

1. Maupin-Furlow JA. Archaeal proteasomes and sarnylation. *Subcell Biochem.* 2013;66:297–327.
2. Glatt S, Zabel R, Kolaj-Robin O, Onuma OF, Baudin F, Graziadei A, et al. Structural basis for tRNA modification by Elp3 from *Dehalococcoides mccartyi*. *Nat Struct Mol Biol.* 2016 Sep;23(9):794–802.
3. Mehlgarten C, Jablonowski D, Wrackmeyer U, Tschitschmann S, Sondermann D, Jäger G, et al. Elongator function in tRNA wobble uridine modification is conserved between yeast and plants. *Molecular Microbiology.* 2010;76(5):1082–94.
4. Selvadurai K, Wang P, Seimetz J, Huang RH. Archaeal Elp3 catalyzes tRNA wobble uridine modification at C5 via a radical mechanism. *Nat Chem Biol.* 2014 Oct;10(10):810–2.
5. Selvadurai K, Wang P, Seimetz J, Huang RH. Archaeal Elp3 catalyzes tRNA wobble uridine modification at C5 via a radical mechanism. *Nat Chem Biol.* 2014 Oct;10(10):810–2.
6. Selvadurai K, Wang P, Seimetz J, Huang RH. Archaeal Elp3 catalyzes tRNA wobble uridine modification at C5 via a radical mechanism. *Nat Chem Biol.* 2014 Oct;10(10):810–2.
7. Wittschieben BØ, Fellows J, Du W, Stillman DJ, Svejstrup JQ. Overlapping roles for the histone acetyltransferase activities of SAGA and Elongator in vivo. *The EMBO Journal.* 2000 Jun 15;19(12):3060–8.
8. Winkler GS, Kristjuhan A, Erdjument-Bromage H, Tempst P, Svejstrup JQ. Elongator is a histone H3 and H4 acetyltransferase important for normal histone acetylation levels in vivo. *PNAS.* 2002 Mar 19;99(6):3517–22.
9. Sylvers LA, Rogers KC, Shimizu M, Ohtsuka E, Soll D. A 2-thiouridine derivative in tRNA^{Glu} is a positive determinant for aminoacylation by *Escherichia coli* glutamyl-tRNA synthetase. *Biochemistry.* 1993 Apr 20;32(15):3836–41.
- 10.

Yarian C, Marszalek M, Sochacka E, Malkiewicz A, Guenther R, Miskiewicz A, et al. Modified Nucleoside Dependent Watson–Crick and Wobble Codon Binding by tRNA^{Lys}UUU Species. *Biochemistry*. 2000 Nov 1;39(44):13390–5.

11.

Ikeuchi Y, Shigi N, Kato J, Nishimura A, Suzuki T. Mechanistic Insights into Sulfur Relay by Multiple Sulfur Mediators Involved in Thiouridine Biosynthesis at tRNA Wobble Positions. *Molecular Cell*. 2006 Jan 6;21(1):97–108.

12.

Huang B, Johansson MJO, Byström AS. An early step in wobble uridine tRNA modification requires the Elongator complex. *RNA*. 2005 Apr 1;11(4):424–36.

13.

Rogers KC, Crescenzo AT, Söll D. Aminoacylation of transfer RNAs with 2-thiouridine derivatives in the wobble position of the anticodon. *Biochimie*. 1995 Jan 1;77(1):66–74.

14.

Dewez M, Bauer F, Dieu M, Raes M, Vandehaute J, Hermand D. The conserved Wobble uridine tRNA thiolase Ctu1–Ctu2 is required to maintain genome integrity. *PNAS*. 2008 Apr 8;105(14):5459–64.

15.

Tyagi K, Pedrioli PGA. Protein degradation and dynamic tRNA thiolation fine-tune translation at elevated temperatures. *Nucleic Acids Res*. 2015 May 19;43(9):4701–12.

16.

Termathe M, Leidel SA. The Uba4 domain interplay is mediated via a thioester that is critical for tRNA thiolation through Urm1 thiocarboxylation. *Nucleic Acids Res*. 2018 Jun 1;46(10):5171–81.

17.

Schmitz J, Chowdhury MM, Hänzelmann P, Nimtz M, Lee E-Y, Schindelin H, et al. The Sulfurtransferase Activity of Uba4 Presents a Link between Ubiquitin-like Protein Conjugation and Activation of Sulfur Carrier Proteins. *Biochemistry*. 2008 Jun 1;47(24):6479–89.

18.

Termathe M, Leidel SA. The Uba4 domain interplay is mediated via a thioester that is critical for tRNA thiolation through Urm1 thiocarboxylation. *Nucleic Acids Res*. 2018 Jun 1;46(10):5171–81.

19.

Schmitz J, Chowdhury MM, Hänzelmann P, Nimtz M, Lee E-Y, Schindelin H, et al. The sulfurtransferase activity of Uba4 presents a link between ubiquitin-like protein

