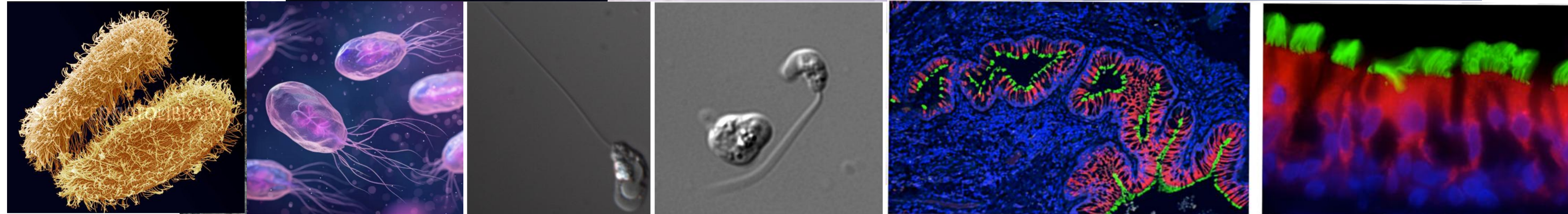


From Pond Scum to Human Disease

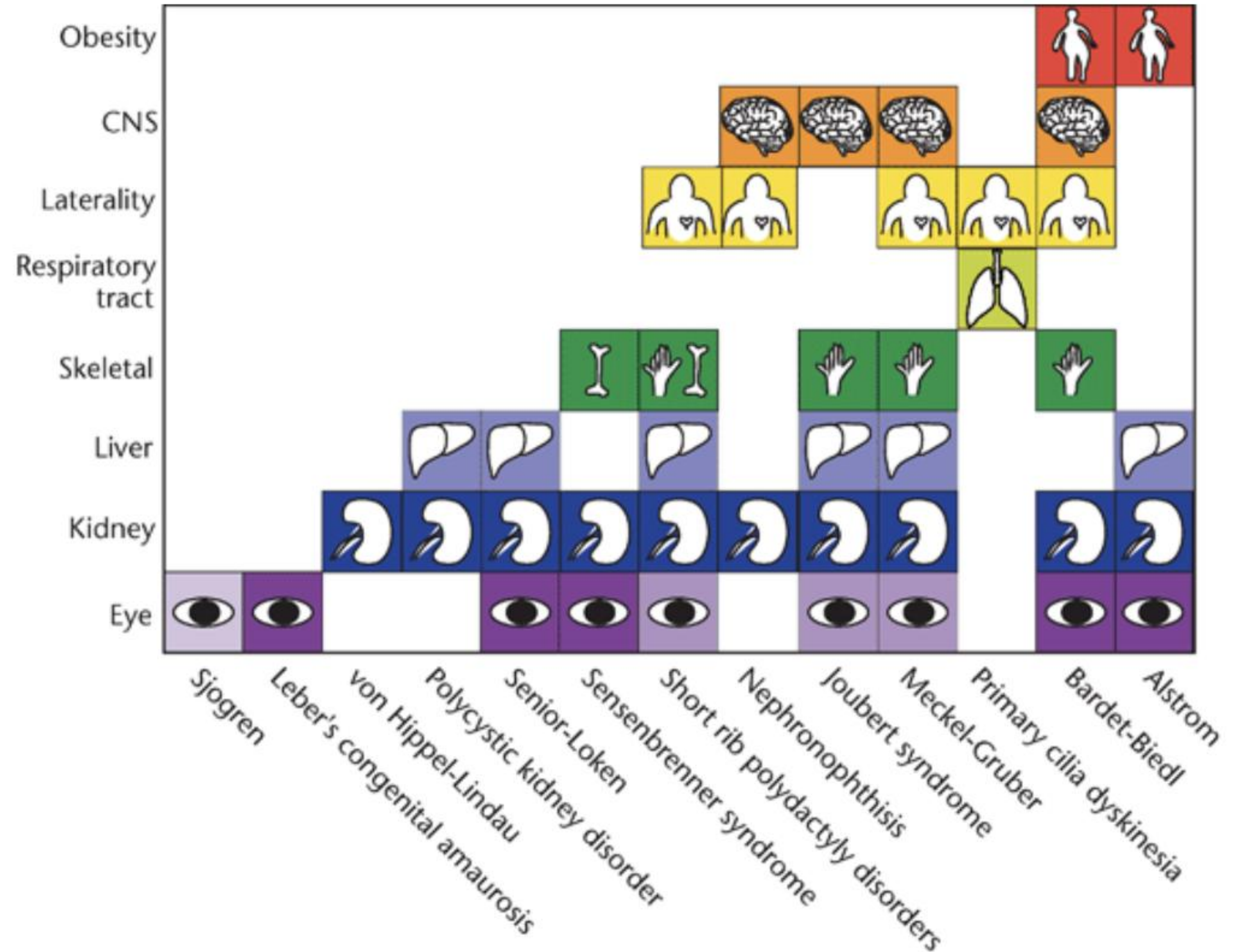


Susan K. Dutcher
Department of Genetics
Washington University School of Medicine

From Pond Scum to Human Disease



William Peck, MD.
Dean, Washington University
Medical School



Acknowledgements

Washington University Cilia and O



Steve Brody
Adult
Pulmonary



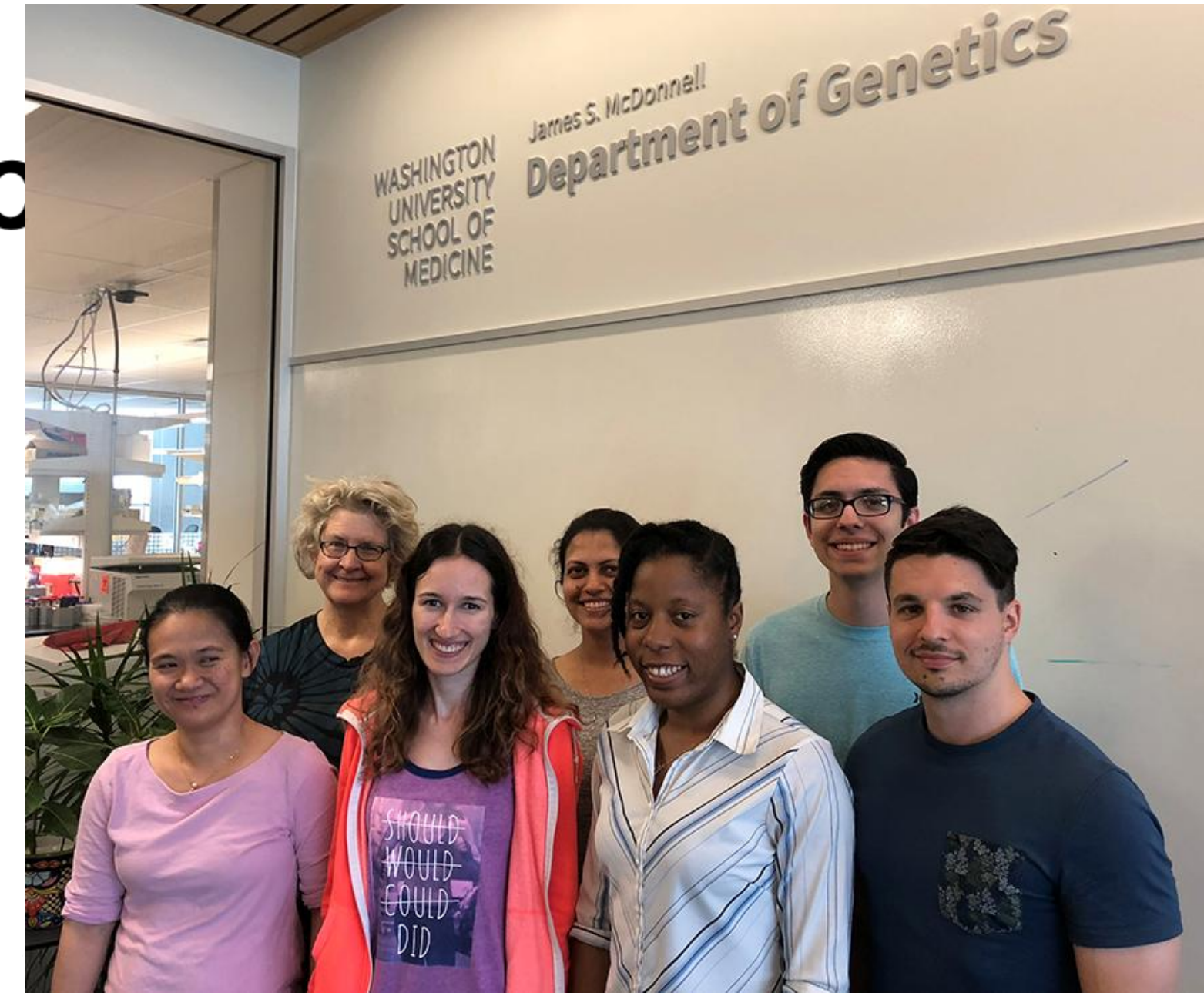
Amjad Horani
Pediatric
Pulmonary



Phil Bayly
Mechanical
Engineering



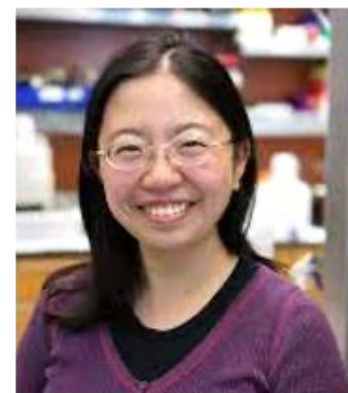
Rui Zhang
Biochemistry



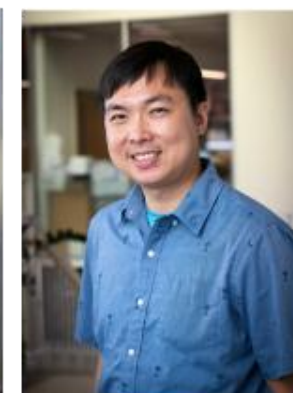
Amber Stratman
Cell Biology



Jenn Strahle
Pediatric
Neurosurgery



Jenn Wang
Biology



Peter Jin
Genetics



Polina Lishko
Cell Biology



Moe Mahjoub
Nephrology



Phil Williams
Ophthalmology



Louis
Woodhams



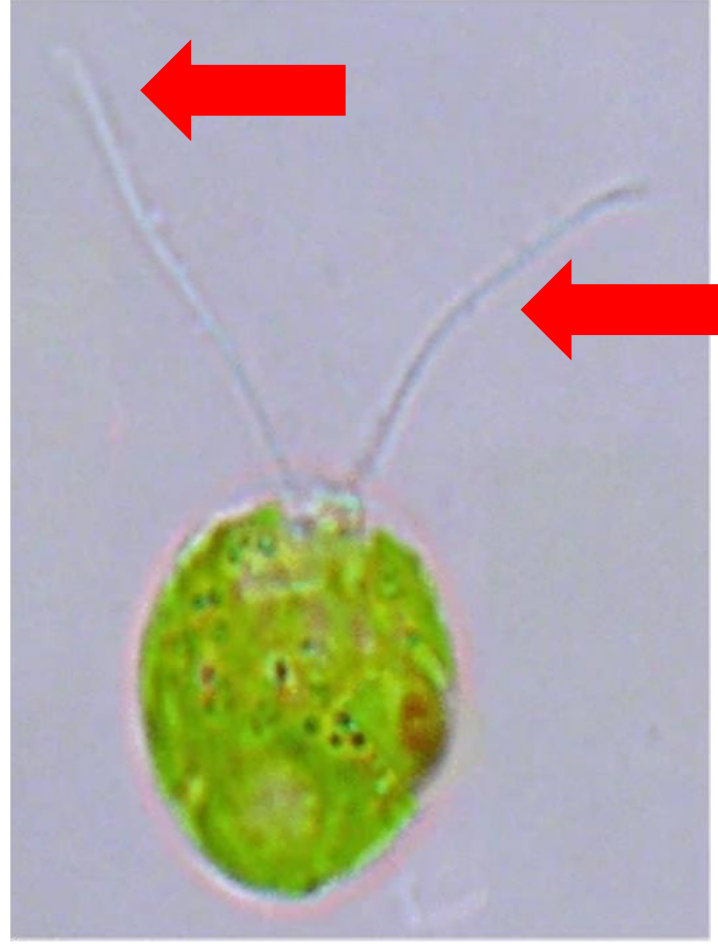
Ben Major
Cell Biology



Yao Chen
Neuroscience



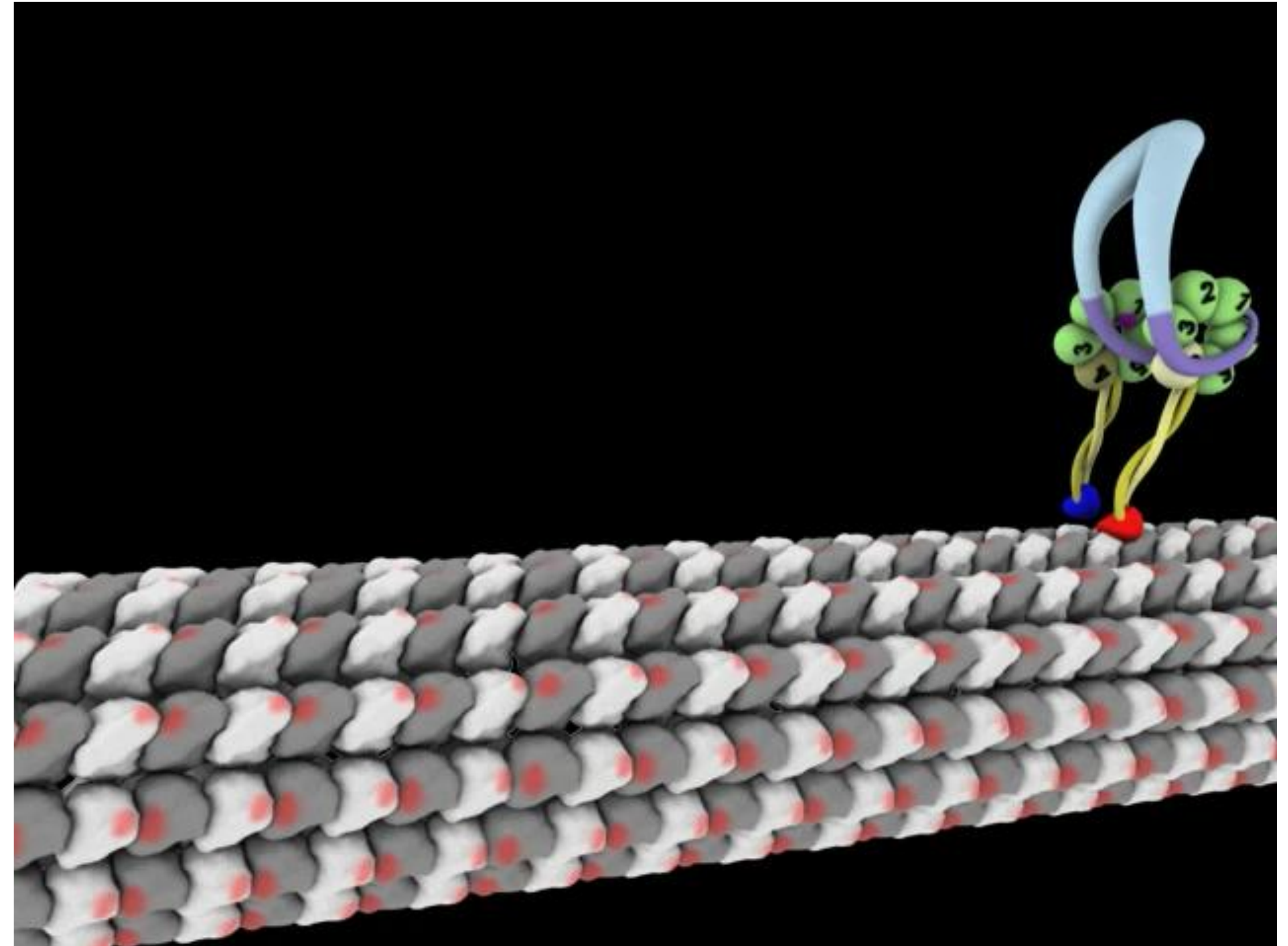
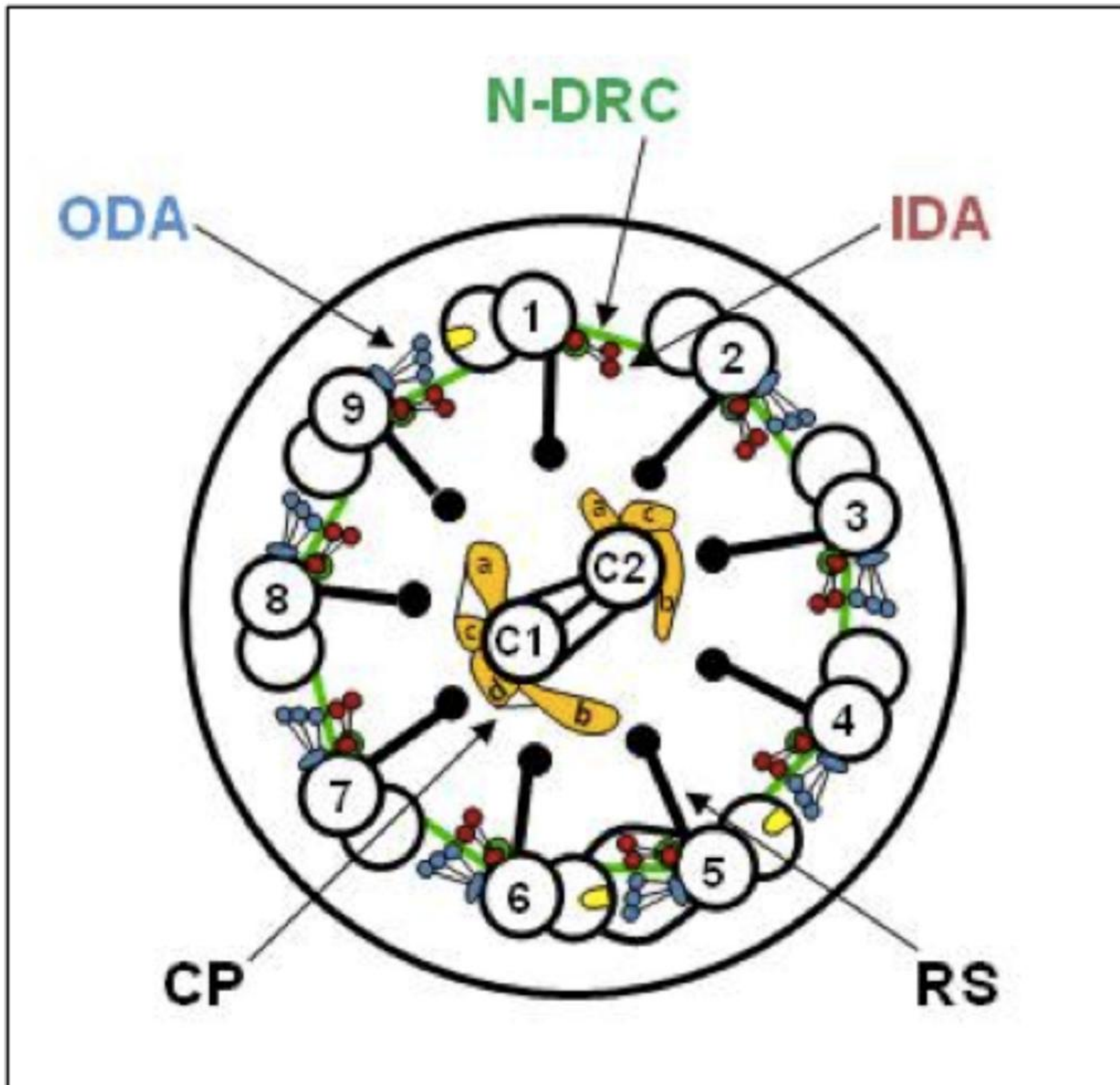
Celia Santi
Ob/Gyn



