antivirulence Agents against Methicillin-Resistant Staphylococcus aureus. Antimicrobial Agents and Chemotherapy, 2013, 57, 3645-3652.	3.2	116
8	Signal peptide of FadA adhesin from Fusobacterium nucleatum plays a novel structural role by modulating the filament's length and width. FEBS Letters, 2012, 586, 1-6.	2.8	30
9	Specificity of Three Vasopressin Receptor Antagonists. Letters in Drug Design and Discovery, 2011, 8, 529-535.	0.7	0
10	Fusobacterium nucleatumadhesin FadA binds vascular endothelial cadherin and alters endothelial integrity. Molecular Microbiology, 2011, 82, 1468-1480.	2.5	216
11	Antivirulence agents against MRSA. Future Medicinal Chemistry, 2011, 3, 775-777.	2.3	23
12	Crystal Structure of FadA Adhesin from Fusobacterium nucleatum Reveals a Novel Oligomerization Motif, the Leucine Chain. Journal of Biological Chemistry, 2009, 284, 3865-3872.	3.4	33
13	Discovery of a Quorum-Sensing Inhibitor of Drug-Resistant Staphylococcal Infections by Structure-Based Virtual Screening. Molecular Pharmacology, 2008, 73, 1578-1586.	2.3	177
14	Arrestin Binding to Calmodulin: A Direct Interaction Between Two Ubiquitous Signaling Proteins. Journal of Molecular Biology, 2006, 364, 955-963.	4.2	72
15	Crystallization and preliminary X-ray data of the FadA adhesin fromFusobacterium nucleatum. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1215-1217.	0.7	4
16	Soluble Mimics of the Cytoplasmic Face of the Human V1-Vascular Vasopressin Receptor Bind Arrestin2 and Calmodulin. Molecular Pharmacology, 2006, 70, 249-258.	2.3	7
17	Mapping the Binding Site of Six Nonpeptide Antagonists to the Human V₂-Renal Vasopressin Receptor. Journal of Pharmacology and Experimental Therapeutics, 2006, 316, 564-571.	2.5	54
18	Prediction of the Structure of the Complex Between the 30S Ribosomal Subunit and Colicin E3 via Weighted-Geometric Docking. Journal of Biomolecular Structure and Dynamics, 2003, 20, 669-675.	3.5	8

#	Article	IF	Citations
19	Structure of decay-accelerating factor bound to echovirus 7: A virus-receptor complex. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10325-10329.	7.1	69
20	On the interaction of colicin E3 with the ribosome. Biochimie, 2002, 84, 447-454.	2.6	18
21	Bulk Production and Functional Analyses of Mouse CD55's Native and Deglycosylated Active Domains. Archives of Biochemistry and Biophysics, 2001, 393, 67-72.	3.0	10
22	Crystal Structure of Colicin E3. Molecular Cell, 2001, 8, 1053-1062.	9.7	143
23	Crystal structure of colicin E3 immunity protein: an inhibitor of a ribosome-inactivating RNase. Structure, 1999, 7, 1365-1372.	3.3	14
24	Crystal structure of a thermophilic alcohol dehydrogenase substrate complex suggests determinants of substrate specificity and thermostability. , 1999, 37, 619-627.		59
25	Multiple Wavelength Anomalous Diffraction (MAD) Crystal Structure of Rusticyanin: a Highly Oxidizing Cupredoxin with Extreme Acid Stability. Journal of Molecular Biology, 1996, 263, 730-751.	4.2	127
26	Insights into protein adaptation to a saturated salt environment from the crystal structure of a halophilic 2Fe-2S ferredoxin. Nature Structural Biology, 1996, 3, 452-458.	9.7	207
27	Molecular modeling and mechanism of action of human decay-accelerating factor. Protein Engineering, Design and Selection, 1996, 9, 1143-1149.	2.1	48
28	Structural diversity in a conserved cholera toxin epitope involved in ganglioside binding. Protein Science, 1995, 4, 841-848.	7.6	8
29	Crystal Structure of an Anticholera Toxin Peptide Complex at 2Â·3 Ã.... Journal of Molecular Biology, 1993, 232, 1169-1175.	4.2	76
30	Crystallization and preliminary X-ray crystallographic studies of rusticyanin from Thiobacillus ferrooxidans. Journal of Molecular Biology, 1992, 227, 581-582.	4.2	22
31	A structural model for human dihydrolipoamide dehydrogenase. Proteins: Structure, Function and Bioinformatics, 1992, 14, 88-101.	2.6	27
32	Crystal parameters and molecular replacement of an anticholera toxin peptide complex. Proteins: Structure, Function and Bioinformatics, 1991, 11, 218-222.	2.6	7