- conjugation and activation of sulfur carrier proteins. *Biochemistry*. 2008 Jun 17;47(24):6479–89. 20.
- Dahl J-U, Urban A, Bolte A, Sriyabhaya P, Donahue JL, Nimtz M, et al. The Identification of a Novel Protein Involved in Molybdenum Cofactor Biosynthesis in *Escherichia coli*. *J Biol Chem*. 2011 Oct 14;286(41):35801–12. 21.
- Matthies A, Nimtz M, Leimkühler S. Molybdenum Cofactor Biosynthesis in Humans: Identification of a Persulfide Group in the Rhodanese-like Domain of MOCS3 by Mass Spectrometry. *Biochemistry*. 2005 May 1;44(21):7912–20. 22.
- Schulman BA, Wade Harper J. Ubiquitin-like protein activation by E1 enzymes: the apex for downstream signalling pathways. *Nature Reviews Molecular Cell Biology*. 2009 May;10(5):319–31. 23.
- Ubiquitin-like protein activation by E1 enzymes: the apex for downstream signalling pathways | *Nature Reviews Molecular Cell Biology* [Internet]. [cited 2020 Jul 12]. Available from: <https://www.nature.com/articles/nrm2673> 24.
- Lake MW, Wuebbens MM, Rajagopalan KV, Schindelin H. Mechanism of ubiquitin activation revealed by the structure of a bacterial MoeB–MoaD complex. *Nature*. 2001 Nov;414(6861):325–9. 25.
- Prunetti L, Reuter CJ, Hepowit NL, Wu Y, Barrueto L, Miranda HV, et al. Structural and biochemical properties of an extreme ‘salt-loving’ proteasome activating nucleotidase from the archaeon *Haloferax volcanii*. *Extremophiles*. 2014 Mar;18(2):283–93. 26.
- Ye K, Liao S, Zhang W, Fan K, Zhang X, Zhang J, et al. Ionic strength-dependent conformations of a ubiquitin-like small archaeal modifier protein (SAMP1) from *Haloferax volcanii*. *Protein Science*. 2013;22(9):1174–82. 27.
- Forouzan D, Ammelburg M, Hobel CF, Ströh LJ, Sessler N, Martin J, et al. The Archaeal Proteasome Is Regulated by a Network of AAA ATPases. *J Biol Chem*. 2012 Nov 9;287(46):39254–62. 28.

Darwin KH. Prokaryotic ubiquitin-like protein (Pup), proteasomes and pathogenesis. *Nature Reviews Microbiology*. 2009 Jul;7(7):485–91.

29.

Barthelme D, Sauer RT. Identification of the Cdc48•20S Proteasome as an Ancient AAA+ Proteolytic Machine. *Science*. 2012 Aug 17;337(6096):843–6.

30.

Stolz A, Hilt W, Buchberger A, Wolf DH. Cdc48: a power machine in protein degradation. *Trends in Biochemical Sciences*. 2011 Oct 1;36(10):515–23.

31.

Wilson HL, Ou MS, Aldrich HC, Maupin-Furlow J. Biochemical and Physical Properties of the *Methanococcus jannaschii* 20S Proteasome and PAN, a Homolog of the ATPase (Rpt) Subunits of the Eucaryal 26S Proteasome. *Journal of Bacteriology*. 2000 Mar 15;182(6):1680–92.

32.

Zwickl P, Ng D, Woo KM, Klenk H-P, ||, Goldberg AL. An Archaeobacterial ATPase, Homologous to ATPases in the Eukaryotic 26 S Proteasome, Activates Protein Breakdown by 20 S Proteasomes. *J Biol Chem*. 1999 Sep 10;274(37):26008–14.

33.

Oinonen C, Rouvinen J. Structural comparison of Ntn-hydrolases. *Protein Science*. 2000;9(12):2329–37.

34.

Bochtler M, Ditzel L, Groll M, Hartmann C, Huber R. The Proteasome. *Annual Review of Biophysics and Biomolecular Structure*. 1999;28(1):295–317.

35.

THE PROTEASOME | Annual Review of Biophysics [Internet]. [cited 2020 Jul 11]. Available

from: https://www.annualreviews.org/doi/full/10.1146/annurev.biophys.28.1.295?url_ver=Z39.88-2003&rfr_id=ori%3Arid%3Acrossref.org&rfr_dat=cr_pub++0pubmed

36.

Bochtler M, Ditzel L, Groll M, Hartmann C, Huber R. The proteasome. *Annu Rev Biophys Biomol Struct*. 1999;28:295–317.

37.

Bar-Nun S, Glickman MH. Proteasomal AAA-ATPases: structure and function. *Biochim Biophys Acta*. 2012 Jan;1823(1):67–82.

38.

Maupin-Furlow JA, Humbard MA, Kirkland PA, Li W, Reuter CJ, Wright AJ, et al. Proteasomes from Structure to Function: Perspectives from Archaea. In: Current Topics in Developmental Biology [Internet]. Academic Press; 2006 [cited 2020 Jul 11]. p. 125–69. Available from: <http://www.sciencedirect.com/science/article/pii/S0070215306750050>

39.

Volker C, Lupas AN. Molecular Evolution of Proteasomes. In: Zwickl P, Baumeister W, editors. The Proteasome — Ubiquitin Protein Degradation Pathway [Internet]. Berlin, Heidelberg: Springer; 2002 [cited 2020 Jul 11]. p. 1–22. (Current Topics in Microbiology and Immunology). Available from: https://doi.org/10.1007/978-3-642-59414-4_1

40.

Burns KE, Liu W-T, Boshoff HIM, Dorrestein PC, Barry CE. Proteasomal protein degradation in Mycobacteria is dependent upon a prokaryotic ubiquitin-like protein. *J Biol Chem*. 2009 Jan 30;284(5):3069–75.

41.

Pearce MJ, Mintseris J, Ferreyra J, Gygi SP, Darwin KH. Ubiquitin-like protein involved in the proteasome pathway of *Mycobacterium tuberculosis*. *Science*. 2008 Nov 14;322(5904):1104–7.

42.

Burns KE, Darwin KH. Pupylation versus ubiquitylation: tagging for proteasome-dependent degradation. *Cellular Microbiology*. 2010;12(4):424–31.

43.

Pedrioli PGA, Leidel S, Hofmann K. Urm1 at the crossroad of modifications. *EMBO reports*. 2008 Dec 1;9(12):1196–202.

44.

Pickart CM, Eddins MJ. Ubiquitin: structures, functions, mechanisms. *Biochimica et Biophysica Acta (BBA) - Molecular Cell Research*. 2004 Nov 29;1695(1):55–72.

45.

Maupin-Furlow J. Proteasomes and protein conjugation across domains of life. *Nature Reviews Microbiology*. 2012 Feb;10(2):100–11.

46.