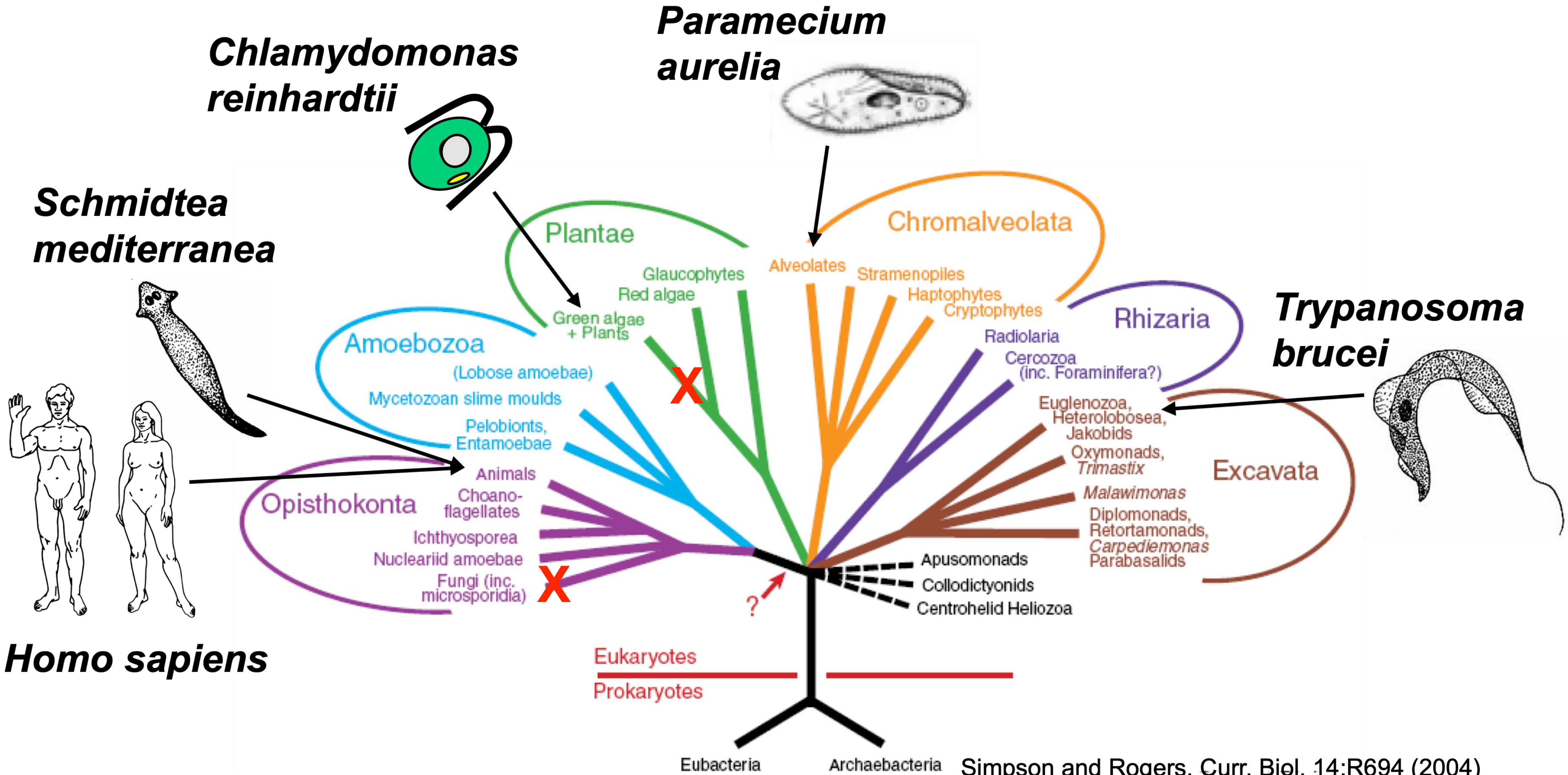
Chlamydomonas



Amherst MA 1942

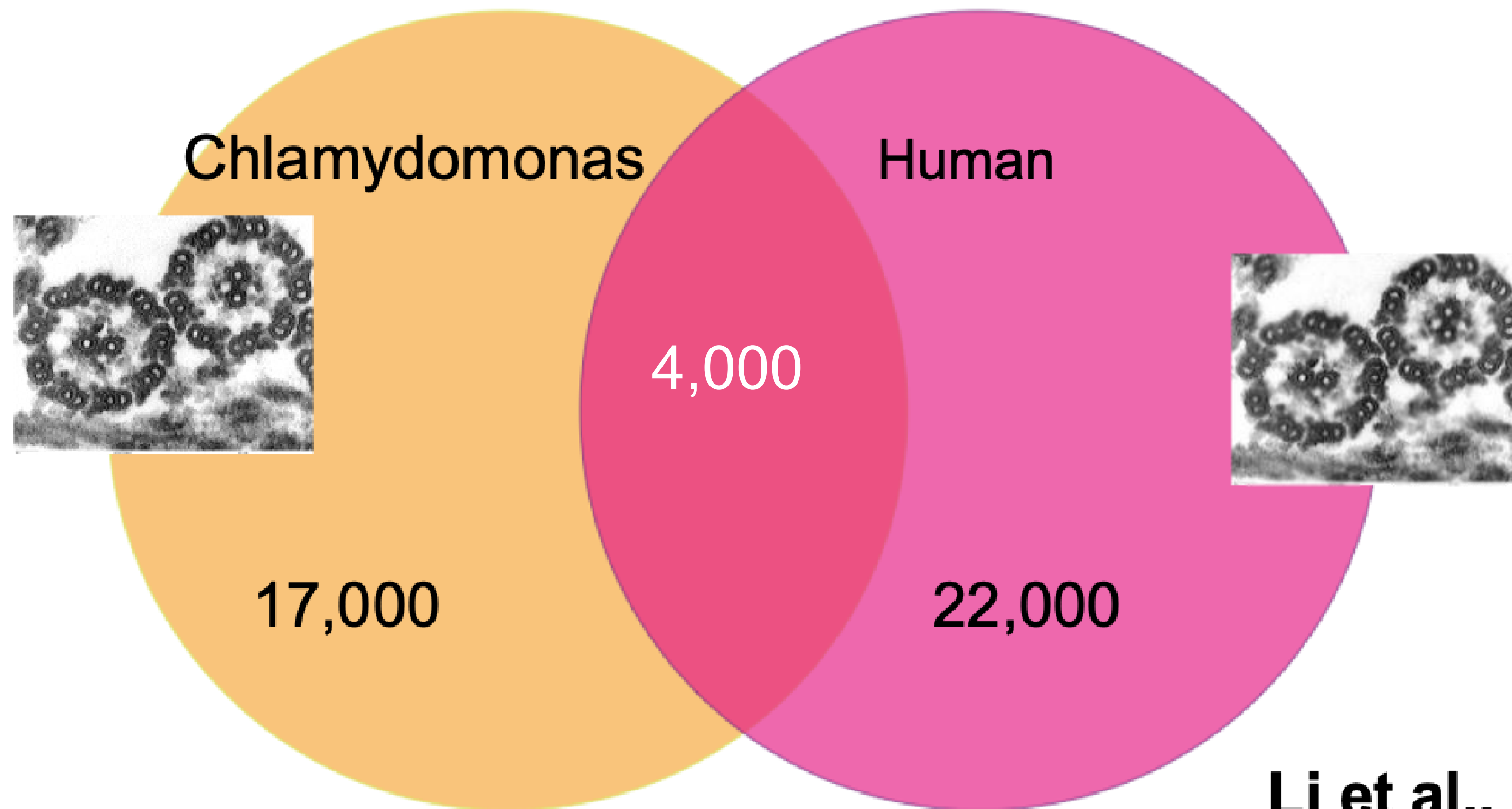


Cilia in Eukaryotes



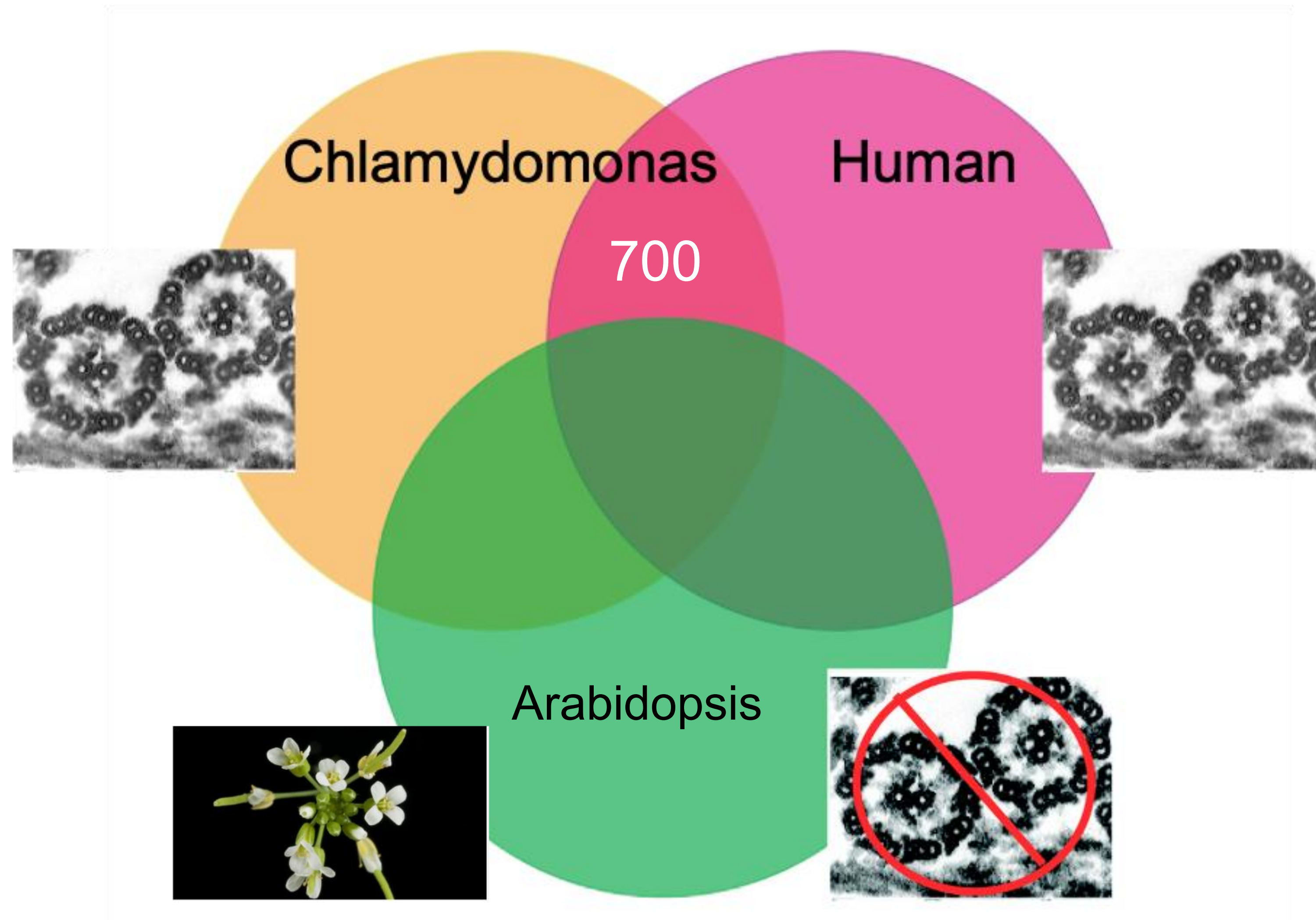
Simpson and Rogers, Curr. Biol. 14:R694 (2004)

Comparative genomics to find genes for cilia

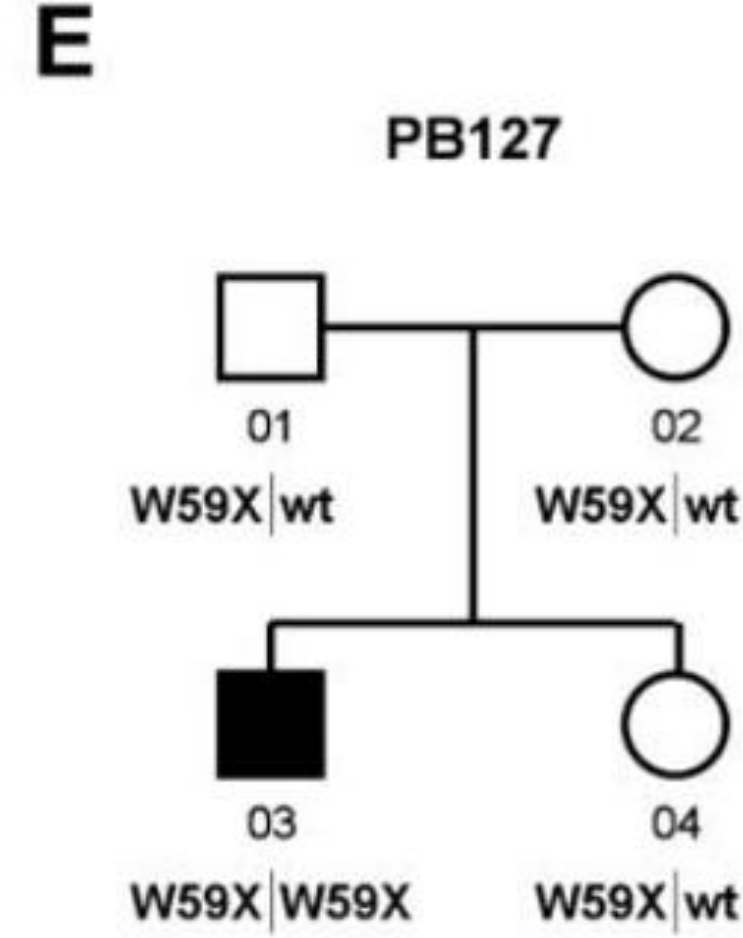
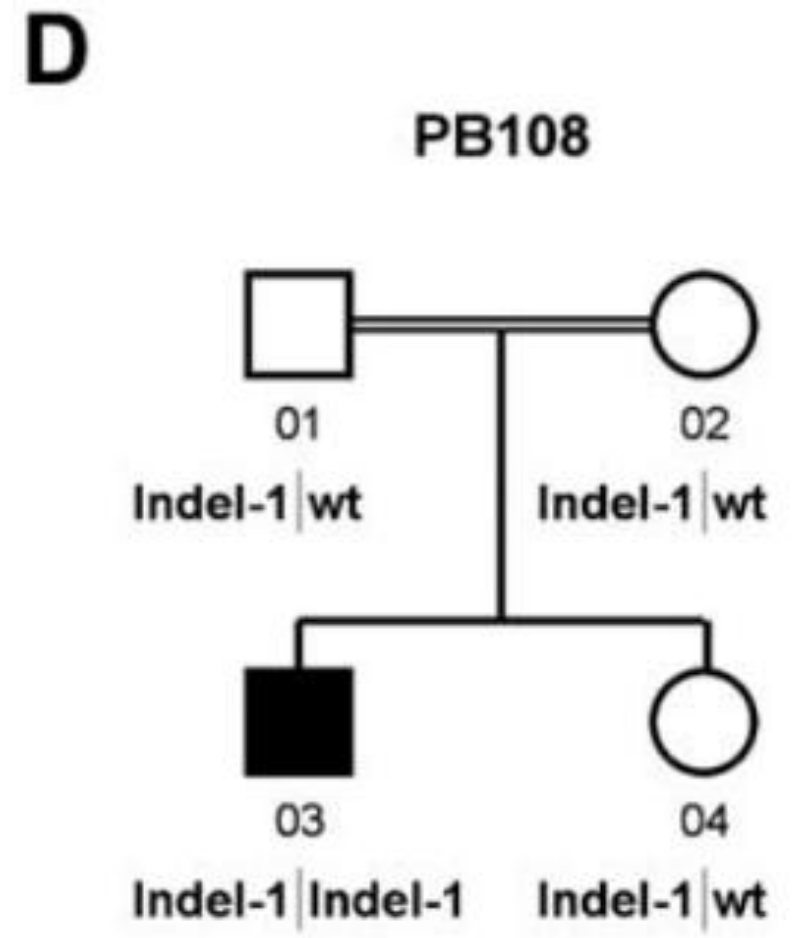
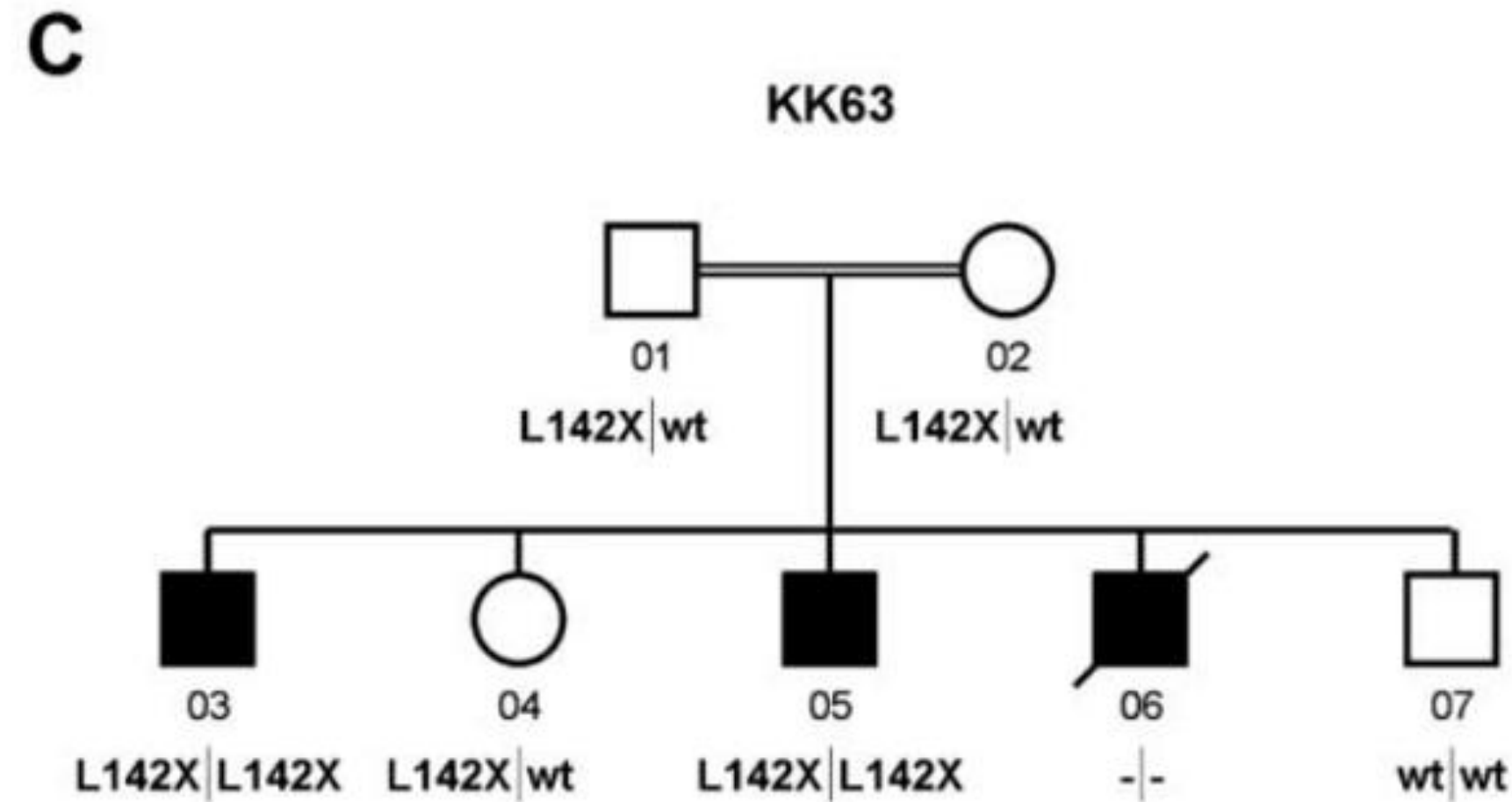
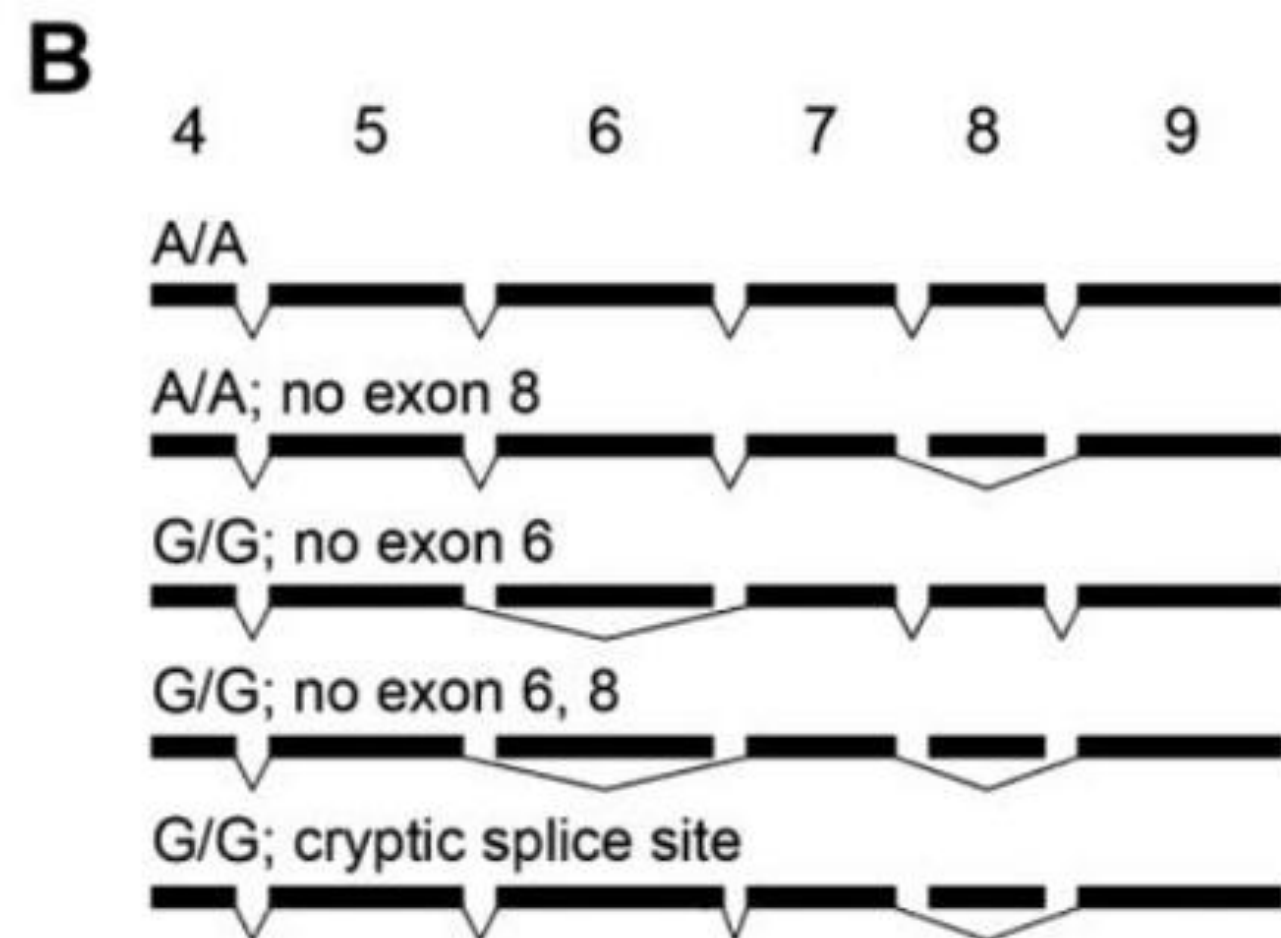
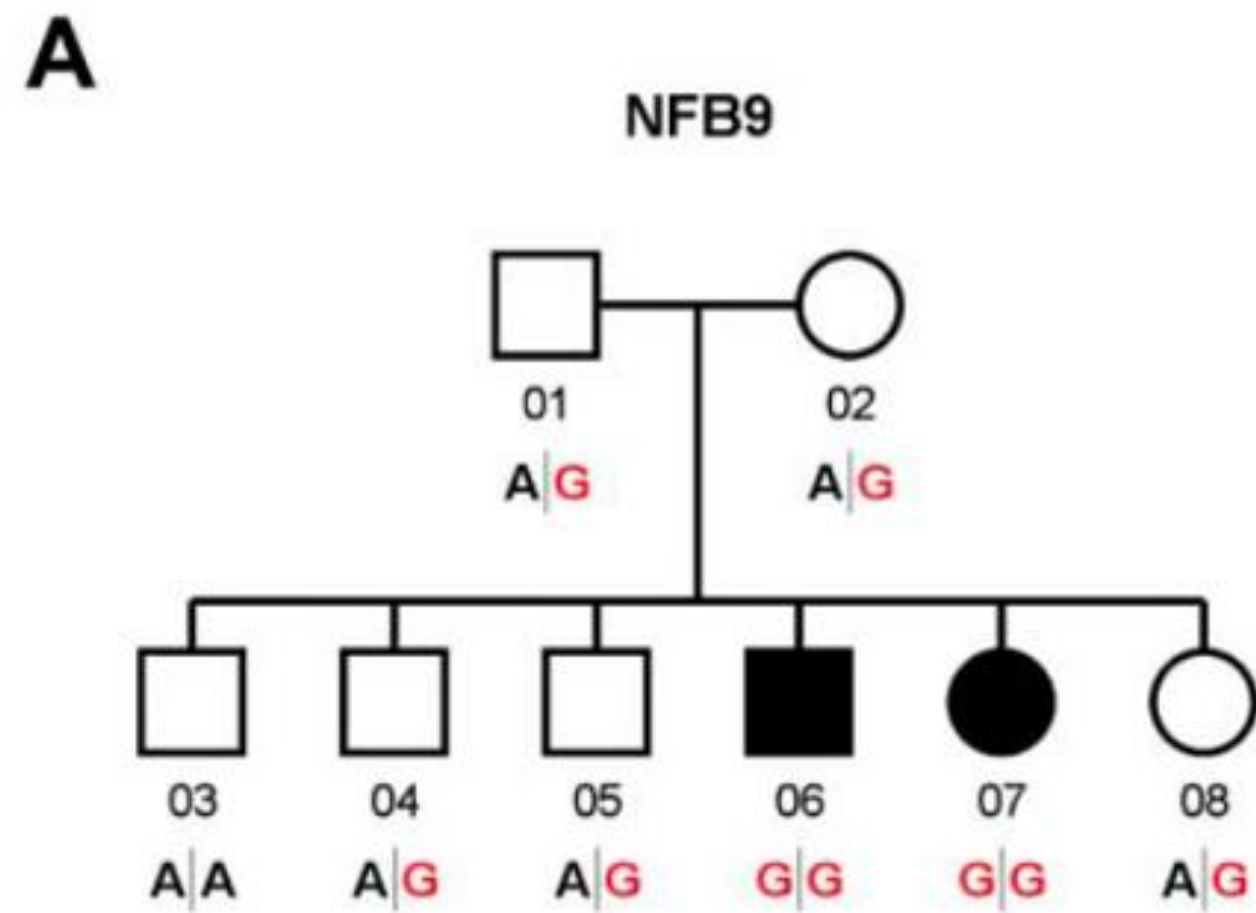


