

Osnat Herzberg

List of Publications by Year in descending order

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papers

2,066
citations

304743

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39
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all docs

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docs citations

43
times ranked

2550
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of the wide-spectrum binuclear zinc β -lactamase from <i>Bacteroides fragilis</i> . Structure, 1996, 4, 823-836.	3.3	402
2	Crosslinking of mammalian lectin (galectin-1) by complex biantennary saccharides. Nature Structural and Molecular Biology, 1994, 1, 863-870.	8.2	218
3	Analysis of the steric strain in the polypeptide backbone of protein molecules. Proteins: Structure, Function and Bioinformatics, 1991, 11, 223-229.	2.6	216
4	Structure of Human Hyaluronidase-1, a Hyaluronan Hydrolyzing Enzyme Involved in Tumor Growth and Angiogenesis. Biochemistry, 2007, 46, 6911-6920.	2.5	148
5	Gene polymorphism linked to increased asthma and IBD risk alters gasdermin-B structure, a sulfatide and phosphoinositide binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1128-E1137.	7.1	135
6	Intracellular Delivery of an Antibody Targeting Gasdermin-B Reduces HER2 Breast Cancer Aggressiveness. Clinical Cancer Research, 2019, 25, 4846-4858.	7.0	79
7	Hydrological applications of noble gases and temperature measurements in underground water systems: Examples from Israel. Journal of Hydrology, 1979, 41, 217-231.	5.4	57
8	Challenging the state of the art in protein structure prediction: Highlights of experimental target structures for the 10th Critical Assessment of Techniques for Protein Structure Prediction Experiment CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 26-42.	2.6	53
9	Structural Basis for Inactivation of <i>Giardia lamblia</i> Carbamate Kinase by Disulfiram. Journal of Biological Chemistry, 2014, 289, 10502-10509.	3.4	51
10	Crystal structure of YbaK protein from <i>Haemophilus influenzae</i> (HI1434) at 1.8 Å resolution: Functional implications. , 2000, 40, 86-97.		47
11	Characterization, Kinetics, and Crystal Structures of Fructose-1,6-bisphosphate Aldolase from the Human Parasite, <i>Giardia lamblia</i> . Journal of Biological Chemistry, 2007, 282, 4859-4867.	3.4	45
12	High-Throughput <i>Giardia lamblia</i> Viability Assay Using Bioluminescent ATP Content Measurements. Antimicrobial Agents and Chemotherapy, 2011, 55, 667-675.	3.2	43
13	Crystal structures of the cadmium- and mercury-substituted metallo- β -lactamase from <i>Bacteroides fragilis</i> . Protein Science, 1997, 6, 2671-2676.	7.6	42
14	Computational models in the service of X-ray and cryo-electron microscopy structure determination. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1633-1646.	2.6	37
15	Pyruvate Site of Pyruvate Phosphate Dikinase: Crystal Structure of the Enzyme-Phosphonopyruvate Complex, and Mutant Analysis. Biochemistry, 2002, 41, 780-787.	2.5	36
16	Troponin-C mutants with increased calcium affinity. FEBS Journal, 1993, 213, 599-604.	0.2	34
17	Crystal Structure of the Sema-PSI Extracellular Domain of Human RON Receptor Tyrosine Kinase. PLoS ONE, 2012, 7, e41912.	2.5	33
18	Discovery of Novel Antigiardiasis Drug Candidates. Antimicrobial Agents and Chemotherapy, 2014, 58, 7303-7311.	3.2	33

