OMB No. 0925-0001 and 0925-0002 (Rev. 10/2021 Approved Through 01/31/2026)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
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NAME: Conway, James F.

eRA COMMONS USER NAME (credential, e.g., agency login): JXC100

POSITION TITLE: Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Massey University, New Zealand.	B.Sc. (hons)	12/1985	Physics & biophysics
Massey University, New Zealand.	Ph.D.	12/1989	Protein structure
NIH (NIAMS), Bethesda Maryland. USA. (Post Doc)		1990-1995	Structural biology

A. Personal Statement

I have been working on determining the structure of protein assemblies using cryo-electron microscopy (cryoEM) and image reconstruction since 1993, including those of virus capsids such as herpesviruses and dsDNA bacteriophages. I have extensive experience with cryo-EM data collection and analysis, and I have designed and equipped the cryo-EM suite in the University of Pittsburgh School of Medicine for which I am currently responsible. Work on the capsids of HK97 and other viruses includes my development of new image analysis methods that led to a breakthrough in achievable resolution to below 1nm (10 Ångstroms) achieved first with the hepatitis B (HBV) capsid and published in Nature in 1997. Labeling of the HBV capsid protein augmented the value of the high-resolution cryoEM density map considerably, including the mapping of an immuno-dominant epitope and the structure of a conformational epitope. My subsequent work modeling the HK97 procapsid with the mature capsid subunit crystal structure includes a publication in Science (2001), and more recent studies on herpesvirus capsids have definitively identified proteins involved in capsid maturation and DNA retention. Current work on our in-house Krios microscope is yielding structures of protein complexes to 2Å resolution, including a test sample of apoferritin to 1.8Å and a capsid structure of AAV2 to 2.2Å. My recent work on bacteriophage and herpesvirus structures focuses on understanding the organization of the non-icosahedral portal vertex and the structural and functional role of the symmetry mis-match between the 12-subunit portal ring, through which the viral DNA is packaged and released, and the 5-fold icosahedral vertex it occupies. In addition, I have brought cryoEM to a number of projects as a collaborator, as reflected in publications and current grant support, and expect to continue spreading the utility of this technique to the local science community. I look forward to working with Professor Teschke on detecting intermediates in the capsid maturation pathway of bacteriophage P22, developing high-resolution structures from cryoEM data that I will collect, and visualizing the molecular changes that accompany maturation including at the capsid portal vertex.

Ongoing projects that I would like to highlight include:

R01 GM144981 Conway (PI) 9/23/2022 – 8/31/2026

Structure and assembly of dsDNA tailed bacteriophages.

R01 AI154646 Conway, Homa (co-PIs) 4/15/2021 – 3/31/2026

Structure and function of the portal vertex on the herpes simplex virus capsid.

R01 AI173044 Silva (PI), Role: co-investigator 7/01/2024 – 6/30/2029

Molecular mechanisms governing chikungunya virus binding, tropism and Pathogenesis.

R01 GM112686 Calero (PI), Role: co-investigator 1/15/2015 – 3/31/2025

Structural Studies of RNA Polymerase II transcription initiation and elongation.

Citations that I would like to highlight include:

1. Huet A, Makhov AM, Huffman JB, Vos M, Homa FL & **Conway JF**. (2016) Nat Struct Mol Biol **23**, 531-539, 2016. PMCID: PMC4899274. Extensive subunit contacts underpin herpesvirus capsid stability and interior-to-exterior allostery.
2. Huet A, Duda RL, Boulanger P, **Conway JF**. Capsid expansion of bacteriophage T5 revealed by high resolution cryoelectron microscopy. Proc Natl Acad Sci USA 116, 21037-46 (2019).
3. Huet A, Huffman JB, C**onway JF** and Homa FL. (2020). J Virol **94**, e01534-20. PMCID: PMC7925205. The role of the herpes simplex virus CVSC proteins at the capsid portal vertex.
4. Huet A, Oh B, Maurer J, Duda RL & **Conway JF** (2023) Sci Adv **9**, eadg8868. PMCID: PMC10275583. A symmetry mismatch unraveled: How phage HK97 scaffold flexibly accommodates a 12-fold pore at a 5-fold viral capsid vertex.