Li et al., 2004

Comparative genomics identifies ~700 proteins that are only in organisms with cilia



Human disease genes (BBS5, MKS1, LRRC6) in the cilia comparative genomics list



Bardel Biedl Syndrome

Central Obesity

Retinal Degeneration

Kidney Disease

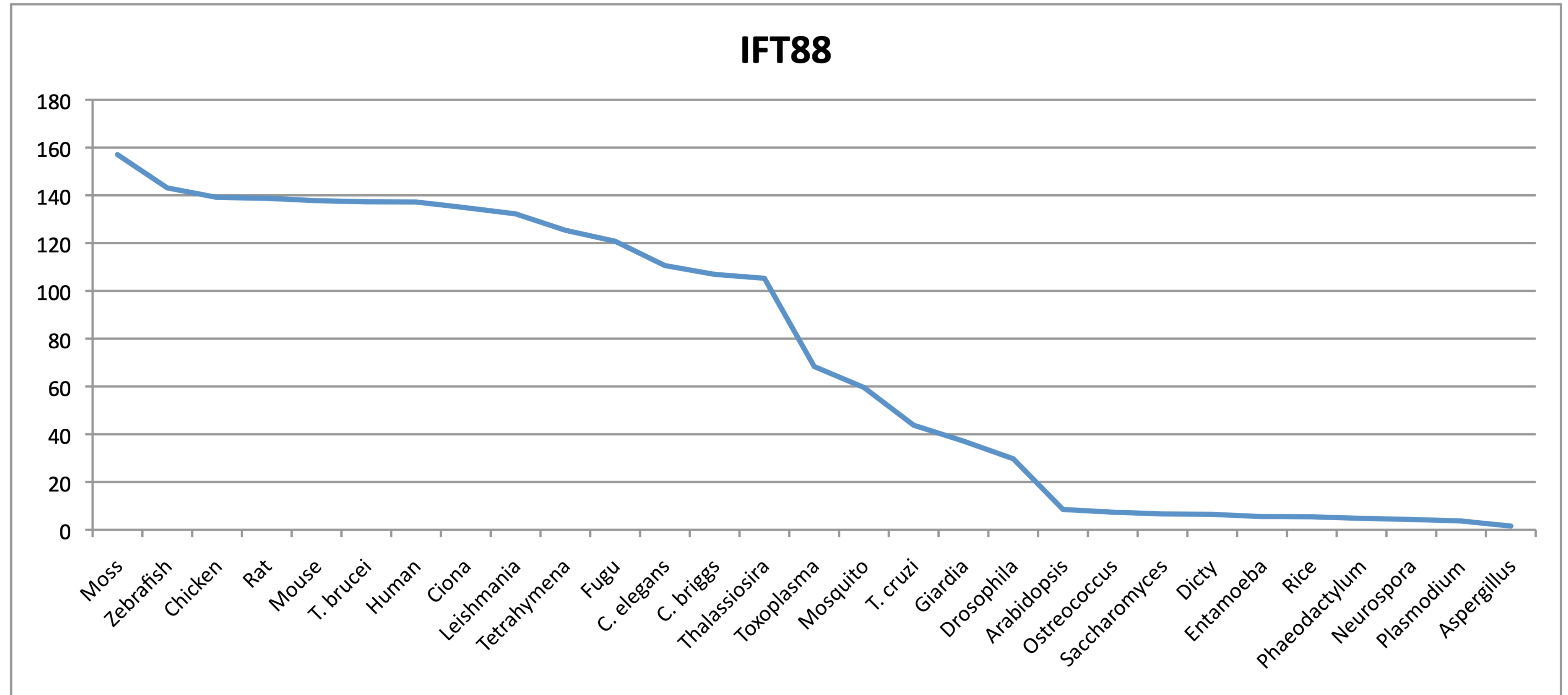
Mental Retardation

Li et al., 2004

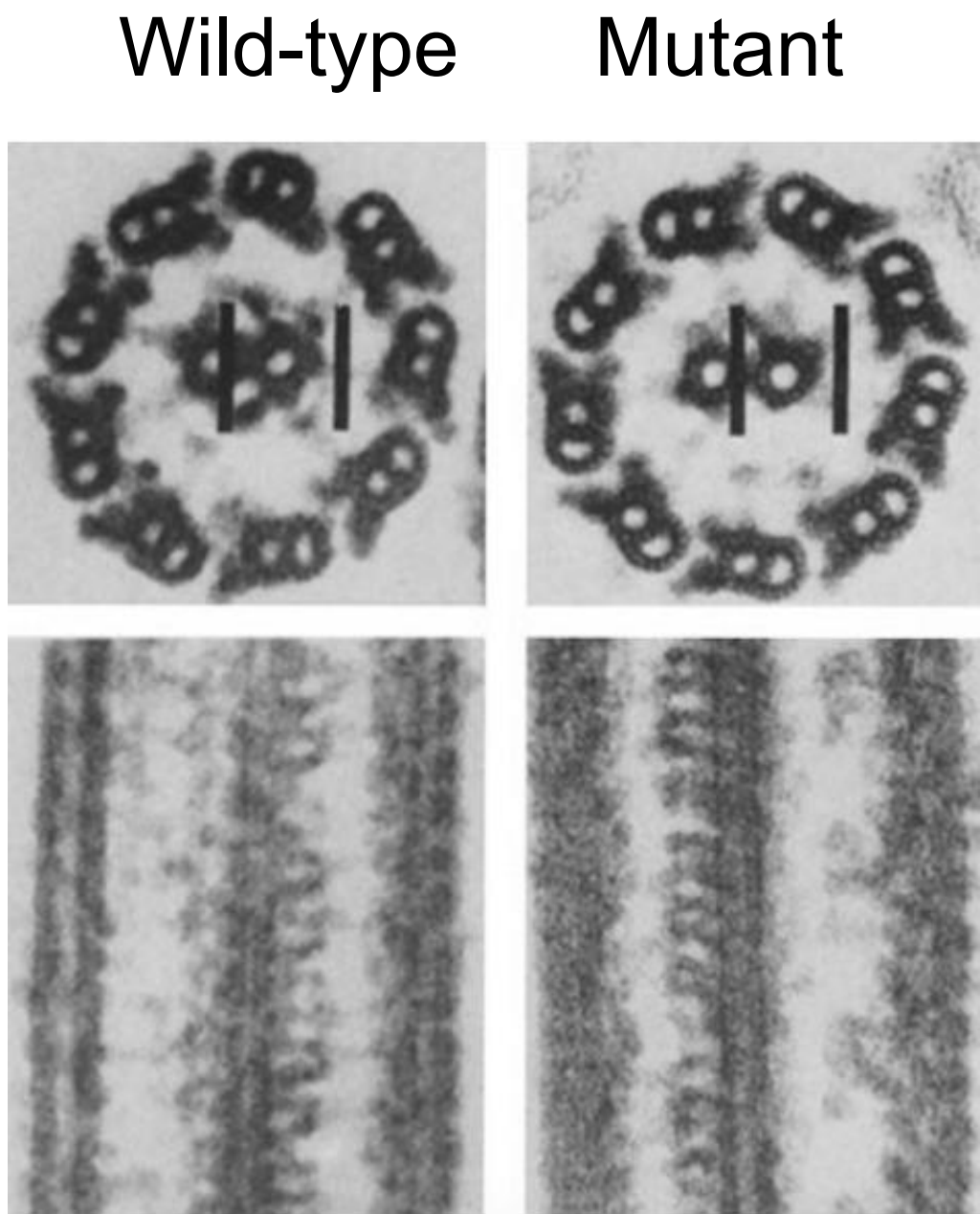
Kyattala et al., 2013

Horani et al., 2013

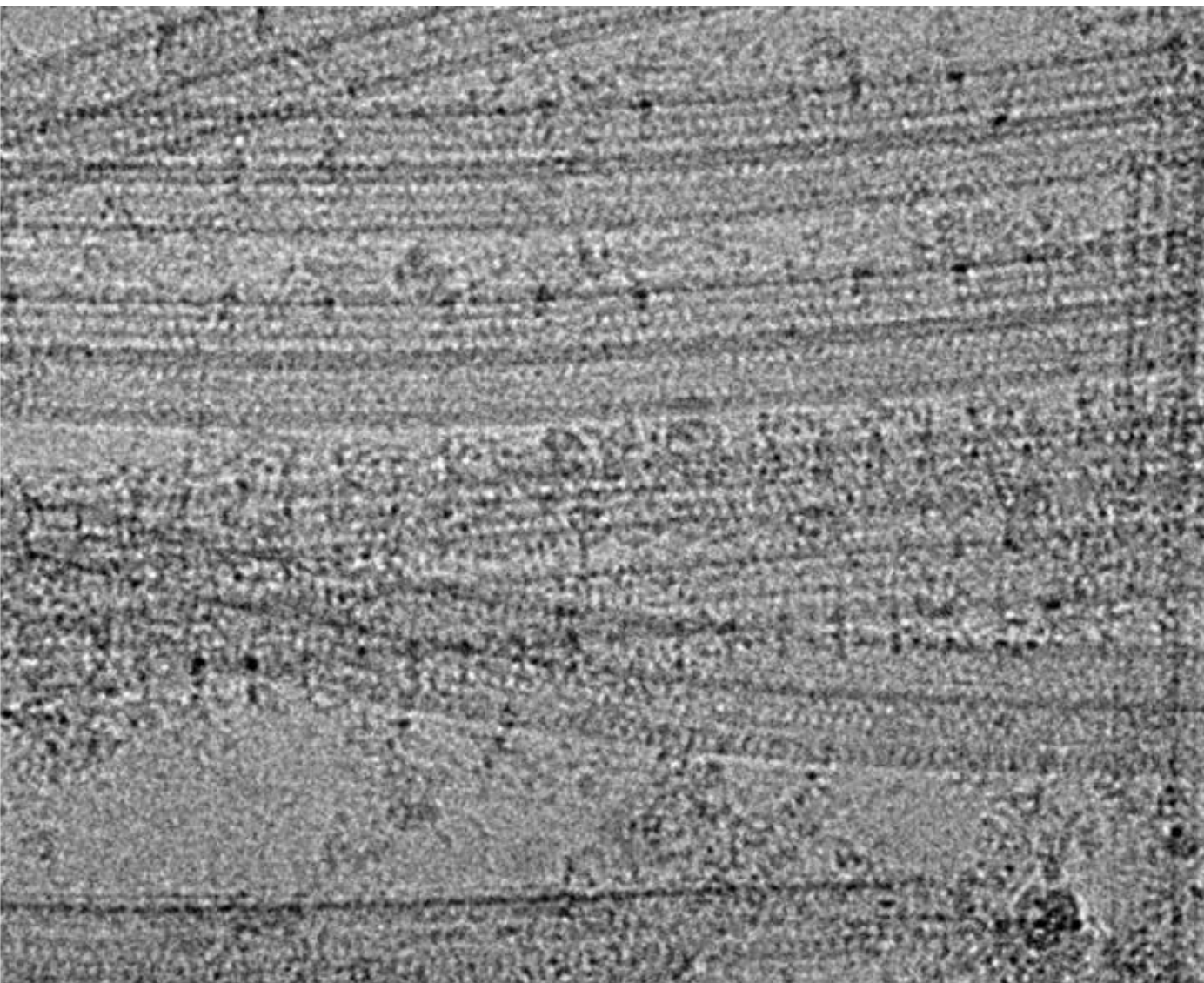
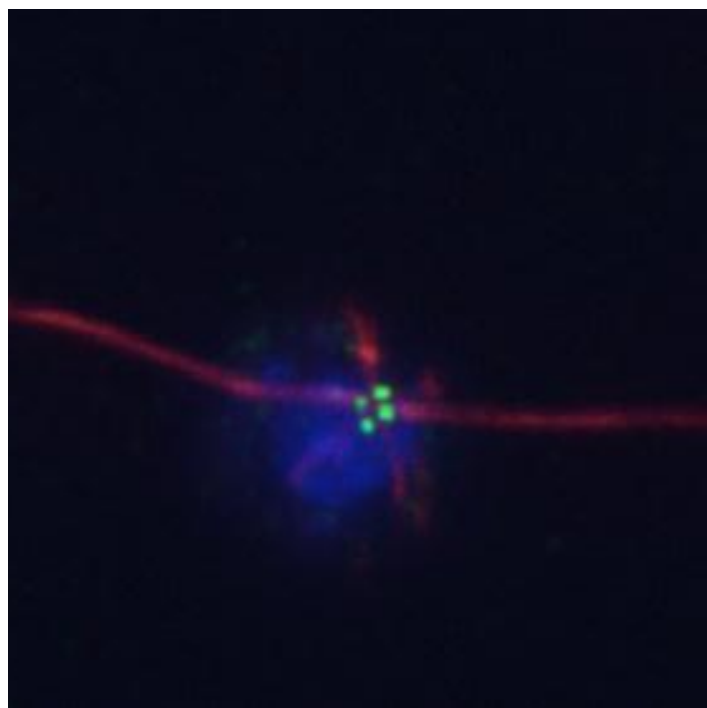
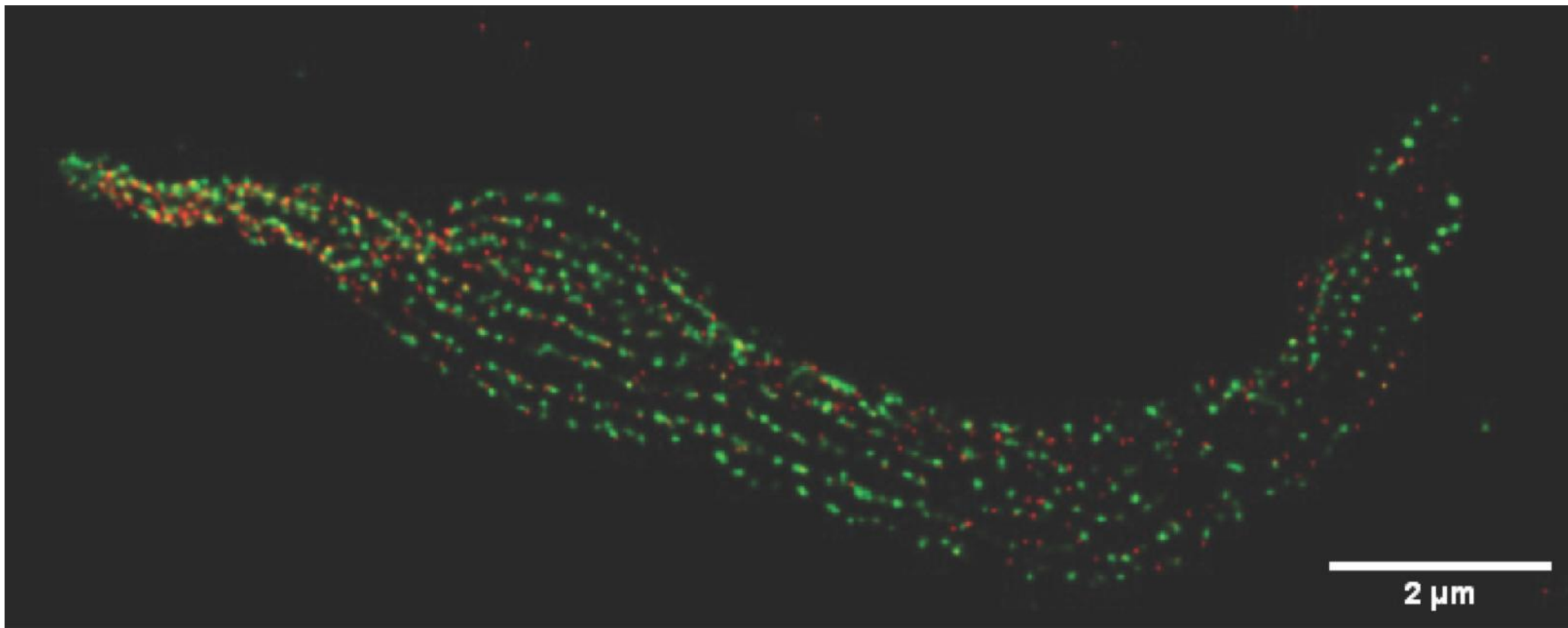
Many proteins show this cilia-specific pattern over 40 species



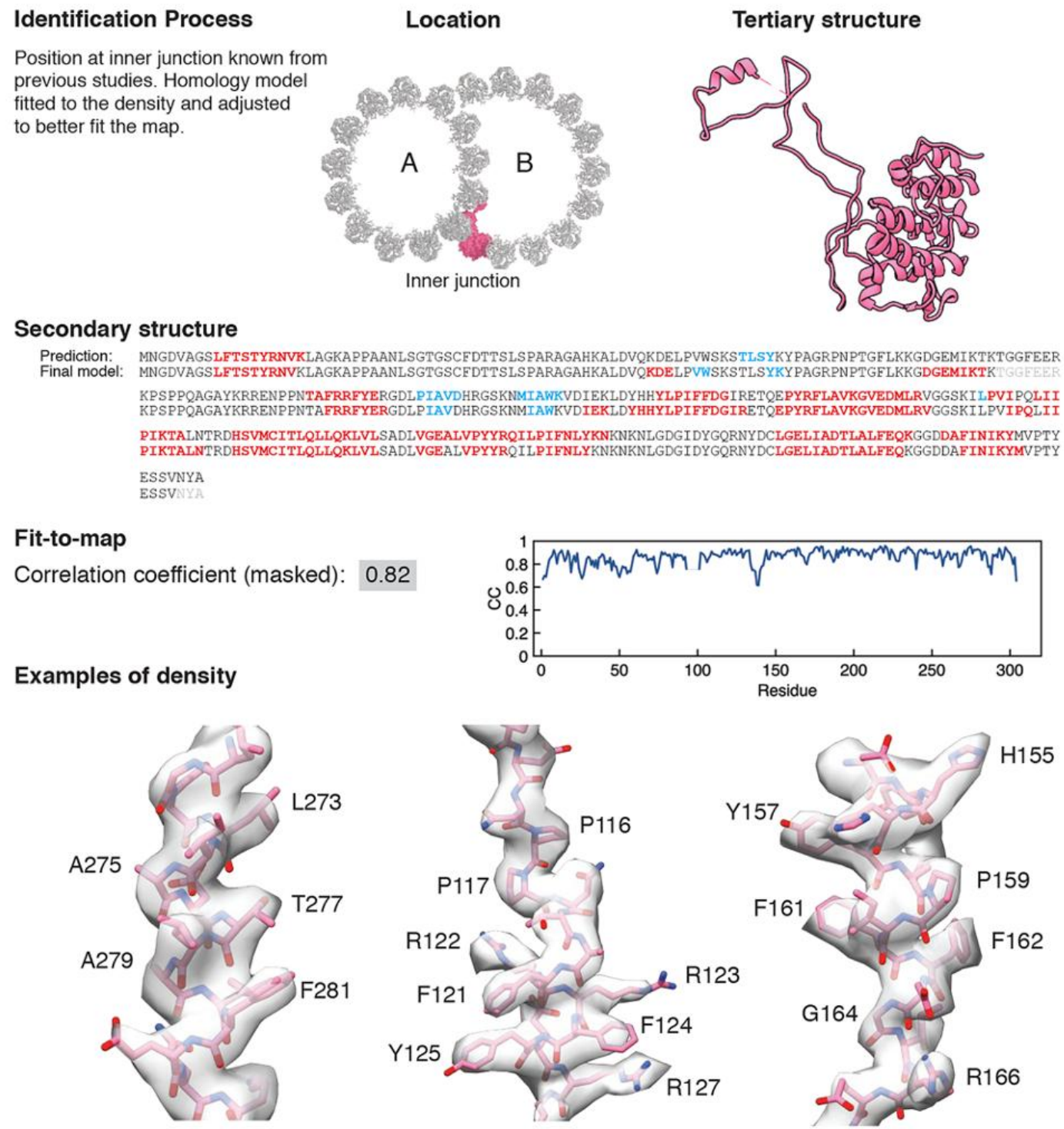
Changing Technologies: Single particle cryo-electron microscopy



