

**Dr. Christian H. Ahrens**

Senior Scientist Genomics &amp; Bioinformatics

Group Leader SIB Swiss Institute of Bioinformatics: <http://www.isb-sib.ch/ahrens-christian/>Federal Department of Economic Affairs,  
Education and Research EAER**Agroscope**

Methods Development &amp; Analytics

Müller-Thurgau-Str. 29, 8820 Wädenswil, Switzerland

Phone: +41 58 460 6114

Email: christian.ahrens@agroscope.admin.ch

Fax: +41 58 460 6341

**Publications****Status: September 2021****Peer-reviewed articles (original publications)**

\* = equal contribution / # = co-corresponding author / IF = Impact factor (basis: Journal Citation Report)

76. C.H. Ahrens<sup>#</sup>, J.T. Wade<sup>#</sup>, M.C. Champion<sup>#</sup>, J.D. Langer<sup>#</sup>. A Practical Guide to Small Protein Discovery and Characterization using Mass Spectrometry. **J Bacteriol.** 2021, *in press*. (IF 3.2)
75. J. Mayerhofer, B. Thuerig, T. Oberhaensli, E. Enderle, S. Lutz, C.H. Ahrens, J.G. Fuchs, F. Widmer. Indicative bacterial communities and taxa of disease suppressing and growth promoting composts and their associations to the rhizoplane. **FEMS Microbiol Ecol.** 2021, 97(10). doi: 10.1093/femsec/fiab134. (IF 3.7)
74. M.P. Rueda-Mejia, L. Nägeli, S. Lutz, R.D. Hayes, A.R. Varadarajan, I.V. Grigoriev, C.H. Ahrens, F.M. Freimoser. Genome, transcriptome and secretome analyses of the antagonistic, yeast-like fungus *Aureobasidium pullulans* to identify potential biocontrol genes. **Microb Cell.** 2021, 8:184-202. (IF 4.0)
73. S. Hug, Y. Liu, B. Heiniger, A. Bailly, C.H. Ahrens, L. Eberl, G. Pessi. Differential Expression of *Paraburkholderia phymatum* Type VI Secretion Systems (T6SS) Suggests a Role of T6SS-b in Early Symbiotic Interaction. **Front Plant Sci.** 2021, 12:699590. (IF 5.7).
72. S. Fuchs, M. Kucklick, E. Lehmann, A. Beckmann, M. Wilkens, B. Kolte, A. Mustafayeva, T. Ludwig, M. Diwo, J. Wissing, L. Jänsch, C.H. Ahrens, Z. Ignatova, S. Engelmann. Towards the characterization of the hidden world of small proteins in *Staphylococcus aureus*, a proteogenomics approach. **PLoS Genet.** 2021, 17:e1009585. (IF 5.5)
71. H. Petruschke\*, C. Schori\*, S. Canzler, S. Riesbeck, A. Poehlein, R. Daniel, D. Frei, T. Segessemann, J. Zimmerman, G. Marinos, C. Kaleta, N. Jehmlich, C.H. Ahrens<sup>\*\*</sup>, M. von Bergen<sup>\*\*</sup>. Discovery of novel community-relevant small proteins in a simplified human intestinal microbiome. **Microbiome.** 2021, 9:55 (IF 13.6).
70. A.R. Varadarajan, R.N. Allan, J.D.P. Valentin, O.E. Castaneda Ocampo, V. Somerville, F. Pietsch, M.T. Buhmann, J. West, P.J. Skipp, H.C. van der Mei, Q. Ren, F. Schreiber, J.S. Webb, C.H. Ahrens. An integrated model system to gain mechanistic insights into biofilm-associated antimicrobial resistance in *Pseudomonas aeruginosa* MPAO1. **NPJ Biofilms and Microbiomes.** 2020, 6:46. (IF 7.1)
69. G.D. Koutsovoulos, M. Pouillet, A. Elshahry, D.K.L. Kozlowski, E. Sallet, M. Da Rocha, L. Perfus-Barbeoch, C. Martin-Jimenez, J.E. Frey, C.H. Ahrens, S. Kiewnick, E.G.J. Danchin. Genome assembly and annotation of *Meloidogyne enterolobii*, an emerging parthenogenetic root-knot nematode. **Sci Data.** 2020, 7:324. (IF 5.5)