B. Positions, Scientific Appointments, and Honors

Positions

2024-: Interim Chair, Department of Structural Biology, University of Pittsburgh School of Medicine.

2017-:Professor, University of Pittsburgh School of Medicine, Pittsburgh PA, USA.

2007-2017: Associate Professor, University of Pittsburgh School of Medicine, Pittsburgh PA, USA. 2005-2007: Visiting Associate Professor, University of Pittsburgh School of Medicine, Pittsburgh PA. 2002-2005: Group Leader, *Laboratoire de Microscopie Électronique Structurale*, IBS Grenoble, France. 2000-2005: *Directeur de Recherche* - CNRS, *Institut de Biologie Structurale* (IBS), Grenoble, France.
1996-1999: Visiting Associate/Staff Scientist, NIH, Bethesda MD, USA.

1990-1995: Visiting Fellow, National Institutes of Health (NIH), Bethesda MD, USA.

Membership on review committees

- NIH Fellowship Review Panel 2024/05 ZRG1 F04-S (20), Feb 2024.
- NIH Study Section “Biochemistry and Biophysics of Membranes” – member, 2017-2021.
- Canadian Foundation for Infrastructure: Expert Committee, Imaging, structural biology, Jan 2017, Jan 2023.
- NIH Study Section “Biochemistry and Biophysics of Membranes” – *ad hoc* member, 2006-2016.
- Austrian Science Fund (FWF) Austrian Doctoral Programme (DK) review of "Integrative Structure Biology", Feb 2015 & Oct 2019.
- NIH Special Emphasis Panel ZRG1 BCMB-P (40), Oct 2015.
- NIH Special Emphasis Panel IDM-B (02) – *ad hoc* member, Jul 2014.
- NIH Special Emphasis Panel ZRG1 BCMB P (40) – *ad hoc* member, Mar 2014.
- NIH Special Emphasis Panel ZRG1 CB-R (30) I – *ad hoc* member, Jul 2013.
- NIH Special Emphasis Panel ZRG1 GGG-A (02) – *ad hoc* member, Oct 2012.
- NIH Special Emphasis Panel ZRG1 IDM-S (02) – *ad hoc* member, May 2012.
- NIH Special Emphasis Panel NIGMS-ZGM1 CBCB-3 (BI) – *ad hoc* member, Jul 2009.
- NIH Study Section “Macromolecular Structure and Function - C” – *ad hoc* member, Feb 2008.

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
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NAME: TESCHKE, CAROLYN

eRA COMMONS USER NAME (credential, e.g., agency login): cmteschke

POSITION TITLE: Department Head

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
University of Wisconsin-Eau Claire, Eau Claire, WI	BS	05/1983	Chemistry
Washington State University, Pullman, WA	PHD	09/1990	Biochemistry
Massachusetts Institute of Technology, Cambridge, MA	Postdoctoral Fellow	08/1994	biochemistry/biophysics/protein folding/capsid assembly

A. Personal Statement

My lab's primary research objective focuses on elucidating the role of protein:protein interactions in the precise assembly of an icosahedral virus, particularly employing the model dsDNA virus bacteriophage P22 and its relatives. I have been studying the folding and assembly mechanisms of phage P22 capsid proteins since my post-doc, so I have extensive expertise in this field. Over the years, my team and I have identified pivotal research questions where our contributions could make a substantial impact in the field of viral capsid assembly. For instance, our research established the reversibility of procapsid assembly—a milestone that enabled the rigorous application of thermodynamic analysis to a two-protein assembly system. This rigorous thermodynamic analysis yielded broadly applicable insights into virus assembly. We found that while the individual interactions among procapsid subunits are weak, their cumulative effect results in a substantial association energy. In addition, we pinpointed the specific site of interaction between coat and scaffolding proteins, demonstrating that their co-assembly hinges on a simple electrostatic interaction. We also worked to understand how the coat protein governs capsid morphology. We engineered coat mutants that formed tubes and petite particles, correlating these distinctive phenotypes with the coat protein's structure. Presently, our focus is on unraveling how the scaffolding protein, acting as the catalyst for the assembly process, orchestrates the assembly of all other capsid proteins to attain the proper assembly outcome. We are also investigating how portal proteins signal to the rest of the capsid proteins the extent of DNA packaged into the capsid. Another recent focus is delving into some of the relatively underexplored phage:host interactions within P22. For instance, our work revealed that the SieA protein is located in the inner membrane in P22 lysogens and is by itself sufficient to exclude infection by P22-like phages.