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19	Circularly Permuted β -Lactamase from <i>Staphylococcus aureus</i> PC1. <i>Biochemistry</i> , 1997, 36, 8767-8774.	2.5	31
20	Insight into the Mechanism of Phosphoenolpyruvate Mutase Catalysis Derived from Site-Directed Mutagenesis Studies of Active Site Residues. <i>Biochemistry</i> , 1999, 38, 14165-14173.	2.5	28
21	Crystal structure of Yeco from <i>Haemophilus influenzae</i> (HI0319) reveals a methyltransferase fold and a bound S-adenosylhomocysteine. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 397-407.	2.6	27
22	Protein Characterization of a Candidate Mechanism SNP for Crohn's Disease: The Macrophage Stimulating Protein R689C Substitution. <i>PLoS ONE</i> , 2011, 6, e27269.	2.5	24
23	Structure and tailspike glycosidase machinery of ORF212 from <i>E. coli</i> O157:H7 phage CBA120 (TSP3). <i>Scientific Reports</i> , 2019, 9, 7349.	3.3	23
24	Structural Basis for the Mechanism and Substrate Specificity of Glycoamine Kinase, a Phosphagen Kinase Family Member. <i>Biochemistry</i> , 2010, 49, 2031-2041.	2.5	22
25	Location of the Phosphate Binding Site within <i>Clostridium symbiosum</i> Pyruvate Phosphate Dikinase. <i>Biochemistry</i> , 1998, 37, 13463-13474.	2.5	21
26	Crystal Structure of ORF210 from <i>E. coli</i> O157:H1 Phage CBA120 (TSP1), a Putative Tailspike Protein. <i>PLoS ONE</i> , 2014, 9, e93156.	2.5	18
27	For the record: Structural consequences of the active site substitution Cys181 \rightarrow Ser in metallo- β -lactamase from <i>Bacteroides fragilis</i> . <i>Protein Science</i> , 1999, 8, 249-252.	7.6	17
28	Structural Basis for the Binding Specificity of Human Recepteur d'Origine Nantais (RON) Receptor Tyrosine Kinase to Macrophage-stimulating Protein. <i>Journal of Biological Chemistry</i> , 2014, 289, 29948-29960.	3.4	17
29	A Homogenous Luminescence Assay Reveals Novel Inhibitors for <i>Giardia lamblia</i> Carbamate Kinase. <i>Current Chemical Genomics</i> , 2012, 6, 93-102.	2.0	16
30	Structure and function of bacteriophage CBA120 ORF211 (TSP2), the determinant of phage specificity towards <i>E. coli</i> O157:H7. <i>Scientific Reports</i> , 2020, 10, 15402.	3.3	15
31	Topography of the Interaction of HPr(Ser) Kinase with HPr. <i>Biochemistry</i> , 1998, 37, 11762-11770.	2.5	14
32	An engineered <i>Staphylococcus aureus</i> PCI β -lactamase that hydrolyses third-generation cephalosporins. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 1275-1285.	2.1	12
33	X-ray structure and characterization of carbamate kinase from the human parasite <i>Giardia lamblia</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 386-390.	0.7	11
34	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	2.6	11
35	Relocation of the catalytic carboxylate group in class A β -lactamase: the structure and function of the mutant enzyme Glu166 \rightarrow Gln:Asn170 \rightarrow Asp. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 573-579.	2.1	10
36	Structure of <i>Escherichia coli</i> O157:H7 bacteriophage CBA120 tailspike protein 4 baseplate anchor and tailspike assembly domains (TSP4-N). <i>Scientific Reports</i> , 2022, 12, 2061.	3.3	10

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37	Cryo-EM structure of the ancient eukaryotic ribosome from the human parasite <i>Giardia lamblia</i> . Nucleic Acids Research, 2022, 50, 1770-1782.	14.5	9
38	A protein-protein interaction dictates Borrelial infectivity. Scientific Reports, 2017, 7, 2932.	3.3	8
39	Discovery and Preclinical Development of Antigiardiasis Fumagillol Derivatives. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	6
40	Crystal Structures of Carbamate Kinase from <i>Giardia lamblia</i> Bound with Citric Acid and AMP-PNP. PLoS ONE, 2013, 8, e64004.	2.5	4
41	Reply to HU et al.: On the interpretation of gasdermin-B expression quantitative trait loci data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7863-E7864.	7.1	0