

# Walid A Houry

## List of Publications by Year in descending order

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102  
papers

9,642  
citations

66343

42  
h-index

39675

94  
g-index

119  
all docs

119  
docs citations

119  
times ranked

11132  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	12.6	1,937
2	Navigating the Chaperone Network: An Integrative Map of Physical and Genetic Interactions Mediated by the Hsp90 Chaperone. <i>Cell</i> , 2005, 120, 715-727.	28.9	729
3	Identification of in vivo substrates of the chaperonin GroEL. <i>Nature</i> , 1999, 402, 147-154.	27.8	501
4	Polypeptide Flux through Bacterial Hsp70. <i>Cell</i> , 1999, 97, 755-765.	28.9	399
5	In Vivo Observation of Polypeptide Flux through the Bacterial Chaperonin System. <i>Cell</i> , 1997, 90, 491-500.	28.9	338
6	Mechanisms of Acid Resistance in <i>Escherichia coli</i> . <i>Annual Review of Microbiology</i> , 2013, 67, 65-81.	7.3	279
7	Inhibition of the Mitochondrial Protease ClpP as a Therapeutic Strategy for Human Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2015, 27, 864-876.	16.8	265
8	The AAA+ superfamily of functionally diverse proteins. <i>Genome Biology</i> , 2008, 9, 216.	9.6	215
9	Mitochondrial ClpP-Mediated Proteolysis Induces Selective Cancer Cell Lethality. <i>Cancer Cell</i> , 2019, 35, 721-737.e9.	16.8	206
10	An atlas of chaperone-protein interactions in <i>Saccharomyces cerevisiae</i> : implications to protein folding pathways in the cell. <i>Molecular Systems Biology</i> , 2009, 5, 275.	7.2	202
11	Quantitative NMR spectroscopy of supramolecular complexes: Dynamic side pores in ClpP are important for product release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16678-16683.	7.1	195
12	ClpP: A distinctive family of cylindrical energy-dependent serine proteases. <i>FEBS Letters</i> , 2007, 581, 3749-3757.	2.8	185
13	Linkage between the bacterial acid stress and stringent responses: the structure of the inducible lysine decarboxylase. <i>EMBO Journal</i> , 2011, 30, 931-944.	7.8	166
14	Molecular chaperone Hsp90 stabilizes Pih1/Nop17 to maintain R2TP complex activity that regulates snoRNA accumulation. <i>Journal of Cell Biology</i> , 2008, 180, 563-578.	5.2	159
15	The role of Hsp90 in protein complex assembly. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 674-682.	4.1	154
16	Direct binding targets of the stringent response alarmone (p)ppGpp. <i>Molecular Microbiology</i> , 2012, 85, 1029-1043.	2.5	153
17	The R2TP complex: Discovery and functions. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 101-107.	4.1	127
18	The Role of ClpP Protease in Bacterial Pathogenesis and Human Diseases. <i>ACS Chemical Biology</i> , 2018, 13, 1413-1425.	3.4	122

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19	Hsp90: a chaperone for protein folding and gene regulation. <i>Biochemistry and Cell Biology</i> , 2005, 83, 703-710.	2.0	120
20	Acid stress response in enteropathogenic gammaproteobacteria: an aptitude for survivalThis paper is one of a selection of papers published in this special issue entitled "Canadian Society of Biochemistry, Molecular & Cellular Biology 52nd Annual Meeting " Protein Folding: Principles and Diseases" and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 301-314.	2.0	120
21	Chaperone-Assisted Protein Folding in the Cell Cytoplasm. <i>Current Protein and Peptide Science</i> , 2001, 2, 227-244.	1.4	116
22	AAA+ proteins: diversity in function, similarity in structure. <i>Biochemical Society Transactions</i> , 2008, 36, 72-77.	3.4	115
23	The ClpP Double Ring Tetradecameric Protease Exhibits Plastic Ring-Ring Interactions, and the N Termini of Its Subunits Form Flexible Loops That Are Essential for ClpXP and ClpAP Complex Formation. <i>Journal of Biological Chemistry</i> , 2005, 280, 16185-16196.	3.4	111
24	The Role of Pontin and Reptin in Cellular Physiology and Cancer Etiology. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 58.	3.5	97
25	The N-terminal Zinc Binding Domain of ClpX Is a Dimerization Domain That Modulates the Chaperone Function. <i>Journal of Biological Chemistry</i> , 2003, 278, 48981-48990.	3.4	96
26	Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2014, 10, e1004120.	3.5	96
27	A processive rotary mechanism couples substrate unfolding and proteolysis in the ClpXP degradation machinery. <i>ELife</i> , 2020, 9, .	6.0	94
28	Activators of Cylindrical Proteases as Antimicrobials: Identification and Development of Small Molecule Activators of ClpP Protease. <i>Chemistry and Biology</i> , 2011, 18, 1167-1178.	6.0	86
29	Yeast Rvb1 and Rvb2 are ATP-Dependent DNA Helicases that Form a Heterohexameric Complex. <i>Journal of Molecular Biology</i> , 2008, 376, 1320-1333.	4.2	82
30	Chaperone networks in bacteria: analysis of protein homeostasis in minimal cells. <i>Journal of Structural Biology</i> , 2004, 146, 79-89.	2.8	81
31	The Clp Chaperones and Proteases of the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Journal of Molecular Biology</i> , 2010, 404, 456-477.	4.2	81
32	Chaperone-like activity of the AAA+ proteins Rvb1 and Rvb2 in the assembly of various complexes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20110399.	4.0	81
33	MoxR AAA+ ATPases: A novel family of molecular chaperones?. <i>Journal of Structural Biology</i> , 2006, 156, 200-209.	2.8	75
34	The Enzymatic Activities of the <i>Escherichia coli</i> Basic Aliphatic Amino Acid Decarboxylases Exhibit a pH Zone of Inhibition. <i>Biochemistry</i> , 2011, 50, 9388-9398.	2.5	74
35	Acyldepsipeptide Analogs Dysregulate Human Mitochondrial ClpP Protease Activity and Cause Apoptotic Cell Death. <i>Cell Chemical Biology</i> , 2018, 25, 1017-1030.e9.	5.2	72
36	Molecular Interaction Network of the Hsp90 Chaperone System. , 2007, 594, 27-36.		72