Contributions to the scientific community: Co-Chair Phage/Virus assembly conference 2025; Councilor American Society of Virology, elected 2023-2026; AAAS Council Delegate, Section on Biological Sciences, nationally elected 2020-2023; Editorial Board, Journal of Virology 2020-2026; Associate Editor, Science Advances, AAAS 2018-; Committee on the Status of Women, American Society of Microbiology 2018-2024; Basic Science Awards Nominating Committee, Amer. Society of Microbiology 2016-2019; Jefferson Science Fellow, serving at the U.S. State Dept. 2015-2016; Embassy Science Fellow 2016; AAAS Kavli Science Journalism awards Screener 2020-2024; Co-chair the FASEB Summer Conference on Virus Assembly and Structure 2014

Grant Reviewer for: Stage 2 Editorial Board reviewer for the NIH Director’s New Innovator Award 2022;

Ad hoc reviewer, Biotechnology & Biological Sciences Research Council (BBSRC), UK 2020; NSF ad hoc reviewer 2017, 2019, 2020, 2020; NIH Ad Hoc reviewer Prokaryotic Molecular and Cell Biology study section 2008, 2009, 2010, 2016; Ad hoc reviewer for NIH F31 fellowship in Molecular Genetics 2007; University of Kansas Cobre grants 2007, 2016; Ad hoc reviewer for United States-Israel Binational Science Foundation 1998, 2004, 2006

Ongoing projects that I would like to highlight include:

R01GM076661 Teschke (PI) 09/23/2019 – 06/30/2025 Understanding the Protein: Protein Interactions Required for Virus Assembly

R21AI156838 Simon White (PI), Teschke (coI), Michael Lynes (coI) 12/1/2020 – 11/30/2024 Characterization of long-circulating phages isolated from in vivo mouse studies

Defense Health Agency Teschke (CoI) Robin Bogner(CoI),Physical Sciences, Inc (PI) Stabilized, Freeze Dried Bacteriophage for use in Austere Environments

1. Leavitt JC, Woodbury BM, Gilcrease EB, Bridges CM, Teschke CM, Casjens SR. Bacteriophage P22 SieA-mediated superinfection exclusion. mBio. 2024 Feb 14;15(2):e0216923. PubMed Central PMCID: PMC10883804.
2. Woodbury BM, Motwani T, Leroux MN, Barnes LF, Lyktey NA, Banerjee S, Dedeo CL, Jarrold MF, Teschke CM. Tryptophan Residues Are Critical for Portal Protein Assembly and Incorporation in Bacteriophage P22. Viruses. 2022 Jun 27;14(7) PubMed Central PMCID: PMC9320234.
3. Whitehead RD 3rd, Teschke CM, Alexandrescu AT. NMR Mapping of Disordered Segments from a Viral Scaffolding Protein Enclosed in a 23 MDa Procapsid. Biophys J. 2019 Oct 15;117(8):1387-1392. PubMed Central PMCID: PMC6817520.
4. Motwani T, Teschke CM. Architect of Virus Assembly: the Portal Protein Nucleates Procapsid Assembly in Bacteriophage P22. J Virol. 2019 May 1;93(9) PubMed Central PMCID: PMC6475791.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2022 -	Department Head, University of Connecticut, Dept. of Molecular and Cell Biology, Storrs, CT
2021 - 2021	Interim Department Head, University of Connecticut, Dept. of Molecular and Cell Biology, Storrs, CT
2016 - 2021	Associate Department Head , University of Connecticut, Dept. of Molecular and Cell Biology, Storrs, CT
2008 -	Professor, Univeristy of Connecticut, Depts. of Molcular and Cell Biology, and Chemistry, Storrs, CT
2000 - 2008	Associate Professor, University of Connecticut, Dept. of Molecular and Cell Biology, Storrs, CT
1994 - 2000	Assistant Professor, University of Connecticut, Dept. of Molecular and Cell Biology, Storrs, CT
1991 - 1994	Post-doctoral Associate, Massachusetts Institute of Technology, Advisor: Dr. Jonathan A. King, Cambridge, MA
1983 - 1990	Doctoral Graduate Student, Washington State University, Advisor: Dr. Linda L. Randall, Pullman, WA

