

Curriculum Vitae

Charlotte Uetrecht

W2 / Associate Professor Biochemistry Dynamics of viral Structures
Center for Structural Systems Biology (CSSB),
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Research positions and education

2021-present W2 / Associate Professor for Biochemistry, Faculty V: School of Life Sciences, position associated to DESY and LIV (formerly HPI), research group at CSSB Hamburg

2020-2021 Associate member, CSSB, Hamburg, Germany

2014-2021 Junior group leader “Dynamics of viral Structures”, LIV, Hamburg, Germany

2011-present Postdoc (2013-2014) /guest scientist, Sample Environment, European XFEL GmbH

2011-2013 Postdoc on EMBO longterm fellowship, Molecular Biophysics, Uppsala University, Sweden

2006–2010 PhD student/postdoc, Biomolecular Mass Spectrometry and Proteomics, Utrecht University, the Netherlands
Analysing macromolecular structures with native mass spectrometry:
Insights to virus structure and assembly, supervisor: Prof. Dr. A.J.R. Heck, Graduation: Nov 2010 with cum laude

2001-2006 Diplom Biochemistry, University of Potsdam, Germany,
Thesis supervisors: Prof. Dr. R. Seckler and Dr. S. Barbirz
Specialisation: physical biochemistry and structural biology

Awards/Grants

2010 PhD with Cum Laude (highest degree in the Netherlands awarded to < 5%)

2011-2013	EMBO Longterm Fellowship ALTF 1531-2010
2011	H.G.K. Westenbrink prize 2011
2013-2015	PIER Ideenfonds together with Prof. Dr. H. Schlüter, UKE: "Towards a prototype mass spectrometer for delivery of biological samples at X-ray Free-Electron Lasers"
2014-2017	Leibniz Association, Leibniz Competition 2014, Women in academic leadership positions, SAW-2014-HPI-4: "Advanced mass spectrometric tools to elucidate structures involved in viral infection"
2015-2017	Co-applicant LFF-Deligrath graduate school, speaker: Prof. Dr. J. Kehr
2016-2019	Co-applicant Joachim-Herz-Stiftung, project leader: Prof. Dr. M. Kolbe
2016-2022	Co-applicant DFG research unit Virocarb FOR 2327, speaker: Prof. Dr. T. Stehle
2016-2020	Coordinator BMBF "VisaVix" 05K16BH1
2016-2022	Co-applicant, H2020-FETPROACT-2016, Viruscan (731868), coordinator: Dr. J. Tamayo
2018-2023	ERC-2017-STG, SPOCK'S MS (759661)
2018-2023	Coordinator H2020-FETOPEN-1-2016-2017, MS SPIDOC (801406)
2019-2022	LCI stipend project with Maria Rosenthal
2019-2023	Leibniz Science Campus Interact, co-applicant and member board of directors
2020	BMG Rapid response grant
2020-2021	BMBF RTK-Struktur
2020-2023	LFF ZeMeIn, co-applicant
2021-2025	Co-applicant, H2020-FETOPEN, ARIADNE
2021-2022	LIV SIP together with Maya Topf
2022	Mattauch-Herzog Award of the DGMS
2022-2025	BMBF VirMScan project with Pietro Scaturro
2022-2026	RAC SAXFELS project with Carl Coleman and Erik Marklund
2022-2027	Co-applicant DFG RTG "Humans and microbes"

Memberships/other

German Biophysical Society (DGfB)
 German Mass Spectrometry Society (DGMS)
 Society for Virology (GfV)
 International Society of HDX-MS
 World Society of Virology (WSV)
 Jury member Wolfgang-Paul-Studienpreis of the DGMS (since 2017)
 Active external expert for European Commission and other funding agencies in Europe
 Elected chair at the 2023 GRC Physical Virology Conference
 Deputy chair scientific council of HPI (2019-2021)
 Internal Advisory Board of the CSSB Multi-User CryoEM Facility (since 2020)
 Select Member Virology Division, Microbiology Society, UK (since 2021)
 Member Academia.net, platform for excellent women researchers (since 2021)
 Analytical Chemistry Early Career Board, American Chemical Society (2022 – 2024)

Research Focus

My group is interested in the structure and dynamics of viral protein complexes to elucidate, how these complex machineries function. A main focus is the replication/transcription machine of coronaviruses. Since these protein complexes often exist in many different states to mediate a diverse set of functions, single particle-like approaches are best suited to deduce structural information. We therefore use and develop mass spectrometry (MS) based techniques, which allow revealing coexisting states in a time-resolved manner. Another interest lies in the dynamic structure of viral capsids, where we focus on noroviruses. MS coupled to X-ray free-electron lasers for sample delivery will in the near future allow high resolution single particle imaging of transient states in functional cycles or capsid assembly as our new system will allow the selective imaging of specific states.