67. S. Lutz, B. Thuerig, T. Oberhaensli, J. Mayerhofer, J.G. Fuchs, F. Widmer, F.M. Freimoser, C.H. Ahrens. Harnessing the Microbiomes of Suppressive Composts for Plant Protection: From Metagenomes to Beneficial Microorganisms and Reliable Diagnostics. **Front Microbiol.** 2020, 11:1810. (IF 4.1)
66. J. Bartel, A.R. Varadarajan, T. Sura, C.H. Ahrens, S. Maass, D. Becher. Optimized proteomics workflow for the detection of small proteins. **J Prot Res.** 2020, 19:4004-4018. (IF 4.3)
65. O.N. Reva, S.A. Larisa, A.D. Mwakilili, D. Tibuhwa, S. Lyantagaye, W.Y. Chan, S. Lutz, C.H. Ahrens, J. Vater, R. Borriss. Complete genome sequence and epigenetic profile of *Bacillus velezensis* UCMB5140 used for plant and crop protection in comparison with other plant-associated *Bacillus* strains. **Appl Microbiol Biotechnol.** 2020, 104:7643-7656. (IF 3.7)
64. H. Melior, S. Maass, S. Li, K.U. Förstner, S. Azarderakhsh, A.R. Varadarajan, M. Stötzel, M. Elhossary, S. Barth-Weber, C.H. Ahrens, D. Becher, E. Evgenieva-Hackenberg. The leader peptide peTrpL forms antibiotic-containing ribonucleoprotein complexes for posttranscriptional regulation of multiresistance genes. **mBio.** 2020, 11:e01027-20. (IF 6.8)
63. M. De Vrieze\*, A.R. Varadarajan\*, K. Schneeberger, A. Bailly, R.P. Rohr, C.H. Ahrens<sup>#\*</sup>, L. Weisskopf<sup>#\*</sup>. Linking comparative genomics of nine potato-associated *Pseudomonas* isolates with their differing biocontrol potential against late blight. **Front Microbiol.** 2020, 11:857. (IF 4.1)
62. A.R. Varadarajan\*, S. Goetze\*, M.P. Pavlou\*, V. Grosboillot, Y. Shen, M.J. Loessner, C.H. Ahrens<sup>#\*</sup>, B. Wollscheid<sup>#\*</sup>. A proteogenomic resource enabling integrated analysis of *Listeria* genotype-proteotype-phenotype relationships. **J Prot Res.** 2020, 19:1647-1662. (IF 4.3)
61. O.N. Reva, D.Z.H. Swanevelder, L. Mwita, A.D. Mwakilili, D. Muzondiwa, M. Joubert, W-Y. Chan, S. Lutz, C.H. Ahrens, L.V. Avdeeva, M.A. Kharkhota, D. Tibuhwa, S. Lyantagaye, J. Vater, R. Borriss, J. Meijer. Genetic, epigenetic and phenotypic diversity of four *Bacillus velezensis* strains used for plant protection or as probiotics. **Front Microbiol.** 2019, 10:2610. (IF 4.1)
60. V. Somerville, S. Lutz, M. Schmid, D. Frei, A. Moser, S. Irmiler, J.E. Frey, C.H. Ahrens. Long-read based *de novo* assembly of low-complexity metagenome samples results in finished genomes and reveals insights into strain diversity and an active phage system. **BMC Microbiol.** 2019, 19:143. (IF 2.8)
