

# 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	Substrates and interactors of the ClpP protease in the mitochondria. <i>Current Opinion in Chemical Biology</i> , 2022, 66, 102078.	6.1	19
2	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
3	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
4	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
5	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
6	<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
7	Functional cooperativity between the trigger factor chaperone and the ClpXP proteolytic complex. <i>Nature Communications</i> , 2021, 12, 281.	12.8	16
8	Development of Antibiotics That Dysregulate the <i>Neisseria</i> ClpP Protease. <i>ACS Infectious Diseases</i> , 2020, 6, 3224-3236.	3.8	15
9	AAA+ proteins. <i>Current Biology</i> , 2020, 30, R251-R257.	3.9	36
10	Sorafenib as an Inhibitor of RUVBL2. <i>Biomolecules</i> , 2020, 10, 605.	4.0	13
11	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
12	A processive rotary mechanism couples substrate unfolding and proteolysis in the ClpXP degradation machinery. <i>ELife</i> , 2020, 9, .	6.0	94
13	Chemical Modulation of Human Mitochondrial ClpP: Potential Application in Cancer Therapeutics. <i>ACS Chemical Biology</i> , 2019, 14, 2349-2360.	3.4	26
14	Mitochondrial ClpP-Mediated Proteolysis Induces Selective Cancer Cell Lethality. <i>Cancer Cell</i> , 2019, 35, 721-737.e9.	16.8	206
15	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
16	<i>Plasmodium falciparum</i> R2TP complex: driver of parasite Hsp90 function. <i>Biophysical Reviews</i> , 2019, 11, 1007-1015.	3.2	16
17	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
18	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

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19	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
20	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
21	Molecular Basis of ClpP Protease Activation by Small Molecules. <i>FASEB Journal</i> , 2019, 33, 466.6.	0.5	0
22	Systems analysis of the genetic interaction network of yeast molecular chaperones. <i>Molecular Omics</i> , 2018, 14, 82-94.	2.8	14
23	The PAQosome, an R2TP-Based Chaperone for Quaternary Structure Formation. <i>Trends in Biochemical Sciences</i> , 2018, 43, 4-9.	7.5	67
24	Computational Analysis of the Chaperone Interaction Networks. <i>Methods in Molecular Biology</i> , 2018, 1709, 275-291.	0.9	2
25	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
26	Editorial: The Role of AAA+ Proteins in Protein Repair and Degradation. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 85.	3.5	12
27	The Role of ClpP Protease in Bacterial Pathogenesis and Human Diseases. <i>ACS Chemical Biology</i> , 2018, 13, 1413-1425.	3.4	122
28	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
29	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
30	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
31	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
32	Features of the Chaperone Cellular Network Revealed through Systematic Interaction Mapping. <i>Cell Reports</i> , 2017, 20, 2735-2748.	6.4	47
33	The Role of Pontin and Reptin in Cellular Physiology and Cancer Etiology. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 58.	3.5	97
34	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
35	Structural insights into the Escherichia coli lysine decarboxylases and molecular determinants of interaction with the AAA+ ATPase RavA. <i>Scientific Reports</i> , 2016, 6, 24601.	3.3	36
36	Mechanism of Amyloidogenesis of a Bacterial AAA+ Chaperone. <i>Structure</i> , 2016, 24, 1095-1109.	3.3	12

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37	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
38	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
39	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
40	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
41	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
42	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
43	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
44	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
45	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
46	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
47	Chaperones and Proteases of <i>Plasmodium falciparum</i> . , 2014, , 161-187.		5
48	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
49	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
50	PIH1D1 interacts with mTOR complex 1 and enhances ribosome RNA transcription. <i>FEBS Letters</i> , 2013, 587, 3303-3308.	2.8	25
51	The control of spindle length by Hsp70 and Hsp110 molecular chaperones. <i>FEBS Letters</i> , 2013, 587, 1067-1072.	2.8	12
52	Mechanisms of Acid Resistance in <i>Escherichia coli</i> . <i>Annual Review of Microbiology</i> , 2013, 67, 65-81.	7.3	279
53	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
54	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