Archaeal Proteasomes and Sanylation | SpringerLink [Internet]. [cited 2020 Jul 9]. Available from: https://link.springer.com/chapter/10.1007/978-94-007-5940-4_11

47.

Darwin KH, Hofmann K. SAMPyling proteins in archaea. *Trends in Biochemical Sciences*. 2010 Jun 1;35(6):348–51.

48. Burns KE, Darwin KH. Pupylation: Proteasomal Targeting by a Protein Modifier in Bacteria. In: Dohmen RJ, Scheffner M, editors. Ubiquitin Family Modifiers and the Proteasome: Reviews and Protocols [Internet]. Totowa, NJ: Humana Press; 2012 [cited 2020 Jul 9]. p. 151–60. (Methods in Molecular Biology). Available from: https://doi.org/10.1007/978-1-61779-474-2_10
49. Barandun J, Delley CL, Weber-Ban E. The pupylation pathway and its role in mycobacteria. *BMC Biology*. 2012 Nov 30;10(1):95.
50. Maupin-Furlow JA. Prokaryotic Ubiquitin-Like Protein Modification. *Annual Review of Microbiology*. 2014;68(1):155–75.
51. Seth-Pasricha M, Bidle KA, Bidle KD. Specificity of archaeal caspase activity in the extreme halophile *Haloferax volcanii*. *Environ Microbiol Rep*. 2013 Apr;5(2):263–71.
52. Zhou G, Kowalczyk D, Humbard MA, Rohatgi S, Maupin-Furlow JA. Proteasomal components required for cell growth and stress responses in the haloarchaeon *Haloferax volcanii*. *J Bacteriol*. 2008 Dec;190(24):8096–105.
53. Gomez M, Leung W, Dantuluri S, Pillai A, Gani Z, Hwang S, et al. Molecular Factors of Hypochlorite Tolerance in the Hypersaline Archaeon *Haloferax volcanii*. *Genes (Basel)* [Internet]. 2018 Nov 20 [cited 2020 Jul 9];9(11). Available from: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6267482/>
54. Jones DL, Baxter BK. DNA Repair and Photoprotection: Mechanisms of Overcoming Environmental Ultraviolet Radiation Exposure in Halophilic Archaea. *Front Microbiol* [Internet]. 2017 [cited 2020 Jul 9];8. Available from: <https://www.frontiersin.org/articles/10.3389/fmicb.2017.01882/full>
55. Xu X, Wang T, Niu Y, Liang K, Yang Y. The ubiquitin-like modification by ThiS and ThiF in *Escherichia coli*. *International Journal of Biological Macromolecules*. 2019 Dec 1;141:351–7.
56. Delley CL, Müller AU, Ziemski M, Weber-Ban E. Prokaryotic Ubiquitin-Like Protein and Its Ligase/Delgase Enzymes. *Journal of Molecular Biology*. 2017 Nov 10;429(22):3486–99.

57. Schwertman P, Bekker-Jensen S, Mailand N. Regulation of DNA double-strand break repair by ubiquitin and ubiquitin-like modifiers. *Nature Reviews Molecular Cell Biology*. 2016 Jun;17(6):379–94.
58. Regulation of DNA double-strand break repair by ubiquitin and ubiquitin-like modifiers | *Nature Reviews Molecular Cell Biology* [Internet]. [cited 2020 Jul 8]. Available from: <https://www.nature.com/articles/nrm.2016.58>
59. Wang Z, Zhu W-G, Xu X. Ubiquitin-like modifications in the DNA damage response. *Mutat Res*. 2017;803–805:56–75.
60. Han Z-J, Feng Y-H, Gu B-H, Li Y-M, Chen H. The post-translational modification, SUMOylation, and cancer (Review). *International Journal of Oncology*. 2018 Apr 1;52(4):1081–94.
61. Swatek KN, Komander D. Ubiquitin modifications. *Cell Research*. 2016 Apr;26(4):399–422.
62. Kirkland PA, Gil MA, Karadzic IM, Maupin-Furlow JA. Genetic and Proteomic Analyses of a Proteasome-Activating Nucleotidase A Mutant of the Haloarchaeon *Haloferax volcanii*. *Journal of Bacteriology*. 2008 Jan 1;190(1):193–205.
63. Humbard MA, Stevens SM, Maupin-Furlow JA. Posttranslational Modification of the 20S Proteasomal Proteins of the Archaeon *Haloferax volcanii*. *Journal of Bacteriology*. 2006 Nov 1;188(21):7521–30.
64. Heyer R, Dörr M, Jellen-Ritter A, Späth B, Babski J, Jaschinski K, et al. High throughput sequencing reveals a plethora of small RNAs including tRNA derived fragments in *Haloferax volcanii*. *RNA Biology*. 2012 Jul 1;9(7):1011–8.
65. Norais C, Hawkins M, Hartman AL, Eisen JA, Myllykallio H, Allers T. Genetic and Physical Mapping of DNA Replication Origins in *Haloferax volcanii*. *PLOS Genetics*. 2007 May 18;3(5):e77.
66. Allers T. Overexpression and purification of halophilic proteins in *Haloferax volcanii*. *Bioengineered Bugs*. 2010 Jul;1(4):290–2.