Full list of publications

See also: ResearcherID D-1883-2010 or ORCID 0000-0002-1991-7922

Peer-review original articles

- 1) In-solution structure and oligomerization of human histone deacetylase 6 - an integrative approach. Shukla S, Komarek J, Novakova Z, Nedvedova J, Ustinova K, Vankova P, Kadek A, **Uetrecht C**, Mertens H, Barinka C. (2022) FEBS J, accepted.
- 2) NMR experiments provide insights into ligand-binding to the SARS-CoV-2 spike protein receptor-binding domain. Creutzmacher R, Maass T, Veselkova B, Ssebyatika G, Krey T, Empting M, Tautz N, Frank M, Koelbel K, **Uetrecht C**, Peters T. (2022) J Am Chem Soc, DOI: 10.1021/jacs.2c05603.
- 3) Distinct dissociation rates of murine and human norovirus P domain dimers suggest a role of dimer stability in virus-host interactions. Creutzmacher R, Maass T, Dülfer J, Feldmann C, Hartmann V, Lane MS, Knickmann J, Westermann LT, Thiede L, Smith TJ, **Uetrecht C**, Mallagaray A, Waudby CA, Taube S, Peters T. (2022) Commun Biol, <https://doi.org/10.1038/s42003-022-03497-4>.
- 4) Dissociation of β_2m from MHC Class I Triggers Formation of Noncovalent, Transient Heavy Chain Dimers. Dirscherl C, Loechte S, Hein Z, Kopicki JD, Harders AR, Linden N, Karner A, Preiner J, Weghuber J, Garcia-Alai M, **Uetrecht C**, Zacharias M, Piehler J, Lanzerstorfer P, Springer S. (2022) J Cell Sci, jcs.259498.
- 5) Opening opportunities for K_d determination and screening of MHC peptide complexes. Kopicki JD, Saikia A, Niebling S, Günther C, Anjanappa R, Garcia-Alai MM, Springer S#, **Uetrecht C#**. (2022) Commun Biol, 5:488, doi: 10.1038/s42003-022-03366-0, #corresponding authors
- 6) Assignment of Ala, Ile, LeuproS, Met, and ValproS methyl groups of the protruding domain of murine norovirus capsid protein VP1 using methyl-methyl NOEs, site directed mutagenesis, and pseudocontact shifts. Maass T, Westermann LT, Creutzmacher R, Mallagaray A, Dülfer J, **Uetrecht C**, Peters T. (2022) Biomol NMR Assign, DOI: 10.1007/s12104-022-10066-7
- 7) Caldendrin/myosinV regulate spine apparatus localization via ER-stabilization in dendritic spines. Konietzny A, Grendel J, Kadek A, Bucher M, Han Y, Hertrich N, Dekkers DHW, Demmers JAA, Grünewald K, **Uetrecht C**, Mikhaylova M. (2022) EMBO J, 41:e106523, doi: 10.15252/embj.2020106523
- 8) Protein secondary structure affects glycan clustering in native mass spectrometry. Yan H, Lockhauserbäumer J, Szekeres GP, Mallagaray A, Creutzmacher R, Taube S, Peters T, Pagel K, **Uetrecht C**. (2021) Life, 11:554.
- 9) Glycan-induced protein dynamics in human norovirus P dimers depend on virus strain and deamidation status. Dülfer J, Yan H, Brodmerkel MN, Creutzmacher R, Mallagaray A, Peters T, Coleman C, Marklund EG, **Uetrecht C**. (2021) Molecules, 26:2125.
- 10) X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. Günther S, Reinke PYA, Fernández-García Y, Lieske J, Lane TJ, Ginn HM, Koua FHM, Ehart C, Ewert W, Oberthuer D, Yefanov O, Meier S, Lorenzen K, Krichel B, Kopicki JD, Gelisio L, Brehm W, Dunkel I, Seychell B, Gieseler H, Norton-Baker B, Escudero-Pérez B, Domaracky M, Saouane S, Tolstikova A, White TA, Hänle A, Groessler M, Fleckenstein H, Trost F, Galchenkova M, Gevorkov Y, Li C, Awel S, Peck A, Barthelmess M, Schlünzen F, Xavier PL, Werner N, Andaleeb H, Ullah N, Falke S, Srinivasan V, Alves Franca B, Schwinzer M, Brognaro H, Rogers C, Melo D, Zaitsev-Doyle JJ, Knoska J, Peña Murillo GE, Rahmani Mashhour A, Hennicke V, Fischer P, Hakanpää J, Meyer J, Gribbon P, Ellinger B, Kuzikov M, Wolf M, Beccari AR, Bourenkov G, von Stetten D, Pompidor G, Bento I, Panneerselvam S, Karpics I, Schneider TR, Garcia Alai MM, Niebling S, Günther C, Schmidt C, Schubert R, Han H, Boger J, Monteiro DCF, Zhang L, Sun X, Pletzer-Zelgert J, Wollenhaupt J, Feiler CG, Weiss MS, Schulz EC, Mehrabi P, Karničar K, Usenik A, Loboda J, Tidow H, Chari A, Hilgenfeld R, **Uetrecht C**, Cox R, Zaliani A, Beck T, Rarey M, Günther S, Turk D, Hinrichs W, Chapman HN, Pearson AR, Betzel C, Meents A. (2021) Science, 372:642-

