



From proteins to people: understanding Huntington's disease at the molecular level

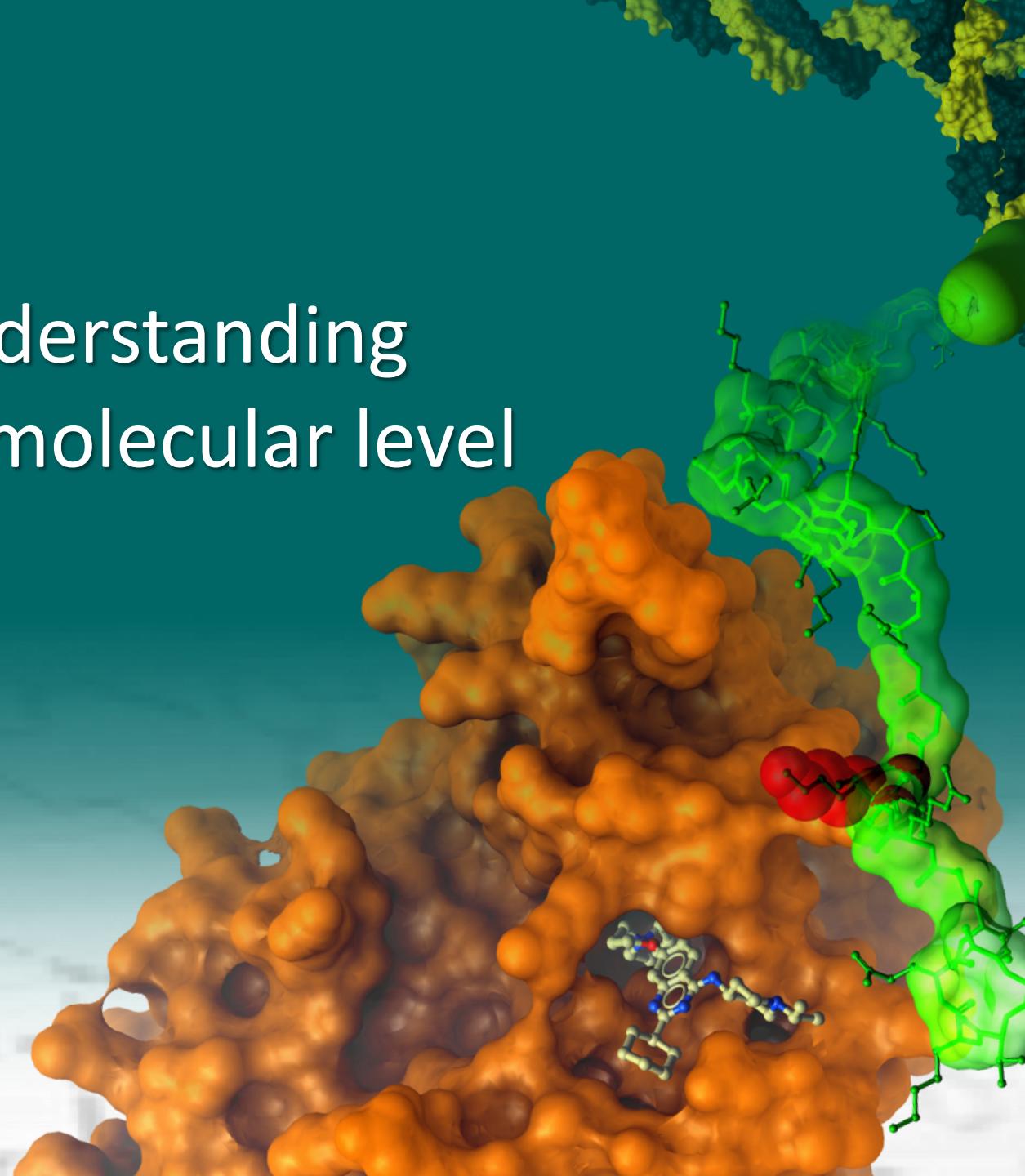
Dr Rachel J. Harding
HDSA Convention, Boston MA
28th June 2019



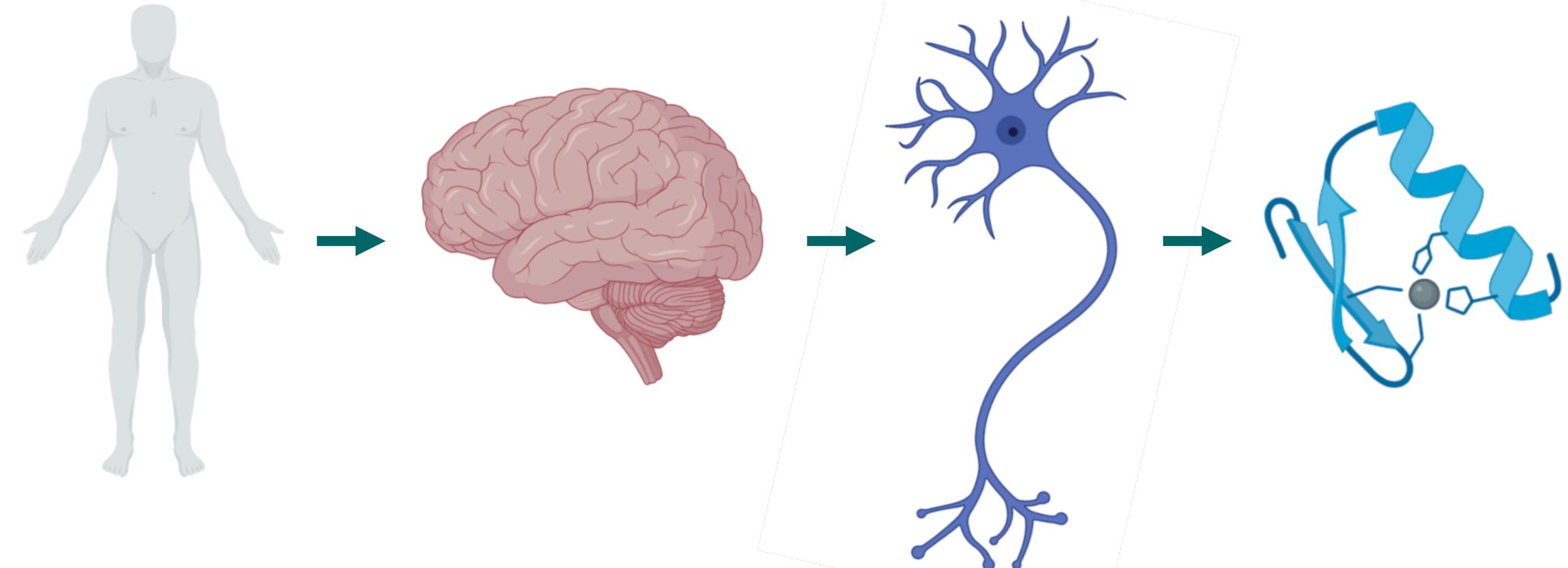
McGill



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Understanding biology at the molecular level



