

Amnon Horovitz

List of Publications by Year in descending order

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83
papers

4,746
citations

136950

32
h-index

102487

66
g-index

87
all docs

87
docs citations

87
times ranked

3571
citing authors

#	ARTICLE	IF	CITATIONS
1	Strength and co-operativity of contributions of surface salt bridges to protein stability. <i>Journal of Molecular Biology</i> , 1990, 216, 1031-1044.	4.2	410
2	Estimating the contribution of engineered surface electrostatic interactions to protein stability by using double-mutant cycles. <i>Biochemistry</i> , 1990, 29, 9343-9352.	2.5	390
3	Strategy for analysing the co-operativity of intramolecular interactions in peptides and proteins. <i>Journal of Molecular Biology</i> , 1990, 214, 613-617.	4.2	338
4	Nested cooperativity in the ATPase activity of the oligomeric chaperonin GroEL. <i>Biochemistry</i> , 1995, 34, 5303-5308.	2.5	298
5	Allostery in Its Many Disguises: From Theory to Applications. <i>Structure</i> , 2019, 27, 566-578.	3.3	285
6	Double-mutant cycles: a powerful tool for analyzing protein structure and function. <i>Folding & Design</i> , 1996, 1, R121-R126.	4.5	284
7	Mapping pathways of allosteric communication in GroEL by analysis of correlated mutations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 611-617.	2.6	175
8	Allosteric regulation of chaperonins. <i>Current Opinion in Structural Biology</i> , 2005, 15, 646-651.	5.7	132
9	Allosteric mechanisms can be distinguished using structural mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7235-7239.	7.1	131
10	Review: Allostery in Chaperonins. <i>Journal of Structural Biology</i> , 2001, 135, 104-114.	2.8	118
11	Two Lines of Allosteric Communication in the Oligomeric Chaperonin GroEL are Revealed by the Single Mutation Arg196→Ala. <i>Journal of Molecular Biology</i> , 1994, 243, 397-401.	4.2	108
12	Allosteric Control by ATP of Non-folded Protein Binding to GroEL. <i>Journal of Molecular Biology</i> , 1996, 255, 356-361.	4.2	106
13	Sequential ATP-induced allosteric transitions of the cytoplasmic chaperonin containing TCP-1 revealed by EM analysis. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 233-237.	8.2	100
14	Non-additivity in protein-protein interactions. <i>Journal of Molecular Biology</i> , 1987, 196, 733-735.	4.2	87
15	Allosteric Mechanisms in Chaperonin Machines. <i>Chemical Reviews</i> , 2016, 116, 6588-6606.	47.7	85
16	Equivalent Mutations in the Eight Subunits of the Chaperonin CCT Produce Dramatically Different Cellular and Gene Expression Phenotypes. <i>Journal of Molecular Biology</i> , 2010, 401, 532-543.	4.2	83
17	Mutation Ala2 → Ser Destabilizes Intersubunit Interactions in the Molecular Chaperone GroEL. <i>Journal of Molecular Biology</i> , 1993, 231, 58-64.	4.2	71
18	Transient Kinetic Analysis of Adenosine 5'-Triphosphate Binding-Induced Conformational Changes in the Allosteric Chaperonin GroEL. <i>Biochemistry</i> , 1998, 37, 7083-7088.	2.5	70

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19	Detection and reduction of evolutionary noise in correlated mutation analysis. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 247-253.	2.1	62
20	Nested allosteric interactions in the cytoplasmic chaperonin containing TCP-1. <i>Protein Science</i> , 2001, 10, 445-449.	7.6	61
21	Structural aspects of GroEl function. <i>Current Opinion in Structural Biology</i> , 1998, 8, 93-100.	5.7	58
22	ATP-Induced Allostery in the Eukaryotic Chaperonin CCT Is Abolished by the Mutation G345D in CCT4 that Renders Yeast Temperature-Sensitive for Growth. <i>Journal of Molecular Biology</i> , 2008, 377, 469-477.	4.2	55
23	Structural basis of allosteric changes in the GroEL mutant Arg197â†’Ala. <i>Nature Structural Biology</i> , 1997, 4, 690-694.	9.7	52
24	The MitCHAP-60 Disease Is Due to Entropic Destabilization of the Human Mitochondrial Hsp60 Oligomer. <i>Journal of Biological Chemistry</i> , 2009, 284, 28198-28203.	3.4	49
25	Inter-ring Communication is Disrupted in the GroEL Mutant Arg13 â†’ Gly; Ala126 â†’ Val with Known Crystal Structure. <i>Journal of Molecular Biology</i> , 1996, 258, 732-735.	4.2	48
26	Transient Kinetic Analysis of ATP-induced Allosteric Transitions in the Eukaryotic Chaperonin containing TCP-1. <i>Journal of Molecular Biology</i> , 2003, 326, 981-987.	4.2	45
27	GroES Promotes the T to R Transition of the GroEL Ring Distal to GroES in the GroELâ”GroES Complexâ€. <i>Biochemistry</i> , 1997, 36, 12276-12281.	2.5	44
28	Prediction of an Inter-residue Interaction in the Chaperonin GroEL from Multiple Sequence Alignment is Confirmed by Double-mutant Cycle Analysis. <i>Journal of Molecular Biology</i> , 1994, 238, 133-138.	4.2	40
29	Mapping the Transition State of the Allosteric Pathway of GroEL by Protein Engineering. <i>Journal of the American Chemical Society</i> , 1998, 120, 13262-13263.	13.7	40
30	What distinguishes GroEL substrates from other <i>Escherichia coli</i> proteins?. <i>FEBS Journal</i> , 2012, 279, 543-550.	4.7	40
31	Different subunits belonging to the same protein complex often exhibit discordant expression levels and evolutionary properties. <i>Current Opinion in Structural Biology</i> , 2014, 26, 113-120.	5.7	39
32	Conversion of the allosteric transition of GroEL from concerted to sequential by the single mutation Asp-155 -> Ala. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13797-13802.	7.1	36
33	Trade-off between Positive and Negative Design of Protein Stability: From Lattice Models to Real Proteins. <i>PLoS Computational Biology</i> , 2009, 5, e1000592.	3.2	36
34	Probing allosteric mechanisms using native mass spectrometry. <i>Current Opinion in Structural Biology</i> , 2015, 34, 7-16.	5.7	34
35	Double-mutant cycles: new directions and applications. <i>Current Opinion in Structural Biology</i> , 2019, 58, 10-17.	5.7	33
36	Interactions of subunit CCT3 in the yeast chaperonin CCT/TRiC with Q/N-rich proteins revealed by high-throughput microscopy analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18833-18838.	7.1	32