59. N. Fernández\*, J.J. Cabrera\*, A.R. Varadarajan\*, S. Lutz, R. Ledermann, B. Roschitzki, L. Eberl, H.-M. Fischer, G. Pessi, C.H. Ahrens<sup>#</sup>, S. Mesa<sup>#</sup>. An Integrated Systems Approach Unveils New Aspects of Microoxia-Mediated Regulation in *Bradyrhizobium diazoefficiens*. **Front Microbiol.** 2019, 10:924. (IF 4.1)
58. D. Gore-Lloyd\*, I. Sumann\*, A.O. Brachmann, K. Schneeberger, R.A. Ortiz-Merino, M. Moreno-Beltrán, M. Schläfli, P. Kirner, A. Santos Kron, M.P. Rueda-Mejia, V. Somerville, K.H. Wolfe, J. Piel, C.H. Ahrens, D. Henk\*, F.M. Freimoser\*. Snf2 controls pulcherriminic acid biosynthesis and antifungal activity of the biocontrol yeast *Metschnikowia pulcherrima*. **Mol Microbiol.** 2019, 112:317-332. (IF 3.8)
57. M. Schmid, D. Frei, A. Patrignani, R. Schlapbach, J.E. Frey, M.N.P. Remus-Emsermann, C.H. Ahrens. Pushing the limits of *de novo* genome assembly for complex prokaryotic genomes harboring very long, near identical repeats. **Nucleic Acids Res.** 2018, 46, 8953-8965. (IF 10.2)
56. M. Lardi, Y. Liu, G. Giudice, C.H. Ahrens, N. Zamboni, G. Pessi. Metabolomics and Transcriptomics Identify Multiple Downstream Targets of *Paraburkholderia phymatum*  $\sigma$ 54 During Symbiosis with *Phaseolus vulgaris*. **Int J Mol Sci.** 2018, 19, 1049. (IF 3.2)
55. S. Huntscha, M.A. Stravs, A. Bühlmann, C.H. Ahrens, J.E. Frey, F. Pomati, J. Hollender, I.J. Buerge, M.E. Balmer, T. Poiger. Seasonal Dynamics of Glyphosate and AMPA in Lake Greifensee: Rapid Microbial Degradation in the Epilimnion During Summer. **Environ Sci Technol.** 2018, 52, 4641-4649. (IF 6.2)
54. M. Schmid, J. Muri, D. Melidis, A.R. Varadarajan, V. Somerville, A. Wicki, A. Moser, M. Bourqui, C. Wenzel, E. Eugster-Meier, J.E. Frey, S. Irmiler, C.H. Ahrens. Comparative genomics of completely sequenced *Lactobacillus helveticus* genomes provides insights into strain-specific genes and resolves metagenomics data down to the strain level. **Front Microbiol.** 2018, 9:63. (IF 4.1)
53. V. Zengerer, M. Schmid, B. Marco, D.C. Müller, M.N.P. Remus-Emsermann, C.H. Ahrens, C. Pelludat. *Pseudomonas orientalis* F9: a potent antagonist against phytopathogens with phytotoxic effect in the apple flower. **Front Microbiol.** 2018, 9:145. (IF 4.1)