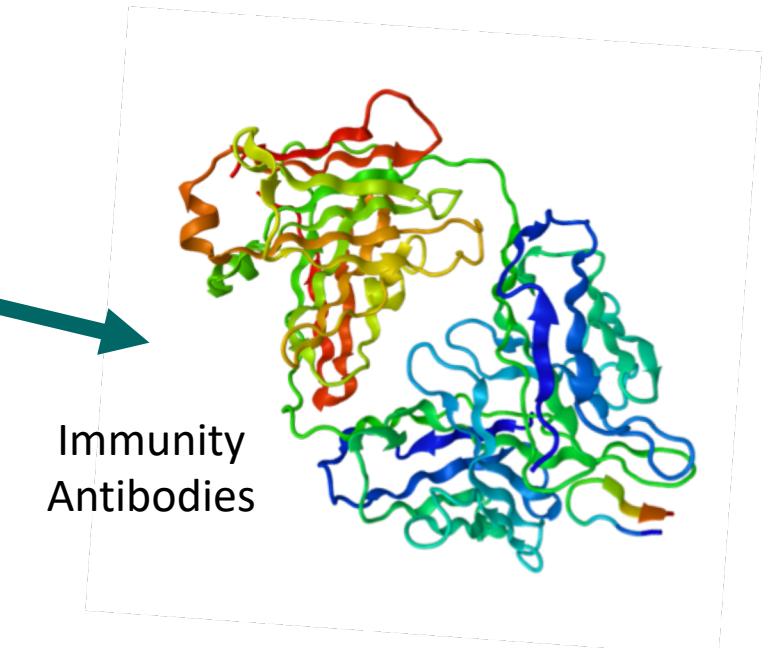
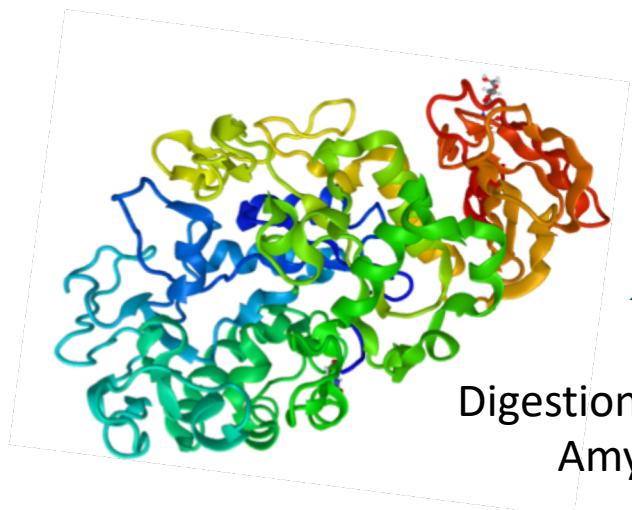
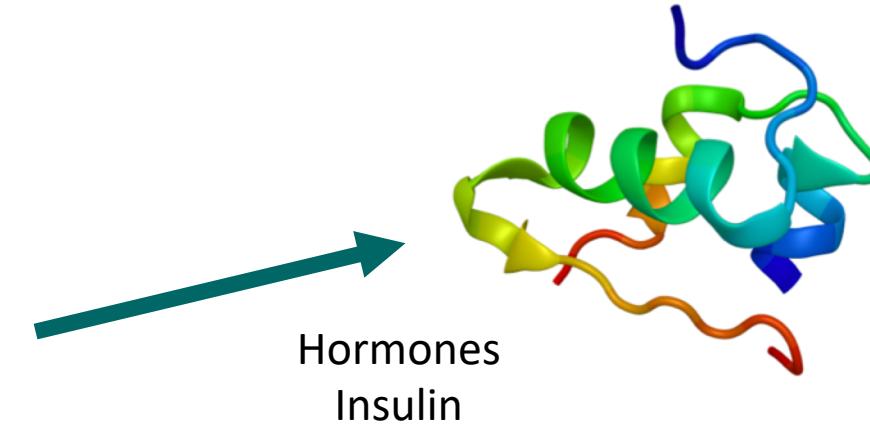
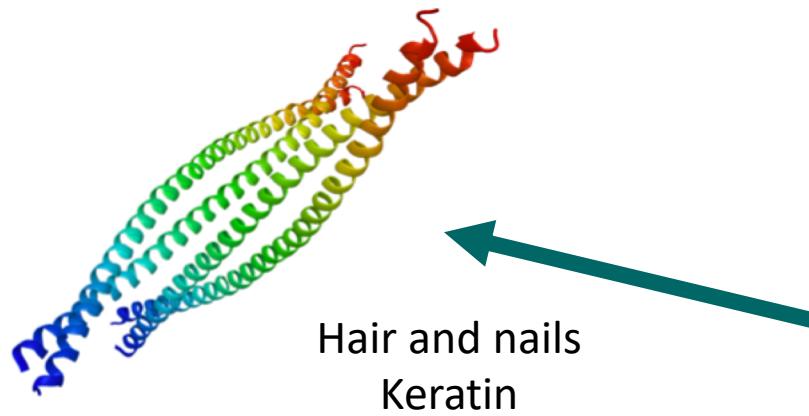
2 metres
0.2 m