Dutcher et al., 1984

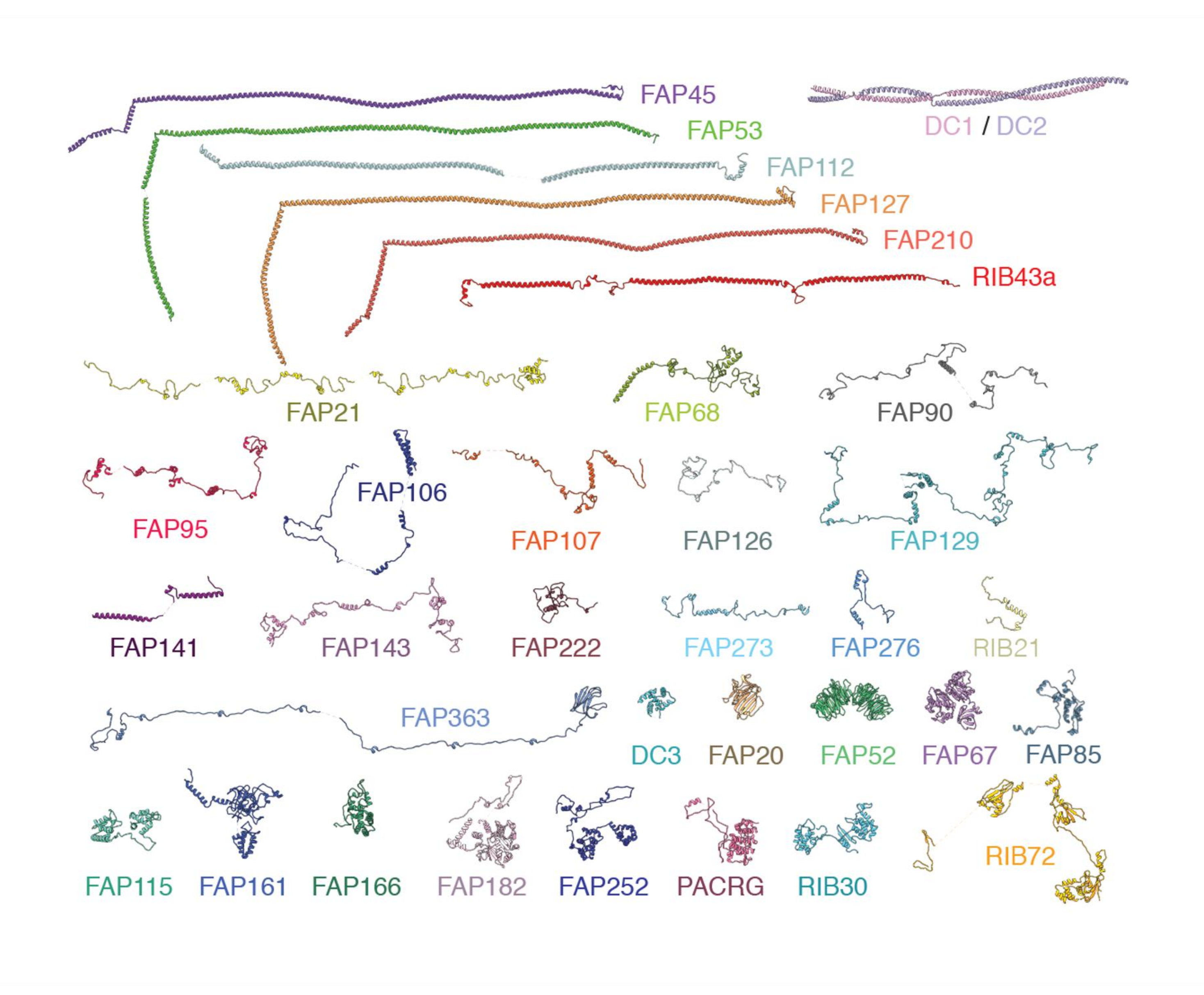
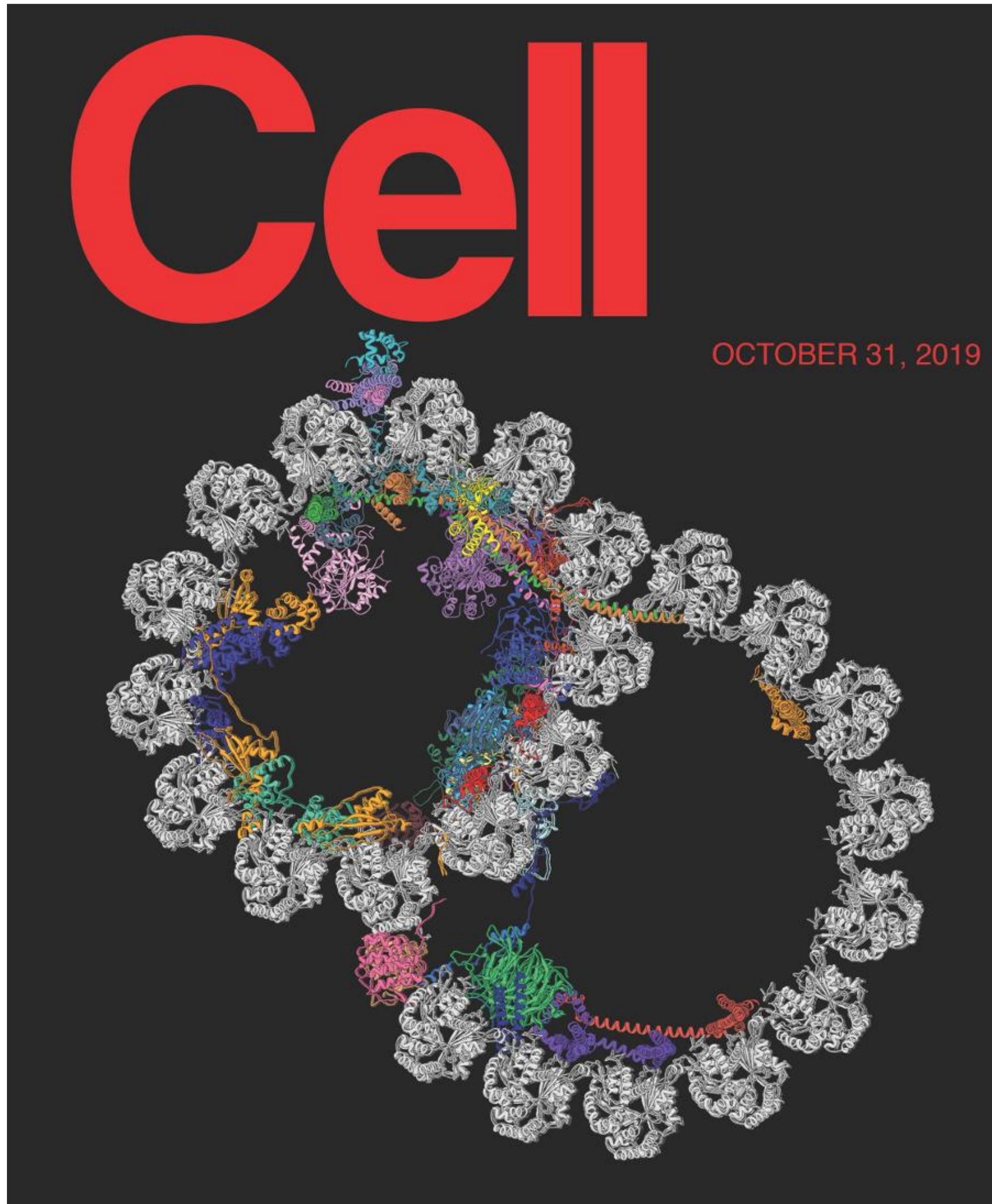


Ma et al., 2019

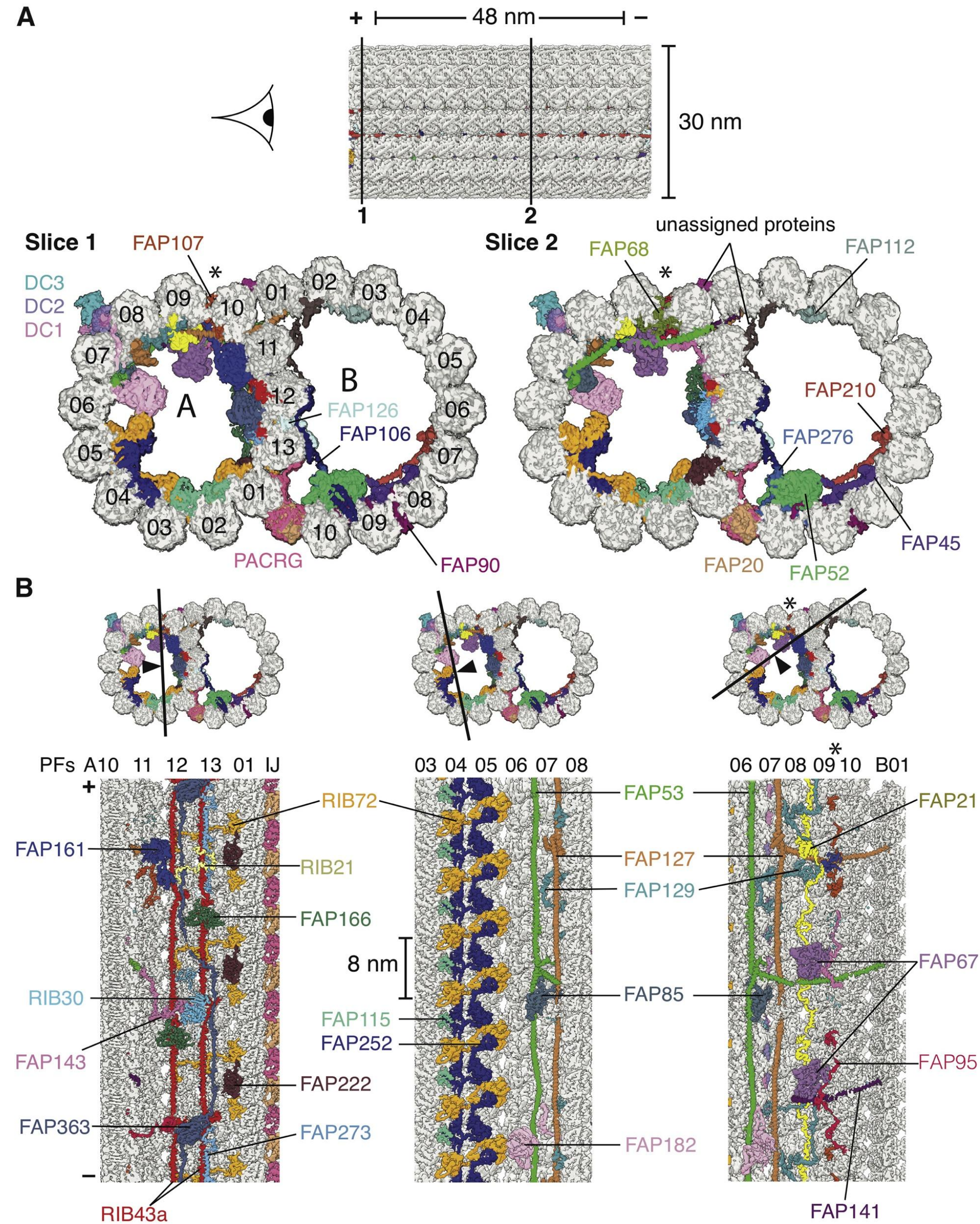


Rui Zhang

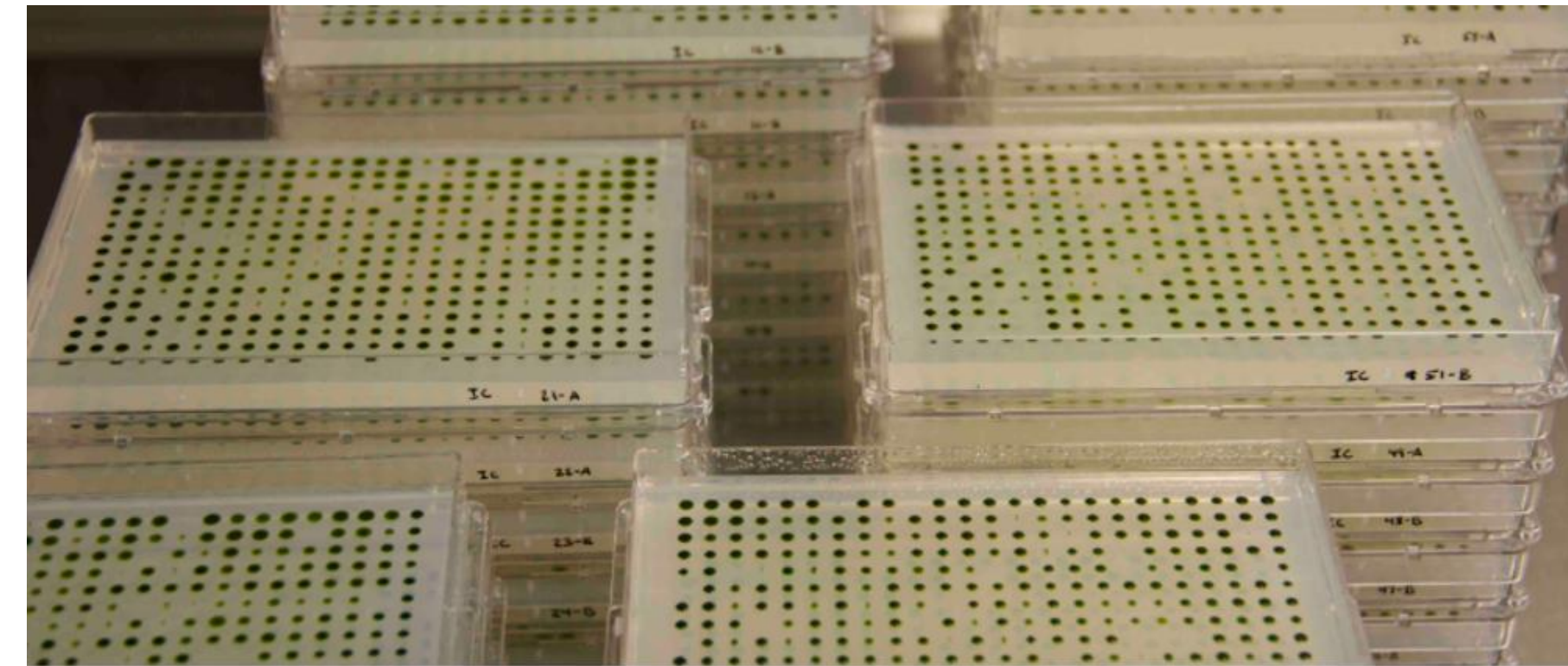
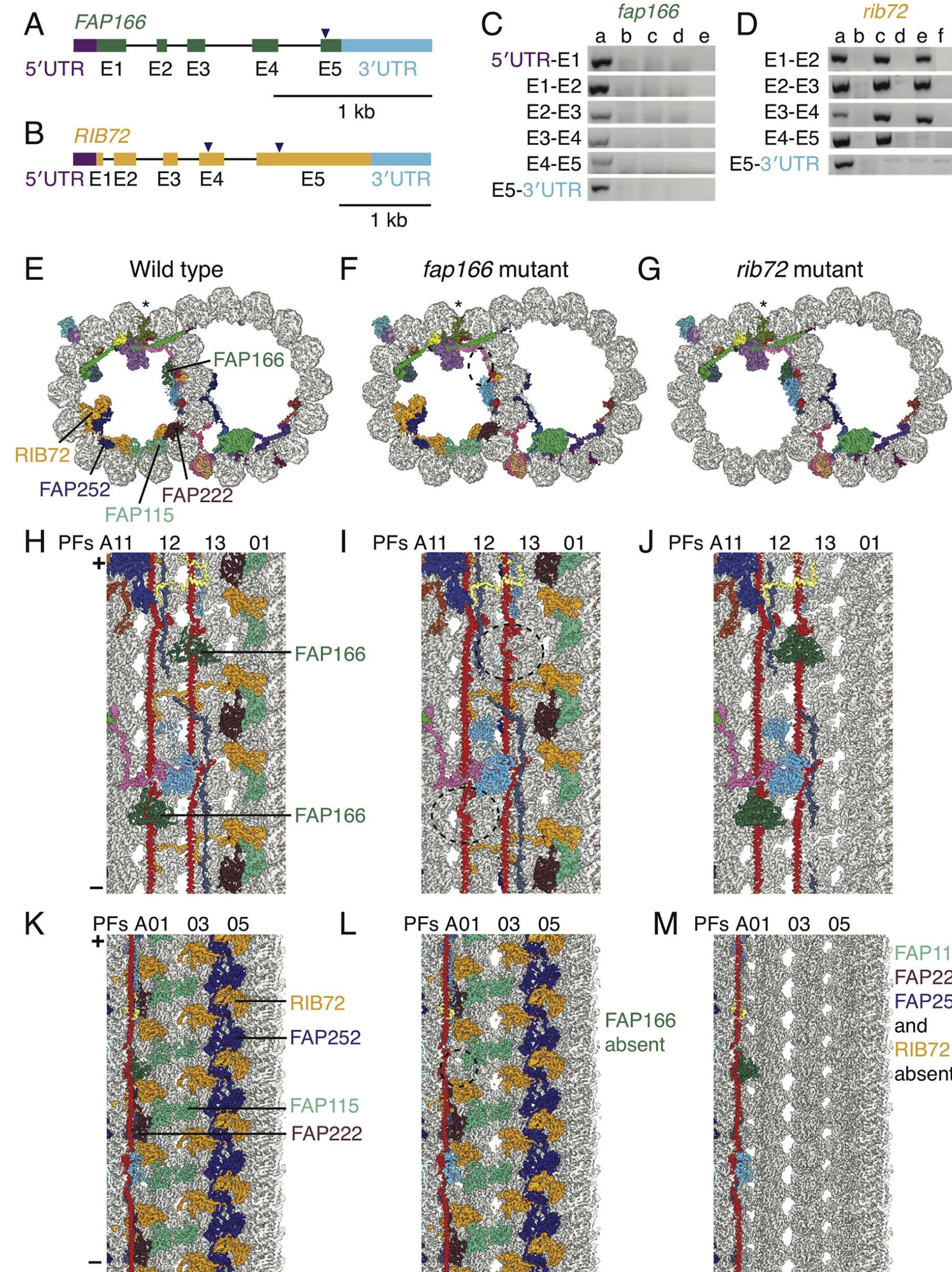
Microtubule Inner Proteins



Microtubule Inner Proteins —MIPS



Mutants in *MIP* genes

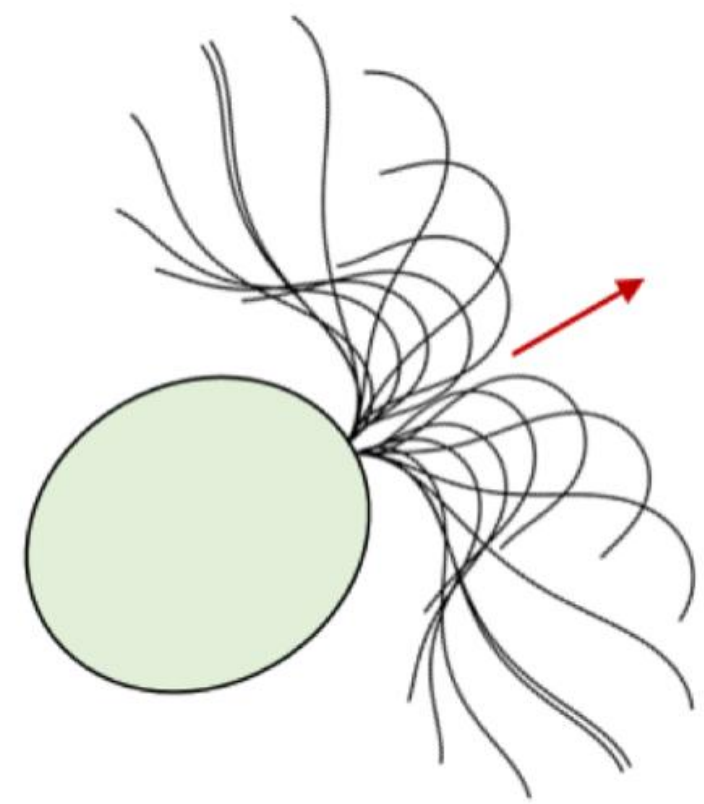


The *fap166* mutant is missing only one protein: FAP166

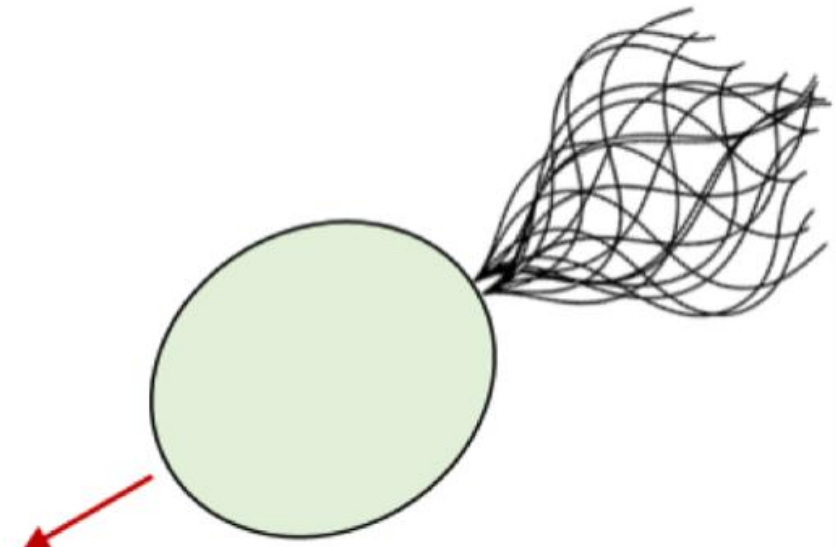
The *rib72* mutant is missing four proteins: RIB72, FAP115, FAP222, and FAP252