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37	Analysing the origin of long-range interactions in proteins using lattice models. <i>BMC Structural Biology</i> , 2009, 9, 4.	2.3	27
38	Thermodynamic Protein Destabilization by GFP Tagging: A Case of Interdomain Allostery. <i>Biophysical Journal</i> , 2015, 109, 1157-1162.	0.5	27
39	Out-of-equilibrium conformational cycling of GroEL under saturating ATP concentrations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6270-6274.	7.1	26
40	Local energetic frustration affects the dependence of green fluorescent protein folding on the chaperonin GroEL. <i>Journal of Biological Chemistry</i> , 2017, 292, 20583-20591.	3.4	26
41	Different mechanistic requirements for prokaryotic and eukaryotic chaperonins: a lattice study. <i>Bioinformatics</i> , 2007, 23, i240-i248.	4.1	25
42	Probing Water Density and Dynamics in the Chaperonin GroEL Cavity. <i>Journal of the American Chemical Society</i> , 2014, 136, 9396-9403.	13.7	25
43	A Method for Removing Effects of Nonspecific Binding on the Distribution of Binding Stoichiometries: Application to Mass Spectroscopy Data. <i>Biophysical Journal</i> , 2010, 99, 1645-1649.	0.5	24
44	Low folding propensity and high translation efficiency distinguish <i>in vivo</i> substrates of GroEL from other <i>Escherichia coli</i> proteins. <i>Bioinformatics</i> , 2007, 23, 3276-3279.	4.1	23
45	Sequential allosteric mechanism of ATP hydrolysis by the CCT/TRiC chaperone is revealed through Arrhenius analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5189-5194.	7.1	23
46	Å value analysis of heterogeneity in pathways of allosteric transitions: Evidence for parallel pathways of ATP-induced conformational changes in a GroEL ring. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14095-14097.	7.1	22
47	Concerted ATP-induced allosteric transitions in GroEL facilitate release of protein substrate domains in an all-or-none manner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3119-3124.	7.1	22
48	Comparative study of the effectiveness and limitations of current methods for detecting sequence coevolution. <i>Bioinformatics</i> , 2015, 31, 1929-1937.	4.1	22
49	Measuring inter-protein pairwise interaction energies from a single native mass spectrum by double-mutant cycle analysis. <i>Nature Communications</i> , 2017, 8, 212.	12.8	22
50	Glu257 in GroEL is a sensor involved in coupling polypeptide substrate binding to stimulation of ATP hydrolysis. <i>Protein Science</i> , 2006, 15, 1270-1276.	7.6	21
51	Kinetic Analysis of ATP-dependent Inter-ring Communication in GroEL. <i>Journal of Molecular Biology</i> , 2004, 338, 979-988.	4.2	20
52	Extending the New Generation of Structure Predictors to Account for Dynamics and Allostery. <i>Journal of Molecular Biology</i> , 2021, 433, 167007.	4.2	20
53	Dissociation of the GroEL~GroES Asymmetric Complex Is Accelerated by Increased Cooperativity in ATP Binding to the GroEL Ring Distal to GroES. <i>Biochemistry</i> , 2002, 41, 5938-5944.	2.5	19
54	Unpicking allosteric mechanisms of homo-oligomeric proteins by determining their successive ligand binding constants. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170176.	4.0	18

