

# Thorsten Allers

## List of Publications by Year in descending order

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53  
papers

3,804  
citations

172207

29  
h-index

189595

50  
g-index

55  
all docs

55  
docs citations

55  
times ranked

2671  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cas1 and Fen1 Display Equivalent Functions During Archaeal DNA Repair. <i>Frontiers in Microbiology</i> , 2022, 13, 822304.	1.5	3
2	The lanthipeptide biosynthetic clusters of the domain Archaea. <i>Microbiological Research</i> , 2021, 253, 126884.	2.5	9
3	<i>Haloferax volcanii</i> for biotechnology applications: challenges, current state and perspectives. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 1371-1382.	1.7	38
4	Adaptation induced by self-targeting in a type I-B CRISPR-Cas system. <i>Journal of Biological Chemistry</i> , 2020, 295, 13502-13515.	1.6	6
5	SnapShot: Microbial Extremophiles. <i>Cell</i> , 2020, 180, 818-818.e1.	13.5	26
6	<i>Haloferax volcanii</i> – a model archaeon for studying DNA replication and repair. <i>Open Biology</i> , 2020, 10, 200293.	1.5	16
7	Characterisation of a solvent-tolerant haloarchaeal (R)-selective transaminase isolated from a Triassic period salt mine. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 5727-5737.	1.7	15
8	Cyclic nucleotides in archaea: Cyclic diAMP in the archaeon <i>Haloferax volcanii</i> and its putative role. <i>MicrobiologyOpen</i> , 2019, 8, e00829.	1.2	32
9	<i>Haloferax volcanii</i> as immobilised whole cell biocatalyst: new applications for halophilic systems. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3807-3817.	1.7	17
10	Evolution of Genome Architecture in Archaea: Spontaneous Generation of a New Chromosome in <i>Haloferax volcanii</i> . <i>Molecular Biology and Evolution</i> , 2018, 35, 1855-1868.	3.5	19
11	Structural and functional adaptation of <i>Haloferax volcanii</i> TFE <sup>±</sup> /I <sup>2</sup> . <i>Nucleic Acids Research</i> , 2018, 46, 2308-2320.	6.5	7
12	DNA repair in the archaea – an emerging picture. <i>FEMS Microbiology Reviews</i> , 2018, 42, 514-526.	3.9	49
13	Cdc48a AAA-ATPase and its association with ubiquitin-like SAMP1 and DNA repair in Archaea. <i>FASEB Journal</i> , 2018, 32, 786.10.	0.2	0
14	High tolerance to self-targeting of the genome by the endogenous CRISPR-Cas system in an archaeon. <i>Nucleic Acids Research</i> , 2017, 45, 5208-5216.	6.5	44
15	RadB acts in homologous recombination in the archaeon <i>Haloferax volcanii</i> , consistent with a role as recombination mediator. <i>DNA Repair</i> , 2017, 55, 7-16.	1.3	10
16	Finally, Archaea Get Their CRISPR-Cas Toolbox. <i>Trends in Microbiology</i> , 2017, 25, 430-432.	3.5	13
17	Diversity of DNA Replication in the Archaea. <i>Genes</i> , 2017, 8, 56.	1.0	24
18	Production of halophilic proteins using <i>Haloferax volcanii</i> H1895 in a stirred-tank bioreactor. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 1183-1195.	1.7	21