- 11) Hallmarks of Alpha- and Betacoronavirus non-structural protein 7+8 complexes. Krichel B, Bylapudi G, Schmidt C, Blanchet C, Schubert R, Brings L, Koehler M, Zenobi R, Svergun D, Lorenzen K, Madhugiri R, Ziebuhr J, **Uetrecht C**. (2021) *Sci Adv*, 7:eabf1004.
- 12) N-terminal VP1 truncations favor $T=1$ norovirus-like particles. Pogan R, Weiss VU, Bond K, Dülfer J, Krisp C, Lykтей N, Mueller-Guhl J, Zoratto S, Allmaier G, Jarrold MF, Munoz-Fontela C, Schlüter H, **Uetrecht C**. (2020) *Vaccines*, 9:8
- 13) The XBI BioLab for life science experiments at the European XFEL. Han H, Round E, Schubert R, Gül Y, Makroczynova J, Meza D, Heuser P, Apfelbacher M, Barak I, Betzel C, Fromme P, Kursula I, Nissen P, Tereschenko E, Schulz J, **Uetrecht C**, Ulicny J, Wilmanns M, Hajdu J, Lamzin VS, Lorenzen K. (2021) *J Appl Cryst*, 54:7-21.
- 14) The crystal structure of mycobacterial Epoxide Hydrolase A. Schulz EC, Henderson SR, Illarionov B, Crosskey T, Southall SM, Krichel B, **Uetrecht C**, Fischer M, Wilmanns M. (2020) *Sci Rep*, 10:16539.
- 15) Megahertz single-particle imaging at the European XFEL. Sobolev E, Zolotarev S, Giewekemeyer K, Bielecki J, Okamoto K, Reddy HKN, Andreasson J, Ayyer K, Barak I, Bari S, Barty A, Bean R, Bobkov S, Chapman HN, Chojnowski G, Daurer BJ, Dörner K, Ekeberg T, Flückiger L, Galzitskaya O, Gelisio L, Hauf S, Hogue BG, Horke DA, Hosseinizadeh A, Ilyin V, Jung C, Kim C, Kim Y, Kirian RA, Kirkwood H, Küpper J, Kulyk O, Letrun R, Loh D, Messerschmidt M, Mühlig K, Ourmazd A, Raab N, Rode AV, Rose M, Round A, Sato T, Schubert R, Schwander P, Sellberg JA, Sikorski M, Silenzi A, Song C, Spence JCH, Stern S, Sztuk-Dambietz J, Teslyuk A, Timneanu N, Trebbin M, **Uetrecht C**, Weinhausen B, Williams GJ, Xavier PL, Xu C, Vartanyants I, Lamzin V, Mancuso A, Maia FRNC. (2020) *Commun Phys*, 3:97.
- 16) Methylation of Salmonella Typhimurium flagella promotes bacterial adhesion and host cell invasion. Horstmann JA, Lunelli M, Cazzola H, Heidemann J, Kühne C, Steffen P, Szefs S, Rossi C, Lokareddy RK, Wang C, Hughes KT, **Uetrecht C**, Schlüter H, Grassl GA, Stradal TEB, Rossez Y, Kolbe M, Erhardt M. (2020) *Nat Commun*, 11:2013.