Ma et al., 2019
Li et al., 2018

Mutants in Microtubule Inner Proteins

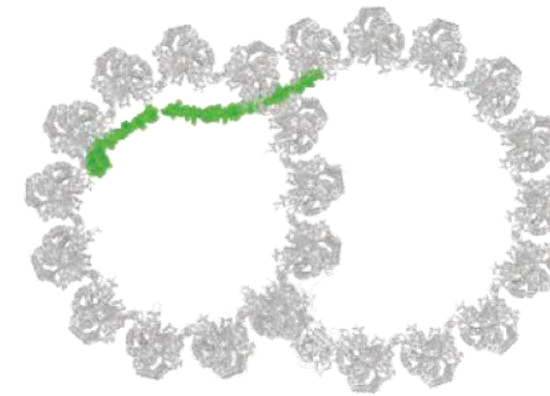


Forward

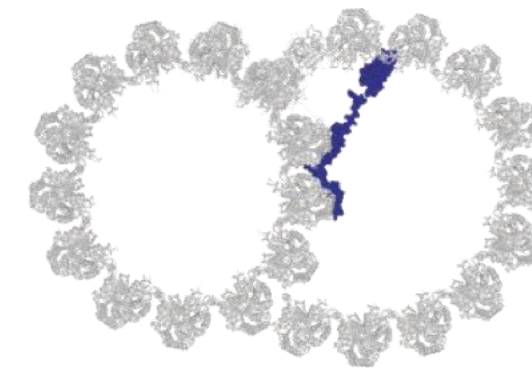


Reverse

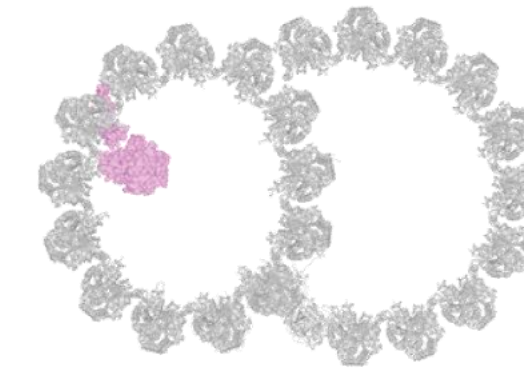
FAP53
CCDC11



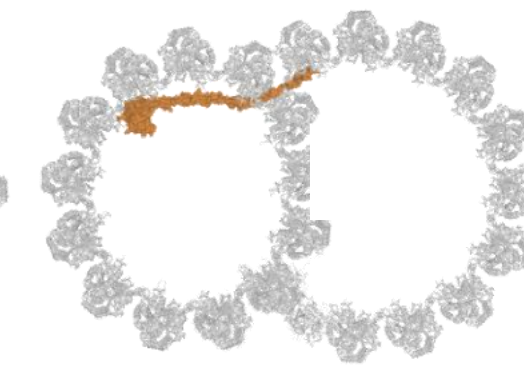
FAP106
Enkurin



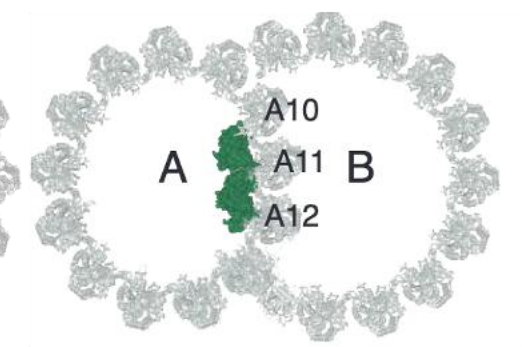
FAP127
MNS1



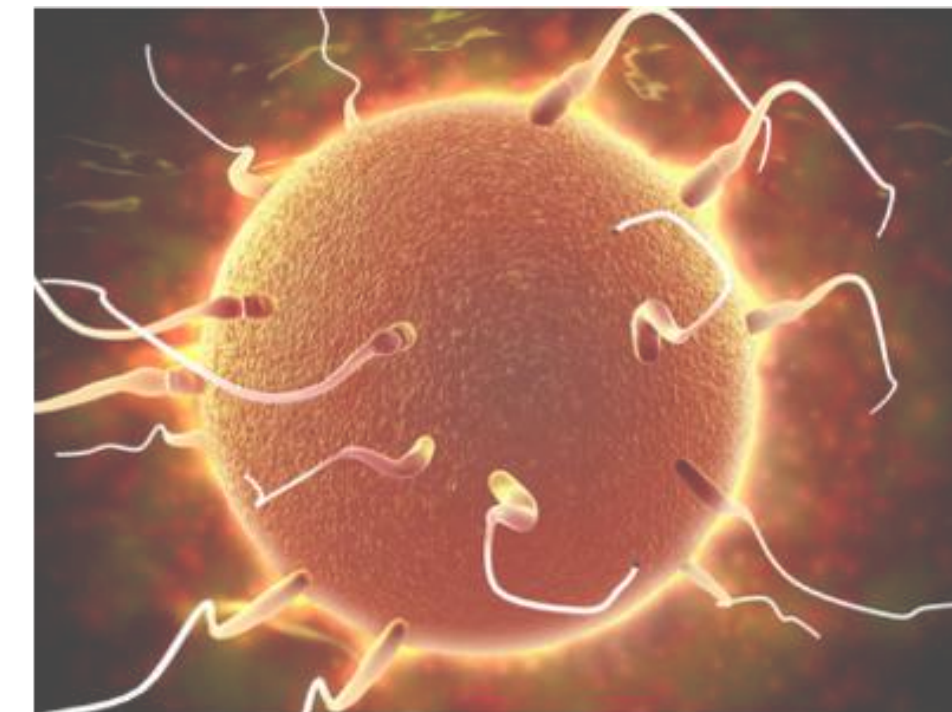
FAP184
Pierce



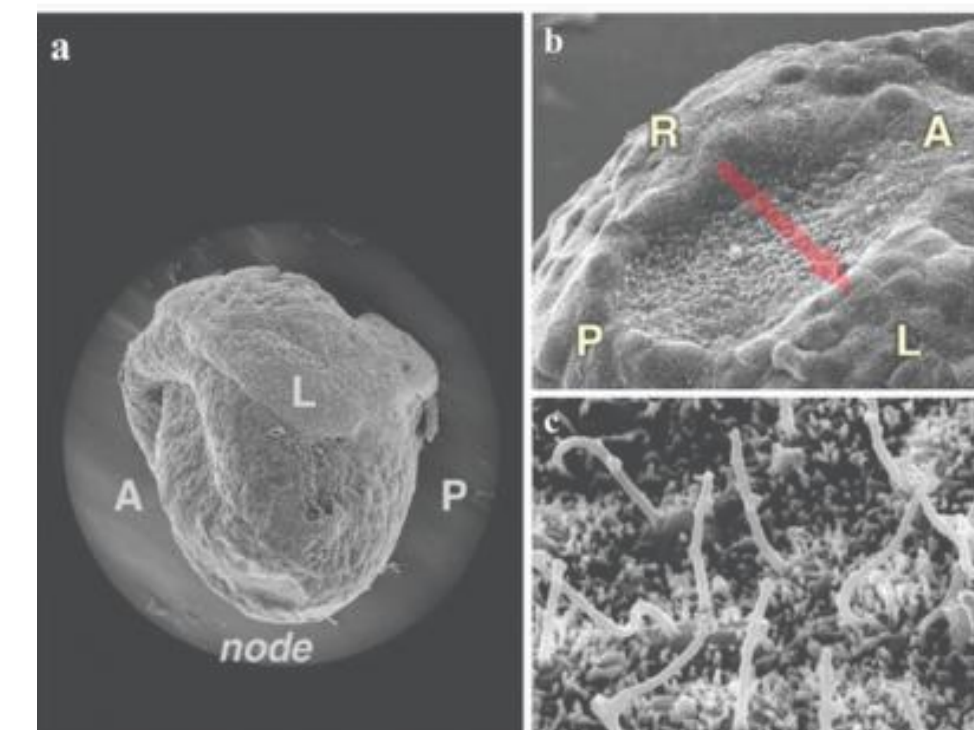
FAP166



Genotype	Low Light	Hight Light
Wild-type	Swim (WT)	Reverse Swimming
<i>fap53</i>	Swim (WT)	Immotile
<i>fap106</i>	Swim (WT)	Immotile
<i>fap127</i>	Swim (WT)	Immotile
<i>fap184</i>	Swim (WT)	Immotile
<i>fap166</i>	Swim (WT)	Slow Reverse Swimming



• Sperm



• The node

The study of human biology as discussed in Nature, News and Views, 1986

The proper study of mankind

Molecular biology has made the human genome accessible to laboratory investigation. But does that mean that the sequence of the human genome would be worth the effort?

THERE IS NO scientific reason for studying man. Thus one of the 120 speakers at this year's Cold Spring Harbor Symposium on the molecular biology of *Homo sapiens* from 28 May to 4 June. The issue arises because, as the programme was designed to demonstrate, there are now few fundamental questions in biology that cannot be explored using human genes and human cells.

This in itself is scarcely sufficient reason for overlooking the rather obvious shortcomings of man as an object of investigation. But there is one reason, just the same: the human species alone preserves its rare defective variants. Mouse mothers, whose matings are manipulable and whose generation times are manage-

and Goldstein have built up a picture of the cellular and, more recently, the molecular biology of receptor-mediated endocytosis which has provided fundamental insights into these processes as well as clarifying the mechanism of atherosclerosis.

This has been possible only because Brown and Goldstein worked up to the molecular biology from classical genetics via biochemistry. More characteristic of latter-day triumphs were the papers presented by Louis Kunkel (Boston Children's Hospital) and Stuart Orkin (Harvard Medical School), both published in this issue of *Nature* (pp 73 and 32). They have arrived directly at the genes responsible for two human genetic diseases without engaging with the intervening bio-

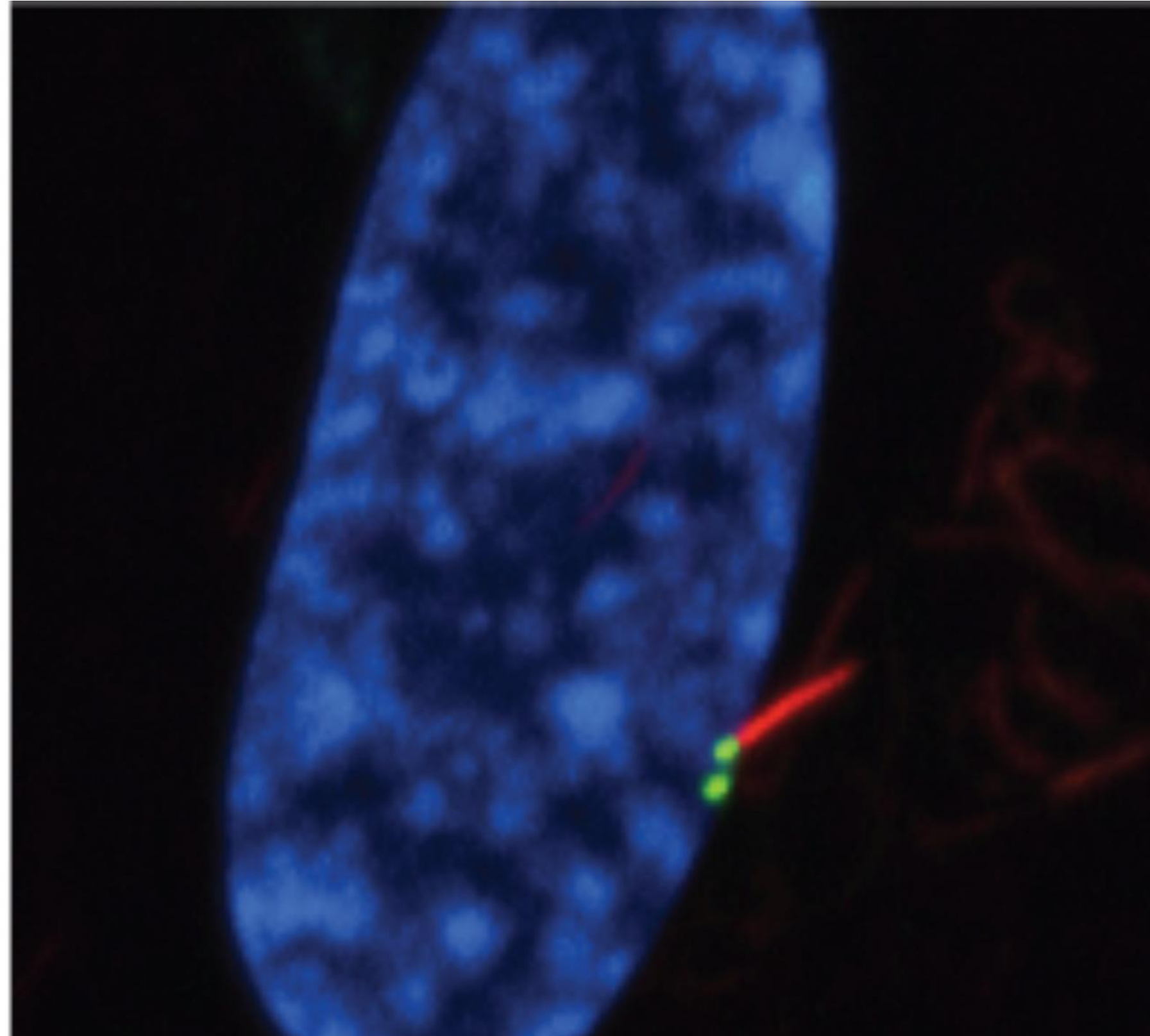
may require some ingenuity, as well as some biochemistry, to discover.

The substantial challenge now facing Orkin and Kunkel and their collaborators is in no sense a reflection on the quality of the work or the validity of their approach. But it is an inevitable consequence of approaching the DNA directly, and thus has a direct bearing on the desirability of sequencing the rest of the human genome.

In the discussion on that topic at the symposium, Paul Berg (Stanford) set out the issues — is it feasible, who will pay and is it worth it? Walter Gilbert (Harvard) seraphically chalked up the tally — three thousand million bases at 10^5 bases per year equals 30,000 person-years or, at the current rate of 2×10^6 bases per year, but

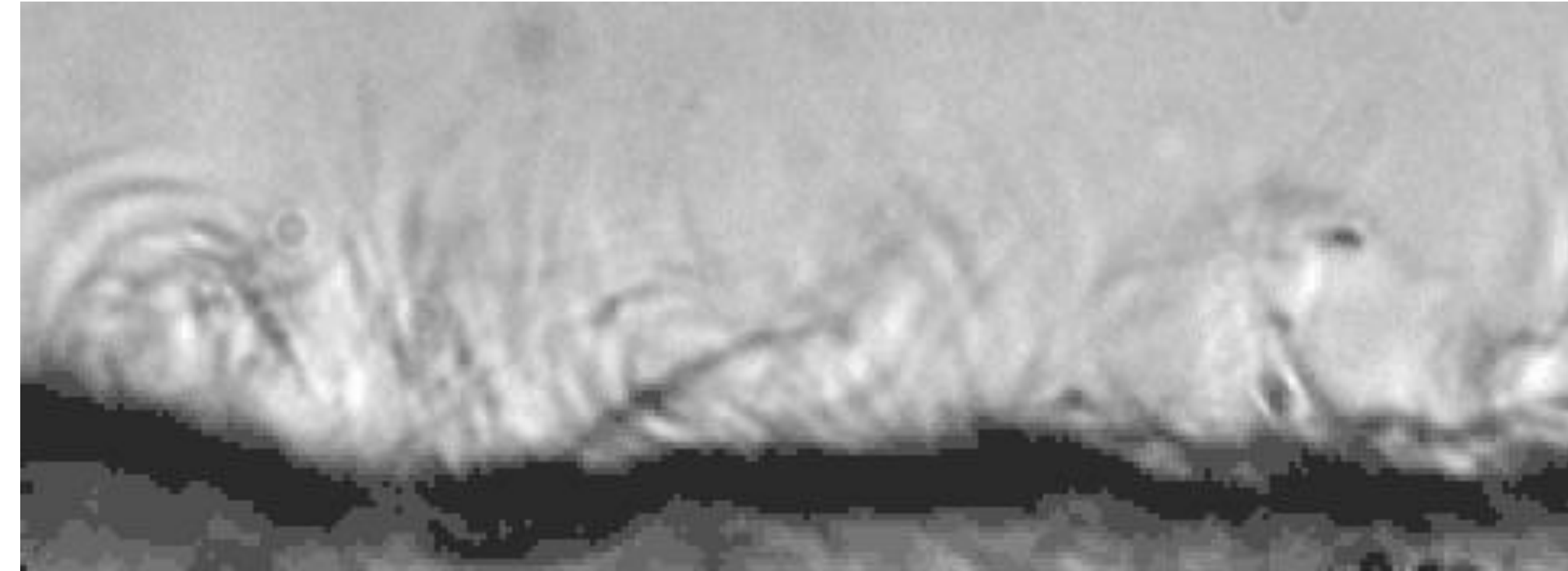
The human species preserves its rare variants

Two Types of Mammalian Cilia

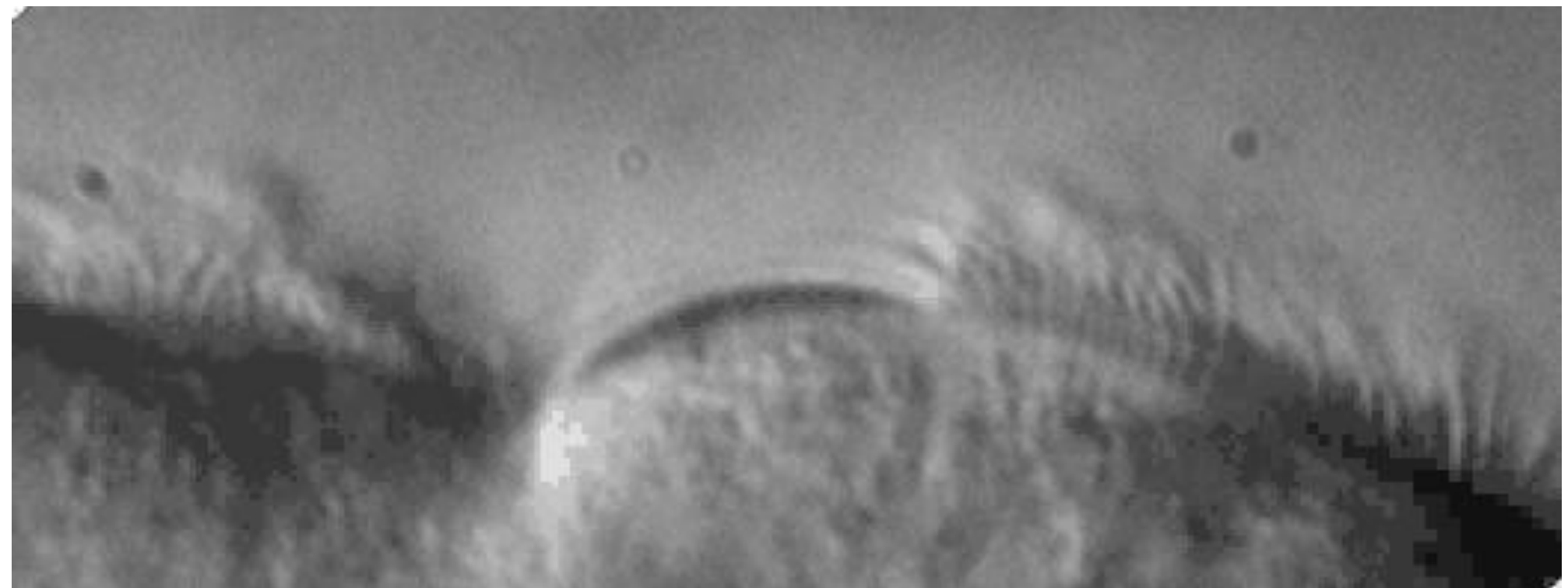


Alison Albee

Sensory Cilia



Mouse Ependymal Cilia

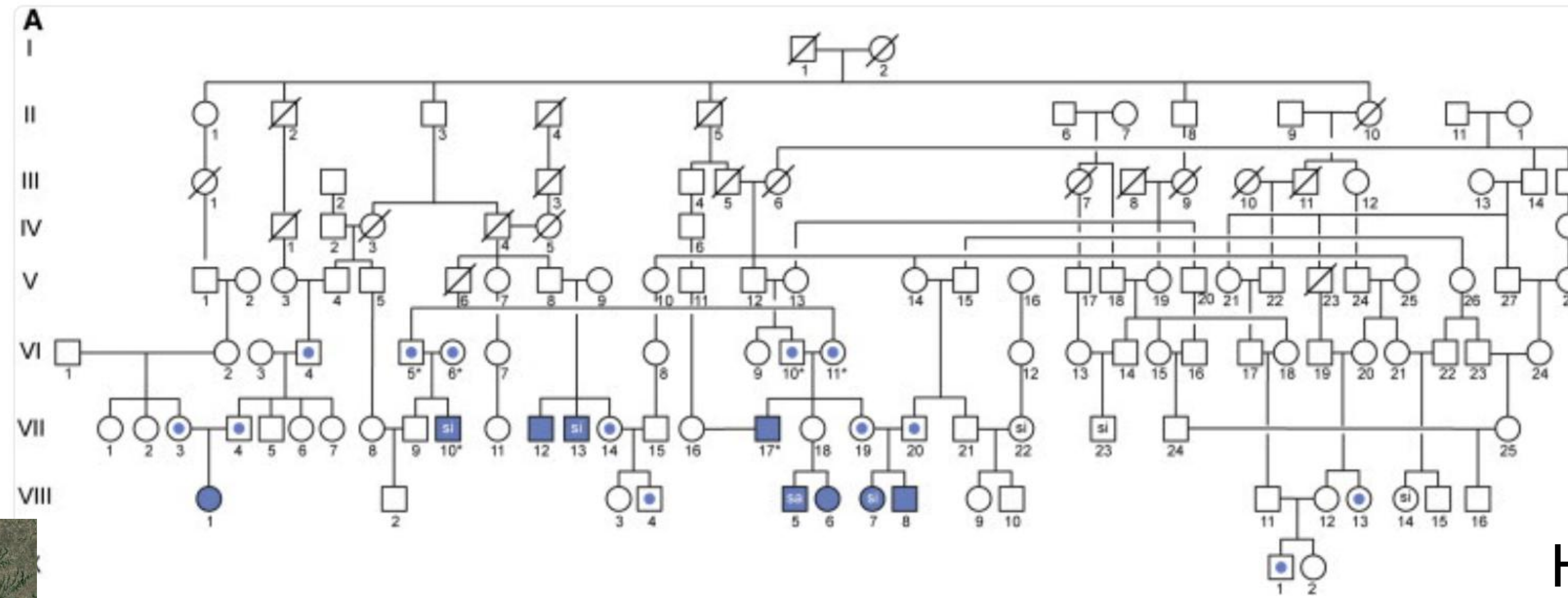


Mouse Tracheal Cilia

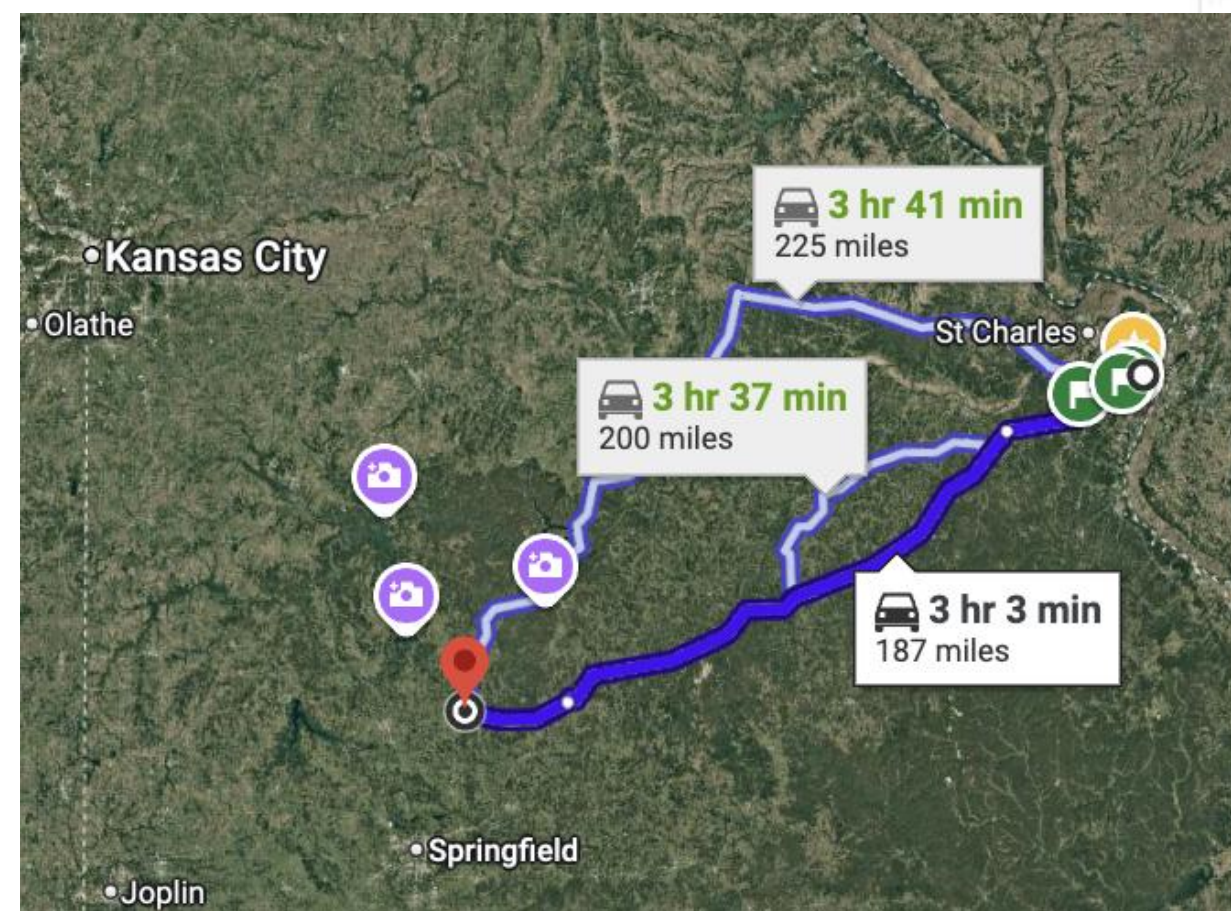
Karl Lecktreck

Motile Cilia

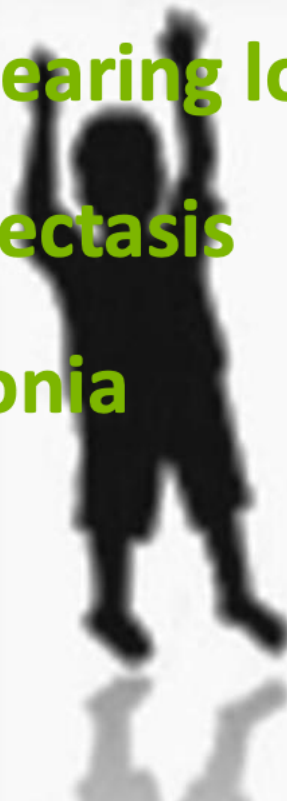
Primary Ciliary Dyskinesia (PCD)