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37	Rvb1 and Rvb2: essential ATP-dependent helicases for critical complexes. This paper is one of a selection of papers published in this special issue entitled 8th International Conference on AAA Proteins and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 29-40.	2.0	67
38	The PAQosome, an R2TP-Based Chaperone for Quaternary Structure Formation. <i>Trends in Biochemical Sciences</i> , 2018, 43, 4-9.	7.5	67
39	Dynamics of the ClpP serine protease: A model for self-compartmentalized proteases. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2014, 49, 400-412.	5.2	61
40	Structural and Theoretical Studies Indicate that the Cylindrical Protease ClpP Samples Extended and Compact Conformations. <i>Structure</i> , 2010, 18, 798-808.	3.3	59
41	Reversible inhibition of the ClpP protease via an N-terminal conformational switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6447-E6456.	7.1	56
42	Formation of a Distinctive Complex between the Inducible Bacterial Lysine Decarboxylase and a Novel AAA+ ATPase. <i>Journal of Biological Chemistry</i> , 2006, 281, 1532-1546.	3.4	54
43	Features of the Chaperone Cellular Network Revealed through Systematic Interaction Mapping. <i>Cell Reports</i> , 2017, 20, 2735-2748.	6.4	47
44	Solution Structure of the Dimeric Zinc Binding Domain of the Chaperone ClpX. <i>Journal of Biological Chemistry</i> , 2003, 278, 48991-48996.	3.4	46
45	Structure of RavA MoxR AAA+ protein reveals the design principles of a molecular cage modulating the inducible lysine decarboxylase activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22499-22504.	7.1	45
46	Structure of Minimal Tetratricopeptide Repeat Domain Protein Tah1 Reveals Mechanism of Its Interaction with Pih1 and Hsp90. <i>Journal of Biological Chemistry</i> , 2012, 287, 5698-5709.	3.4	44
47	Development and Characterization of Potent Cyclic Acyldepsipeptide Analogues with Increased Antimicrobial Activity. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 624-646.	6.4	44
48	Novel structural and functional insights into the MoxR family of AAA+ ATPases. <i>Journal of Structural Biology</i> , 2012, 179, 211-221.	2.8	41
49	Nutritional status modulates box C/D snoRNP biogenesis by regulated subcellular relocalization of the R2TP complex. <i>Genome Biology</i> , 2014, 15, 404.	8.8	40
50	Comparison of the multiple oligomeric structures observed for the Rvb1 and Rvb2 proteins. This paper is one of a selection of papers published in this special issue entitled 8th International Conference on AAA Proteins and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 77-88.	2.0	39
51	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2015, 31, 306-310.	4.1	38
52	Alternative Oligomeric States of the Yeast Rvb1/Rvb2 Complex Induced by Histidine Tags. <i>Journal of Molecular Biology</i> , 2010, 404, 478-492.	4.2	37
53	The AAA+ proteins Pontin and Reptin enter adult age: from understanding their basic biology to the identification of selective inhibitors. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 17.	3.5	37
54	Structural insights into the <i>Escherichia coli</i> lysine decarboxylases and molecular determinants of interaction with the AAA+ ATPase RavA. <i>Scientific Reports</i> , 2016, 6, 24601.	3.3	36