- 17) Processing of the SARS-CoV pp1a/ab nsp7-10 region. Krichel B, Falke S, Hilgenfeld R, Redecke L, **Uetrecht C**. (2020) *Biochem J*, 477(5):1009-1019. Cover article.
- 18) Structures of peptide-free and partially loaded MHC class I molecules reveal mechanisms of peptide selection. Anjanappa R, Garcia-Alai M, Kopicki J-D, Lockhauserbäumer J, Aboelmagd M, Hinrichs J, Nemtanu IM, **Uetrecht C**, Zacharias M, Springer S, Meijers R. (2020) *Nat Commun*, 11:1314.
- 19) Further insights from structural mass spectrometry into endocytosis adaptor protein assemblies. Heidemann J, Kölbel K, Konijnenberg A, Van Dyck J, Garcia-Alai M, Meijers R, Sobott F, **Uetrecht C**. (2020) *Int J Mass Spectrom*, 447: 116240. Cover article, IJMS Best Student Paper Award 2019.
- 20) Structural analysis of ligand-bound states of the Salmonella type III secretion system ATPase InvC. Bernal I, Römermann J, Flacht L, Lunelli M, **Uetrecht C**, Kolbe M. (2019) *Protein Sci*, 28:1888-1901.
- 21) Molecular Organization of Soluble Type III Secretion System Sorting Platform Complexes. Bernal I§, Börnicke J§, Heidemann J§, Svergun D, Horstmann JA, Erhardt M, Tuukkanen A#, **Uetrecht C**#, Kolbe M#. (2019) *J Mol Biol*, 431:3787-3803. §equal contribution, #corresponding authors
- 22) Virus-like particle size and molecular weight/mass determination applying gas-phase electrophoresis (native nES GEMMA). Weiss VU§, Pogan R§, Zoratto S, Bond K, Boulanger P, Jarrold MF, Lykтей N, Pahl D, Puffer N, Schelhaas M, Selivanovitch E, **Uetrecht C**, Allmaier G. (2019) *Anal Bioanal Chem*, 411:5951-5962. §equal contribution
- 23) Synthesis and characterization of α -carboxynitrobenzyl photocaged L-aspartates for applications in time-resolved structural biology. Zaitsev-Doyle JJ, Puchert A, Pfeifer Y, Yan H, Yorke BA, Müller-Werkmeister HM, **Uetrecht C**, Rehbein J, Huse N, Pearson AR, Sans M. (2019) *RSC Advances*, 9, 8695-8699.