15 centimetres
0.15 m

20 micrometres
0.00002 m

5 nanometres
0.00000005 m

Proteins are the molecules which do the work in cells of our bodies

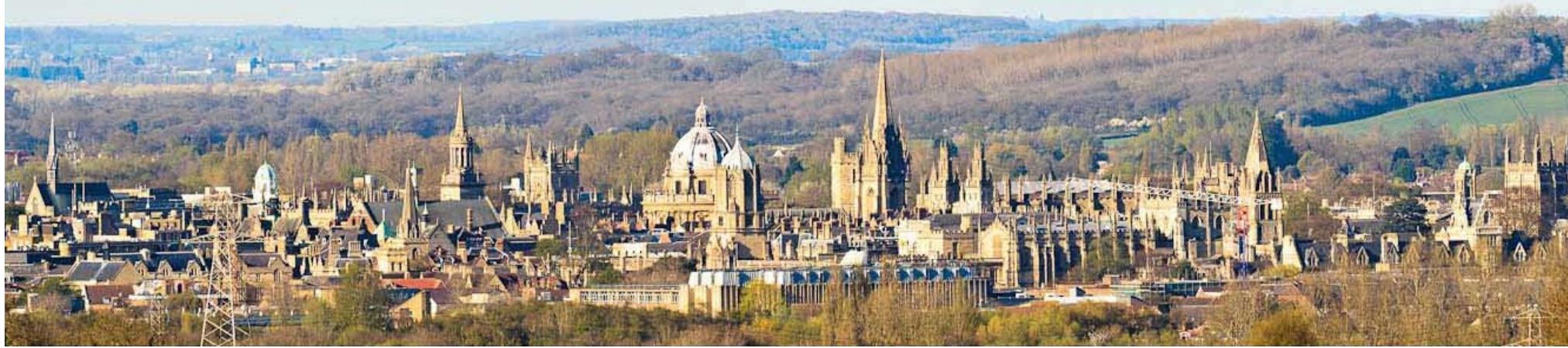


Understanding protein molecules: the devil is in the details



Understanding protein molecules: the devil is in the details



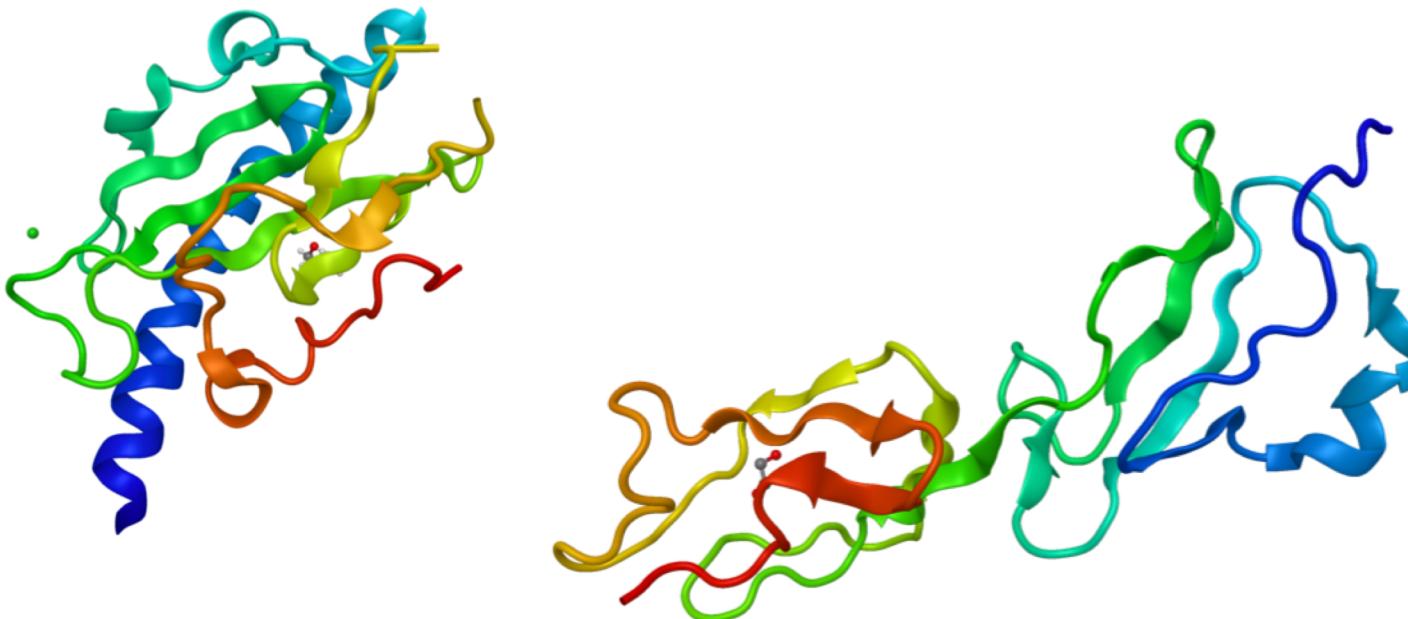


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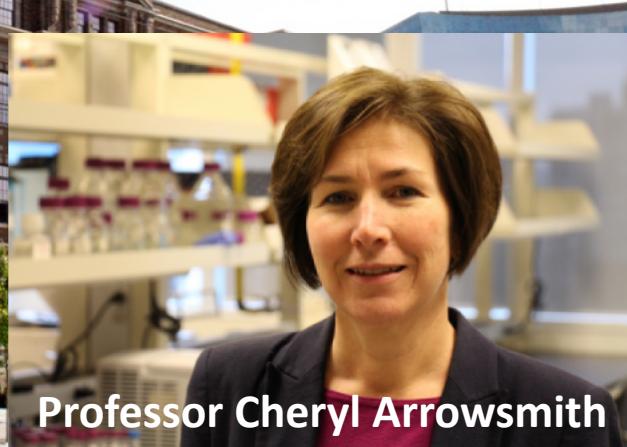
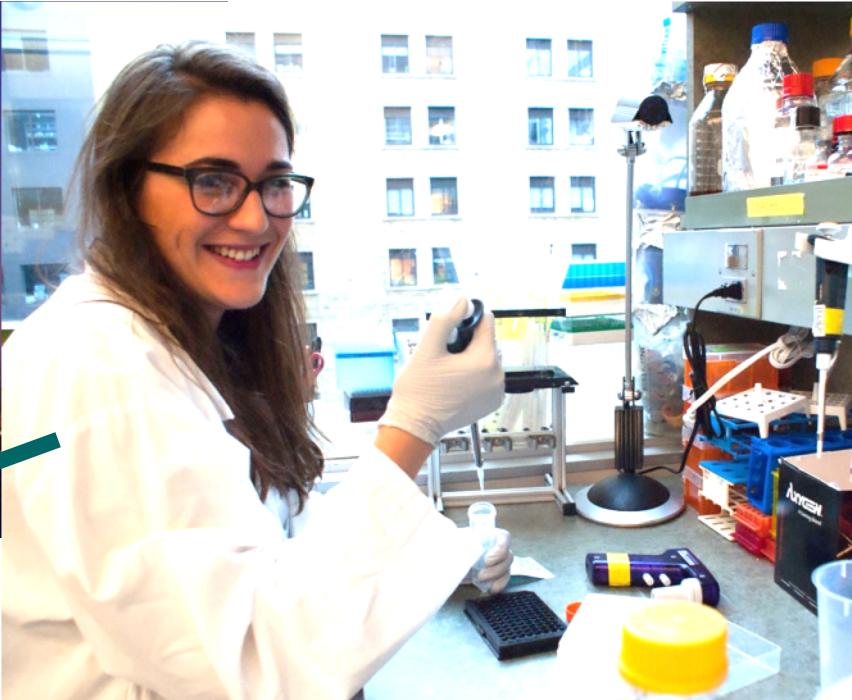
Thesis

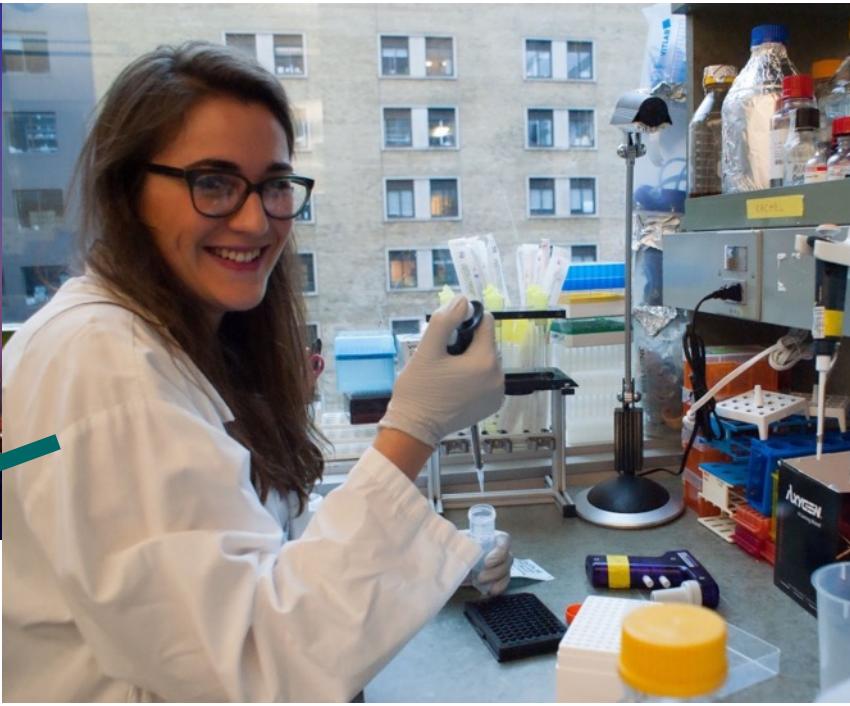
Interactions of *Neisseria meningitidis* with the human immune system