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55	AAA+ proteins. <i>Current Biology</i> , 2020, 30, R251-R257.	3.9	36
56	The MoxR ATPase RavA and Its Cofactor ViaA Interact with the NADH:Ubiquinone Oxidoreductase I in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2014, 9, e85529.	2.5	34
57	Specificity in substrate and cofactor recognition by the N-terminal domain of the chaperone ClpX. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17724-17729.	7.1	30
58	Large nucleotide-dependent movement of the N-terminal domain of the ClpX chaperone. <i>EMBO Journal</i> , 2006, 25, 3367-3376.	7.8	28
59	The RavA-ViaA Chaperone-Like System Interacts with and Modulates the Activity of the Fumarate Reductase Respiratory Complex. <i>Journal of Molecular Biology</i> , 2017, 429, 324-344.	4.2	28
60	Hsp90 at the crossroads of genetics and epigenetics. <i>Cell Research</i> , 2006, 16, 742-749.	12.0	26
61	Total Synthesis and Antibacterial Testing of the A54556 Cyclic Acyldepsipeptides Isolated from <i>Streptomyces hawaiiensis</i> . <i>Journal of Natural Products</i> , 2014, 77, 2170-2181.	3.0	26
62	Chemical Modulation of Human Mitochondrial ClpP: Potential Application in Cancer Therapeutics. <i>ACS Chemical Biology</i> , 2019, 14, 2349-2360.	3.4	26
63	PIH1D1 interacts with mTOR complex 1 and enhances ribosome RNA transcription. <i>FEBS Letters</i> , 2013, 587, 3303-3308.	2.8	25
64	Structural Insights into the Inactive Subunit of the Apicoplast-localized Caseinolytic Protease Complex of <i>Plasmodium falciparum</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 1022-1031.	3.4	25
65	Architecture and Nucleotide-Dependent Conformational Changes of the Rvb1-Rvb2 AAA+ Complex Revealed by Cryoelectron Microscopy. <i>Structure</i> , 2016, 24, 657-666.	3.3	25
66	Substrate Interaction Networks of the <i>Escherichia coli</i> Chaperones: Trigger Factor, DnaK and GroEL. <i>Advances in Experimental Medicine and Biology</i> , 2015, 883, 271-294.	1.6	23
67	Recent structural insights into the mechanism of ClpP protease regulation by AAA+ chaperones and small molecules. <i>Journal of Biological Chemistry</i> , 2022, 298, 101781.	3.4	22
68	The Stability of the Small Nucleolar Ribonucleoprotein (snoRNP) Assembly Protein Pih1 in <i>Saccharomyces cerevisiae</i> Is Modulated by Its C Terminus. <i>Journal of Biological Chemistry</i> , 2012, 287, 43205-43214.	3.4	21
69	ClpP protease activation results from the reorganization of the electrostatic interaction networks at the entrance pores. <i>Communications Biology</i> , 2019, 2, 410.	4.4	20
70	Assembly principles of a unique cage formed by hexameric and decameric <i>E. coli</i> proteins. <i>ELife</i> , 2014, 3, e03653.	6.0	20
71	Hsp110 is required for spindle length control. <i>Journal of Cell Biology</i> , 2012, 198, 623-636.	5.2	19
72	Substrates and interactors of the ClpP protease in the mitochondria. <i>Current Opinion in Chemical Biology</i> , 2022, 66, 102078.	6.1	19