67.
Bitan-Banin G, Ortenberg R, Mevarech M. Development of a Gene Knockout System for the Halophilic Archaeon *Haloferax volcanii* by Use of the *pyrE* Gene. *Journal of Bacteriology*. 2003 Feb 1;185(3):772–8.
68.
Wendoloski D, Ferrer C, Dyall-Smith ML. A new simvastatin (mevinolin)-resistance marker from *Haloarcula hispanica* and a new *Haloferax volcanii* strain cured of plasmid pHV2. The GenBank accession number for the sequence reported in this paper is AF123438. *Microbiology*. 2001;147(4):959–64.
69.
Charlebois RL, Lam WL, Cline SW, Doolittle WF. Characterization of pHV2 from *Halobacterium volcanii* and its use in demonstrating transformation of an archaeobacterium. *PNAS*. 1987 Dec 1;84(23):8530–4.
70.
Hartman AL, Norais C, Badger JH, Delmas S, Haldenby S, Madupu R, et al. The Complete Genome Sequence of *Haloferax volcanii* DS2, a Model Archaeon. Friedberg I, editor. *PLoS ONE*. 2010 Mar 19;5(3):e9605.
71.
Mullakhanbhai MF, Larsen H. *Halobacterium volcanii* spec. nov., a Dead Sea halobacterium with a moderate salt requirement. *Arch Microbiol*. 1975 Jan 1;104(1):207–14.
72.
Woese CR, Fox GE. Phylogenetic structure of the prokaryotic domain: The primary kingdoms. *PNAS*. 1977 Nov 1;74(11):5088–90.
73.
Hepowit NL, Uthandi S, Miranda HV, Toniutti M, Prunetti L, Olivarez O, et al. Archaeal JAB1/MPN/MOV34 metalloenzyme (HvJAMM1) cleaves ubiquitin-like small archaeal modifier proteins (SAMPs) from protein-conjugates. *Mol Microbiol*. 2012 Nov;86(4):971–87.
74.
Cao S, Hepowit N, Maupin-Furlow JA. Ubiquitin-Like Protein SAMP1 and JAMM/MPN+ Metalloprotease HvJAMM1 Constitute a System for Reversible Regulation of Metabolic Enzyme Activity in Archaea. *PLoS ONE*. 2015;10(5):e0128399.
- 75.

Rogers KC, Crescenzo AT, Söll D. Aminoacylation of transfer RNAs with 2-thiouridine derivatives in the wobble position of the anticodon. *Biochimie*. 1995 Jan 1;77(1):66–74.

76.

Dantuluri S, Wu Y, Hepowit NL, Chen H, Chen S, Maupin-Furlow JA. Proteome targets of ubiquitin-like sanylation are associated with sulfur metabolism and oxidative stress in *Haloferax volcanii*. *Proteomics*. 2016 Apr;16(7):1100–10.

77.

Pandey A, Golla R, Yoon H, Dancis A, Pain D. Persulfide formation on mitochondrial cysteine desulfurase: enzyme activation by a eukaryote-specific interacting protein and Fe–S cluster synthesis. *Biochem J*. 2012 Dec 1;448(2):171–87.

78.

Rocha AG, Knight SAB, Pandey A, Yoon H, Pain J, Pain D, et al. Cysteine desulfurase is regulated by phosphorylation of Nfs1 in yeast mitochondria. *Mitochondrion*. 2018 May 1;40:29–41.

79.

Liu Y, Zhu X, Nakamura A, Orlando R, Söll D, Whitman WB. Biosynthesis of 4-thiouridine in tRNA in the methanogenic archaeon *Methanococcus maripaludis*. *J Biol Chem*. 2012 Oct 26;287(44):36683–92.

80.

Petroski MD, Salvesen GS, Wolf DA. Urm1 couples sulfur transfer to ubiquitin-like protein function in oxidative stress: Fig. 1. *Proc Natl Acad Sci USA*. 2011 Feb 1;108(5):1749–50.

81.

Schmitz J, Chowdhury MM, Hänzelmann P, Nimitz M, Lee E-Y, Schindelin H, et al. The Sulfurtransferase Activity of Uba4 Presents a Link between Ubiquitin-like Protein Conjugation and Activation of Sulfur Carrier Proteins. *Biochemistry*. 2008 Jun 1;47(24):6479–89.

82.

Shigi N. Posttranslational Modification of Cellular Proteins by a Ubiquitin-like Protein in Bacteria. *J Biol Chem*. 2012 May 18;287(21):17568–77.

83.

Termathe M, Leidel SA. The Uba4 domain interplay is mediated via a thioester that is critical for tRNA thiolation through Urm1 thiocarboxylation. *Nucleic Acids Res*. 2018 Jun 1;46(10):5171–81.

84.

Čavuzić M, Liu Y. Biosynthesis of Sulfur-Containing tRNA Modifications: A Comparison of Bacterial, Archaeal, and Eukaryotic Pathways. *Biomolecules*. 2017 11;7(1).

85.

Selvadurai K, Wang P, Seimetz J, Huang RH. Archaeal Elp3 catalyzes tRNA wobble uridine modification at C5 via a radical mechanism. *Nat Chem Biol*. 2014 Oct;10(10):810–2.

86.

Humbard MA, Zhou G, Maupin-Furlow JA. The N-terminal penultimate residue of 20S proteasome alpha1 influences its N(alpha) acetylation and protein levels as well as growth rate and stress responses of *Haloferax volcanii*. *J Bacteriol*. 2009 Jun;191(12):3794–803.

87.

Maupin-Furlow JA. Ubiquitin-like proteins and their roles in archaea. *Trends in Microbiology*. 2013 Jan 1;21(1):31–8.

88.

Leidel S, Pedrioli PGA, Bucher T, Brost R, Costanzo M, Schmidt A, et al. Ubiquitin-related modifier Urm1 acts as a sulphur carrier in thiolation of eukaryotic transfer RNA. *Nature*. 2009 Mar;458(7235):228–32.

89.

Bedford L, Lowe J, Dick LR, Mayer RJ, Brownell JE. Ubiquitin-like protein conjugation and the ubiquitin–proteasome system as drug targets. *Nature Reviews Drug Discovery*. 2011 Jan;10(1):29–46.

90.

Kar G, Keskin O, Fraternali F, Gursoy A. Emerging Role of the Ubiquitin-proteasome System as Drug Targets. *Current Pharmaceutical Design*. 2013 Jun 1;19(18):3175–89.

91.