52. U. Omasits, A.R. Varadarajan, M. Schmid, S. Goetze, D. Melidis, M. Bourqui, O. Nikolayeva, M. Quebatte, A. Patrignani, C. Dehio, J.E. Frey, M.D. Robinson, B. Wollscheid, C.H. Ahrens. An integrative strategy to identify the entire protein coding potential of prokaryotic genomes by proteogenomics. **Genome Res.** 2017, 27(12): 2083 -2095. (IF 11.9)
51. R. Marti, M. Schmid, S. Kulli, K. Schneeberger, J. Naskova, S. Knöchel, C.H. Ahrens, J. Hummerjohann. Biofilm Formation Potential of Heat Resistant *Escherichia coli* Dairy Isolates and Complete Genome of MDR Heat Resistant Strain FAM21845. **Appl Environ Microbiol.** 2017, 83(15): e00628-17. (IF 3.8)
50. D. Montes Vidal, A.L. von Rymon-Lipinski, S. Ravella, U. Groenhagen, J. Herrmann, N. Zaburanyi, P.H. Zarbin, A.R. Varadarajan, C.H. Ahrens, L. Weisskopf, R. Müller, S. Schulz. Long-Chain Alkyl Cyanides: Unprecedented Volatile Compounds Released by *Pseudomonas* and *Micromonospora* Bacteria. **Angew Chem Int Ed Engl.** 2017, 56(15):4342-4346. (IF 12.0)
49. M. Hilber-Bodmer, M. Schmid, C.H. Ahrens, F.M. Freimoser. Competition assays and physiological experiments of soil and phyllosphere yeasts identify *Candida subhashii* as a novel antagonist of filamentous fungi. **BMC Microbiol.** 2017, 17(1):4. (IF 2.6)
48. M.N.P. Remus-Emsermann, M. Schmid, M.T. Gekenidis, C. Pelludat, J.E. Frey, C.H. Ahrens<sup>#</sup>, D. Drissner<sup>#</sup>. Complete genome sequence of *Pseudomonas citronellolis* P3B5, a candidate for microbial phyllo-remediation of hydrocarbon-contaminated sites. **Stand Genomic Sci.** 2016, 11: 75. (IF 1.2)
47. R. Marti, M. Muniesa, M. Schmid, C.H. Ahrens, J. Naskova, J. Hummerjohann. Short communication: Heat-resistant *Escherichia coli* as potential persistent reservoir of extended-spectrum  $\beta$ -lactamases and Shiga toxin-encoding phages in dairy. **J Dairy Sci.** 2016, 99(11):8622-8632. (IF 2.4)
46. M. Lardi, V. Murset, H.M. Fischer, S. Mesa, C.H. Ahrens, N. Zamboni, G. Pessi. Metabolomic Profiling of *Bradyrhizobium diazoefficiens*-Induced Root Nodules Reveals Both Host Plant-Specific and Developmental Signatures. **Int J Mol Sci.** 2016, 17(6), 815. (IF 3.2)
45. J. Čuklina, J. Hahn, M. Imakaev, U. Omasits, K.U. Förstner, N. Ljubimov, M. Goebel, G. Pessi, H.M. Fischer, C.H. Ahrens<sup>#</sup>, M.S. Gelfand, E. Evgenieva-Hackenberg. Genome-wide transcription start site mapping of *Bradyrhizobium japonicum* grown free-living or in symbiosis - a rich resource to identify new transcripts, proteins and to study gene regulation. **BMC Genomics.** 2016, 17:302. (IF 3.7)
44. L. Turnbull, M. Toyofuku, A.L. Hynen, M. Kurosawa, G. Pessi, N.K. Petty, S.R. Osvath, G. Cárcamo-Oyarce, E.S. Gloag, R. Shimoni, U. Omasits, S. Ito, X. Yap, L.G. Monahan, R. Cavaliere, C.H. Ahrens, I.G. Charles, N. Nomura, L. Eberl, C.B. Whitchurch. Explosive cell lysis as a mechanism for the biogenesis of bacterial membrane vesicles and biofilms. **Nat Commun.** 2016, 7:11220. (IF 12.1)
43. M. Urfer, J. Bogdanovic, F. Lo Monte, K. Moehle, K. Zerbe, U. Omasits, C.H. Ahrens, G. Pessi, L. Eberl, J.A. Robinson. A peptidomimetic antibiotic targets outer membrane proteins and disrupts selectively the outer membrane in *Escherichia coli*. **J Biol Chem.** 2016, 291:1921-1932. (IF 4.1)
42. SIB Swiss Institute of Bioinformatics Members. The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. **Nucleic Acids Res.** 2016, 44:D27-37. (IF 10.2)
41. M. De Vrieze, P. Pandey, T. Bucheli, A.R. Varadarajan, C.H. Ahrens, L. Weisskopf, A. Bailly. Volatile organic compounds from native potato-associated *Pseudomonas* as potential anti-oomycete agents. **Front Microbiol.** 2015, 6:1295. (IF 4.1)
40. M. Lardi, C. Aguilar, A. Pedrioli, U. Omasits, A. Suppiger, G. Cárcamo-Oyarce, N. Schmid, C.H. Ahrens, L. Eberl\*, G. Pessi\*.  $\sigma^{54}$ -dependent response to nitrogen limitation and virulence in *Burkholderia cenocepacia* H111. **Appl Environ Microbiol.** 2015, 81:4077-4089. (IF 3.8)
39. E. Qeli\*, U. Omasits\*, S. Götze, D.J. Stekhoven, J.E. Frey, K. Basler, B. Wollscheid, E. Brunner, C.H. Ahrens. Improved prediction of peptide detectability for targeted proteomics using a rank-based algorithm and organism-specific data. **J Proteomics.** 2014, 108:269-283. (IF 3.9)
38. D.J. Stekhoven\*, U. Omasits\*, M. Quebatte, C. Dehio, C.H. Ahrens. Proteome-wide identification of predominant subcellular protein localizations in a bacterial model organism. **J Proteomics.** 2014, 99:123-137. (IF 3.9)