Honors

2022	Member, CT Academy of Science and Engineering, elected, CT Academy of Science and Engineering

2022 Fulbright Scholar, University of York, UK, Fulbright
2018 Alice C. Evans Award for the Advancement of Women, American Society of Microbiology
2016 Embassy Science Fellow, Okinawa Consulate, U.S. State Department
2015 Fellow of the AAAS, elected, AAAS
2015 Jefferson Science Fellow, U.S. State Dept, National Academies of Science

C. Contribution to Science

1. We investigate the ability of viral proteins to assemble into complexes Specifically, we study the assembly of viruses primarily using bacteriophage P22 as a model system. Our goal is to understand how icosahedral viruses assemble, which will allow the design of inhibitors of the assembly process. My lab has also studied chaperoned protein folding. Below I describe in broad strokes five major projects my lab has worked on and the significant contributions arising from each:

   Viral capsid assembly—investigations of capsids: Assembly of a virus is a highly coordinated process involving sequential addition of multiple proteins, ultimately leading to an infectious virion. How do interactions between individual proteins support assembly of a whole virus? Our work addresses how viruses assemble precisely into the proper size and shape, given their capsid proteins are pliable by design. We use bacteriophage P22 as a model dsDNA virus. In bacteriophage P22, herpesviruses, adenoviruses, and many other dsDNA viruses, the initial product of assembly is a proteinaceous precursor capsid known as the procapsid, which undergoes a coordinated series of interactions to arrive at the final mature capsid. Assembly of phage P22 is a particularly tractable model where we can apply phage genetics with rigorous biochemical, biophysical and structural analyses of the reaction and assembly products. For instance, in collaboration with Martin Jarrold's lab, we have determined the mass of entire phages. My lab played a major role in a collaborative effort to solve strctures of coat protein and tail machines. In addition, my laboratory established procapsid assembly is a reversible reaction. This discovery was significant because it allowed the first application of rigorous, thermodynamic analysis to a complex assembly system. We found that the individual coat protein subunit interactions in a procapsid are weak but because of the additive nature of the interactions, the association energy of procapsids is very large.

   a. Iglesias SM, Lokareddy RK, Yang R, Li F, Yeggoni DP, David Hou CF, Leroux MN, Cortines JR, Leavitt JC, Bird M, Casjens SR, White S, Teschke CM, Cingolani G. Molecular Architecture of Salmonella Typhimurium Virus P22 Genome Ejection Machinery. J Mol Biol. 2023 Dec 15;435(24):168365. PubMed Central PMCID: PMC10842050.
   b. Leavitt JC, Gilcrease EB, Woodbury BM, Teschke CM, Casjens SR. Intravirion DNA Can Access the Space Occupied by the Bacteriophage P22 Ejection Proteins. Viruses. 2021 Jul 30;13(8) PubMed Central PMCID: PMC8402733.
   c. Asija K, Teschke CM. A Hydrophobic Network: Intersubunit and Intercapsomer Interactions Stabilizing the Bacteriophage P22 Capsid. J Virol. 2019 Jul 15;93(14) PubMed Central PMCID: PMC6600197.
   d. Keifer DZ, Motwani T, Teschke CM, Jarrold MF. Measurement of the accurate mass of a 50 MDa infectious virus. Rapid Commun Mass Spectrom. 2016 Sep 15;30(17):1957-62. PubMed Central PMCID: PMC5137368.