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73	Yeast Rvb1 and Rvb2 Proteins Oligomerize As a Conformationally Variable Dodecamer with Low Frequency. <i>Journal of Molecular Biology</i> , 2015, 427, 1875-1886.	4.2	18
74	Recent Advances in Targeting Human Mitochondrial AAA+ Proteases to Develop Novel Cancer Therapeutics. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1158, 119-142.	1.6	17
75	Role of the N-Terminal Domain of the Chaperone ClpX in the Recognition and Degradation of Lambda Phage Protein O. <i>Journal of Physical Chemistry B</i> , 2012, 116, 6717-6724.	2.6	16
76	The Multiple Functions of the PAQosome: An R2TP- and URI1 Prefoldin-Based Chaperone Complex. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1106, 37-72.	1.6	16
77	<i>Plasmodium falciparum</i> R2TP complex: driver of parasite Hsp90 function. <i>Biophysical Reviews</i> , 2019, 11, 1007-1015.	3.2	16
78	Functional cooperativity between the trigger factor chaperone and the ClpXP proteolytic complex. <i>Nature Communications</i> , 2021, 12, 281.	12.8	16
79	Tamoxifen Enhances the Hsp90 Molecular Chaperone ATPase Activity. <i>PLoS ONE</i> , 2010, 5, e9934.	2.5	16
80	Development of Antibiotics That Dysregulate the <i>Neisseria</i> ClpP Protease. <i>ACS Infectious Diseases</i> , 2020, 6, 3224-3236.	3.8	15
81	Systems analysis of the genetic interaction network of yeast molecular chaperones. <i>Molecular Omics</i> , 2018, 14, 82-94.	2.8	14
82	Multiple functionalities of molecular chaperones revealed through systematic mapping of their interaction networks. <i>Journal of Biological Chemistry</i> , 2019, 294, 2142-2150.	3.4	13
83	Sorafenib as an Inhibitor of RUVBL2. <i>Biomolecules</i> , 2020, 10, 605.	4.0	13
84	Assembly principles of the human R2TP chaperone complex reveal the presence of R2T and R2P complexes. <i>Structure</i> , 2022, 30, 156-171.e12.	3.3	13
85	The control of spindle length by Hsp70 and Hsp110 molecular chaperones. <i>FEBS Letters</i> , 2013, 587, 1067-1072.	2.8	12
86	Mechanism of Amyloidogenesis of a Bacterial AAA+ Chaperone. <i>Structure</i> , 2016, 24, 1095-1109.	3.3	12
87	Editorial: The Role of AAA+ Proteins in Protein Repair and Degradation. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 85.	3.5	12
88	The Thiazole-5-Carboxamide GPS491 Inhibits HIV-1, Adenovirus, and Coronavirus Replication by Altering RNA Processing/Accumulation. <i>Viruses</i> , 2022, 14, 60.	3.3	10
89	Exosome-Bound WD Repeat Protein Monad Inhibits Breast Cancer Cell Invasion by Degrading Amphiregulin mRNA. <i>PLoS ONE</i> , 2013, 8, e67326.	2.5	9
90	Mechanism of substrate recognition by the chaperonin GroEL. <i>Biochemistry and Cell Biology</i> , 2001, 79, 569-77.	2.0	8

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91	Strategies for purification of the bacteriophage HK97 small and large terminase subunits that yield pure and homogeneous samples that are functional. <i>Protein Expression and Purification</i> , 2019, 160, 45-55.	1.3	6
92	Targeting the Mammalian Mitochondrial Clpp (mClpP) As a Novel Therapeutic Strategy for Acute Myeloid Leukemia. <i>Blood</i> , 2012, 120, 3603-3603.	1.4	6
93	Heat shock protein 90 kDa (Hsp90) from <i>Aedes aegypti</i> has an open conformation and is expressed under heat stress. <i>International Journal of Biological Macromolecules</i> , 2020, 156, 522-530.	7.5	5
94	Chaperones and Proteases of <i>Plasmodium falciparum</i> . , 2014, , 161-187.		5
95	<i>Leishmania major</i> RUVBL1 has a hexameric conformation in solution and, in the presence of RUVBL2, forms a heterodimer with ATPase activity. <i>Archives of Biochemistry and Biophysics</i> , 2021, 703, 108841.	3.0	4
96	Computational Analysis of the Chaperone Interaction Networks. <i>Methods in Molecular Biology</i> , 2018, 1709, 275-291.	0.9	2
97	Purification and characterization of a novel and conserved TPR-domain protein that binds both Hsp90 and Hsp70 and is expressed in all developmental stages of <i>Leishmania major</i> . <i>Biochimie</i> , 2021, 182, 51-60.	2.6	2
98	Development of Small Molecules to Modulate the Activity of the ATP-Dependent ClpP Protease as a Novel Antibacterial and Anticancer Drug Target. <i>Medicinal Chemistry Reviews</i> , 2019, , 379-404.	0.1	1
99	The role of Hsp90-TP complex in snoRNP assembly and ribosomal RNA processing. <i>FASEB Journal</i> , 2012, 26, 90.2.	0.5	0
100	Targeting The Mitochondrial ClpP As a Novel Therapeutic Strategy For Acute Myeloid Leukemia. <i>Blood</i> , 2013, 122, 3937-3937.	1.4	0
101	Dysregulation of Human Mitochondrial ClpP Protease Activity by Acyldepsipeptides Analogs Leads to Apoptotic Cell Death. <i>FASEB Journal</i> , 2018, 32, 653.3.	0.5	0
102	Molecular Basis of ClpP Protease Activation by Small Molecules. <i>FASEB Journal</i> , 2019, 33, 466.6.	0.5	0