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55	On the Relationship Between the Hill Coefficients for Steady-state and Transient Kinetic Data: A Criterion for Concerted Transitions in Allosteric Proteins. <i>Bulletin of Mathematical Biology</i> , 2000, 62, 241-246.	1.9	17
56	Concerted Release of Substrate Domains from GroEL by ATP Is Demonstrated with FRET. <i>Journal of Molecular Biology</i> , 2008, 380, 717-725.	4.2	17
57	Estimating Interprotein Pairwise Interaction Energies in Cell Lysates from a Single Native Mass Spectrum. <i>Analytical Chemistry</i> , 2018, 90, 10090-10094.	6.5	17
58	Single-molecule spectroscopy exposes hidden states in an enzymatic electron relay. <i>Nature Communications</i> , 2015, 6, 8624.	12.8	16
59	A model of a gp120â€ƒv3 peptide in complex with an HIV-neutralizing antibody based on NMR and mutant cycle-derived constraints. <i>FEBS Journal</i> , 2000, 267, 767-779.	0.2	15
60	Chaperonin Mechanisms: Multiple and (Mis)Understood?. <i>Annual Review of Biophysics</i> , 2022, 51, 115-133.	10.0	15
61	Allostery and molecular machines. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170173.	4.0	14
62	In Vivo and in Vitro Function of GroEL Mutants with Impaired Allosteric Properties. <i>Journal of Biological Chemistry</i> , 2000, 275, 37951-37956.	3.4	13
63	Reconciling the controversy regarding the functional importance of bullet- and football-shaped GroE complexes. <i>Journal of Biological Chemistry</i> , 2019, 294, 13527-13529.	3.4	13
64	Design of an Optical Switch for Studying Conformational Dynamics in Individual Molecules of GroEL. <i>Bioconjugate Chemistry</i> , 2008, 19, 1339-1341.	3.6	11
65	Discriminating between Concerted and Sequential Allosteric Mechanisms by Comparing Equilibrium and Kinetic Hill Coefficients. <i>Journal of Physical Chemistry B</i> , 2021, 125, 70-73.	2.6	11
66	GroEL Allostery Illuminated by a Relationship between the Hill Coefficient and the MWC Model. <i>Biophysical Journal</i> , 2019, 117, 1915-1921.	0.5	10
67	Slowdown of Water Dynamics from the Top to the Bottom of the GroEL Cavity. <i>Journal of Physical Chemistry Letters</i> , 2021, 12, 5723-5730.	4.6	10
68	Measuring protein stability in the GroEL chaperonin cage reveals massive destabilization. <i>ELife</i> , 2020, 9, .	6.0	10
69	Contact Order Is a Determinant for the Dependence of GFP Folding on the Chaperonin GroEL. <i>Biophysical Journal</i> , 2019, 116, 42-48.	0.5	9
70	N-Terminal Domains in Two-Domain Proteins Are Biased to Be Shorter and Predicted to Fold Faster Than Their C-Terminal Counterparts. <i>Cell Reports</i> , 2013, 3, 1051-1056.	6.4	8
71	Intracellular Proteinâ€ƒDrug Interactions Probed by Direct Mass Spectrometry of Cell Lysates. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 19637-19642.	13.8	8
72	Codon-level information improves predictions of inter-residue contacts in proteins by correlated mutation analysis. <i>ELife</i> , 2015, 4, e08932.	6.0	8

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73	Transient Kinetic Analysis of ATP Hydrolysis by the CCT/TRiC Chaperonin. <i>Journal of Molecular Biology</i> , 2016, 428, 4520-4527.	4.2	7
74	Putting handcuffs on the chaperonin GroEL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10884-10885.	7.1	6
75	Insight into the Autosomal-Dominant Inheritance Pattern of SOD1-Associated ALS from Native Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2020, 432, 5995-6002.	4.2	6
76	Comparative genomic analysis of mollicutes with and without a chaperonin system. <i>PLoS ONE</i> , 2018, 13, e0192619.	2.5	6
77	Converting bleomycin into a prodrug that undergoes spontaneous reactivation under physiological conditions. <i>Toxicology and Applied Pharmacology</i> , 2019, 384, 114782.	2.8	4
78	Partitioning the Hill coefficient into contributions from ligand-promoted conformational changes and subunit heterogeneity. <i>Protein Science</i> , 2022, 31, e4298.	7.6	4
79	The Effects of Mutations on Protein Function: A Comparative Study of Three Databases of Mutations in Humans. <i>Israel Journal of Chemistry</i> , 2013, 53, 217-226.	2.3	2
80	Allostery in chaperonins. <i>Rendiconti Lincei</i> , 2006, 17, 115-131.	2.2	1
81	Fluorescence Correlation Spectroscopy and Allostery: The Case of GroEL. <i>Methods in Molecular Biology</i> , 2012, 796, 205-216.	0.9	1
82	Intracellular Protein-Drug Interactions Probed by Direct Mass Spectrometry of Cell Lysates. <i>Angewandte Chemie</i> , 2021, 133, 19789-19794.	2.0	0
83	Molecular Basis of Allosteric Transitions: GroEL. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2012, , 79-86.	0.5	0