2. Viral capsid assembly—studies of scaffolding protein: A scaffolding protein directs assembly of coat protein and all the other internal proteins to form procapsids. We found a simple interaction between coat and scaffolding protein drives the proper assembly of the complex procapsid shell. Scaffolding protein also catalyzes the assembly of portal rings, and their incorporation into procapsids. In recent years my group has discovered that the protein:protein interactions required to generate a capsid can be disrupted readily, suggesting capsid assembly is a good drug target. We developed a novel method to use NMR to investigate disorder inside a procapsid.

a. Whitehead RD 3rd, Teschke CM, Alexandrescu AT. NMR Mapping of Disordered Segments from a Viral Scaffolding Protein Enclosed in a 23 MDa Procapsid. Biophys J. 2019 Oct 15;117(8):1387-1392. PubMed Central PMCID: PMC6817520.
b. Motwani T, Lokareddy RK, Dunbar CA, Cortines JR, Jarrold MF, Cingolani G, Teschke CM. A viral scaffolding protein triggers portal ring oligomerization and incorporation during procapsid assembly. Sci Adv. 2017 Jul;3(7):e1700423. PubMed Central PMCID: PMC5529062.
c. Cortines JR, Weigele PR, Gilcrease EB, Casjens SR, Teschke CM. Decoding bacteriophage P22 assembly: identification of two charged residues in scaffolding protein responsible for coat protein interaction. Virology. 2011 Dec 5;421(1):1-11. PubMed Central PMCID: PMC3208733.
d. Padilla-Meier GP, Teschke CM. Conformational changes in bacteriophage P22 scaffolding protein induced by interaction with coat protein. J Mol Biol. 2011 Jul 8;410(2):226-40. PubMed Central PMCID: PMC3125579.

3. Viral capsid assembly—studies of portal protein: Portal proteins of dsDNA phages and viruses are essential for both DNA packaging and ejection into host cells. As such, portal proteins are excellent targets for anti-viral compounds. When these viruses assemble, a portal protein complex is incorporated at only one vertex of the capsid. This specificity of assembly is not understood. We are characterizing the assembly of P22 procapsid with the portal ring. We have discovered that scaffolding protein catalyzes portal ring assembly and that portal nucleates assembly of procapsids. The portal also organizes the ejection protein in the DNA filled head.

   a. Woodbury BM, Motwani T, Leroux MN, Barnes LF, Lyktey NA, Banerjee S, Dedeo CL, Jarrold MF, Teschke CM. Tryptophan Residues Are Critical for Portal Protein Assembly and Incorporation in Bacteriophage P22. Viruses. 2022 Jun 27;14(7) PubMed Central PMCID: PMC9320234.
   b. Leavitt JC, Gilcrease EB, Woodbury BM, Teschke CM, Casjens SR. Intravirion DNA Can Access the Space Occupied by the Bacteriophage P22 Ejection Proteins. Viruses. 2021 Jul 30;13(8) PubMed Central PMCID: PMC8402733.
   c. Motwani T, Teschke CM. Architect of Virus Assembly: the Portal Protein Nucleates Procapsid Assembly in Bacteriophage P22. J Virol. 2019 May 1;93(9) PubMed Central PMCID: PMC6475791.
   d. Lokareddy RK, Sankhala RS, Roy A, Afonine PV, Motwani T, Teschke CM, Parent KN, Cingolani G. Portal protein functions akin to a DNA-sensor that couples genome-packaging to icosahedral capsid maturation. Nat Commun. 2017 Jan 30;8:14310. PubMed Central PMCID: PMC5290284.