Professor Susan Lea

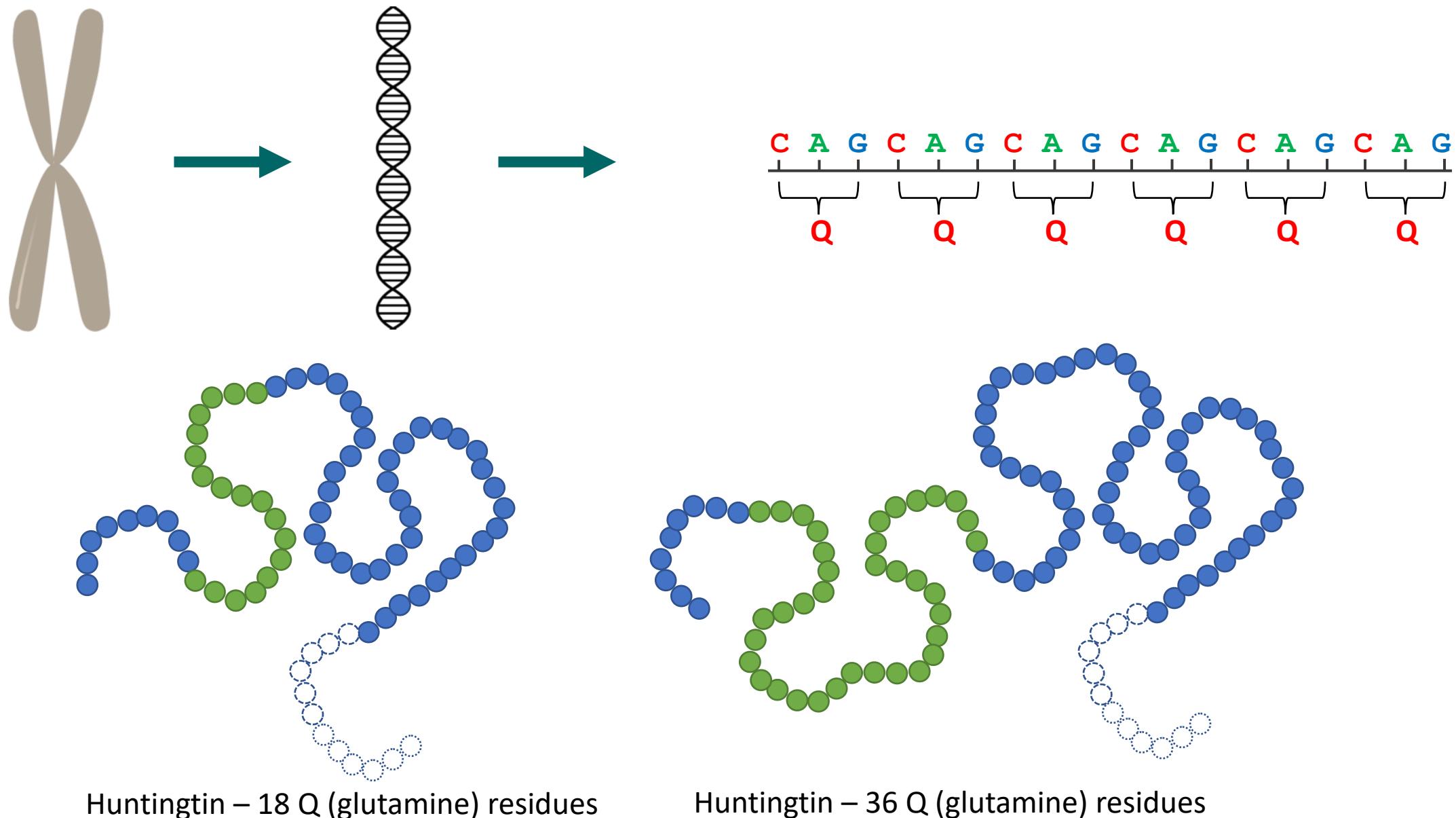






Professor Cheryl Arrowsmith

CAG repeats in the huntingtin gene encode a polyQ repeat in the huntingtin protein



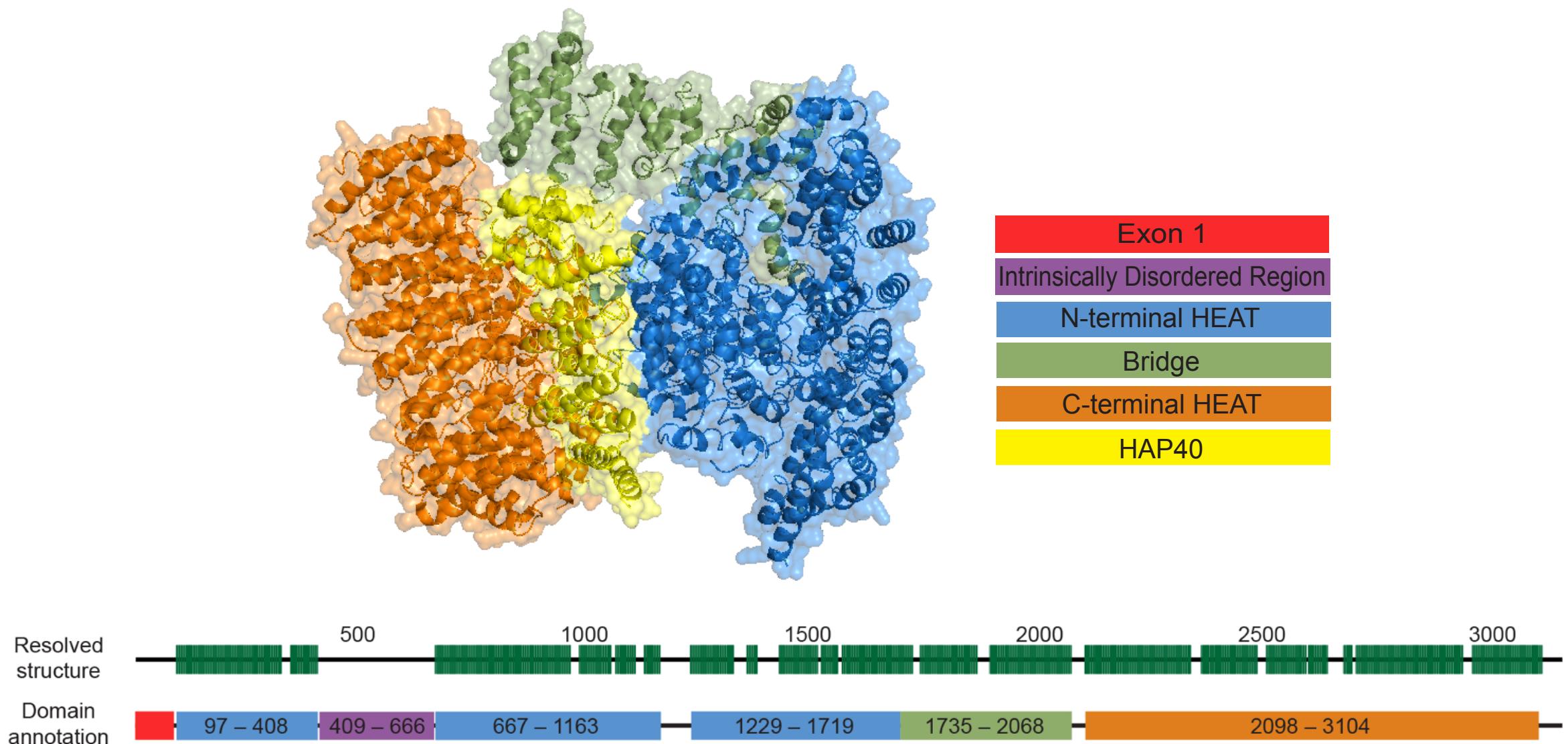
PolyQ lengths above 35 change the function of the huntingtin protein

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TCLRNVHKVTC

PolyQ lengths above 35 change the function of the huntingtin protein

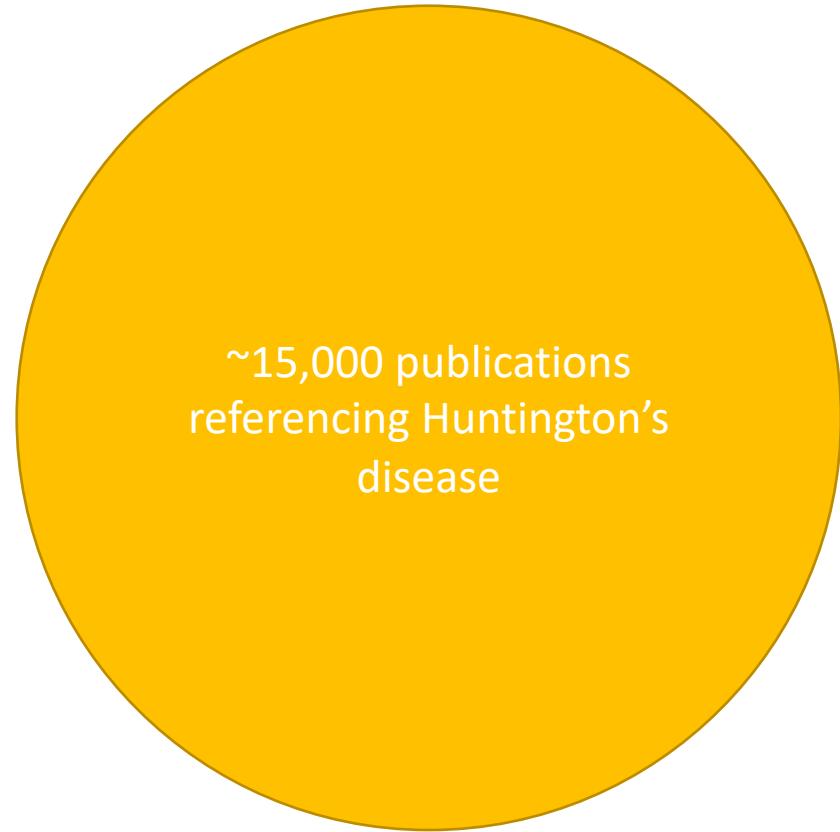
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What does the huntingtin protein look like? What does this tell us about HD?