- 24) Native mass spectrometry provides sufficient ion flux for XFEL single particle imaging. **Uetrecht C#**, Lorenzen K, Kitel M, Heidemann J, Spencer JHR, Schlüter H, Schulz J. (2019) *J Synchrotron Radiat*, 26:653-659. #corresponding author
- 25) Crystal structure of a domain-swapped photoactivatable sfGFP variant provides evidence for GFP folding pathway. Kesgin-Schaefer S, Heidemann J, Puchert A, Koelbel K, Yorke B, Huse N, Pearson AR, **Uetrecht C**, Tidow H. (2019) *FEBS J*, 286:2329-2340.
- 26) A post-translational modification of human Norovirus capsid protein attenuates glycan binding. Mallagaray A, Creutzmacher R, Dülfer J, Mayer P, Grimm L, Orduña J, Trabjerg E, Stehle T, Rand K, Blaum B, **Uetrecht C**, Peters T. (2019) *Nat Commun*, 10:1320.
- 27) Structural basis for activation of plasma-membrane Ca²⁺-ATPase by calmodulin. Nitsche J, Josts I, Heidemann J, Mertens HD, Maric S, Moulin M, Haertlein M, Busch S, Forsyth VT, Svergun DI, **Uetrecht C**, Tidow H. (2018) *Commun Biol*, 1:206.
- 28) Biochemical and structural studies reveal differences and commonalities among cap-snatching endonucleases from segmented negative-strand RNA viruses. Holm T, Kopicki JD, Busch C, Olschewski S, Rosenthal M, **Uetrecht C**, Günther S, Reindl S. (2018) *J Biol Chem*, 293(51):19686-19698.
- 29) Fucose-Functionalized Precision Glycomacromolecules Targeting Human Norovirus Capsid Protein. Bücher KS, Yan H, Creutzmacher R, Ruoff K, Mallagaray A, Grafmüller A, Dirks JS, Kilic T, Weickert S, Rubailo A, Drescher M, Schmidt S, Hansman G, Peters T, **Uetrecht C#**, Hartmann L#. (2018) *Biomacromolecules*, 19(9):3714-3724. #corresponding authors
- 30) Norovirus-like VP1 particles exhibit isolate dependent stability profiles. Pogan R, Schneider C, Reimer R, Hansman G, **Uetrecht C**. (2018) *J Phys Condens Matter*, 30:064006.
- 31) Epsin and Sla2 form assemblies through phospholipid interfaces. Garcia-Alai MM, Heidemann J, Skruzny M, Gieras A, Mertens HDT, Svergun DI, Kaksonen M, **Uetrecht C#**, Meijers R#. (2018) *Nat Comm*, 9:328. #corresponding authors
- 32) Ultra-high mass multimer analysis of protein-1a capping domains by a silicon nanomembrane detector. Shin HC, Deterra D, Park J, Kim H, Nishikiori M, **Uetrecht C**, Ahlquist PG, Arbulu M, Blick RH. (2017) *J Proteomics* 175:5-11.
- 33) Human norovirus GII.4(MI001) P dimer binds fucosylated and sialylated carbohydrates. Wegener H, Mallagaray A, Schöne T, Peters T, Lockhauserbäumer J, Yan H, **Uetrecht C**, Hansman GS, Taube S. (2017) *Glycobiology*, 27:1027-1037.
- 34) A data set from flash X-ray imaging of carboxysomes. Hantke MF, Hasse D, Ekeberg T, John K, Svenda M, Loh D, Martin AV, Timneanu N, Larsson DS, van der Schot G, Carlsson GH, Ingelman M, Andreasson J, Westphal D, Iwan B, **Uetrecht C**, Bielecki J, Liang M, Stellato F, DePonte DP, Bari S, Hartmann R, Kimmel N, Kirian RA, Seibert MM, Mühlig K, Schorb S, Ferguson K, Bostedt C, Carron S, Bozek JD, Rolles D, Rudenko A, Foucar L, Epp SW, Chapman HN, Barty A, Andersson I, Hajdu J, Maia FR. (2016) *Sci Data*, 3:160061.
- 35) Structure and target interaction of a G-quadruplex RNA-aptamer. Szameit K, Berg K, Kruspe S, Valentini E, Magbanua E, Kwiatkowski M, Chauvot de Beauchêne I, Krichel B, Schamoni K, **Uetrecht C**, Svergun DI, Schlüter H, Zacharias M, Hahn U. (2016) *RNA Biol*, 13:973-987.
- 36) Assembly and Mechanical Properties of the Cargo-Free and Cargo-Loaded Bacterial Nanocompartment Encapsulin. Snijder J, Kononova O, Barbu IM, **Uetrecht C**, Rurup WF, Burnley RJ, Koay MS, Cornelissen JJ, Roos WH, Barsegov V, Wuite GJ, Heck AJ. (2016) *Biomacromolecules*, 17:2522-9.
- 37) Crystal Structure of the CTP1L Endolysin Reveals How Its Activity Is Regulated by a Secondary Translation Product. Dunne M, Leicht S, Krichel B, Mertens HD, Thompson A, Krijgsveld J, Svergun DI, Gómez-Torres N, Garde S, **Uetrecht C**, Narbad A, Mayer MJ, Meijers R. (2016) *J Biol Chem*, 291:4882-93.
- 38) Attachment of norovirus to histo blood group antigens: a cooperative multistep