4. Phage P22 coat protein folding and assembly: The cytoplasm of a cell is a crowded environment with DNA, RNA and proteins, all found at very high concentrations, which can lead to misfolding and misassembly of new polypeptide chains. In bacteria there are many molecular chaperones, including GroEL and GroES, to assist in the folding and assembly of substrate polypeptides. but how chaperones recognize substrates remains unclear. The folding of coat protein of phage P22 is a particularly appropriate model for understanding how GroEL/S interact with substrate polypeptides because single amino acid substitutions, which lead to a temperature-sensitive-folding phenotype (tsf), cause coat protein folding intermediates to become substrates for the chaperones. WT coat protein, in contrast, does not require GroEL/S for folding. By investigating the folding of the tsf coat proteins my laboratory defined some of the mechanisms that target proteins to be substrates for chaperones.

   a. Asija K, Teschke CM. Of capsid structure and stability: The partnership between charged residues of E-loop and P-domain of the bacteriophage P22 coat protein. Virology. 2019 Aug;534:45-53. PubMed Central PMCID: PMC6614003.
   b. D'Lima NG, Teschke CM. A Molecular Staple: D-Loops in the I Domain of Bacteriophage P22 Coat Protein Make Important Intercapsomer Contacts Required for Procapsid Assembly. J Virol. 2015 Oct;89(20):10569-79. PubMed Central PMCID: PMC4580156.

c. Suhanovsky MM, Teschke CM. An intramolecular chaperone inserted in bacteriophage P22 coat protein mediates its chaperonin-independent folding. J Biol Chem. 2013 Nov 22;288(47):33772-33783. PubMed Central PMCID: PMC3837121.

d. Parent KN, Teschke CM. GroEL/S substrate specificity based on substrate unfolding propensity. Cell Stress Chaperones. 2007 Spring;12(1):20-32. PubMed Central PMCID: PMC1852890.

5. Folding and NMR studies of P22 coat protein I-domain and other capsid proteins: We completed a solution NMR structure of an inserted domain in P22 coat protein and determined this small domain is crucial for folding and stability of the entire coat protein. The I-domain folds much faster than the remainder of the protein, and provides a folding nucleus for the unusal HK97 fold. We were the first group to ascribe a function for an accessory domain inserted into the HK97 fold. We have also investigated the unusual folding of the phage L decorator protein, and found that its assembly is templated on the DNA filled capsid.

   a. Woodbury BM, Newcomer RL, Alexandrescu AT, Teschke CM. Templated trimerization of the phage L decoration protein on capsids. bioRxiv. 2024 Sep 8; PubMed Central PMCID: PMC11398494.

   b. Tripler TN, Kaplan AR, Alexandrescu AT, Teschke CM. Conservation and Divergence of the I-Domain Inserted into the Ubiquitous HK97 Coat Protein Fold in P22-Like Bacteriophages. J Virol. 2019 May 1;93(9) PubMed Central PMCID: PMC6475800.

   c. Harprecht C, Okifo O, Robbins KJ, Motwani T, Alexandrescu AT, Teschke CM. Contextual Role of a Salt Bridge in the Phage P22 Coat Protein I-Domain. J Biol Chem. 2016 May 20;291(21):11359-72. PubMed Central PMCID: PMC4900280.

   d. Newcomer RL, Fraser LCR, Teschke CM, Alexandrescu AT. Mechanism of Protein Denaturation: Partial Unfolding of the P22 Coat Protein I-Domain by Urea Binding. Biophys J. 2015 Dec 15;109(12):2666-2677. PubMed Central PMCID: PMC4699920.

Complete List of Published Work in My Bibliography:
https://www.ncbi.nlm.nih.gov/myncbi/1fA_Czh9bi2k7/bibliography/public/

- NIH Review Group BST-F 40 (Program Grant in Electron Microscopy) – *ad hoc* member, Dec 2007.
- Human Frontier Science Program – *ad hoc* member, Oct 2007.
- Agence Nationale de la Recherche (Technological platforms for life sciences), France, Jul 2007.
- NIH Study Section "Topics in Bacterial Pathogenesis" – *ad hoc* member, Oct 2006.
- National Research Foundation, South Africa, Oct 2006.
- Comité Scientifique UMR6026, CNRS, France, Feb 2003.