El Yacoubi B, Bailly M, de Crécy-Lagard V. Biosynthesis and Function of Posttranscriptional Modifications of Transfer RNAs. *Annual Review of Genetics*. 2012;46(1):69–95.

92.

Su D, Chan CTY, Gu C, Lim KS, Chionh YH, McBee ME, et al. Quantitative analysis of ribonucleoside modifications in tRNA by HPLC-coupled mass spectrometry. *Nature Protocols*. 2014 Apr;9(4):828–41.

93.

Leihne V, Kirpekar F, Vågbø CB, van den Born E, Krokan HE, Grini PE, et al. Roles of Trm9- and ALKBH8-like proteins in the formation of modified wobble uridines in Arabidopsis tRNA. *Nucleic Acids Res.* 2011 Sep 1;39(17):7688–701.

94.

Chen C, Huang B, Anderson JT, Byström AS. Unexpected Accumulation of mcm5U and mcm5s2U in a trm9 Mutant Suggests an Additional Step in the Synthesis of mcm5U and mcm5s2U. *PLOS ONE.* 2011 Jun 7;6(6):e20783.

95.

Selvadurai K, Wang P, Seimetz J, Huang RH. Archaeal Elp3 catalyzes tRNA wobble uridine modification at C5 via a radical mechanism. *Nature Chemical Biology.* 2014 Oct;10(10):810–2.

96.

Glatt S, Zabel R, Kolaj-Robin O, Onuma OF, Baudin F, Graziadei A, et al. Structural basis for tRNA modification by Elp3 from *Dehalococcoides mccartyi*. *Nature Structural & Molecular Biology.* 2016 Sep;23(9):794–802.

97.

Klassen R, Grunewald P, Thüring KL, Eichler C, Helm M, Schaffrath R. Loss of Anticodon Wobble Uridine Modifications Affects tRNA^{Lys} Function and Protein Levels in *Saccharomyces cerevisiae*. *PLoS One* [Internet]. 2015 Mar 6 [cited 2020 May 20];10(3). Available from: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4352028/>

98.

Klassen R, Grunewald P, Thüring KL, Eichler C, Helm M, Schaffrath R. Loss of Anticodon Wobble Uridine Modifications Affects tRNA^{Lys} Function and Protein Levels in *Saccharomyces cerevisiae*. *PLoS One* [Internet]. 2015 Mar 6 [cited 2020 May 20];10(3). Available from: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4352028/>

99.

Rogers KC, Crescenzo AT, Söll D. Aminoacylation of transfer RNAs with 2-thiouridine derivatives in the wobble position of the anticodon. *Biochimie.* 1995 Jan 1;77(1):66–74.

100.

Rogers KC, Crescenzo AT, Söll D. Aminoacylation of transfer RNAs with 2-thiouridine derivatives in the wobble position of the anticodon. *Biochimie.* 1995 Jan 1;77(1):66–74.

101.

- Weitzel CS, Li L, Zhang C, Eilts KK, Bretz NM, Gatten AL, et al. Duplication of leucyl-tRNA synthetase in an archaeal extremophile may play a role in adaptation to variable environmental conditions. *J Biol Chem*. 2020 Apr 3;295(14):4563–76. 102.
- Godinic-Mikulcic V, Jaric J, Greber BJ, Franke V, Hodnik V, Anderluh G, et al. Archaeal aminoacyl-tRNA synthetases interact with the ribosome to recycle tRNAs. *Nucleic Acids Res*. 2014 Apr 1;42(8):5191–201. 103.
- Banerjee A, Neiner T, Tripp P, Albers S-V. Insights into subunit interactions in the *Sulfolobus acidocaldarius* archaeal cytoplasmic complex. *The FEBS Journal*. 2013;280(23):6141–9. 104.
- McMillan LJ, Hwang S, Farah RE, Koh J, Chen S, Maupin-Furlow JA. Multiplex quantitative SILAC for analysis of archaeal proteomes: a case study of oxidative stress responses. *Environmental Microbiology*. 2018;20(1):385–401. 105.
- Kettenbach AN, Rush J, Gerber SA. Absolute quantification of protein and post-translational modification abundance with stable isotope-labeled synthetic peptides. *Nat Protoc*. 2011 Feb;6(2):175–86. 106.
- Kirkpatrick DS, Gerber SA, Gygi SP. The absolute quantification strategy: a general procedure for the quantification of proteins and post-translational modifications. *Methods*. 2005 Mar 1;35(3):265–73. 107.
- Kirkpatrick DS, Gerber SA, Gygi SP. The absolute quantification strategy: a general procedure for the quantification of proteins and post-translational modifications. *Methods*. 2005 Mar 1;35(3):265–73. 108.
- Martinez-Gomez NC, Palmer LD, Vivas E, Roach PL, Downs DM. The Rhodanese Domain of ThiI Is Both Necessary and Sufficient for Synthesis of the Thiazole Moiety of Thiamine in *Salmonella enterica*. *Journal of Bacteriology*. 2011 Sep 15;193(18):4582–7. 109.
- Wein S, Andrews B, Sachsenberg T, Santos-Rosa H, Kohlbacher O, Kouzarides T, et al. A computational platform for high-throughput analysis of RNA sequences and modifications by mass spectrometry. *Nature Communications*. 2020 Feb 17;11(1):926.