37. M. Koch, C.H. Ahrens\*, N. Delmotte\*, U. Omasits, F. Danza, B. Padhi, V. Murset, O. Braissant, J.A. Vorholt, H. Hennecke, G. Pessi. A link between arabinose utilization and oxalotrophy in *Bradyrhizobium japonicum*. **Appl Environ Microbiol.** 2014, 80:2094-2101. (IF 3.8)
36. U. Omasits, C.H. Ahrens, S. Müller, B. Wollscheid. Protter: interactive protein feature visualization and integration with experimental proteomic data. **Bioinformatics.** 2014, 30:884-886. (IF 7.3)
35. G. Pessi, R. Braunwalder, A. Grunau, U. Omasits, C.H. Ahrens, L. Eberl. Reponse of *Burkholderia cenocepacia* H111 to Micro-Oxia. **PLoS One.** 2013; 8:e72939. (IF 2.8)
34. A. Carlier, U. Omasits, C.H. Ahrens, L. Eberl. Proteomics analysis of *Psychotria* leaf nodule symbiosis: Improved genome annotation and metabolic predictions. **Mol Plant Microbe Interact.** 2013; 26:1325-1333. (IF 4.3)
33. U. Omasits, M. Quebatte, D. Stekhoven, C. Fortes, B. Roschitzki, M.D. Robinson, C. Dehio, C.H. Ahrens. Directed shotgun proteomics guided by saturated RNA-Seq identifies a complete expressed prokaryotic proteome. **Genome Res.** 2013; 23:1916-1927. (IF 11.9)
32. B. Handke, I. Poernbacher, S. Goetze, C.H. Ahrens, U. Omasits, F. Marty, N. Simigdala, I. Meyer, B. Wollscheid, E. Brunner, E. Hafen, C.F. Lehner. The hemolymph proteome of fed and starved *Drosophila* larvae. **PLoS One.** 2013; 20; 8:e67208. (IF 2.8)
31. N. Schmid, G. Pessi, C. Aguilar, Y. Deng, A.L. Carlier, A. Grunau, U. Omasits, L.H. Zhang, C.H. Ahrens, L. Eberl. The AHL- and BDSF-dependent Quorum Sensing Systems control specific and overlapping sets of genes in *Burkholderia cenocepacia* H111. **PLoS One.** 2012; 7:e49966. (IF 2.8)
30. Y. Deng, N. Schmid, C. Wang, J. Wang, G. Pessi, D. Wu, J. Lee, C. Aguilar, C.H. Ahrens, C. Chang, H. Song, L. Eberl, L.-H. Zhang. Cis-2-dodecenoic acid receptor RpfR links quorum-sensing signal perception with regulation of virulence through cyclic dimeric guanosine monophosphate turnover. **Proc Natl Acad Sci USA.** 2012; 109:15479-15484. (IF 9.7)
29. A. Cammarato, C.H. Ahrens, N.N. Alayari, E. Qeli, J. Rucker, M.C. Reedy, C.M. Zmasek, M. Gucek, R.N. Cole, J.E Van Eyk, R. Bodmer, B. O'Rourke, S.I. Bernstein, D.B. Foster. A mighty small heart: the cardiac proteome of adult *Drosophila melanogaster*. **PLoS One.** 2011; 6:e18497. (IF 2.8)
28. S. Gerster, E. Qeli, C.H. Ahrens, P. Bühlmann. Protein and gene model inference based on statistical modeling in k-partite graphs. **Proc Natl Acad Sci USA.** 2010; 107:12101-12106. (IF 9.7)
27. E. Qeli and C.H. Ahrens. PeptideClassifier for protein inference and targeted quantitative proteomics. **Nat Biotechnol.** 2010; 27:647-650. (IF 41.7)
26. C.H. Ahrens, E. Brunner, K. Basler. Quantitative proteomics: An essential technology for systems biology. **J Proteomics.** 2010; 73:820-827. (IF 3.9)
25. N. Delmotte, C.H. Ahrens, C. Knief, E. Qeli, M. Koch, H-M. Fischer, J.A. Vorholt, H. Hennecke, G. Pessi. An integrated proteomics and transcriptomics reference dataset provides new insights into the *Bradyrhizobium japonicum* bacteroid metabolism in soybean root nodules. **Proteomics.** 2010; 10:1391-1400. (IF 4.1)
24. S. Goetze, E. Qeli, C. Mosimann, A. Staes, B. Gerrits, B. Roschitzki, S. Mohanty, E.M. Niederer, E. Laczko, E. Timmerman, V. Lange, E. Hafen, R. Aebersold, J. Vandekerckhove, K. Basler, C.H. Ahrens, K. Gevaert, E. Brunner. Identification and functional characterization of N-terminal protein acetylations in *Drosophila melanogaster*. **PLoS Biol.** 2009; 7:e1000236. (IF 9.8)
23. M.A. Grobei, E. Qeli, H. Rehrauer, E. Brunner, R. Zhang, B. Roschitzki, K. Basler, U. Grossniklaus\*, C.H. Ahrens\*. Deterministic protein inference for shotgun proteomics data of the *Arabidopsis thaliana* mature pollen provides new insights into pollen development and function. **Genome Res.** 2009; 19:1786-1800. (IF 11.9)