Honors

- Fibrous Proteins Merit Award, Massey University, 1986.
- Special Achievement Award, NIAMS/NIH, September 1997: *In recognition and appreciation of special achievement.*
- Group Merit Award, NIAMS/NIH, September 1998: *In recognition of pioneering contributions to image processing, advancing the resolution attainable in biological electron microscopy.*

C. Contributions to Science

1. My work on improving high-resolution structure determination from cryo-electron micrographs was effective in achieving the first sub-nanometer resolution model of a virus capsid by EM in 1997. Such results have now become commonplace, and our subsequent work on the same viral system, hepatitis B, has revealed important details on capsid assembly, structure, and antibody binding.
   a. Conway JF, Cheng N, Zlotnick A, Wingfield PT, Stahl SJ & Steven AC (1997) Nature 386, 91-94, PMID: 9052787. Visualization of a 4-helix bundle in the hepatitis B virus capsid by cryo-electron microscopy.
   b. Conway JF & Steven AC (1999) J Struct Biol 128, 106-118. PMID: 10600565. Methods for reconstructing density maps of single particles from cryoelectron micrographs to subnanometer resolution.
   c. Conway JF, Watts NR, Belnap DM, Cheng N, Stahl SJ, Wingfield PT & Steven AC (2003) J Virol 77, 6466-6473. PMCID: PMC155010. Characterization of a conformational epitope on hepatitis B virus core antigen and quasiequivalent variations in antibody binding.
   d. Watts NR, Conway JF, Cheng N, Stahl SJ, Steven AC & Wingfield PT. (2011) J Mol Biol 409, 202-213. PMCID: PMC3095675. Role of the propeptide in controlling conformation and assembly state of hepatitis B virus e-antigen.

2. Tailed, double-stranded DNA bacteriophages are the largest family of viruses on the planet, and share deep structural connections with herpesviruses and tailed archaeal viruses. One phage in particular, HK97, has been an archetype for capsid structure and maturation, and has been extensively studied to understand how this class of capsid assembles and functions.
   a. Conway JF, Wikoff WR, Cheng N, Duda RL, Hendrix RW, Johnson JE & Steven AC (2001) Science 292, 744-748. PMID: 11326105. Virus maturation involving large subunit rotations and local refolding.
   b. Hua J, Huet A, Lopez CA, Toropova K, Pope WH, Duda RL, Hendrix RW & Conway JF. (2017) mBio 8, e01579-17. PMCID: PMC5646251. Capsids and genomes of jumbo-sized bacteriophages reveal the evolutionary reach of the HK97 fold.
   c. Huet A, Duda RL, Boulanger P & Conway JF. (2019) PNAS 116, 21037-21046. PMCID: PMC6800373. Capsid expansion of bacteriophage T5 revealed by high resolution cryoelectron microscopy.
   d. Huet A, Oh B, Maurer J, Duda RL & Conway JF (2023) Sci Adv 9, eadg8868. PMCID: PMC10275583. A symmetry mismatch unraveled: How phage HK97 scaffold flexibly accommodates a 12-fold pore at a 5-fold viral capsid vertex.