A lack of available biochemical tools have limited investigation of the HTT protein

Data from PubMed
search March 2019 for
“Huntington’s disease” &
“purified huntingtin protein”



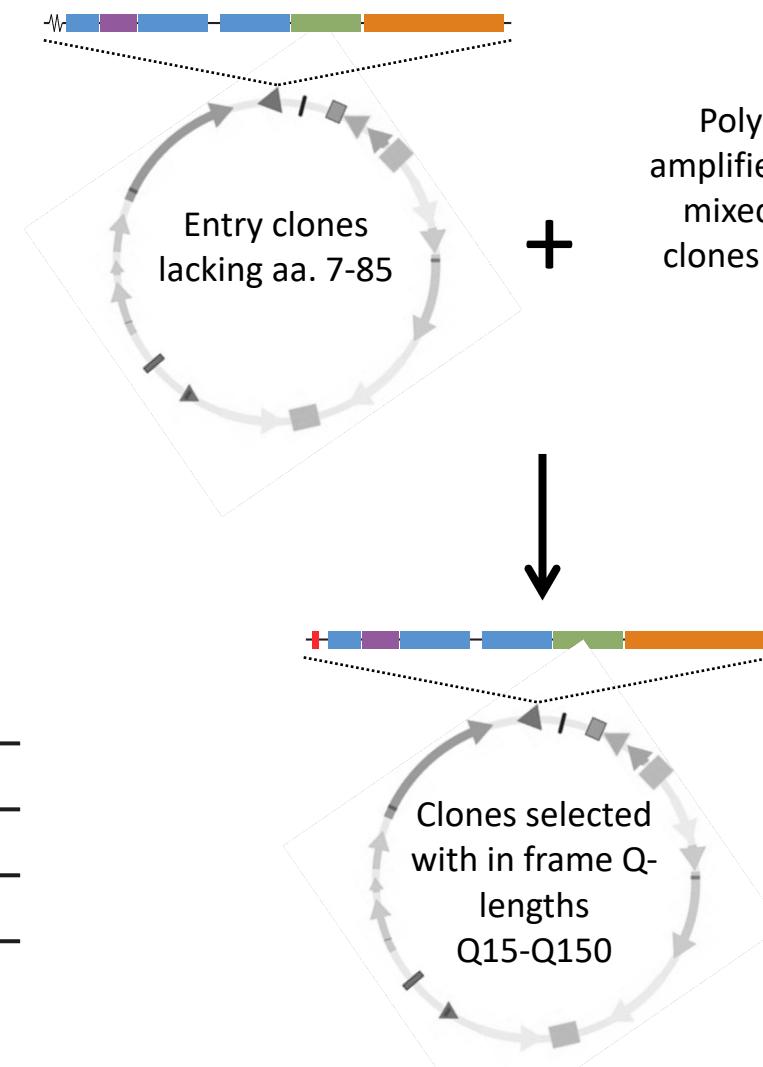
<50 publications referencing
purified full-length
huntingtin protein samples

Aim: Design and characterise an open toolkit of Huntington’s disease research resources for biochemical investigation of full-length HTT

pBacMam full-length huntingtin constructs cloned to freely share with HD community

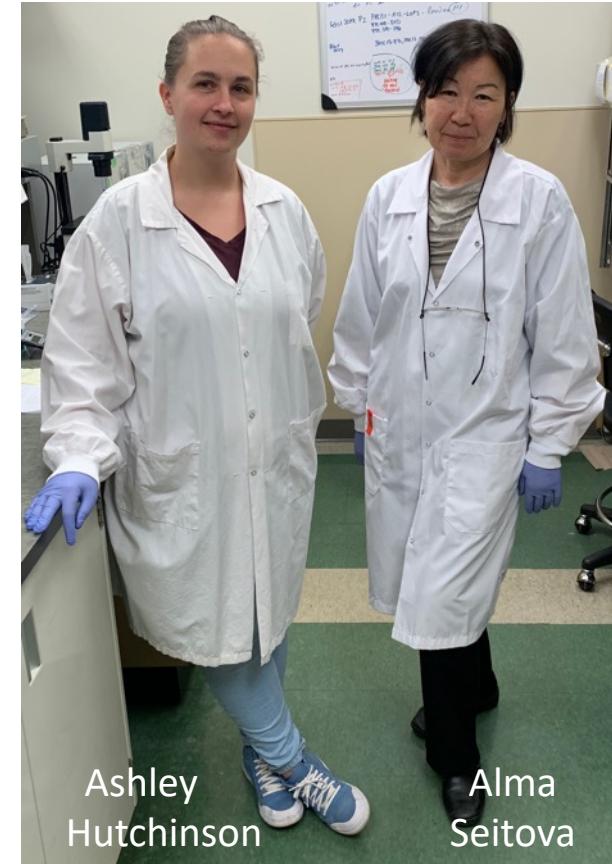
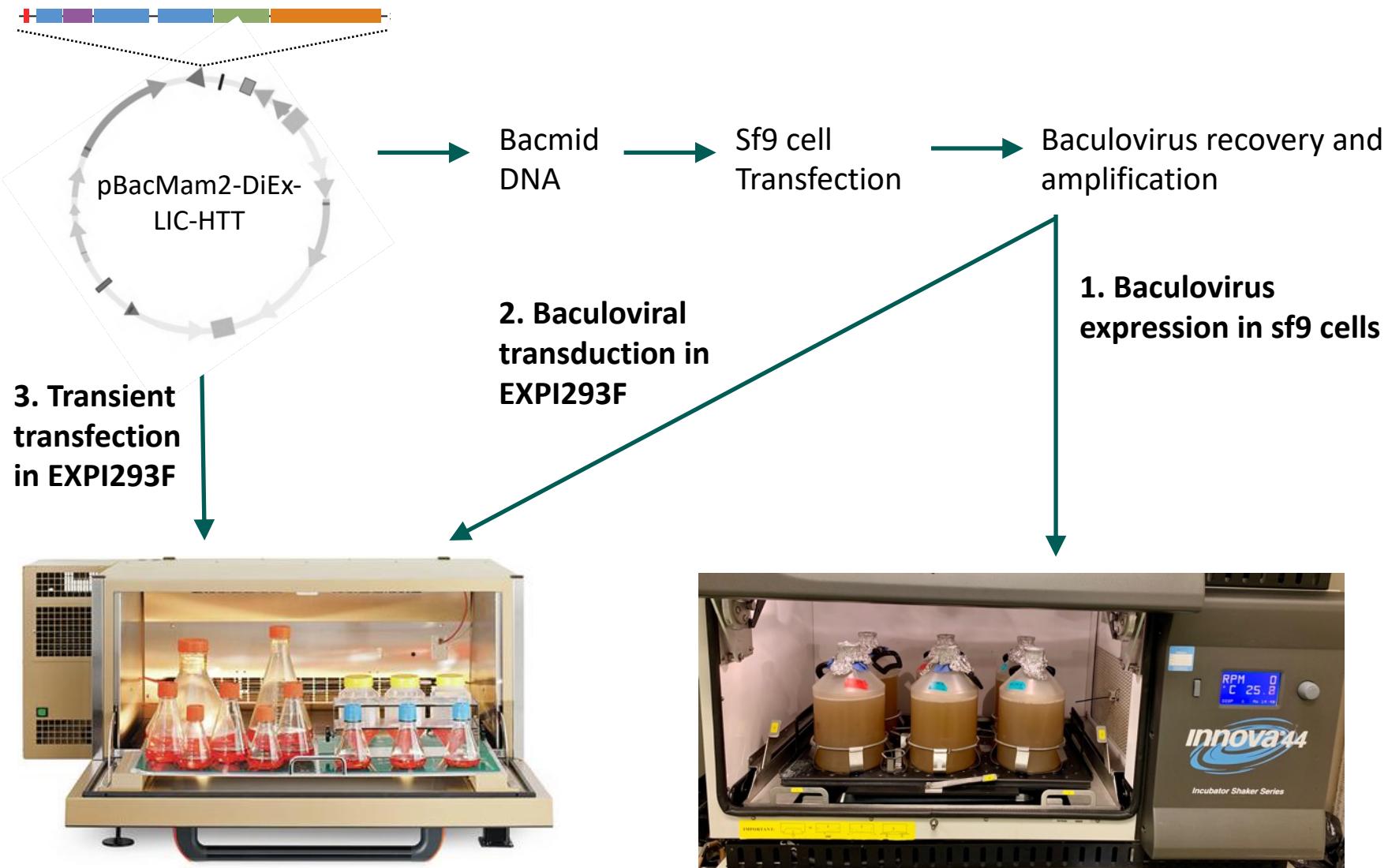