22. S.P. Schimpf, M. Weiss, L. Reiter, C.H. Ahrens, M. Jovanovic, J. Malmström, E. Brunner, S. Mohanty, M.J. Lercher, P.E. Hunziker, R. Aebersold, C. vonMering, M.O. Hengartner. Comparative functional analysis of the *Caenorhabditis elegans* and *Drosophila melanogaster* proteomes. **PLoS Biol.** 2009; 7:e48. (IF 9.8)
21. C.H. Ahrens<sup>\*</sup>, E. Brunner<sup>\*</sup>, E. Hafen, R. Aebersold, K. Basler. A proteome catalog of *Drosophila melanogaster*: An essential resource for targeted quantitative proteomics. **Fly.** 2007; 1:182-186. (IF 0.9)
20. G. Pessi, C.H. Ahrens, H. Rehrauer, A. Lindemann, F. Hauser, H.M. Fischer, H. Hennecke. Genome-wide transcript analysis of *Bradyrhizobium japonicum* bacteroids in soybean root nodules. **Mol Plant Microbe Interact.** 2007; 20:1353-1363. (IF 4.3)
19. E. Brunner<sup>\*</sup>, C.H. Ahrens<sup>#\*</sup>, S. Mohanty<sup>\*</sup>, H. Baetschmann, S. Loevenich, F. Potthast, E.W. Deutsch, C. Panse, U. de Lichtenberg, O. Rinner, H. Lee, P.G.A. Pedrioli, J. Malmstrom, K. Koehler, S. Schimpf, J. Krijgsveld, F. Kregenow, A.J.R. Heck, E. Hafen, R. Schlapbach, R. Aebersold. A high quality map of the *Drosophila melanogaster* proteome. **Nat Biotechnol.** 2007; 25:576-583. (IF 41.7)
18. F. Potthast, B. Gerrits, J. Haekkinen, D. Rutishauser, C.H. Ahrens, B. Roschitzki, K. Baerenfaller, R. Munton, P. Walther, S.N. Loevenich, P. Gehrig, P. Seif, P.H. Seeberger, R. Schlapbach. The mass distance fingerprint: a statistical framework for *de novo* detection of predominant modifications using high-accuracy MS. **J Chromatogr B Analyt Technol Biomed Life Sci.** 2007; 854:173-182. (IF 2.7)
17. D.B. Kristensen, J.C. Brønd, P.A. Nielsen, J.R. Andersen, O.T. Sørensen, V. Jørgensen, K. Budin, J. Matthiesen, P. Venø, H.M. Jespersen, C.H. Ahrens, S. Schandorff, P.T. Ruhoff, J.R. Wisniewski, K.L. Bennett, A.V. Podtelejnikov. Experimental Peptide Identification Repository (EPIR): An integrated peptide-centric platform for validation and mining of tandem mass spectrometry data. **Mol Cell Prot.** 2004; 3:1023-1038. (IF 6.5)
16. L. Thorstensen, C.B. Diep, G.I. Meling, T.H. Aagesen, C.H. Ahrens, T.O. Rognum, R.A. Lothe. WNT-inducible signaling pathway protein-3, Wisp-3, a novel target in colorectal carcinomas with microsatellite instability. **Gastroenterology.** 2001; 121:1275-1280. (IF 18.4)
15. C.H. Ahrens, R. Russell, J.C. Funk, J.T. Evans, S. Harwood, G.F. Rohrmann. The sequence of the *Orygia pseudotsugata* multinucleocapsid nuclear polyhedrosis virus genome. **Virology.** 1997; 229:381-399. (IF 3.4)
14. C.H. Ahrens and G.F. Rohrmann. The DNA polymerase and helicase genes of a baculovirus of *Orygia pseudotsugata*. **J Gen Virol.** 1996; 77:825-837. (IF 2.8)
13. C.H. Ahrens and G.F. Rohrmann. Replication of baculovirus DNA: *lef-2* and *ie-1* are essential, and *ie-2*, *p34* and *Op-iap* are stimulatory genes. **Virology.** 1996; 212:650-662. (IF 3.4)
12. C.H. Ahrens, C. Carlson, G.F. Rohrmann. Identification, sequence and transcriptional analysis of *lef-3*, an essential replication gene of an *Orygia pseudotsugata* baculovirus. **Virology.** 1995; 210:372-382. (IF 3.4)
11. C.H. Ahrens, M.N. Pearson, G.F. Rohrmann. Identification and characterisation of a second putative origin of DNA replication in a baculovirus of *Orygia pseudotsugata*. **Virology.** 1995; 207:572-576. (IF 3.4)
10. C.H. Ahrens and G.F. Rohrmann. Identification of essential trans-acting regions required for DNA replication of the *Orygia pseudotsugata* multinucleocapsid nuclear polyhedrosis virus: *lef-1* is an essential replication gene. **Virology.** 1995; 207:417-428. (IF 3.4)
9. M. Kool, C.H. Ahrens, R.W. Goldbach, G.F. Rohrmann, J.M. Vlak. Identification of genes involved in DNA replication of the *Autographa californica* baculovirus. **Proc Natl Acad Sci USA.** 1994; 91:11212-11216. (IF 9.7)