Horani et al., 2013



- Respiratory distress
- Laterality/CHD
- Nasal obstruction
- Pneumonia
- Chronic cough
- Rhinosinusitis
- Otitis/hearing loss
- Bronchiectasis
- Pneumonia
- Chronic cough
- Rhinosinusitis
- Hearing loss
- Bronchiectasis
- Pneumonia
- Sub/Infertility
- (Hydrocephalus)

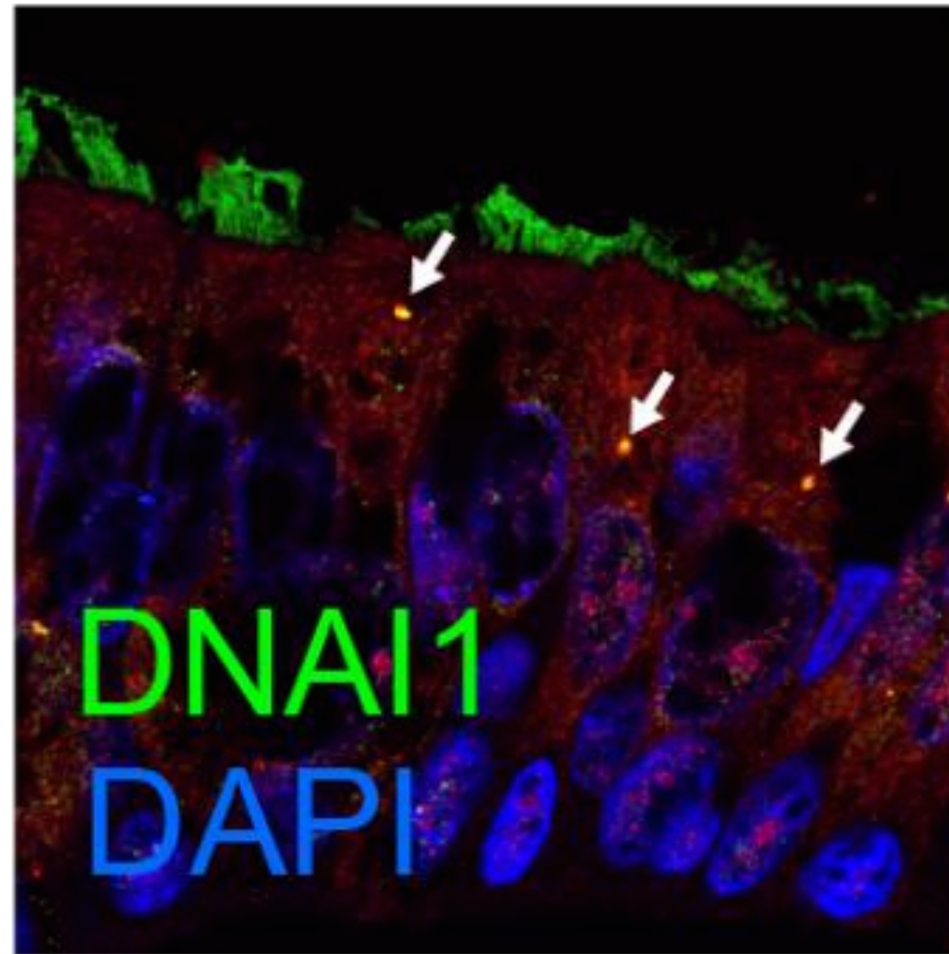


Steve Brody

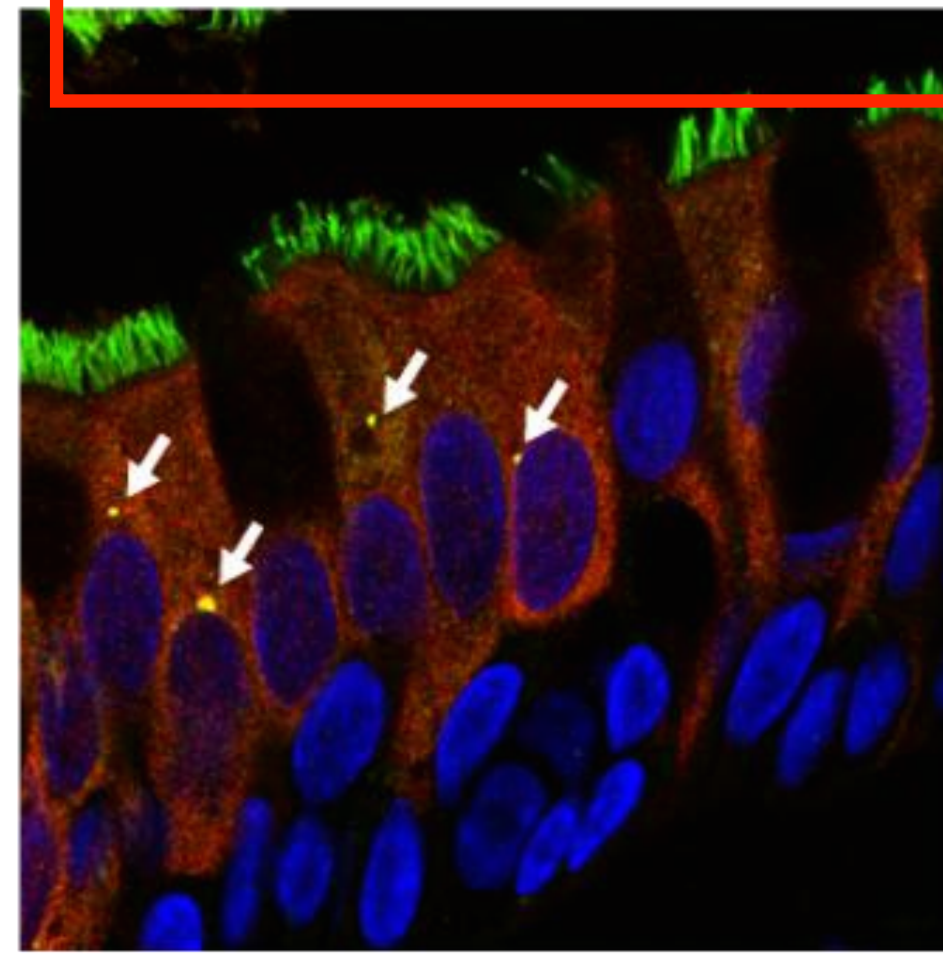
Amjad Horani

Primary Ciliary Dyskinesia (PCD) from a large family in Buffalo Missouri

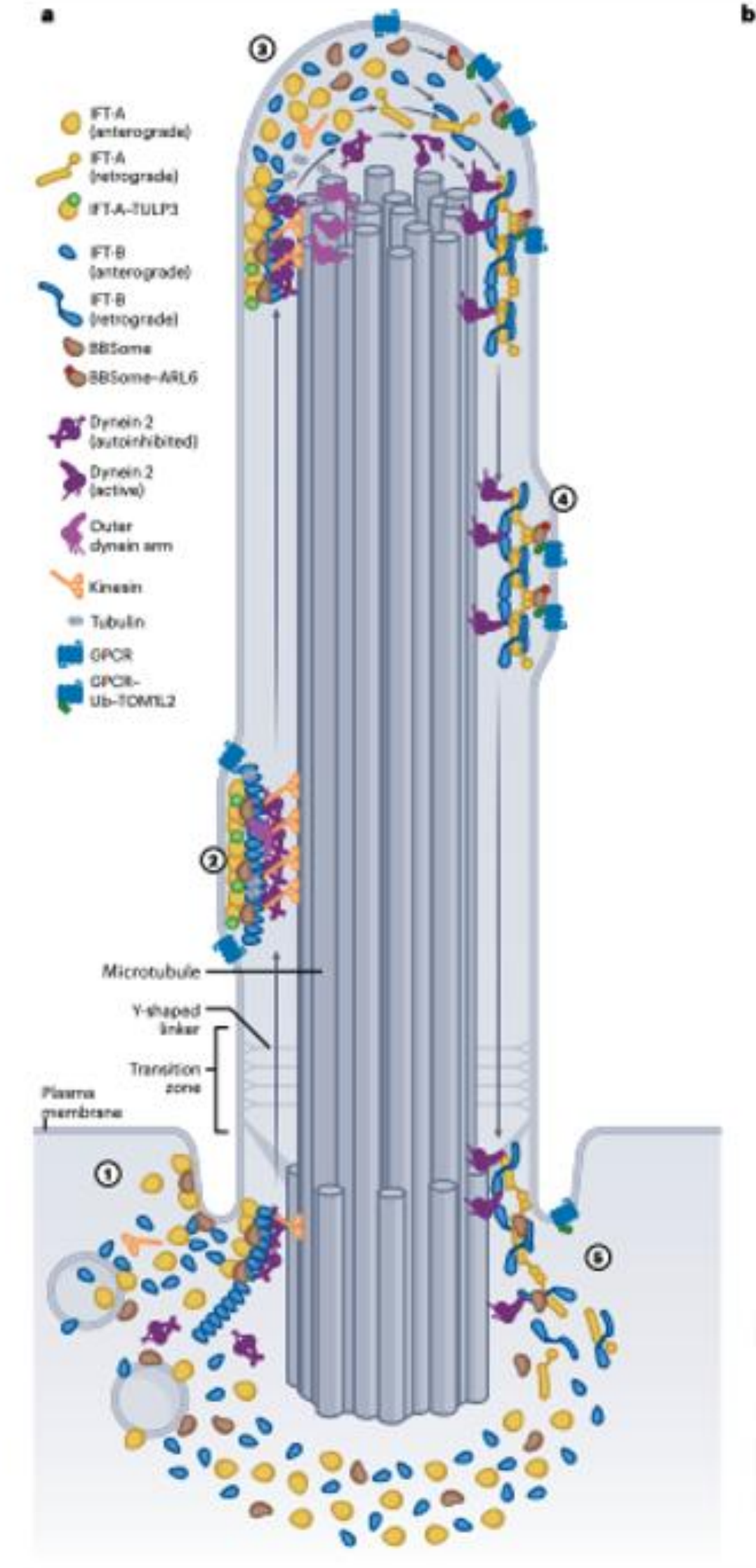
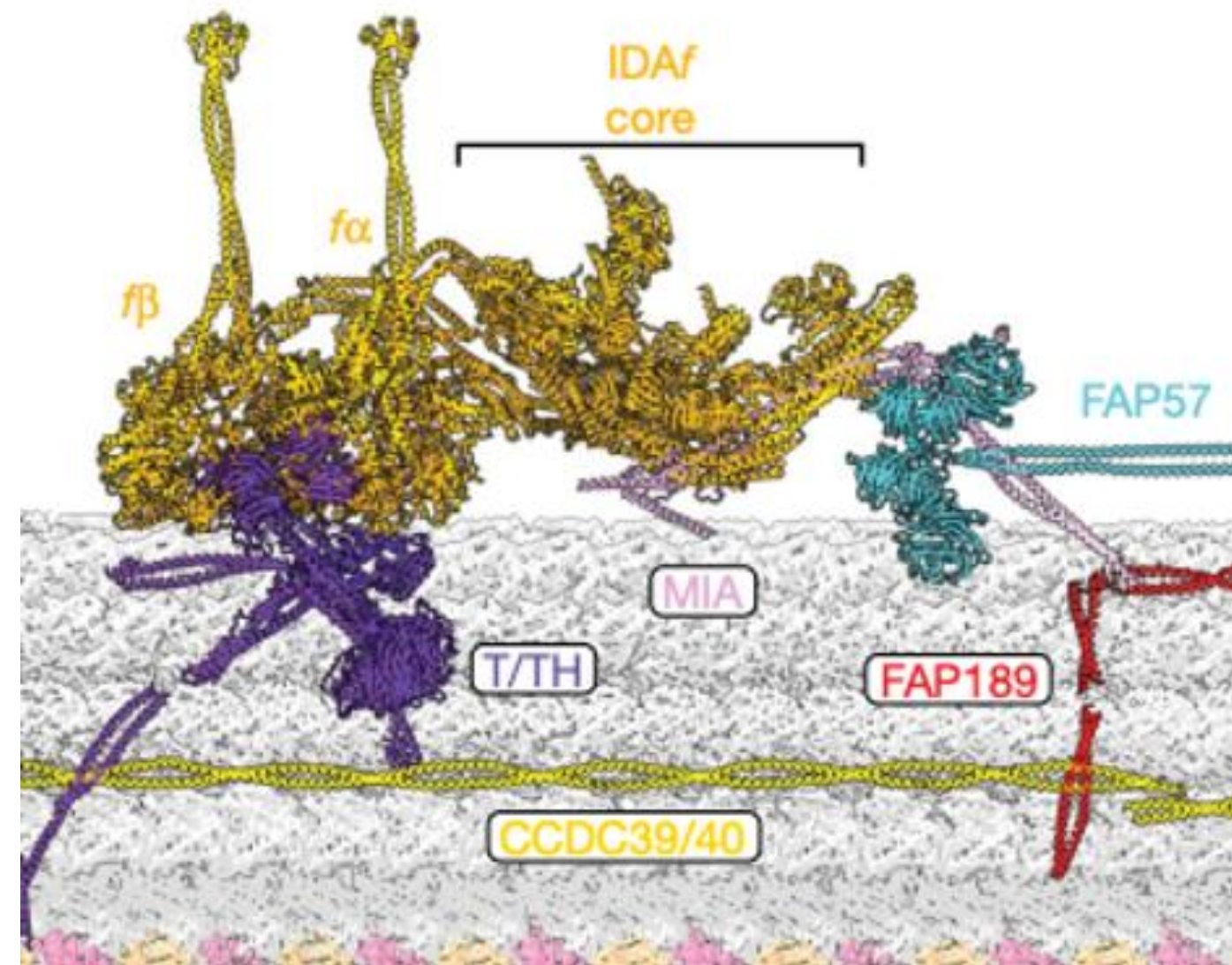
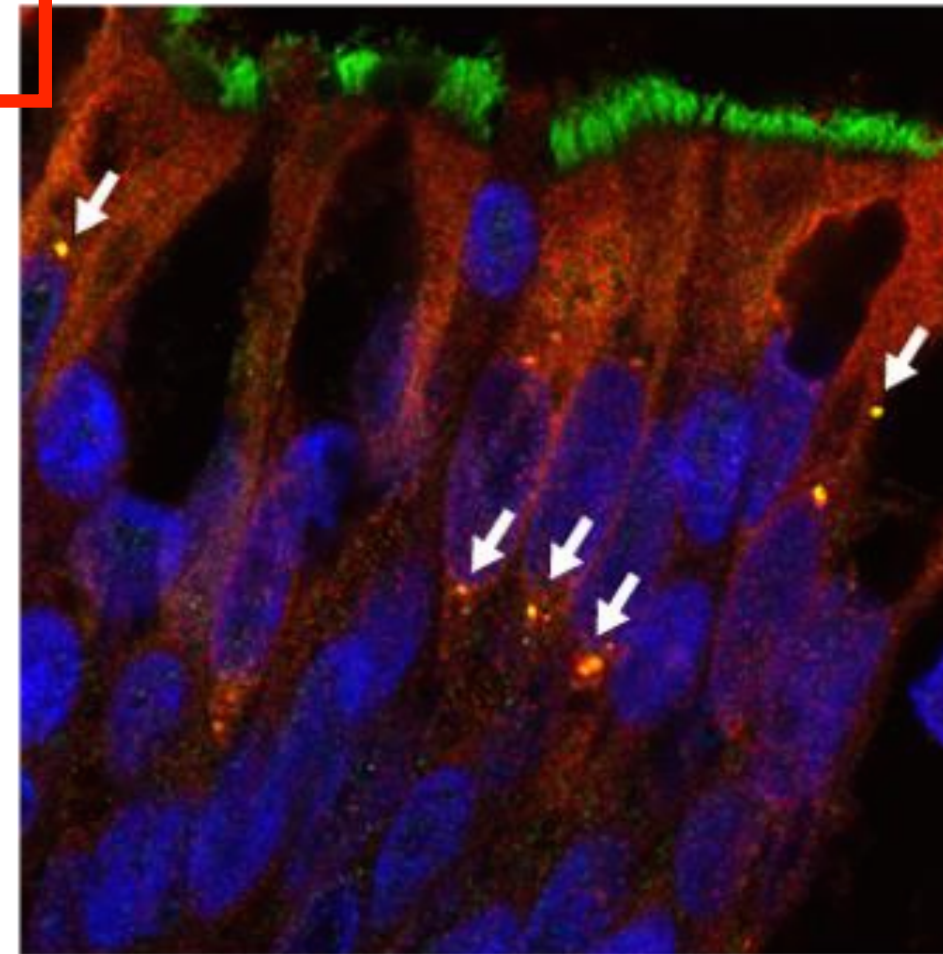
DNAAF2



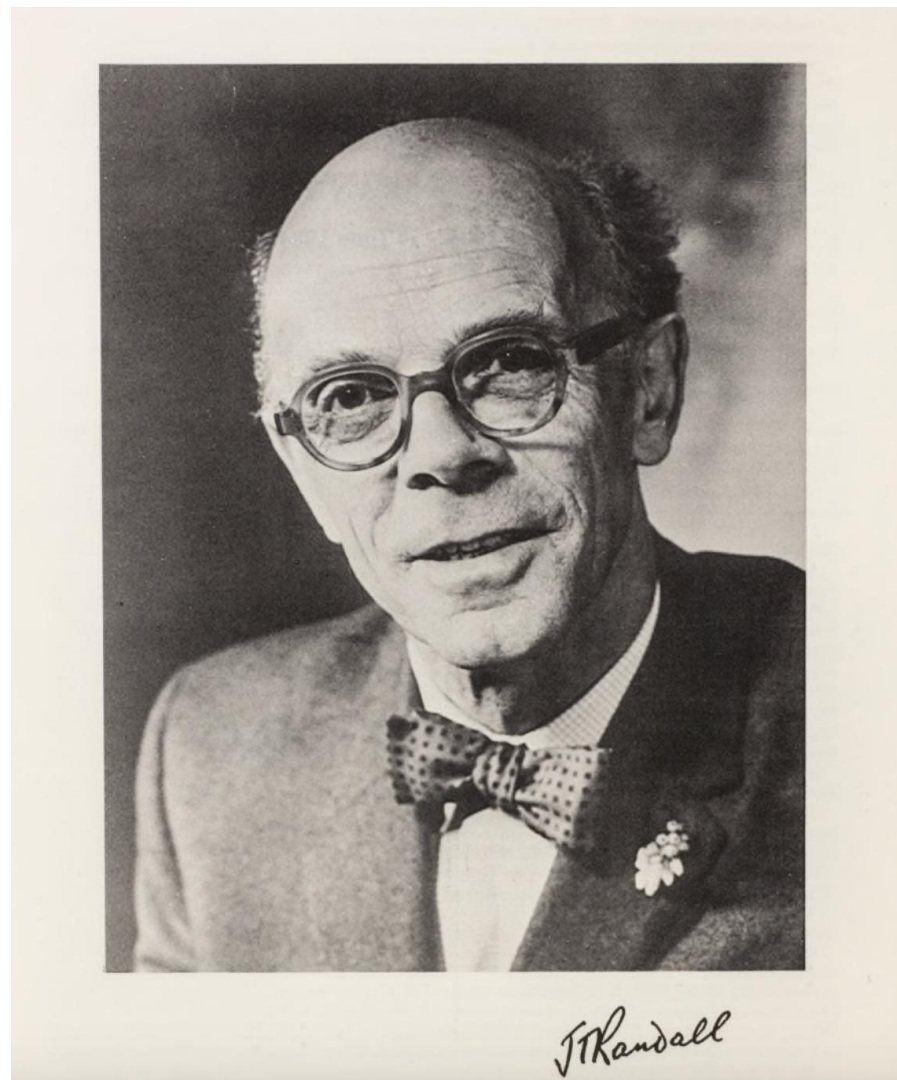
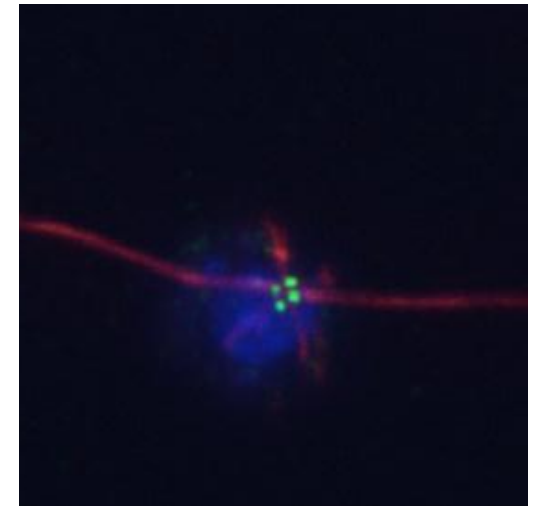
HEATR2