	N-terminal FLAG-tag	C-terminal FLAG-tag
General population	15, 19, 23	19, 23, 24, 25, 30
HD patients		36, 42, 48
Juvenile HD patients	51, 66, 73, 78, 79, 85	52, 54, 60, 66, 73, 79
Extreme expansions	139, 142, 145	109, 145



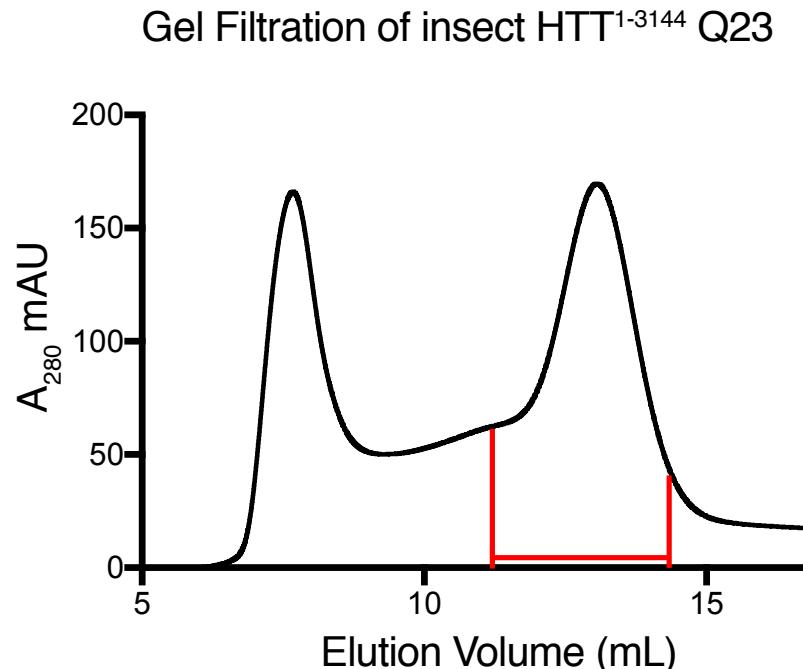
Our series of huntingtin constructs allow you to make any polyQ-length huntingtin

Huntingtin expression in insect and human cells using pBacMam2-DiEx-LIC constructs

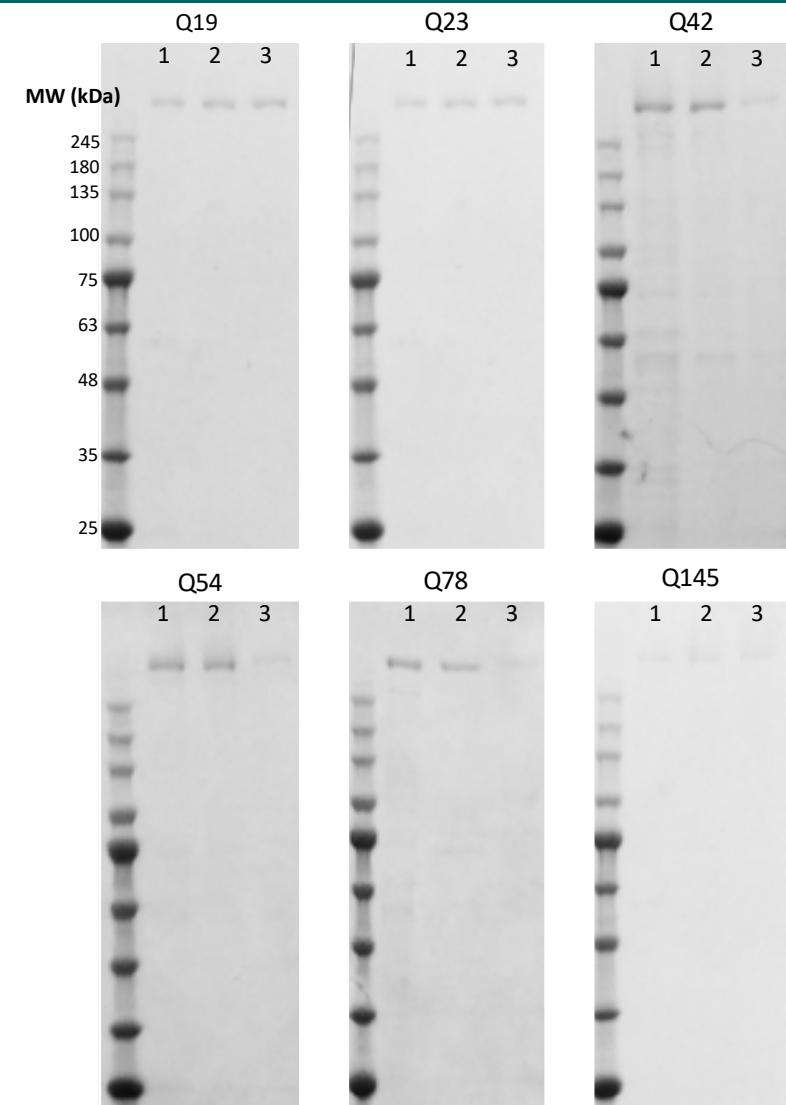
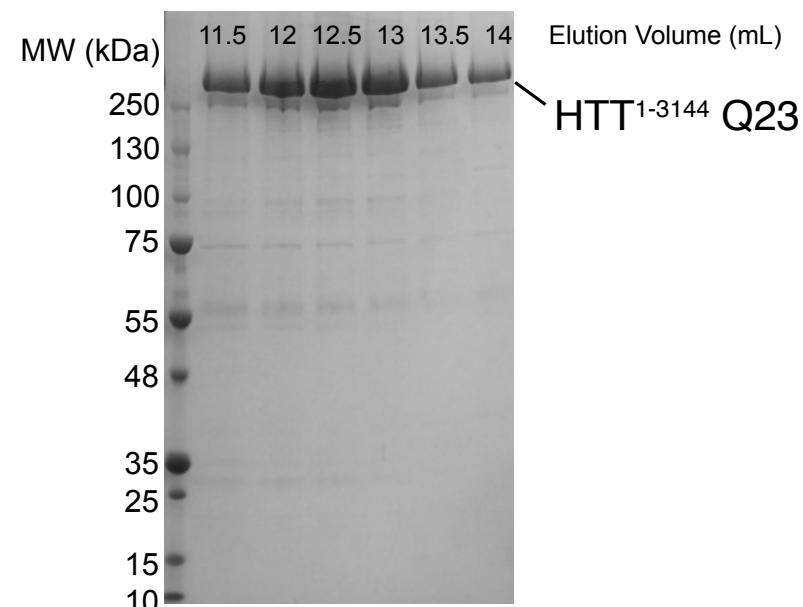


Suspension culture allows scalable production so you can make lots of huntingtin!