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19	Deletion of the Sm1 encoding motif in the lsm gene results in distinct changes in the transcriptome and enhanced swarming activity of Haloferax cells. <i>Biochimie</i> , 2015, 117, 129-137.	1.3	27
20	A Complex of Cas Proteins 5, 6, and 7 Is Required for the Biogenesis and Stability of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-derived RNAs (crRNAs) in <i>Haloferax volcanii</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 7164-7177.	1.6	65
21	A comparison of two novel alcohol dehydrogenase enzymes (ADH1 and ADH2) from the extreme halophile <i>Haloferax volcanii</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 195-203.	1.7	42
22	Phylogenetic- and genome-derived insight into the evolution of N-glycosylation in Archaea. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 327-339.	1.2	53
23	Accelerated growth in the absence of DNA replication origins. <i>Nature</i> , 2013, 503, 544-547.	13.7	129
24	DNA damage induces nucleoid compaction via the Mre11-Rad50 complex in the archaeon <i>Haloferax volcanii</i> . <i>Molecular Microbiology</i> , 2013, 87, 168-179.	1.2	37
25	RecJ-like protein from <i>Pyrococcus furiosus</i> has 3' to 5' exonuclease activity on RNA: implications for proofreading of 3'-mismatched RNA primers in DNA replication. <i>Nucleic Acids Research</i> , 2013, 41, 5817-5826.	6.5	20
26	Genetic and Biochemical Identification of a Novel Single-Stranded DNA-Binding Complex in <i>Haloferax volcanii</i> . <i>Frontiers in Microbiology</i> , 2012, 3, 224.	1.5	43
27	Assigning a function to a conserved archaeal metallo- $\beta$ -lactamase from <i>Haloferax volcanii</i> . <i>Extremophiles</i> , 2012, 16, 333-343.	0.9	8
28	A Genetic Investigation of the KEOPS Complex in Halophilic Archaea. <i>PLoS ONE</i> , 2012, 7, e43013.	1.1	26
29	Swapping genes to survive - a new role for archaeal type IV pili. <i>Molecular Microbiology</i> , 2011, 82, 789-791.	1.2	8
30	Model organisms for genetics in the domain Archaea: methanogens, halophiles, <i>Thermococcales</i> and <i>Sulfolobales</i> . <i>FEMS Microbiology Reviews</i> , 2011, 35, 577-608.	3.9	197
31	The archaeal Xpf/Mus81/FANCM homolog Hef and the Holliday junction resolvase Hjc define alternative pathways that are essential for cell viability in <i>Haloferax volcanii</i> . <i>DNA Repair</i> , 2010, 9, 994-1002.	1.3	56
32	The Complete Genome Sequence of <i>Haloferax volcanii</i> DS2, a Model Archaeon. <i>PLoS ONE</i> , 2010, 5, e9605.	1.1	234
33	The Archaeal Lsm Protein Binds to Small RNAs. <i>Journal of Biological Chemistry</i> , 2010, 285, 34429-34438.	1.6	63
34	Overexpression and purification of halophilic proteins in <i>Haloferax volcanii</i> . <i>Bioengineered Bugs</i> , 2010, 1, 290-292.	2.0	31
35	Improved Strains and Plasmid Vectors for Conditional Overexpression of His-Tagged Proteins in <i>Haloferax volcanii</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 1759-1769.	1.4	181
36	Mre11-Rad50 Promotes Rapid Repair of DNA Damage in the Polyploid Archaeon <i>Haloferax volcanii</i> by Restraining Homologous Recombination. <i>PLoS Genetics</i> , 2009, 5, e1000552.	1.5	77

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37	Stabilization and Electrophoretic Analysis of Meiotic Recombination Intermediates in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2009, 557, 209-234.	0.4	52
38	RecA family proteins in archaea: RadA and its cousins. <i>Biochemical Society Transactions</i> , 2009, 37, 102-107.	1.6	58
39	Maturation of the 5S rRNA 5' end is catalyzed in vitro by the endonuclease tRNase Z in the archaeon <i>H. volcanii</i> . <i>Rna</i> , 2008, 14, 928-937.	1.6	36
40	Genetic and Physical Mapping of DNA Replication Origins in <i>Haloferax volcanii</i> . <i>PLoS Genetics</i> , 2007, 3, e77.	1.5	118
41	Characterization of a tightly controlled promoter of the halophilic archaeon <i>Haloferax volcanii</i> and its use in the analysis of the essential <i>cct1</i> gene. <i>Molecular Microbiology</i> , 2007, 66, 1092-1106.	1.2	94
42	Interactions of RadB, a DNA Repair Protein in Archaea, with DNA and ATP. <i>Journal of Molecular Biology</i> , 2006, 358, 46-56.	2.0	38
43	Regulated Polyploidy in Halophilic Archaea. <i>PLoS ONE</i> , 2006, 1, e92.	1.1	169
44	Archaeal genetics – the third way. <i>Nature Reviews Genetics</i> , 2005, 6, 58-73.	7.7	217
45	Infrequent Co-conversion of Markers Flanking a Meiotic Recombination Initiation Site in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2005, 169, 1353-1367.	1.2	74
46	Genetic and physical mapping of DNA replication origins in <i>Haloferax volcanii</i> . <i>PLoS Genetics</i> , 2005, preprint, e77.	1.5	0
47	Development of Additional Selectable Markers for the Halophilic Archaeon <i>Haloferax volcanii</i> Based on the <i>leuB</i> and <i>trpA</i> Genes. <i>Applied and Environmental Microbiology</i> , 2004, 70, 943-953.	1.4	375
48	New enzymes, new mechanisms?: DNA repair by recombination in the Archaea. <i>Biochemist</i> , 2004, 26, 19-21.	0.2	0
49	Genetic analysis of homologous recombination in Archaea: <i>Haloferax volcanii</i> as a model organism. <i>Biochemical Society Transactions</i> , 2003, 31, 706-710.	1.6	33
50	Intermediates of Yeast Meiotic Recombination Contain Heteroduplex DNA. <i>Molecular Cell</i> , 2001, 8, 225-231.	4.5	137
51	Differential Timing and Control of Noncrossover and Crossover Recombination during Meiosis. <i>Cell</i> , 2001, 106, 47-57.	13.5	657
52	A method for preparing genomic DNA that restrains branch migration of Holliday junctions. <i>Nucleic Acids Research</i> , 2000, 28, 6e-6.	6.5	78
53	DNA Palindromes Adopt a Methylation-resistant Conformation that is Consistent with DNA Cruciform or Hairpin Formation in Vivo. <i>Journal of Molecular Biology</i> , 1995, 252, 70-85.	2.0	22