3. High-resolution cryoEM has been the mainstay of my research efforts and directed at mostly virus capsids, an abundant and biomedically important class of pathogen. A major focus has been on herpesviruses, and detailing the capsid architecture and the structure and function of essential minor capsid proteins.
   a. Toropova K, Huffman JB, Homa FL & Conway JF. (2011) J Virol 85, 7513-7522. PMCID: PMC3147944. The herpes simplex virus 1 UL17 protein is the second constituent of the capsid

vertex-specific component required for DNA packaging and retention.

b. Homa FL, Huffman JB, Toropova K, Lopez HR, Makhov AM & Conway JF. (2013) J Mol Biol 425, 3415-3428. PMCID: PMC3779361. Structure of the pseudorabies virus capsid: comparison with herpes simplex virus type 1 and differential binding of essential minor proteins.
c. Huet A, Makhov AM, Huffman JB, Vos M, Homa FL & Conway JF. (2016) Nat Struct Mol Biol **23**, 531-539, 2016. PMCID: PMC4899274. Extensive subunit contacts underpin herpesvirus capsid stability and interior-to-exterior allostery.
d. Huet A, Huffman JB, Conway JF and Homa FL. (2020). J Virol **94**, e01534-20. PMC7925205. The role of the herpes simplex virus CVSC proteins at the capsid portal vertex.

4. A highly productive collaboration with Dr Susan Hafenstein (Penn State Med School) has led to a series of publications on several viruses, including the following four on enterovirus 71 focusing on differences in structures between procapsid, capsid and A-particle states as visualized directly by cryoEM and through labeling of antibodies that are neutralizing in some cases. These experiments are developing an understanding of capsid function in assembly and infection that will be essential for the design of anti-viral strategies.

a. Shingler KL, Yoder JL, Carnegie MS, Ashley RE, Makhov AM, Conway JF & Hafenstein S. (2013) PLoS Pathog 9: e1003240. PMCID: PMC3605244. The enterovirus 71 A-particle forms a gateway to allow genome release: a cryoem study of picornavirus uncoating.
b. Shingler KL, Cifuente JO, Ashley RE, Makhov AM, Conway JF & Hafenstein S. (2015) J Virol 89, 1900-1908. PMCID: PMC4300772. The enterovirus 71 procapsid binds neutralizing antibodies and rescues virus infection in vitro.
c. Lee H, Shingler KL, Organtini LJ, Ashley RE, Subramanium S, Makhov AM, Conway JF & Hafenstein S. (2016) Science Advances 2, e1501929. PMCID: PMC4996645. The novel asymmetric entry intermediate of a picornavirus captured with nanodiscs.
d. Goetschius DJ, Hartmann SR, Organtini LJ, Callaway H, Huang K, Bator CM, Ashley RE, Makhov AM, Conway JF, Parrish CR, Hafenstein SL. (2021) PNAS USA 118, e2025452118. PMCID: PMC8201801. High-resolution asymmetric structure of a Fab-virus complex reveals overlap with the receptor binding site.

5. I have also been involved in a variety of projects, including cryoEM of amyloid filaments, mitochondria, exosomes, encapsulins, and the SARS-CoV2 spike complexed with neutralizing antibodies, as well as electron microscopy applied to crystal diffraction. Several of many examples are listed here.

a. Stevenson HP, Lin G, Barnes CO, Sutkeviciute I, Krzysiak T, Weiss SC, Reynolds S, Wu Y, Nagarajan V, Makhov AM, Lawrence R, Lamm E, Clark L, Gardella TJ, Hogue BG, Ogata CM, Ahn J, Gronenborn AM, Conway JF, Vilardaga JP, Cohen AE & Calero G. (2016) Acta Crystallogr D Struct Biol, 72, 603-615. PMCID: PMC4854312. Transmission electron microscopy for the evaluation and optimization of crystal growth.
b. Sun D, Sang Z, Kim YJ, Xiang Y, Cohen T, Belford AK, Huet A, Conway JF, Sun J, Taylor DJ, Schneidman-Duhovny D, Zhang C, Huang W, Shi Y. (2021) Nat Commun 12, 4676. PMCID: PMC8333356. Potent neutralizing nanobodies resist convergent circulating variants of SARS-CoV- 2 by targeting diverse and conserved epitopes.
c. Eren E, Watts NR, Conway JF, Wingfield PT. (2024). PNAS 121, e2400426121. PMCID: PMC11126975. *Myxococcus xanthus* encapsulin cargo protein EncD is a flavin-binding protein with ferric reductase activity.
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