- process. Mallagaray A, Lockhauserbäumer J, Hansman G, **Uetrecht C**, Peters T. (2015) *Angew Chem Int Ed Engl*, 54:12014-9.
- 39) A hydrolase-based reporter system to uncover the protein splicing performance of an archaeal intein. von der Heyde A, Lockhauserbäumer J, **Uetrecht C**, Elleuche S. (2015) *Appl Microbiol Biotechnol*, 99:7613-24.
 - 40) An organized co-assembly of clathrin adaptors is essential for endocytosis. Skruzny M, Desfosses A, Prinz S, Dodonova SO, Gieras A, **Uetrecht C**, Jakobi AJ, Abella M, Hagen WJ, Schulz J, Meijers R, Rybin V, Briggs JA, Sachse C, Kaksonen M. (2015) *Dev Cell*, 33:150-62.
 - 41) Game-theory-based search engine to automate the mass assignment in complex native electrospray mass spectra. Tseng YH, **Uetrecht C**, Yang SC, Barendregt A, Heck AJ, Peng WP. (2013) *Anal Chem*, 85:11275-83.
 - 42) Probing the biophysical interplay between a viral genome and its capsid. Snijder J, **Uetrecht C**, Rose RJ, Sanchez-Eugenía R, Marti GA, Agirre J, Guérin DM, Wuite GJ, Heck AJ, Roos WH. (2013) *Nat Chem*, 5:502-9.
 - 43) Single amino acid exchange in bacteriophage HK620 tailspike protein results in thousand-fold increase of its oligosaccharide affinity. Broeker NK, Gohlke U, Müller JJ, **Uetrecht C**, Heinemann U, Seckler R, Barbirz S. (2013) *Glycobiology*, 23:59-68.
 - 44) Structural studies of the O-antigen polysaccharide from *Escherichia coli* TD2158 having O18 serogroup specificity and aspects of its interaction with the tailspike endoglycosidase of the infecting bacteriophage HK620. Zaccheus MV, Broeker NK, Lundborg M, **Uetrecht C**, Barbirz S, Widmalm G. (2012) *Carbohydr Res*, 357:118-25.
 - 45) Prestress strengthens the shell of Norwalk virus nanoparticles. Baclayon M, Shoemaker GK, **Uetrecht C**, Crawford SE, Estes MK, Prasad BV, Heck AJ, Wuite GJ, Roos WH. (2011) *Nano Lett*, 11:4865-9.
 - 46) Encapsulation of phthalocyanine supramolecular stacks into virus-like particles. Brasch M, de la Escosura A, Ma Y, **Uetrecht C**, Heck AJ, Torres T, Cornelissen JJ. (2011) *J Am Chem Soc*, 133:6878-81.
 - 47) Interpreting the charge state assignment in electrospray mass spectra of bioparticles. Tseng YH, **Uetrecht C**, Heck AJ, Peng WP. (2011) *Anal Chem*, 83:1960-8.
 - 48) Interrogating viral capsid assembly with ion mobility-mass spectrometry. **Uetrecht C**, Barbu IM, Shoemaker GK, van Duijn E, Heck AJ. (2011) *Nat Chem*, 3:126-32. Erratum in 2014: *Nat Chem*, 6:745.
 - 49) N-terminal domain of human Hsp90 triggers binding to the cochaperone p23. Karagöz GE, Duarte AM, Ippel H, **Uetrecht C**, Sinnige T, van Rosmalen M, Hausmann J, Heck AJ, Boelens R, Rüdiger SG. (2011) *Proc Natl Acad Sci USA*, 108:580-5.
 - 50) Squeezing protein shells: how continuum elastic models, molecular dynamics simulations, and experiments coalesce at the nanoscale. Roos WH, Gibbons MM, Arkhipov A, **Uetrecht C**, Watts NR, Wingfield PT, Steven AC, Heck AJ, Schulten K, Klug WS, Wuite GJ. (2010) *Biophys J*, 99:1175-81.
 - 51) Subunit exchange rates in Hepatitis B virus capsids are geometry- and temperature-dependent. **Uetrecht C**, Watts NR, Stahl SJ, Wingfield PT, Steven AC, Heck AJ. (2010) *Phys Chem Chem Phys*, 12:13368-71. Cover article.
 - 52) Norwalk virus assembly and stability monitored by mass spectrometry. Shoemaker GK, van Duijn E, Crawford SE, **Uetrecht C**, Baclayon M, Roos WH, Wuite GJ, Estes MK, Prasad BV, Heck AJ. (2010) *Mol Cell Proteomics*, 9:1742-51.
 - 53) A docking model based on mass spectrometric and biochemical data describes phage packaging motor incorporation. Fu CY, **Uetrecht C**, Kang S, Morais MC, Heck AJ, Walter MR, Prevelige PE Jr. (2010) *Mol Cell Proteomics*, 9:1764-73.
 - 54) Crystal structure of *Escherichia coli* phage HK620 tailspike: podoviral tailspike endoglycosidase modules are evolutionarily related. Barbirz S, Müller JJ, **Uetrecht C**, Clark AJ, Heinemann U, Seckler R. (2008) *Mol Microbiol*, 69:303-316. Cover article.
 - 55) Determination of stoichiometry and conformational changes in the first step of the P22 tail assembly. Lorenzen K, Olia AS, **Uetrecht C**, Cingolani G, Heck AJ. (2008) *J Mol Biol*, 379:385-396.