8. M.N. Pearson, R.M. Bjornson, C. Ahrens, G.F. Rohrmann. Identification and characterisation of a putative origin of DNA replication in the genome of a baculovirus pathogenic for *Orgyia pseudotsugata*. **Virology**. 1993; 197:715-725. (IF 3.4)

### Reviews / Editorials / Book Chapters

7. A.M. Jones, R. Aebersold, C.H. Ahrens, R. Apweiler, K. Baerenfaller, E. Bendixen, S. Briggs, P. Brownridge, E. Brunner, M. Daube, et al. The HUPO initiative on Model Organism Proteomes, iMOP. **Proteomics**. 2012; 12:340-345. (IF 4.1)
6. C.H. Ahrens<sup>#</sup>, E. Brunner, E. Qeli, K. Basler, R. Aebersold. Generating and navigating proteome maps by mass spectrometry. Peer-reviewed **review** article. **Nat Rev Mol Cell Biol**. 2010; 11:789-801. (IF 46.6)
5. C.H. Ahrens, S. Schimpf, E. Brunner, R. Aebersold. Model organism proteomics. **J Proteomics**. 2010; 73:2051-2053. (Editorial for a thematic issue for the Journal of Proteomics). (IF 3.9)
4. C.H. Ahrens<sup>\*</sup>, U. Wagner<sup>\*</sup>, H.K. Rehrauer, C. Türker, R. Schlapbach. Current challenges and approaches for the synergistic use of systems biology data in the scientific community. **Book Chapter** in "Plant Systems Biology", **Birkhäuser Press**, 2007. Editors: Sacha Baginsky, Alisdair R. Fernie.
3. C. Ahrens, H.M. Jespersen, S. Schandorff. Bioinformatics for Proteomics. **Book Chapter** in "Industrial Proteomics. Applications for Biotechnology and Pharmaceuticals", **Wiley Press**, 2005. Editor: Daniel Figey.
2. C.H. Ahrens, D.J. Leisy, G.F. Rohrmann. Baculovirus DNA replication. **Book Chapter** in "DNA replication in Eukaryotic Cells", **Cold Spring Harbor Press**, 1996.
1. M. Kool, C.H. Ahrens, J.M. Vlak, G.F. Rohrmann. Replication of Baculovirus DNA. Peer-reviewed **review** article. **J Gen Virol**. 1995; 76:2103-2118. (IF 2.8)

### Publication Repositories/Overviews:

Researcher ID: F-4656-2011  
 Publons: <https://publons.com/researcher/1386936/christian-h-ahrens>  
 ORCID: <http://orcid.org/0000-0002-8148-7257>  
 ResearchGate: [https://www.researchgate.net/profile/Christian\\_Ahrens/](https://www.researchgate.net/profile/Christian_Ahrens/)  
 Google Scholar: [http://scholar.google.ch/citations?user=f17\\_cpkAAAAJ](http://scholar.google.ch/citations?user=f17_cpkAAAAJ)  
 NCBI Publication list:  
<http://www.ncbi.nlm.nih.gov/myncbi/browse/collection/49397441/?sort=date&direction=descending>