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55	Exosome-Bound WD Repeat Protein Monad Inhibits Breast Cancer Cell Invasion by Degrading Amphiregulin mRNA. PLoS ONE, 2013, 8, e67326.	2.5	9
56	Targeting The Mitochondrial ClpP As a Novel Therapeutic Strategy For Acute Myeloid Leukemia. Blood, 2013, 122, 3937-3937.	1.4	0
57	Structure of Minimal Tetratricopeptide Repeat Domain Protein Tah1 Reveals Mechanism of Its Interaction with Pih1 and Hsp90. Journal of Biological Chemistry, 2012, 287, 5698-5709.	3.4	44
58	The Stability of the Small Nucleolar Ribonucleoprotein (snoRNP) Assembly Protein Pih1 in Saccharomyces cerevisiae Is Modulated by Its C Terminus. Journal of Biological Chemistry, 2012, 287, 43205-43214.	3.4	21
59	Hsp110 is required for spindle length control. Journal of Cell Biology, 2012, 198, 623-636.	5.2	19
60	Role of the N-Terminal Domain of the Chaperone ClpX in the Recognition and Degradation of Lambda Phage Protein O. Journal of Physical Chemistry B, 2012, 116, 6717-6724.	2.6	16
61	Novel structural and functional insights into the MoxR family of AAA+ ATPases. Journal of Structural Biology, 2012, 179, 211-221.	2.8	41
62	Direct binding targets of the stringent response alarmone (p)ppGpp. Molecular Microbiology, 2012, 85, 1029-1043.	2.5	153
63	The R2TP complex: Discovery and functions. Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 101-107.	4.1	127
64	The role of Hsp90 in protein complex assembly. Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 674-682.	4.1	154
65	The role of Hsp90&R2TP complex in snoRNP assembly and ribosomal RNA processing. FASEB Journal, 2012, 26, 90.2.	0.5	0
66	Targeting the Mammalian Mitochondrial Clpp (mClpP) As a Novel Therapeutic Strategy for Acute Myeloid Leukemia. Blood, 2012, 120, 3603-3603.	1.4	6
67	The Enzymatic Activities of the <i>Escherichia coli</i> Basic Aliphatic Amino Acid Decarboxylases Exhibit a pH Zone of Inhibition. Biochemistry, 2011, 50, 9388-9398.	2.5	74
68	Linkage between the bacterial acid stress and stringent responses: the structure of the inducible lysine decarboxylase. EMBO Journal, 2011, 30, 931-944.	7.8	166
69	Activators of Cylindrical Proteases as Antimicrobials: Identification and Development of Small Molecule Activators of ClpP Protease. Chemistry and Biology, 2011, 18, 1167-1178.	6.0	86
70	The Genetic Landscape of a Cell. Science, 2010, 327, 425-431.	12.6	1,937
71	Structural and Theoretical Studies Indicate that the Cylindrical Protease ClpP Samples Extended and Compact Conformations. Structure, 2010, 18, 798-808.	3.3	59
72	Structure of RavA MoxR AAA+ protein reveals the design principles of a molecular cage modulating the inducible lysine decarboxylase activity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22499-22504.	7.1	45

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73	The Clp Chaperones and Proteases of the Human Malaria Parasite Plasmodium falciparum. Journal of Molecular Biology, 2010, 404, 456-477.	4.2	81
74	Alternative Oligomeric States of the Yeast Rvb1/Rvb2 Complex Induced by Histidine Tags. Journal of Molecular Biology, 2010, 404, 478-492.	4.2	37
75	Rvb1&Rvb2: essential ATP-dependent helicases for critical complexesThis 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.. Biochemistry and Cell Biology, 2010, 88, 29-40.	2.0	67
76	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.. Biochemistry and Cell Biology, 2010, 88, 301-314.	2.0	120
77	Comparison of the multiple oligomeric structures observed for the Rvb1 and Rvb2 proteinsThis 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.. Biochemistry and Cell Biology, 2010, 88, 77-88.	2.0	39
78	Tamoxifen Enhances the Hsp90 Molecular Chaperone ATPase Activity. PLoS ONE, 2010, 5, e9934.	2.5	16
79	An atlas of chaperone&protein interactions in <i>Saccharomyces cerevisiae</i> : implications to protein folding pathways in the cell. Molecular Systems Biology, 2009, 5, 275.	7.2	202
80	The AAA+ superfamily of functionally diverse proteins. Genome Biology, 2008, 9, 216.	9.6	215
81	Yeast Rvb1 and Rvb2 are ATP-Dependent DNA Helicases that Form a Heterohexameric Complex. Journal of Molecular Biology, 2008, 376, 1320-1333.	4.2	82
82	Molecular chaperone Hsp90 stabilizes Pih1/Nop17 to maintain R2TP complex activity that regulates snoRNA accumulation. Journal of Cell Biology, 2008, 180, 563-578.	5.2	159
83	AAA+ proteins: diversity in function, similarity in structure. Biochemical Society Transactions, 2008, 36, 72-77.	3.4	115
84	ClpP: A distinctive family of cylindrical energy-dependent serine proteases. FEBS Letters, 2007, 581, 3749-3757.	2.8	185
85	Molecular Interaction Network of the Hsp90 Chaperone System. , 2007, 594, 27-36.		72
86	MoxR AAA+ ATPases: A novel family of molecular chaperones?. Journal of Structural Biology, 2006, 156, 200-209.	2.8	75
87	Hsp90 at the crossroads of genetics and epigenetics. Cell Research, 2006, 16, 742-749.	12.0	26
88	Large nucleotide-dependent movement of the N-terminal domain of the ClpX chaperone. EMBO Journal, 2006, 25, 3367-3376.	7.8	28
89	Formation of a Distinctive Complex between the Inducible Bacterial Lysine Decarboxylase and a Novel AAA+ ATPase. Journal of Biological Chemistry, 2006, 281, 1532-1546.	3.4	54
90	Specificity in substrate and cofactor recognition by the N-terminal domain of the chaperone ClpX. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17724-17729.	7.1	30

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91	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
92	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
93	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
94	Hsp90: a chaperone for protein folding and gene regulation. <i>Biochemistry and Cell Biology</i> , 2005, 83, 703-710.	2.0	120
95	Chaperone networks in bacteria: analysis of protein homeostasis in minimal cells. <i>Journal of Structural Biology</i> , 2004, 146, 79-89.	2.8	81
96	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
97	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
98	Chaperone-Assisted Protein Folding in the Cell Cytoplasm. <i>Current Protein and Peptide Science</i> , 2001, 2, 227-244.	1.4	116
99	Mechanism of substrate recognition by the chaperonin GroEL. <i>Biochemistry and Cell Biology</i> , 2001, 79, 569-77.	2.0	8
100	Identification of in vivo substrates of the chaperonin GroEL. <i>Nature</i> , 1999, 402, 147-154.	27.8	501
101	Polypeptide Flux through Bacterial Hsp70. <i>Cell</i> , 1999, 97, 755-765.	28.9	399
102	In Vivo Observation of Polypeptide Flux through the Bacterial Chaperonin System. <i>Cell</i> , 1997, 90, 491-500.	28.9	338