110.
Ross R, Cao X, Yu N, Limbach PA. Sequence mapping of transfer RNA chemical modifications by liquid chromatography tandem mass spectrometry. *Methods*. 2016 Sep 1;107:73–8.
111.
Heiss M, Reichle VF, Kellner S. Observing the fate of tRNA and its modifications by nucleic acid isotope labeling mass spectrometry: NAIL-MS. *RNA Biology*. 2017 Sep 2;14(9):1260–8.
112.
Kimura S, Dedon PC, Waldor MK. Surveying the landscape of tRNA modifications by combining tRNA sequencing and RNA mass spectrometry. *bioRxiv*. 2019 Aug 2;723049.
113.
Lin T-Y, Abbassi NEH, Zakrzewski K, Chramiec-Głębik A, Jemioła-Rzemińska M, Różycki J, et al. The Elongator subunit Elp3 is a non-canonical tRNA acetyltransferase. *Nature Communications*. 2019 Feb 7;10(1):1–12.
114.
Shen Y, Nar R, Fan AX, Aryan M, Hossain MA, Gurumurthy A, et al. Functional interrelationship between TFII-I and E2F transcription factors at specific cell cycle gene loci. *Journal of Cellular Biochemistry*. 2018;119(1):712–22.
115.
Miranda HV, Antelmann H, Hepowit N, Chavarria NE, Krause DJ, Pritz JR, et al. Archaeal Ubiquitin-like SAMP3 is Isopeptide-linked to Proteins via a UbaA-dependent Mechanism. *Molecular & Cellular Proteomics*. 2014 Jan 1;13(1):220–39.
116.
Hepowit NL, Vera IMS de, Cao S, Fu X, Wu Y, Uthandi S, et al. Mechanistic insight into protein modification and sulfur mobilization activities of noncanonical E1 and associated ubiquitin-like proteins of Archaea. *The FEBS Journal*. 2016;283(19):3567–86.
117.
Kravtsova-Ivantsiv Y, Sommer T, Ciechanover A. The Lysine48-Based Polyubiquitin Chain Proteasomal Signal: Not a Single Child Anymore. *Angewandte Chemie International Edition*. 2013;52(1):192–8.
118.
Ciechanover A, Ben-Saadon R. N-terminal ubiquitination: more protein substrates join in. *Trends in Cell Biology*. 2004 Mar 1;14(3):103–6.
- 119.

Streich FC, Lima CD. Structural and Functional Insights to Ubiquitin-Like Protein Conjugation. *Annual Review of Biophysics*. 2014;43(1):357–79.

120.

Schulman BA, Wade Harper J. Ubiquitin-like protein activation by E1 enzymes: the apex for downstream signalling pathways. *Nature Reviews Molecular Cell Biology*. 2009 May;10(5):319–31.

121.

Martins WC, Tasca CI, Cimarosti H. Battling Alzheimer's Disease: Targeting SUMOylation-Mediated Pathways. *Neurochem Res*. 2016 Mar 1;41(3):568–78.

122.

Han Z-J, Feng Y-H, Gu B-H, Li Y-M, Chen H. The post-translational modification, SUMOylation, and cancer (Review). *International Journal of Oncology*. 2018 Apr 1;52(4):1081–94.

123.

Nabavi SF, Atanasov AG, Khan H, Barreca D, Trombetta D, Testai L, et al. Targeting ubiquitin-proteasome pathway by natural, in particular polyphenols, anticancer agents: Lessons learned from clinical trials. *Cancer Letters*. 2018 Oct 10;434:101–13.

124.

Zheng Q, Huang T, Zhang L, Zhou Y, Luo H, Xu H, et al. Dysregulation of Ubiquitin-Proteasome System in Neurodegenerative Diseases. *Front Aging Neurosci* [Internet]. 2016 [cited 2020 Mar 31];8. Available from: <https://www.frontiersin.org/articles/10.3389/fnagi.2016.00303/full>

125.

Lachiondo-Ortega S, Mercado-Gómez M, Serrano-Maciá M, Lopitz-Otsoa F, Salas-Villalobos TB, Varela-Rey M, et al. Ubiquitin-Like Post-Translational Modifications (Ubl-PTMs): Small Peptides with Huge Impact in Liver Fibrosis. *Cells*. 2019 Dec;8(12):1575.

126.

Herrmann Joerg, Lerman Lilach O., Lerman Amir. Ubiquitin and Ubiquitin-Like Proteins in Protein Regulation. *Circulation Research*. 2007 May 11;100(9):1276–91.

127.

Seeler J-S, Dejean A. SUMO and the robustness of cancer. *Nature Reviews Cancer*. 2017 Mar;17(3):184–97.

128.

Dimopoulos MA, Goldschmidt H, Niesvizky R, Joshua D, Chng W-J, Oriol A, et al. Carfilzomib or bortezomib in relapsed or refractory multiple myeloma

(ENDEAVOR): an interim overall survival analysis of an open-label, randomised, phase 3 trial. *The Lancet Oncology*. 2017 Oct 1;18(10):1327–37.

129.

Termathe M, Leidel SA. The Uba4 domain interplay is mediated via a thioester that is critical for tRNA thiolation through Urm1 thiocarboxylation. *Nucleic Acids Res*. 2018 Jun 1;46(10):5171–81.

130.

Jüdes A, Bruch A, Klassen R, Helm M, Schaffrath R. Sulfur transfer and activation by ubiquitin-like modifier system Uba4•Urm1 link protein urmylation and tRNA thiolation in yeast. *Microb Cell*. 2016 Oct 24;3(11):554–64.

131.

Charan M, Singh N, Kumar B, Srivastava K, Siddiqi MI, Habib S. Sulfur Mobilization for Fe-S Cluster Assembly by the Essential SUF Pathway in the *Plasmodium falciparum* Apicoplast and Its Inhibition. *Antimicrobial Agents and Chemotherapy*. 2014 Jun 1;58(6):3389–98.

132.

Leimkühler S, Bühning M, Beilschmidt L. Shared Sulfur Mobilization Routes for tRNA Thiolation and Molybdenum Cofactor Biosynthesis in Prokaryotes and Eukaryotes. *Biomolecules*. 2017 Mar;7(1):5.

133.

Bruch A, Klassen R, Schaffrath R. Unfolded Protein Response Suppression in Yeast by Loss of tRNA Modifications. *Genes (Basel)*. 2018 Oct 23;9(11).

134.

McLennan AG. The Nudix hydrolase superfamily. *Cell Mol Life Sci*. 2006 Jan 1;63(2):123–43.