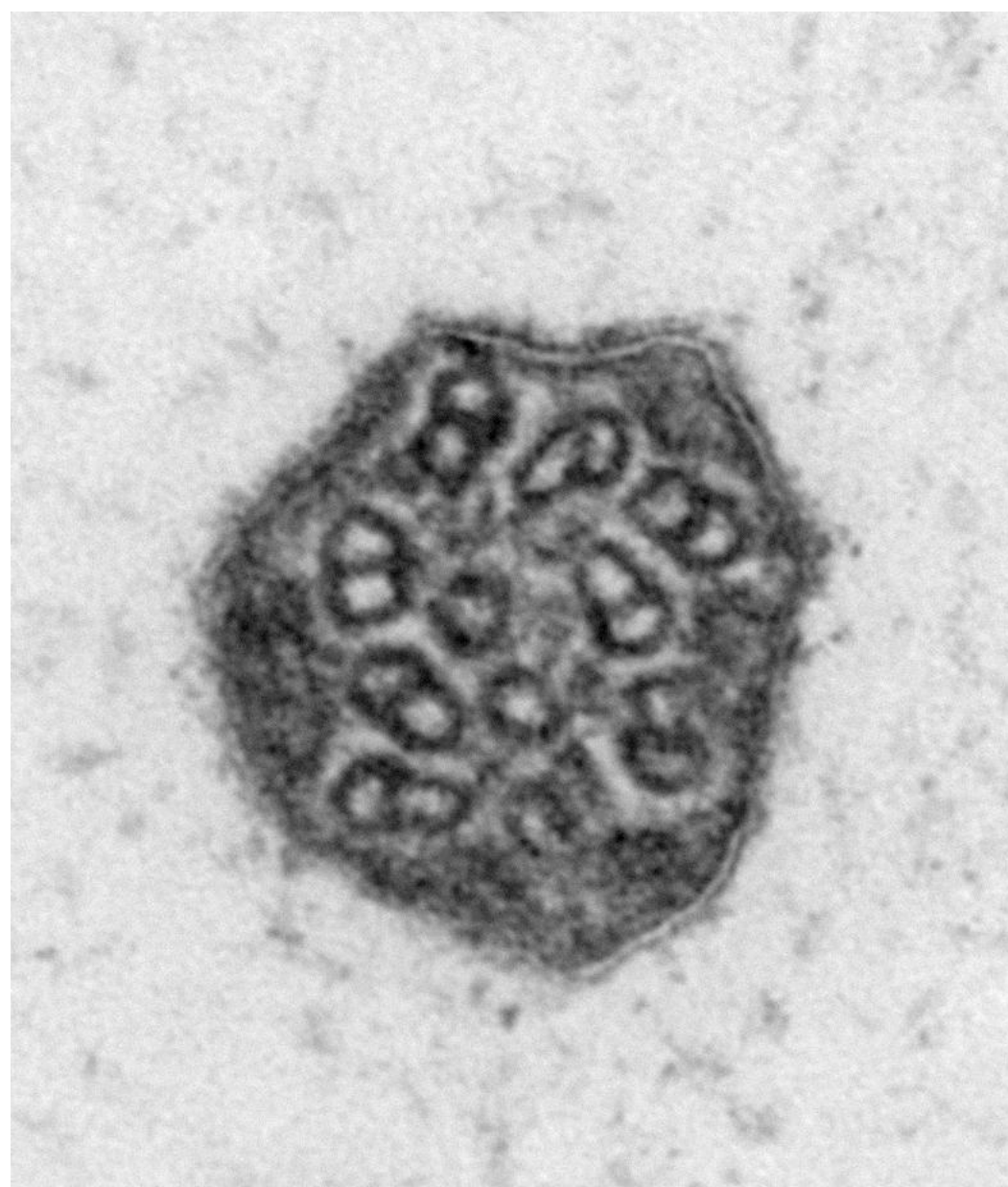
LRRC6



Paralyzed Cilia Collection

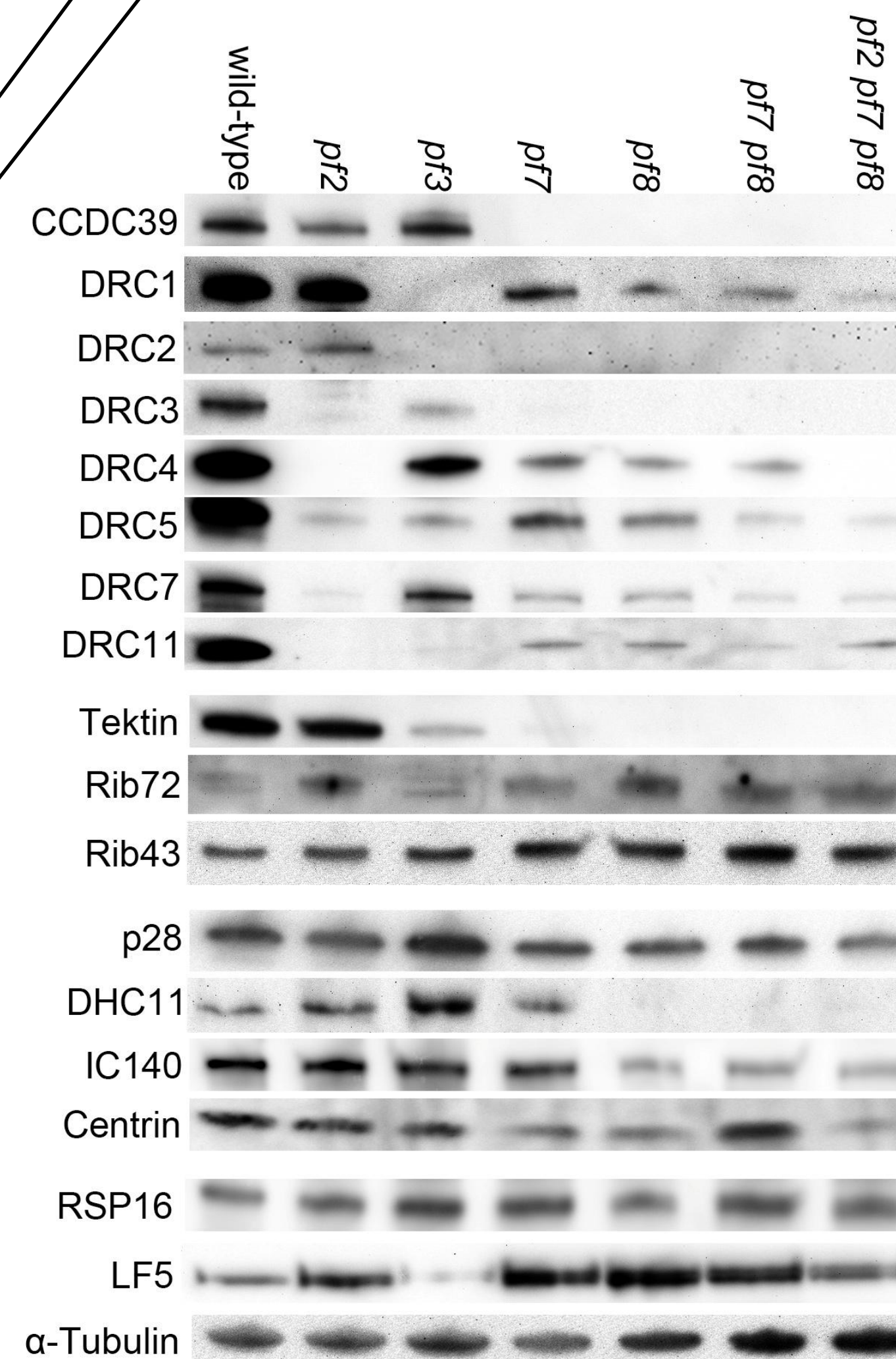


Sir John Randall. University of Edinburgh, 1968-1978

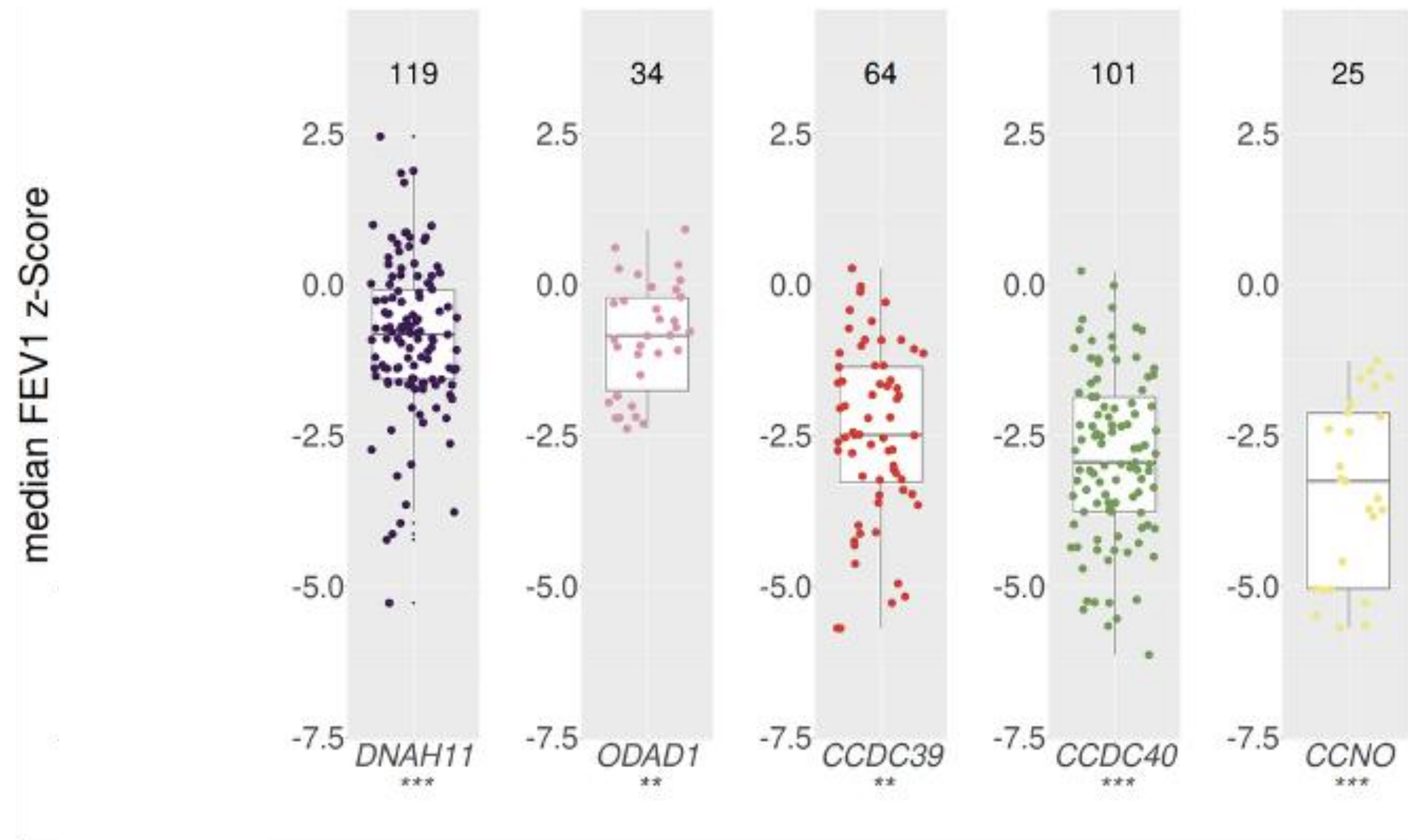
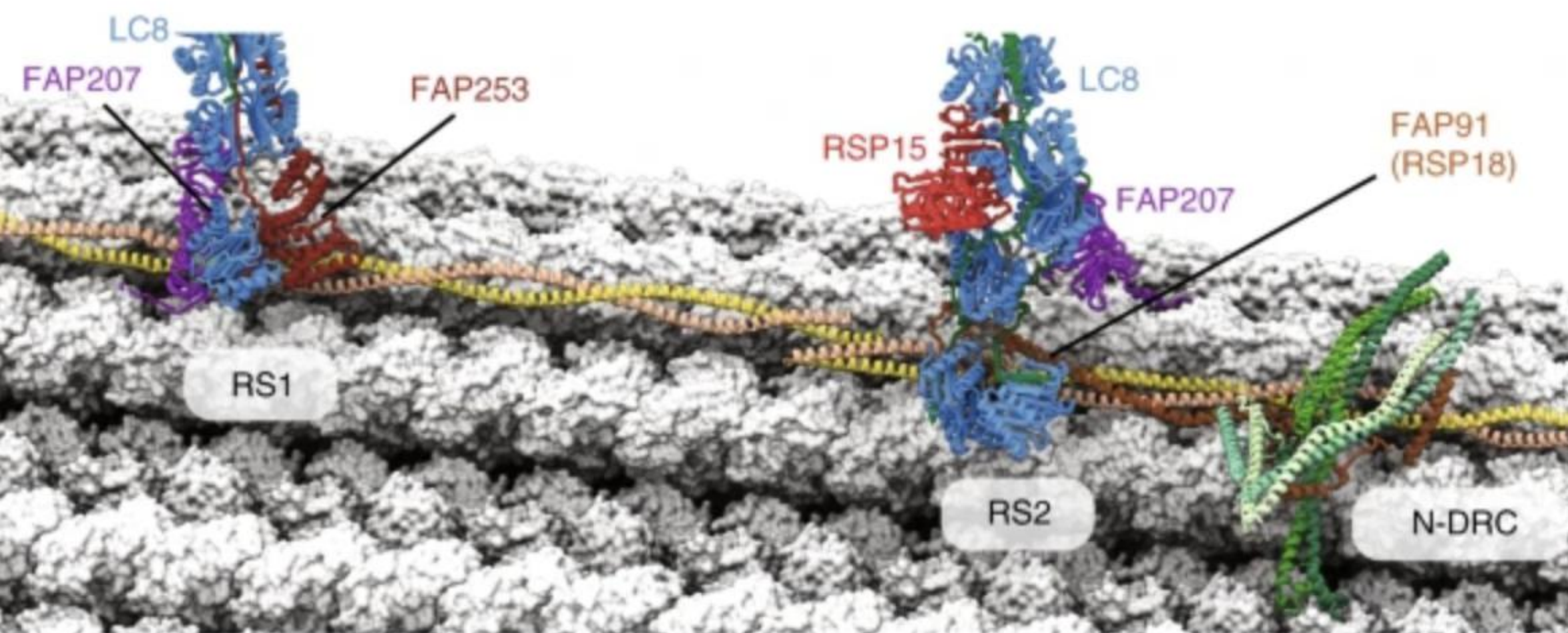
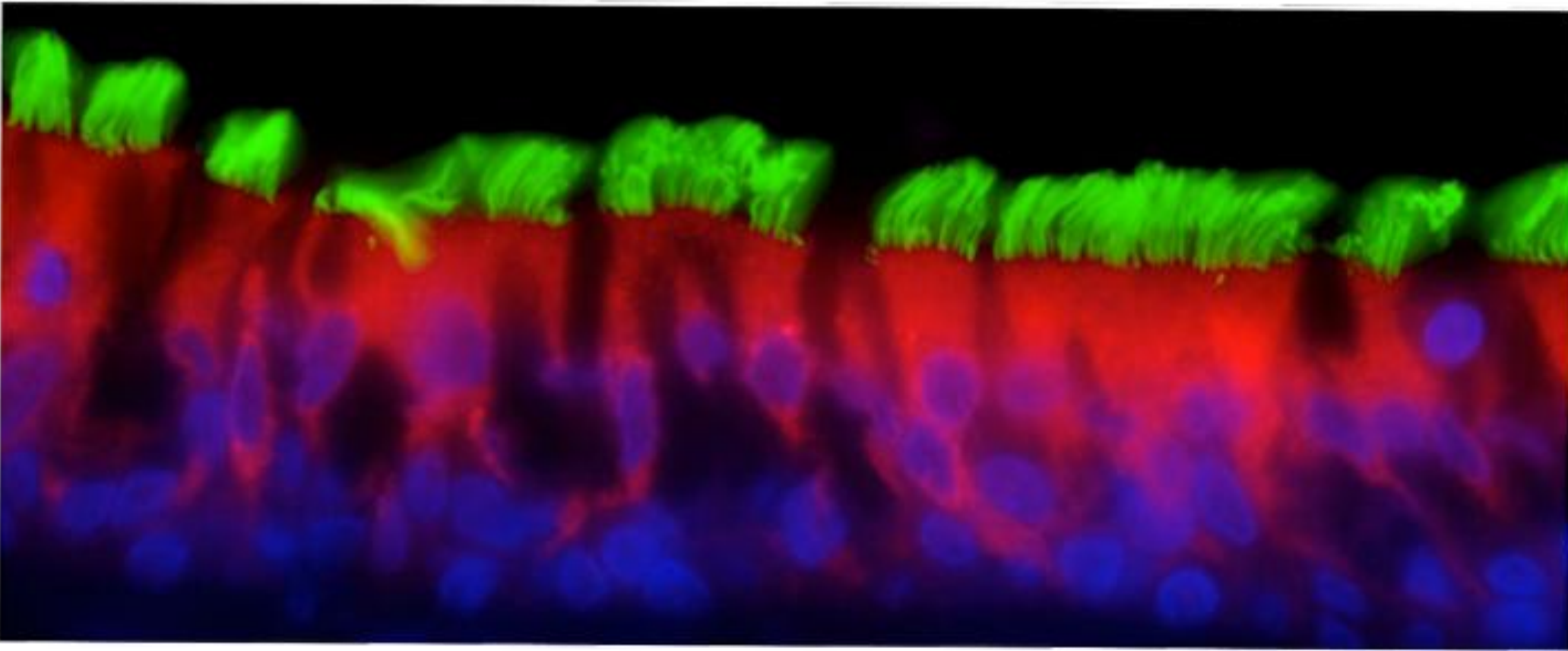


PF1	✓ RSP4	RSPH
PF2	✓ DRC4	N-DRC
PF3	✓ DRC1	N-DRC
PF4	✓ PP2A/IDA	IDA f
PF5	✓ LC8	RSPH
PF6	✓ SPAG17	Central pair
PF7	✓ CCDC39	ADDRESS
PF8	✓ CCDC40	ADDRESS
PF9	✓ DNAH10	IDA f
PF10		UNKNOWN
PF12	✓ PACRG	MIP
PF13	✓ DNAAF2	DNAAF
PF14	✓ RSPH14	RSPH
PF15	✓	Central pair
PF16	✓ SPAG6	Central pair
PF17	✓ RSPH9	RSPH
PF18		Central pair
PF19	✓	Central pair
PF20	✓ SPAG16	Central pair