Full-length huntingtin of different Q-lengths can be trivially purified



4-20% SDS-PAGE of monomer peak fractions

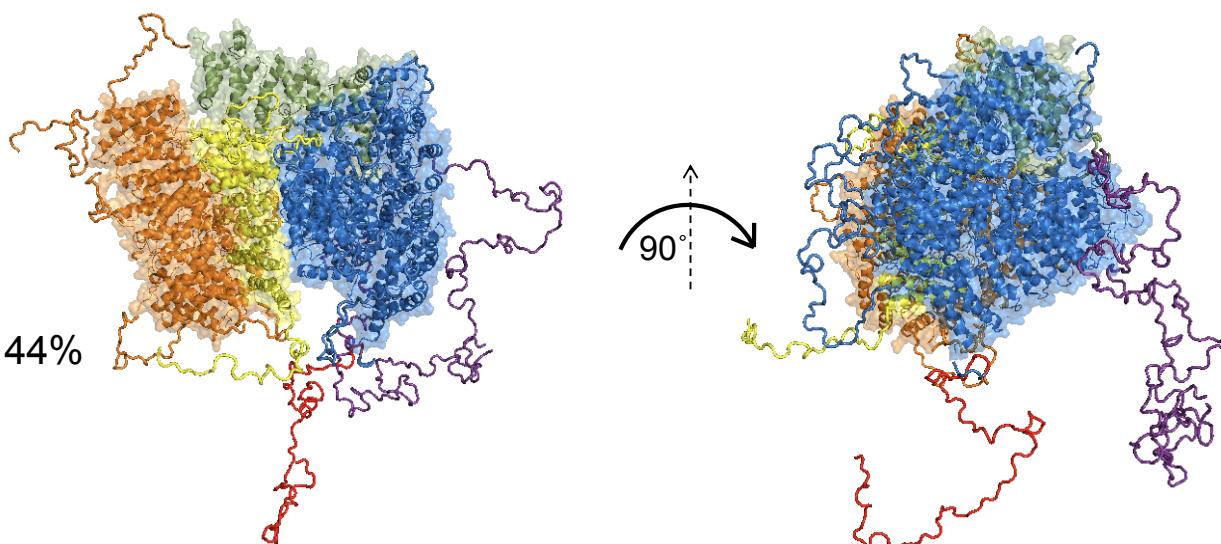


Huntingtin proteins can be extracted to high purity and high yield

- 1 - baculovirus expression in sf9 insect cells
- 2 - transient transfection in mammalian EXPI293F cells
- 3 - transduction in mammalian EXPI293F cells

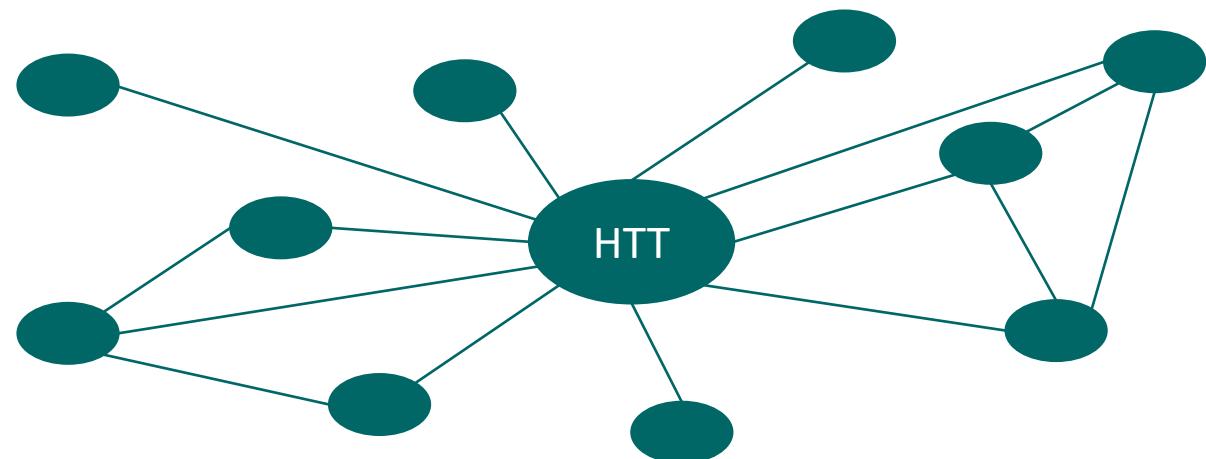
Trying to get a look at the polyQ region of the huntingtin protein molecule

Computational approaches:



44%

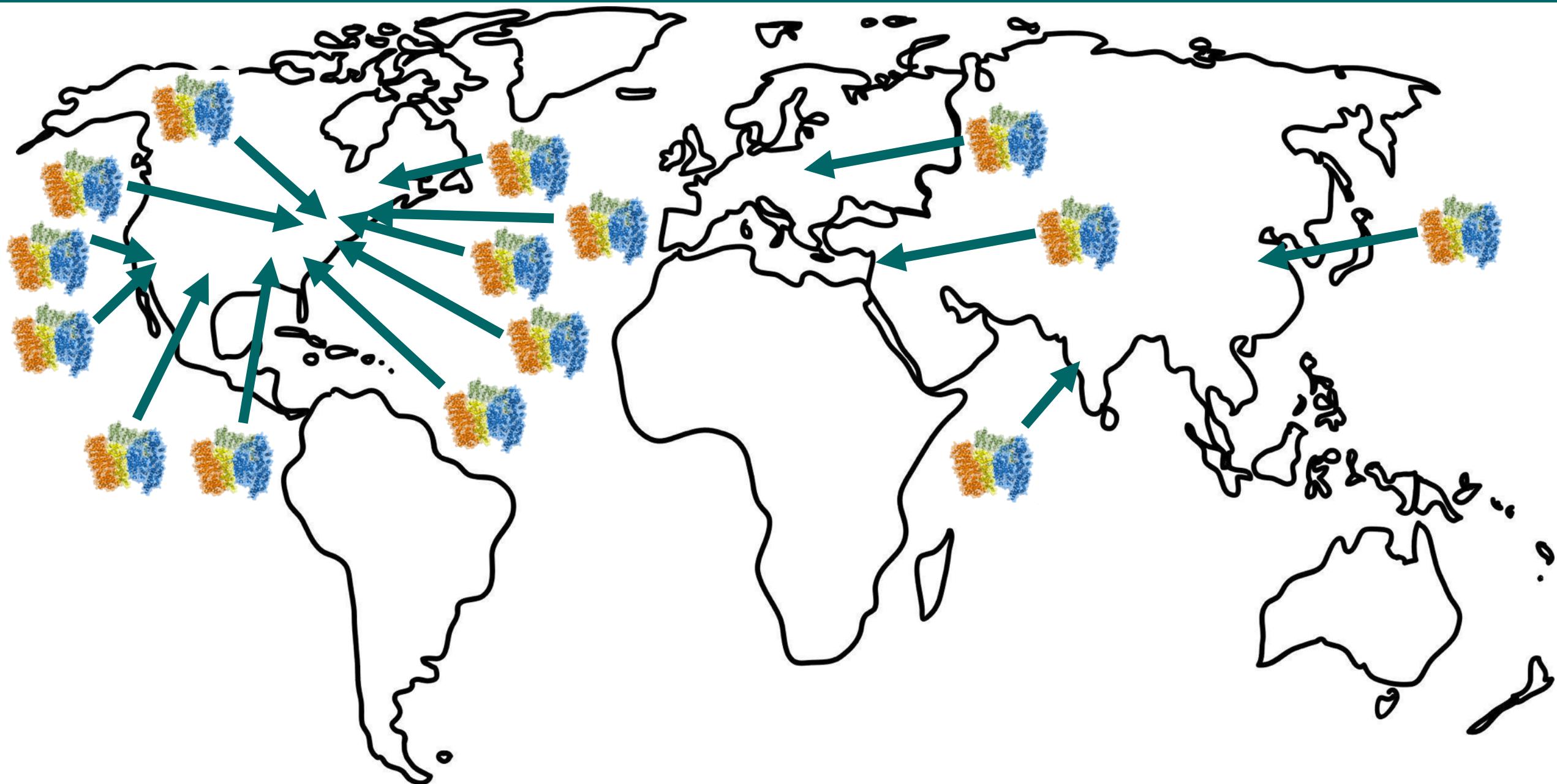
Finding other proteins which bind the huntingtin molecule:



Jacob McAuley

Claudia Alvarez

pBacMam full-length huntingtin constructs freely shared with HD community



All huntingtin plasmids and entry clones from this study are available through the Addgene repository