135.

Trotman JB, Schoenberg DR. A recap of RNA recapping. *WIREs RNA*. 2019;10(1):e1504.

136.

Villahermosa D, Fleck O. Elp3 and Dph3 of *Schizosaccharomyces pombe* mediate cellular stress responses through tRNA^{Lys} UUU modifications. *Sci Rep*. 2017 Dec;7(1):7225.

137.

Lin T-Y, Abbassi NEH, Zakrzewski K, Chramiec-Głąbik A, Jemioła-Rzemińska M, Różycki J, et al. The Elongator subunit Elp3 is a non-canonical tRNA acetyltransferase. *Nature Communications*. 2019 Feb 7;10(1):1–12.

138.
Bento-Abreu A, Jager G, Swinnen B, Rué L, Hendrickx S, Jones A, et al. Elongator subunit 3 (ELP3) modifies ALS through tRNA modification. *Hum Mol Genet.* 2018 Apr 1;27(7):1276–89.
139.
Jüttner M, Weiß M, Ostheimer N, Reglin C, Kern M, Knüppel R, et al. A versatile cis-acting element reporter system to study the function, maturation and stability of ribosomal RNA mutants in archaea. *Nucleic Acids Research.* 2019 Dec 12;gkz1156.
140.
Miranda HV, Antelmann H, Hepowit N, Chavarria NE, Krause DJ, Pritz JR, et al. Archaeal Ubiquitin-like SAMP3 is Isopeptide-linked to Proteins via a UbaA-dependent Mechanism. *Molecular & Cellular Proteomics.* 2014 Jan 1;13(1):220–39.
141.
Cao S, Hepowit N, Maupin-Furlow JA. Ubiquitin-Like Protein SAMP1 and JAMM/MPN+ Metalloprotease HvJAMM1 Constitute a System for Reversible Regulation of Metabolic Enzyme Activity in Archaea. *PLOS ONE.* 2015 May 26;10(5):e0128399.
142.
Chavarria NE, Hwang S, Cao S, Fu X, Holman M, Elbanna D, et al. Archaeal Tuc1/Ncs6 Homolog Required for Wobble Uridine tRNA Thiolation Is Associated with Ubiquitin-Proteasome, Translation, and RNA Processing System Homologs. *PLOS ONE.* 2014 Jun 6;9(6):e99104.
143.
Eichler J, Maupin-Furlow J. Post-translation modification in Archaea: lessons from *Haloferax volcanii* and other haloarchaea. *FEMS Microbiol Rev.* 2013 Jul 1;37(4):583–606.
144.
Babski J, Haas KA, Näther-Schindler D, Pfeiffer F, Förstner KU, Hammelmann M, et al. Genome-wide identification of transcriptional start sites in the haloarchaeon *Haloferax volcanii* based on differential RNA-Seq (dRNA-Seq). *BMC Genomics.* 2016 Aug 12;17(1):629.
145.
Stroud A, Liddell S, Allers T. Genetic and Biochemical Identification of a Novel Single-Stranded DNA-Binding Complex in *Haloferax volcanii*. *Front Microbiol* [Internet]. 2012 [cited 2019 Dec 2];3. Available from: <https://www.frontiersin.org/articles/10.3389/fmicb.2012.00224/full>
- 146.

Rhodanese-Like Domain Protein UbaC and Its Role in Ubiquitin-Like Protein Modification and Sulfur Mobilization in Archaea | Journal of Bacteriology [Internet]. [cited 2019 Dec 2]. Available from: <https://jb.asm.org/content/201/15/e00254-19.abstract>

147.

Zafrilla B, Martínez-Espinosa RM, Esclapez J, Pérez-Pomares F, Bonete MJ. SufS protein from *Haloferax volcanii* involved in Fe-S cluster assembly in haloarchaea. *Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics*. 2010 Jul 1;1804(7):1476–82.

148.

Heyer R, Dörr M, Jellen-Ritter A, Späth B, Babski J, Jaschinski K, et al. High throughput sequencing reveals a plethora of small RNAs including tRNA derived fragments in *Haloferax volcanii*. *RNA Biology*. 2012 Jul 1;9(7):1011–8.

149.

Soppa J, Straub J, Brenneis M, Jellen-Ritter A, Heyer R, Fischer S, et al. Small RNAs of the halophilic archaeon *Haloferax volcanii*. *Biochem Soc Trans*. 2009 Feb 1;37(1):133–6.

150.

Chimileski S, Dolas K, Naor A, Gophna U, Papke RT. Extracellular DNA metabolism in *Haloferax volcanii*. *Front Microbiol* [Internet]. 2014 [cited 2019 Dec 2];5. Available from: <https://www.frontiersin.org/articles/10.3389/fmicb.2014.00057/full>

151.

Warner MD, Lukose V, Lee KH, Lopez K, H. Sazinsky M, Crane EJ. Characterization of an NADH-Dependent Persulfide Reductase from *Shewanella loihica* PV-4: Implications for the Mechanism of Sulfur Respiration via FAD-Dependent Enzymes., *Biochemistry*. 2011 Jan 18;50(2):194–206.

152.

Biondi E, Burke DH. Separating and Analyzing Sulfur-Containing RNAs with Organomercury Gels. In: Jin H, Gassmann W, editors. *RNA Abundance Analysis: Methods and Protocols* [Internet]. Totowa, NJ: Humana Press; 2012 [cited 2019 Oct 29]. p. 111–20. (Methods in Molecular Biology). Available from: https://doi.org/10.1007/978-1-61779-839-9_8

153.

Allers T, Barak S, Liddell S, Wardell K, Mevarech M. Improved Strains and Plasmid Vectors for Conditional Overexpression of His-Tagged Proteins in *Haloferax volcanii*. *Applied and Environmental Microbiology*. 2010 Mar 15;76(6):1759–69.

154.