- 56) High-resolution mass spectrometry of viral assemblies: molecular composition and stability of dimorphic hepatitis B virus capsids. **Uetrecht C**, Versluis C, Watts NR, Roos WH, Wuite GJ, Wingfield PT, Steven AC, Heck AJ. (2008) Proc Natl Acad Sci USA, 105:9216-9220.
- 57) Stability and shape of hepatitis B virus capsids in vacuo. **Uetrecht C**, Versluis C, Watts NR, Wingfield PT, Steven AC, Heck AJ. (2008) Angew Chem Int Ed Engl, 47:6247-6251. Inner cover.

Peer-review review articles

- 58) Norovirus-glycan interactions - How strong are they really? Peters T, Creutzmacher R, Maass T, Mallagaray A, Ogrissek P, Taube S, Thiede L, **Uetrecht C**. (2021) Biochem Soc Trans, 50:347-359. doi: 10.1042/BST20210526.
- 59) In a flash of light: X-ray free electron lasers meet native mass spectrometry. Kádek A, Lorenzen K, **Uetrecht C** for the MS SPIDOC consortium. (2021) Drug Discov Today Technol, 39:89-99.
- 60) Top-Down and Bottom-Up Proteomics Methods to Study RNA Virus Biology. Simanjuntak Y, Schamoni-Kast K, Grün A, **Uetrecht C**, Scaturro P#. (2021) Viruses. 13:668 #corresponding authors
- 61) Structural mass spectrometry goes viral. Dülfer J, Kadek A, Kopicki JD, Krichel B, **Uetrecht C**. (2019) Adv Virus Res, 105:189-238. Cover article.
- 62) Norovirus assembly and stability. Pogan R, Dülfer J, **Uetrecht C**. (2018) Curr Opin Virol, 31:59-65.
- 63) Modern biomolecular mass spectrometry and its role in studying virus structure, dynamics, and assembly. **Uetrecht C**, Heck AJ. (2011) Angew Chem Int Ed Engl, 50:8248-62.
- 64) Ion mobility mass spectrometry of proteins and protein assemblies. **Uetrecht C**, Rose RJ, van Duijn E, Lorenzen K, Heck AJ. (2010) Chem Soc Rev, 39:1633-55.

Manuscripts without peer-review

- 65) Stability and Conformational Memory of Electrosprayed and Rehydrated Bacteriophage Ms2 Virus Coat Proteins. Brodmerkel MN, De Santis E, Coleman C, **Uetrecht C**, Marklund EG. <http://dx.doi.org/10.2139/ssrn.4163357>
- 66) Norovirus Superstar (in English or German). Mischitz V. Editors: Cross A, Wissel S, **Uetrecht C**, Lorenzen K. Comic book of for the EU project MS SPIDOC. Doi: 10.22003/XFEL.EU-COMIC-2021-001-EN / 10.22003/XFEL.EU-COMIC-2021-001-DE
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