31

Total no. samples requested since December 2018

12

No. research groups requesting samples since December 2018

15

No. different constructs (Q-lengths) requested since December 2018



We help provide scientists with huntingtin protein of any Q-length either via collaboration or CRO partnership

12

No. research groups huntingtin protein samples shared through collaboration since October 2017

2

CRO requests for purified HTT protein since January 2019

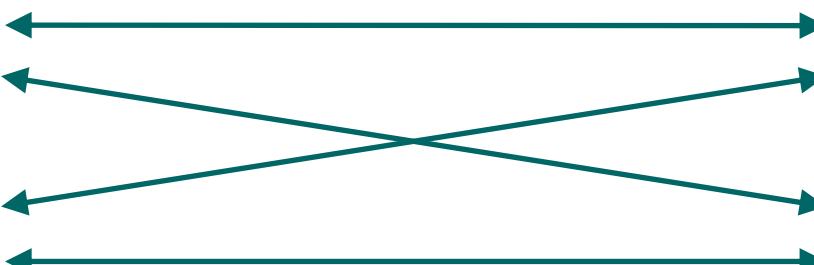
Full-length huntingtin protein interaction investigating collaborative consortium



Rachel Harding and Cheryl Arrowsmith
SGC, University of Toronto



Erich Wanker and Philipp Trepte
Max-Delbrück-Center for Molecular Medicine

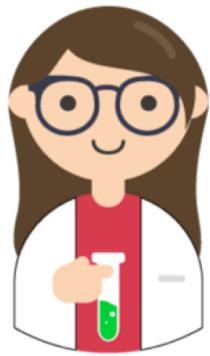


Stefan Kochanek
Ulm University



Christopher Ross and Tamara Ratovitski
John Hopkins University





1. Experiments completed in lab



2. Materials, methods, data and analysis uploaded to <https://zenodo.org> in open notebook community

Successful generation of fragments of the HTT protein and improving the purification procedure for the HTT-HAP40 complex

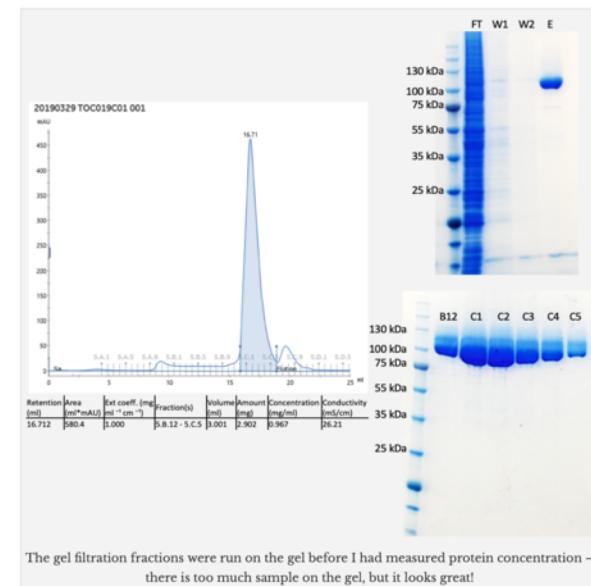
April 3, 2019 · racheljaneharding · Leave a comment · Edit

It has now been almost 2 years since I set out to try and make fragments of the huntingtin protein which might be amenable to structural analysis with X-ray crystallography. X-ray crystallography is a fantastic method and allows us to see the molecules in very fine atomic detail which is important if we are to understand the intricacies of the elusive huntingtin protein molecule. It has been a long hard road with almost none of our extensive cloning efforts producing any expression constructs which made sufficient yields of protein. X-ray crystallography is a protein-expensive method so we need milligram (lots of protein). But finally, I have purified milligrams of different huntingtin fragment protein samples!!!

It should be made very clear that this has been a big team effort with cloner extraordinaire, Peter Loppnau, the eukaryotic production, Ashley Hutchinson and Alma Seitova as well as Linda Lin doing a lot of the heavy lifting on our cloning and eukaryotic production pipeline so I am very grateful for all of their hard work. Turns out that my construct design was fine but the expression vector we used made a huge difference (this is the piece of DNA which we insert different parts of the huntingtin gene). Switching from pFBHOH-MHL to pBMDEL gave us great yields! Here is the C-terminal HEAT domain protein I purified – so much pure protein! All of the other data can be found on [Zenodo](#).



3. Lay summary of experiment including discussion of context, aims and next steps plus links to Zenodo data upload



4. Share open notebook post via Twitter



ACKNOWLEDGEMENTS



SGC and UHN

Jacob McAuley
Claudia Alvarez
Peter Loppnau
Ashley Hutchinson
Alma Seitova
Mani Ravichandran
Levon Halabelian
Suzanne Ackloo
Shili Duan
Sasha Lemak
Linda Lin
Cheryl Arrowsmith
Aled Edwards

Ulm University

Stefan Kochanek

EPFL

Hilal Lashuel
Driss Boudeffa

CHDI Foundation

Leticia Toledo-Sherman
Matt Lee
Liz Doherty

Oxford University

Justin Deme
Susan Lea
Bass Hassan

McMaster University

Ray Truant
Tam Maiuri

Advanced Proton Source

Xiaobing Zuo
Lixin Fan

John Hopkins University

Christopher Ross
Tamara Ratovitski

Western Washington University

Jeff Carroll

A*STAR

Mahmoud Pouladi

Washington University St Louis

Alex Holehouse

Sick Kids Hospital Toronto

Chris Pearson
Terence Gall-Duncan
Babak Koucheki

Max-Delbrück-Center for Molecular Medicine

Erich Wanker
Philipp Trepte
Anne Ast

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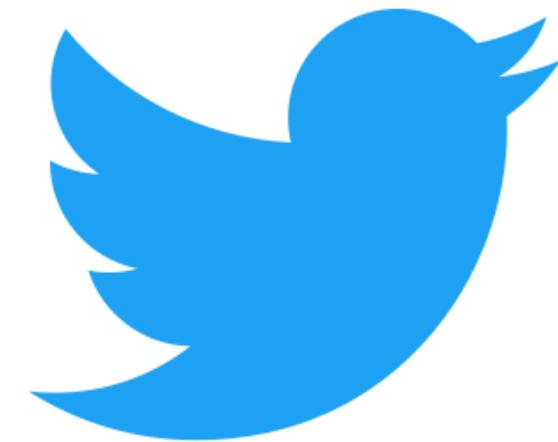
Dr. Harding is the recipient of the Huntington's Disease Society of America Berman Topper Career Development Fellowship which funds and supports this research, in addition to generous funding from the CHDI Foundation and the Huntington Society of Canada. The SGC is a registered charity (number 1097737) that receives funds from AbbVie, Bayer Pharma AG, Boehringer Ingelheim, Canada Foundation for Innovation, Eshelman Institute for Innovation, Genome Canada through Ontario Genomics Institute [OGI-055], Innovative Medicines Initiative (EU/EFPIA) [ULTRA-DD grant no. 115766], Janssen, Merck KGaA, Darmstadt, Germany, MSD, Novartis Pharma AG, Ontario Ministry of Research, Innovation and Science (MRIS), Pfizer, São Paulo Research Foundation-FAPESP, Takeda, and Wellcome.



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Dr. Harding is the recipient of the Huntington's Disease Society of America Berman Topper Career Development Fellowship which funds and supports this research, in addition to generous funding from the CHDI Foundation and the Huntington Society of Canada. The SGC is a registered charity (number 1097737) that receives funds from AbbVie, Bayer Pharma AG, Boehringer Ingelheim, Canada Foundation for Innovation, Eshelman Institute for Innovation, Genome Canada through Ontario Genomics Institute [OGI-055], Innovative Medicines Initiative (EU/EFPIA) [ULTRA-DD grant no. 115766], Janssen, Merck KGaA, Darmstadt, Germany, MSD, Novartis Pharma AG, Ontario Ministry of Research, Innovation and Science (MRIS), Pfizer, São Paulo Research Foundation-FAPESP, Takeda, and Wellcome.