Hepowit NL, Maupin-Furlow JA. Rhodanese-Like Domain Protein UbaC and Its Role in Ubiquitin-Like Protein Modification and Sulfur Mobilization in Archaea. *Journal of Bacteriology*. 2019 Aug 1;201(15):e00254-19.

155.

Nadler WM, Waidelich D, Kerner A, Hanke S, Berg R, Trumpp A, et al. MALDI versus ESI: The Impact of the Ion Source on Peptide Identification. *J Proteome Res*. 2017 Mar 3;16(3):1207–15.

156.

Matthies A, Nimtz M, Leimkühler S. Molybdenum Cofactor Biosynthesis in Humans: Identification of a Persulfide Group in the Rhodanese-like Domain of MOCS3 by Mass Spectrometry †. *Biochemistry*. 2005 May;44(21):7912–20.

157.

Longen S, Richter F, Köhler Y, Wittig I, Beck K-F, Pfeilschifter J. Quantitative Persulfide Site Identification (qPerS-SID) Reveals Protein Targets of H₂S Releasing Donors in Mammalian Cells. *Sci Rep*. 2016 Sep;6(1):29808.

158.

Miranda HV, Nembhard N, Su D, Hepowit N, Krause DJ, Pritz JR, et al. E1- and ubiquitin-like proteins provide a direct link between protein conjugation and sulfur transfer in archaea. *PNAS*. 2011 Mar 15;108(11):4417–22.

159.

Biondi E, Burke DH. Separating and Analyzing Sulfur-Containing RNAs with Organomercury Gels. In: Jin H, Gassmann W, editors. *RNA Abundance Analysis: Methods and Protocols* [Internet]. Totowa, NJ: Humana Press; 2012 [cited 2019 Apr 23]. p. 111–20. (Methods in Molecular Biology). Available from: https://doi.org/10.1007/978-1-61779-839-9_8

160.

Matthies A, Rajagopalan KV, Mendel RR, Leimkuhler S. Evidence for the physiological role of a rhodanese-like protein for the biosynthesis of the molybdenum cofactor in humans. *Proceedings of the National Academy of Sciences*. 2004 Apr 20;101(16):5946–51.

161.

Bell SD. Initiating DNA replication: a matter of prime importance. *Biochemical Society Transactions*. 2019 Feb 28;47(1):351–6.

162.

Maupin-Furlow J. Proteasomes and protein conjugation across domains of life. *Nature Reviews Microbiology*. 2012 Feb;10(2):100–11.

163.

Allers T, Ngo H-P, Mevarech M, Lloyd RG. Development of Additional Selectable Markers for the Halophilic Archaeon *Haloferax volcanii* Based on the *leuB* and *trpA* Genes. *Appl Environ Microbiol.* 2004 Feb 1;70(2):943–53.

164.

Hepowit NL, Vera IMS de, Cao S, Fu X, Wu Y, Uthandi S, et al. Mechanistic insight into protein modification and sulfur mobilization activities of noncanonical E1 and associated ubiquitin-like proteins of Archaea. *The FEBS Journal.* 2016;283(19):3567–86.

165.

Humbard MA, Miranda HV, Lim J-M, Krause DJ, Pritz JR, Zhou G, et al. Ubiquitin-like small archaeal modifier proteins (SAMPs) in *Haloferax volcanii*. *Nature.* 2010 Jan;463(7277):54–60.

166.

Fu X, Liu R, Sanchez I, Silva-Sanchez C, Hepowit NL, Cao S, et al. Ubiquitin-Like Proteasome System Represents a Eukaryotic-Like Pathway for Targeted Proteolysis in Archaea. *mBio.* 2016 Jul 6;7(3):e00379-16.

167.

Costa MI, Cerletti M, Paggi RA, Trötschel C, De Castro RE, Poetsch A, et al. *Haloferax volcanii* Proteome Response to Deletion of a Rhomboid Protease Gene. *J Proteome Res.* 2018 Mar 2;17(3):961–77.

168.

Allers T, Barak S, Liddell S, Wardell K, Mevarech M. Improved Strains and Plasmid Vectors for Conditional Overexpression of His-Tagged Proteins in *Haloferax volcanii*. *Appl Environ Microbiol.* 2010 Mar 15;76(6):1759–69.

169.

Stachler A-E, Marchfelder A. Gene Repression in Haloarchaea Using the CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)-Cas I-B System. *J Biol Chem.* 2016 Jul 15;291(29):15226–42.

170.

Zhou G, Kowalczyk D, Humbard MA, Rohatgi S, Maupin-Furlow JA. Proteasomal Components Required for Cell Growth and Stress Responses in the Haloarchaeon *Haloferax volcanii*. *Journal of Bacteriology.* 2008 Dec 15;190(24):8096–105.

171.

Seth-Pasricha M, Senn S, Sanman LE, Bogyo M, Nanda V, Bidle KA, et al. Catalytic linkage between caspase activity and proteostasis in Archaea. *Environmental Microbiology.* 2019;21(1):286–98.

172.

Eichler J, Maupin-Furlow J. Post-translation modification in Archaea: lessons from *Haloferax volcanii* and other haloarchaea. *FEMS Microbiol Rev.* 2013 Jul 1;37(4):583–606.

173.

Barthelme D, Chen JZ, Grabenstatter J, Baker TA, Sauer RT. Architecture and assembly of the archaeal Cdc48·20S proteasome. *PNAS.* 2014 Apr 29;111(17):E1687–94.

174.

Barthelme D, Sauer RT. Identification of the Cdc48·20S Proteasome as an Ancient AAA+ Proteolytic Machine. *Science.* 2012 Aug 17;337(6096):843–6.

175.

Barthelme D, Sauer RT. Origin and Functional Evolution of the Cdc48/p97/VCP AAA+ Protein Unfolding and Remodeling Machine. *Journal of Molecular Biology.* 2016 May 8;428(9, Part B):1861–9.