CCDC39 and CCDC40 mutants

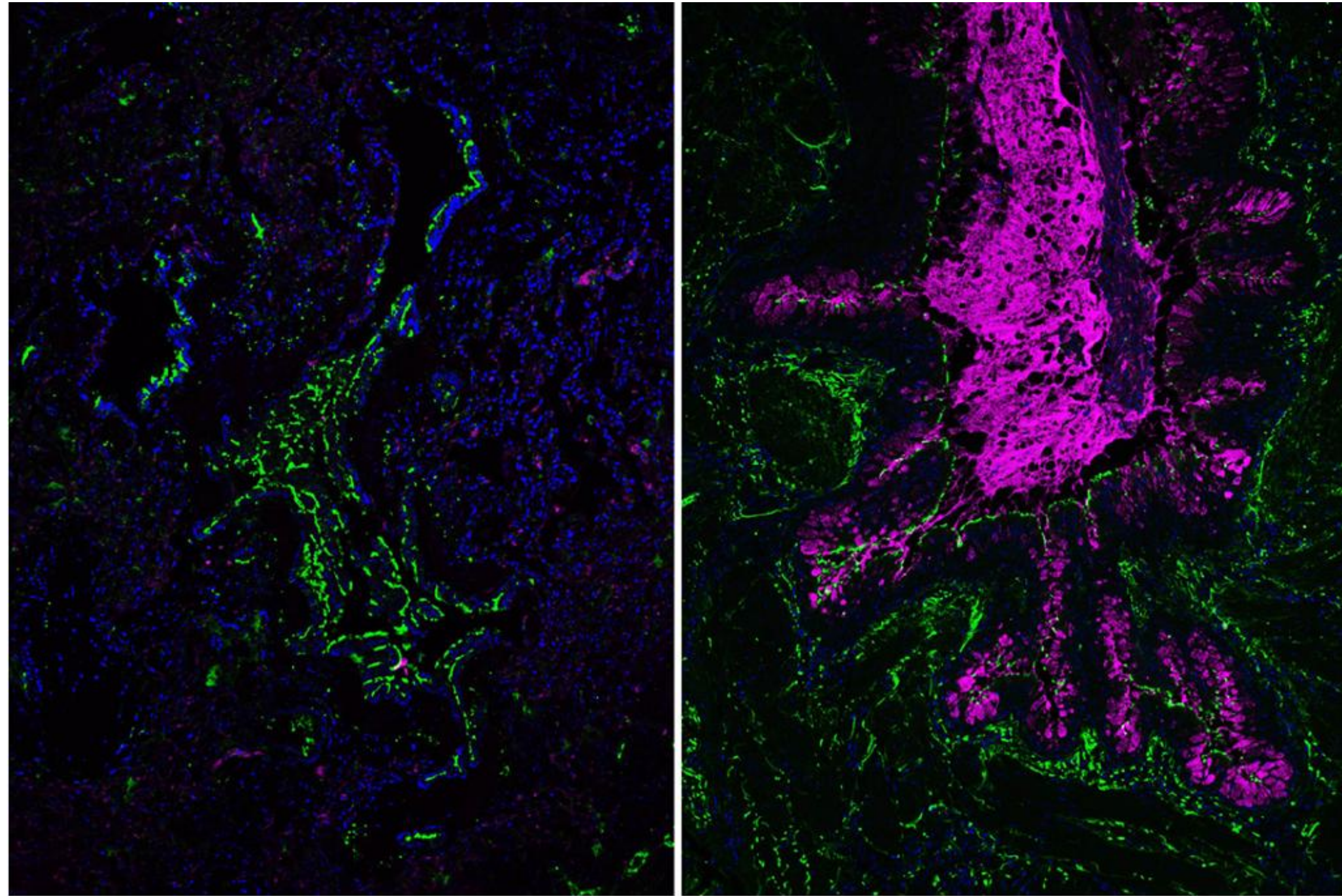


CCDC39 and CCDC40 are a 96 nm long heterodimer



Raidt et al., 2025

CCDC39 and *CCDC40* patients have more mucus in their small airways



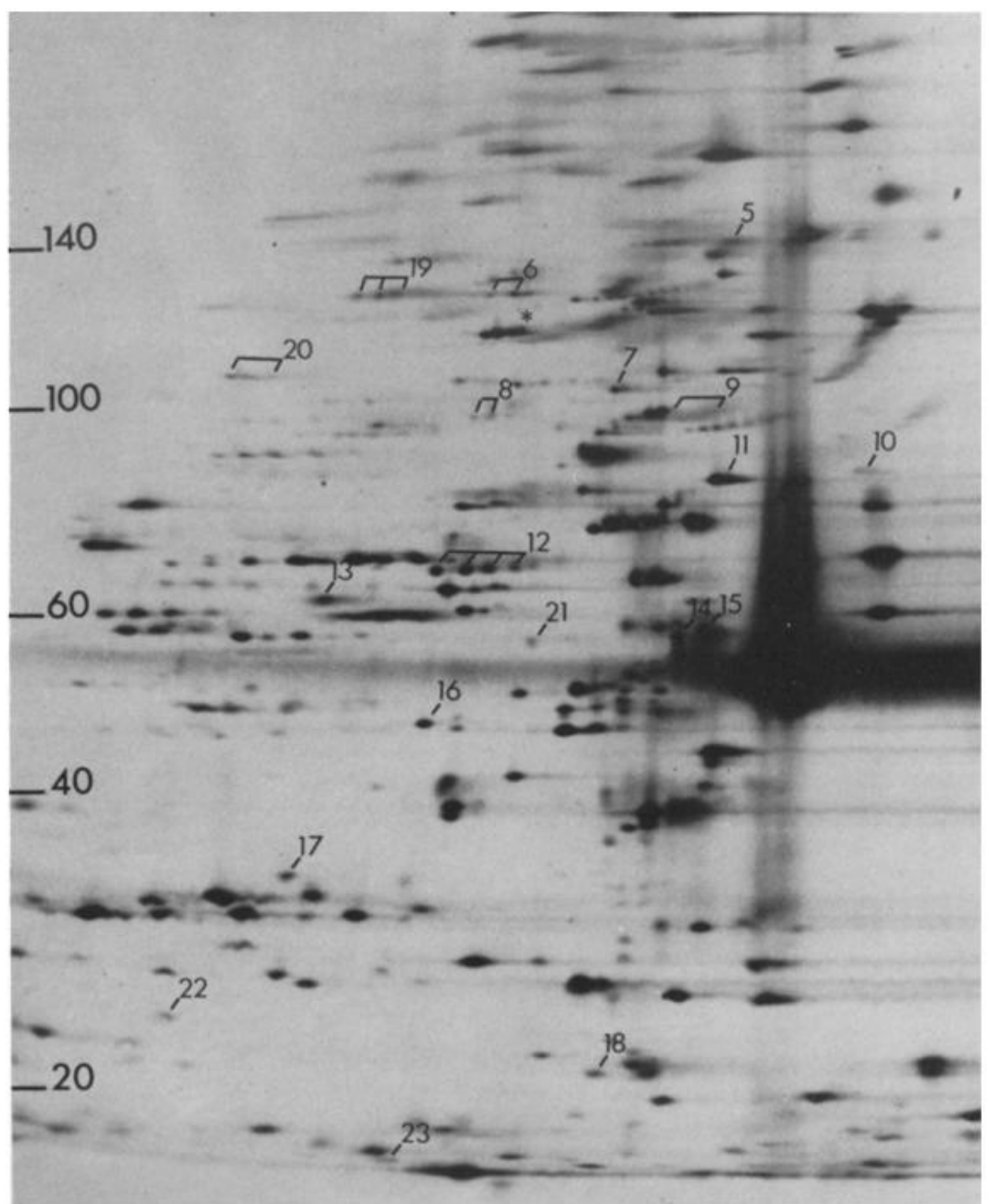
■ Cilia ■ Mucus ■ DNA

Control

CCDC39^{-/-}

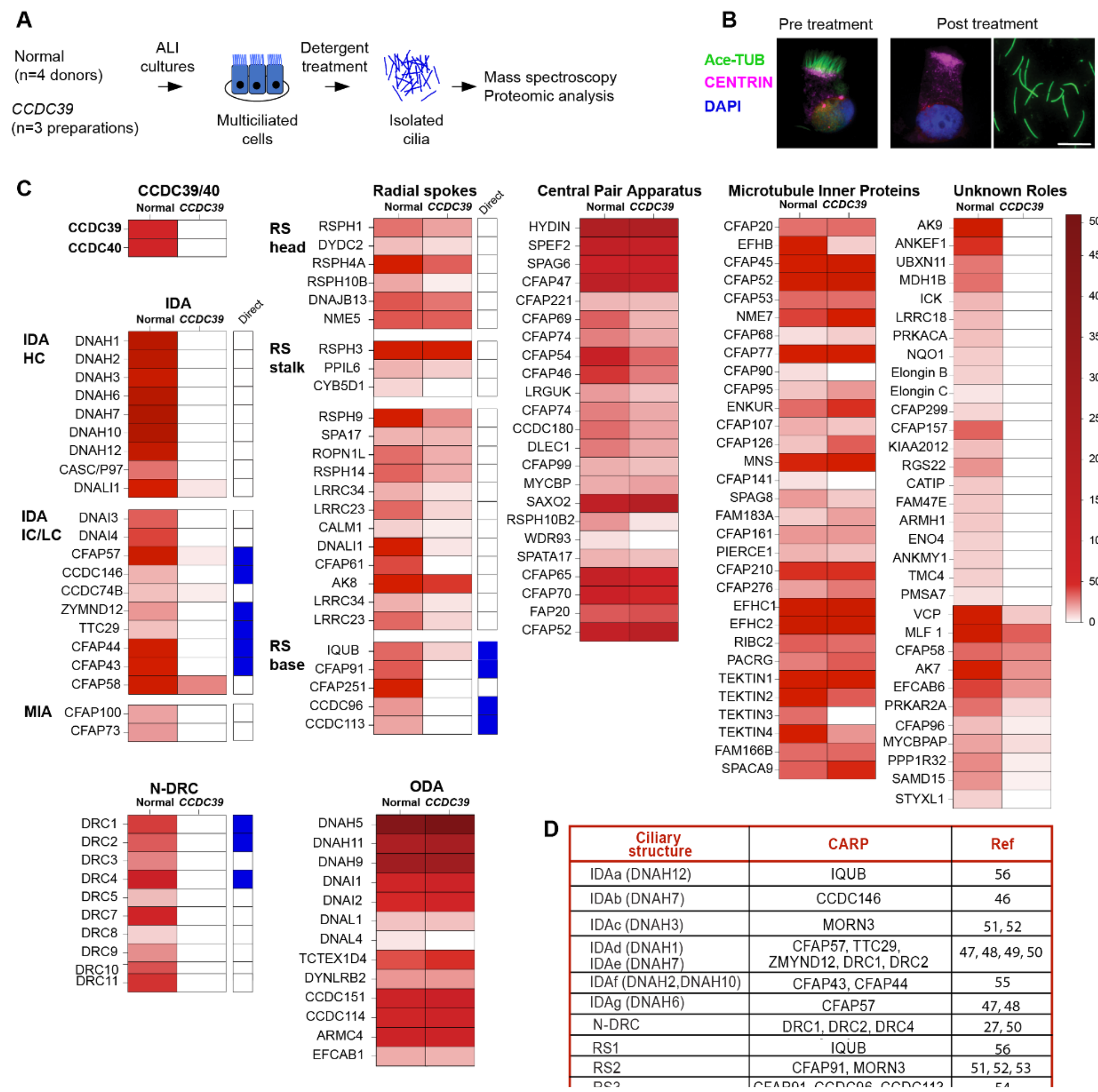
Changing Technologies: 2D gels to Proteomics

$\times 10^{-3}$



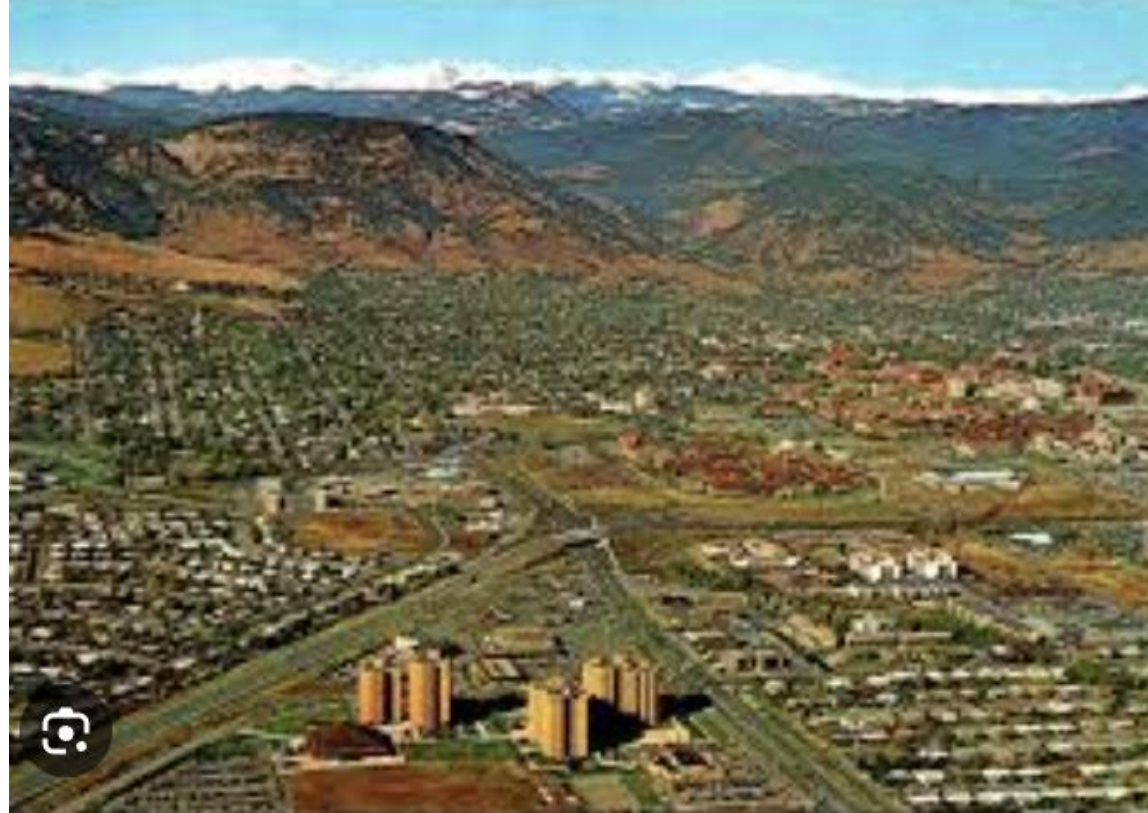
Dutcher et al., 1984

Figure 2

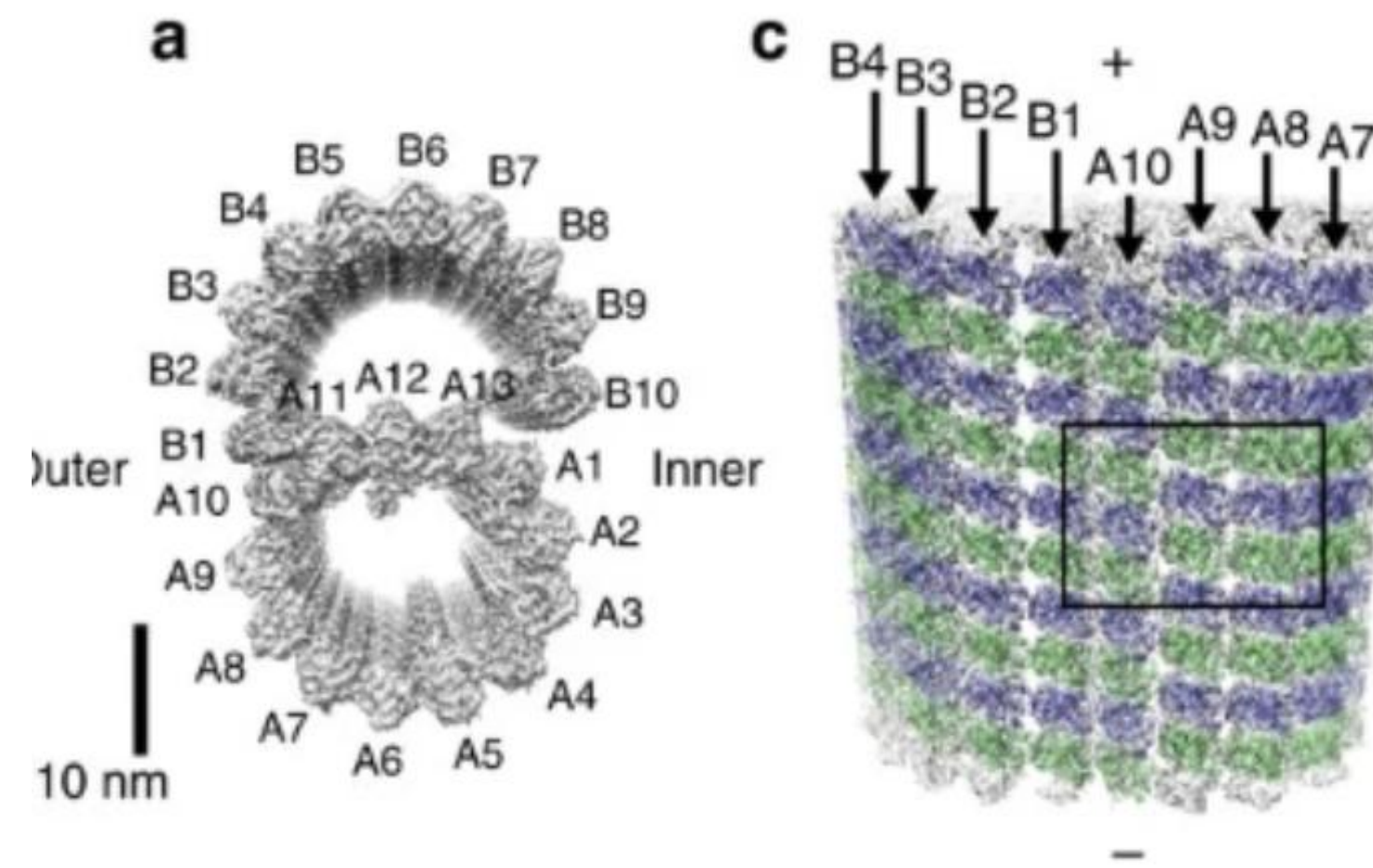


Brody et al., 2025

Finding addresses for ciliary proteins

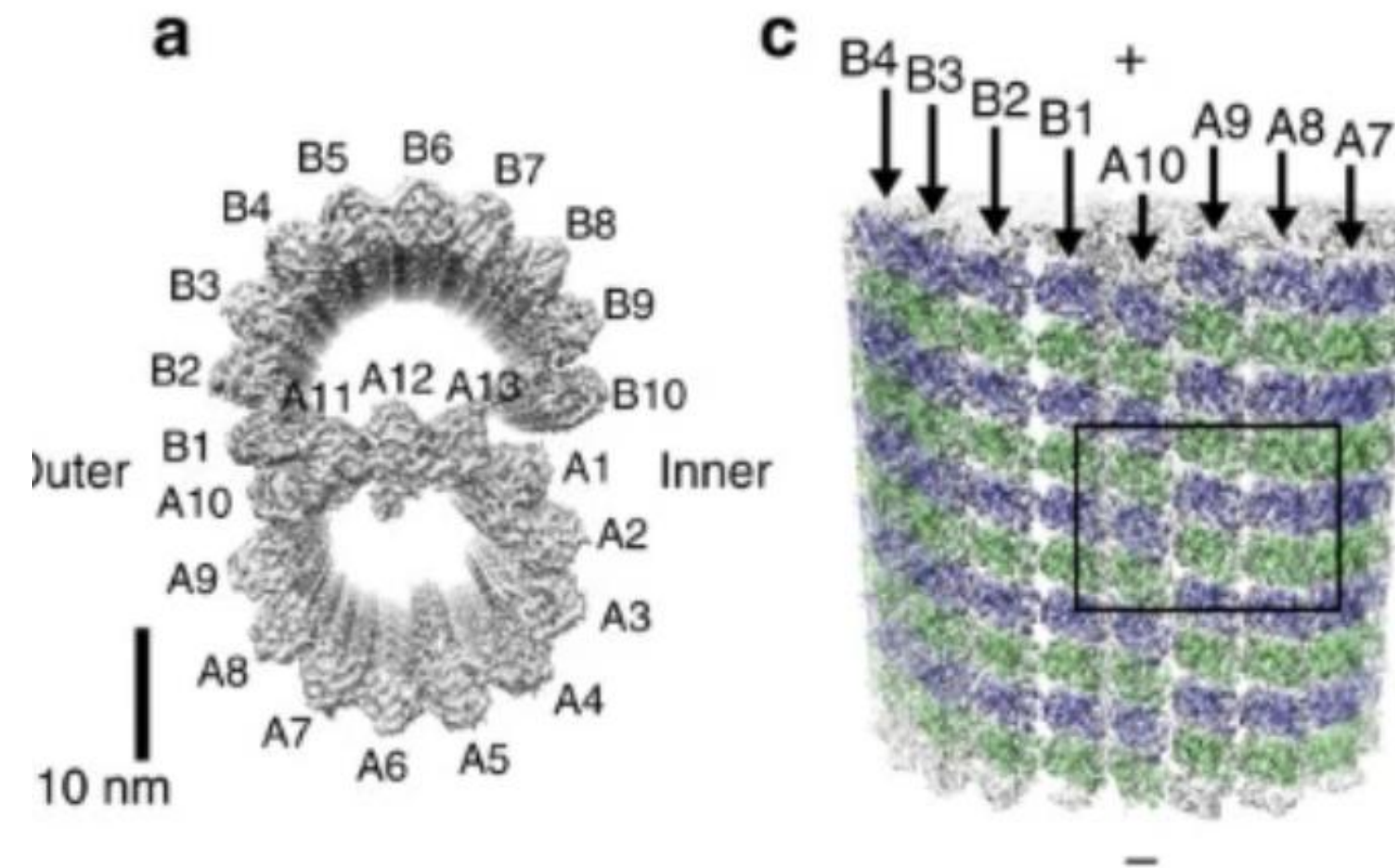


Finding addresses for ciliary proteins



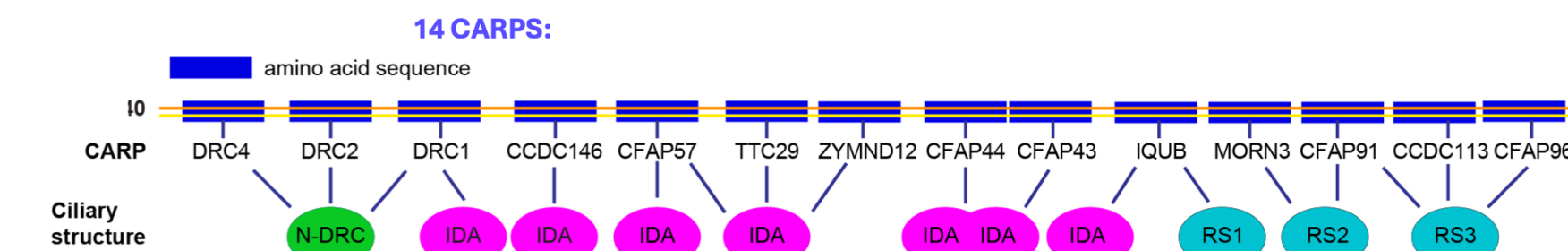


Finding addresses for ciliary proteins



CCDC39/CCDC40
heterodimer

CARPS: Cilia Address Recognition Proteins attached to CCDC39/40 heterodimer



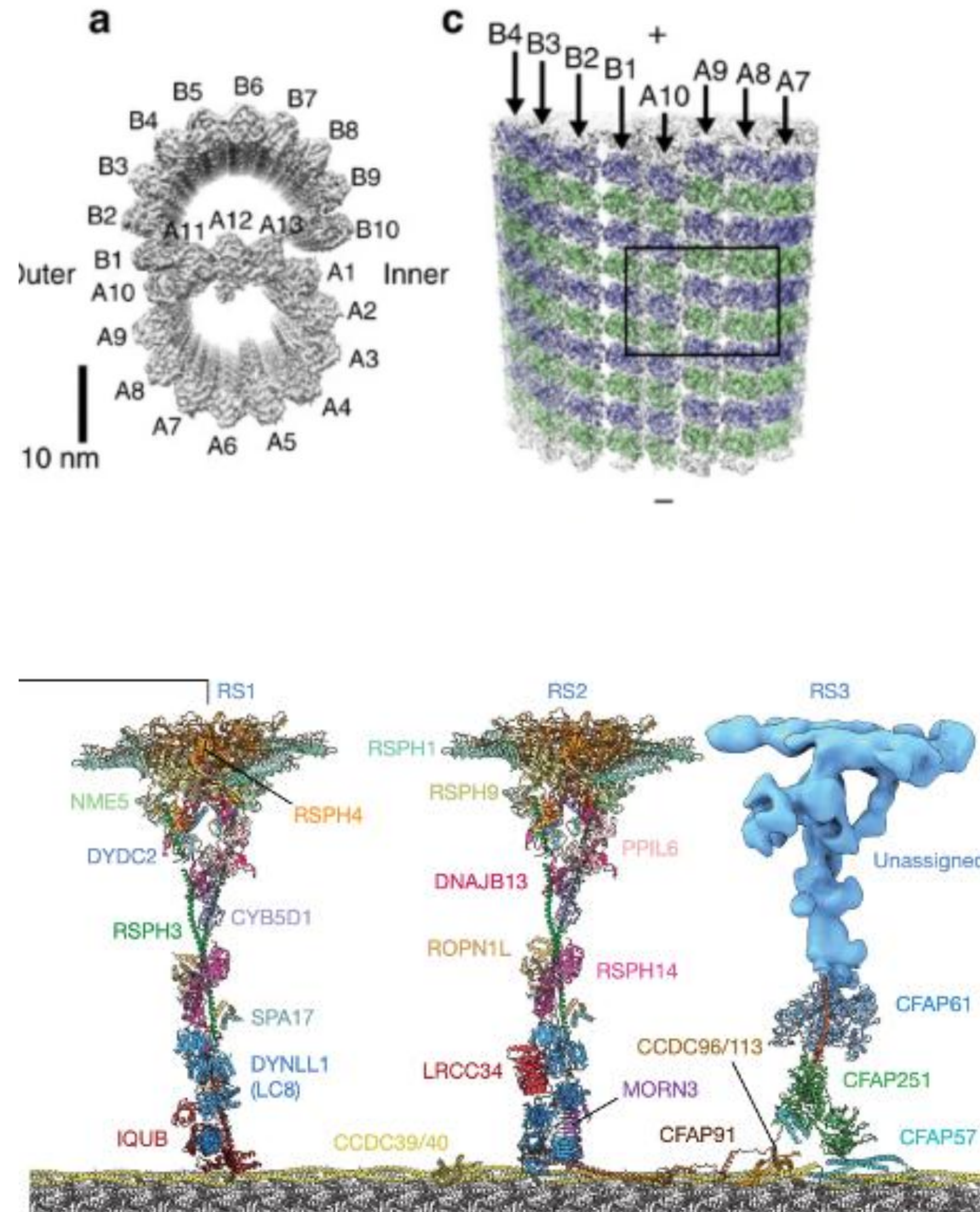
Major structures missing:

- Nexin-dynein regulatory complex
- Inner dynein arms
- Radial spokes

Brody et al., 2025

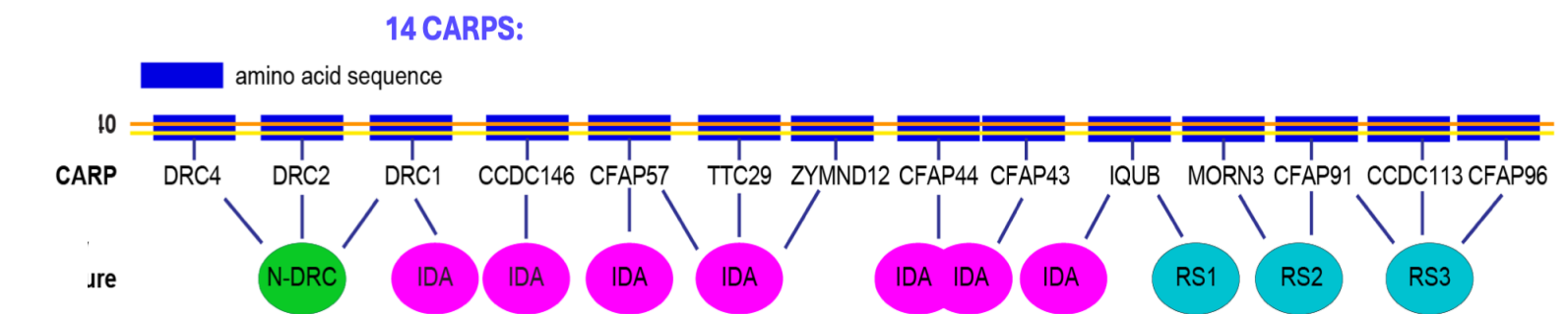


Finding addresses for ciliary proteins



CCDC39/CCDC40 heterodimer

CARPS: Cilia Address Recognition Proteins attached to CCDC39/40 heterodimer

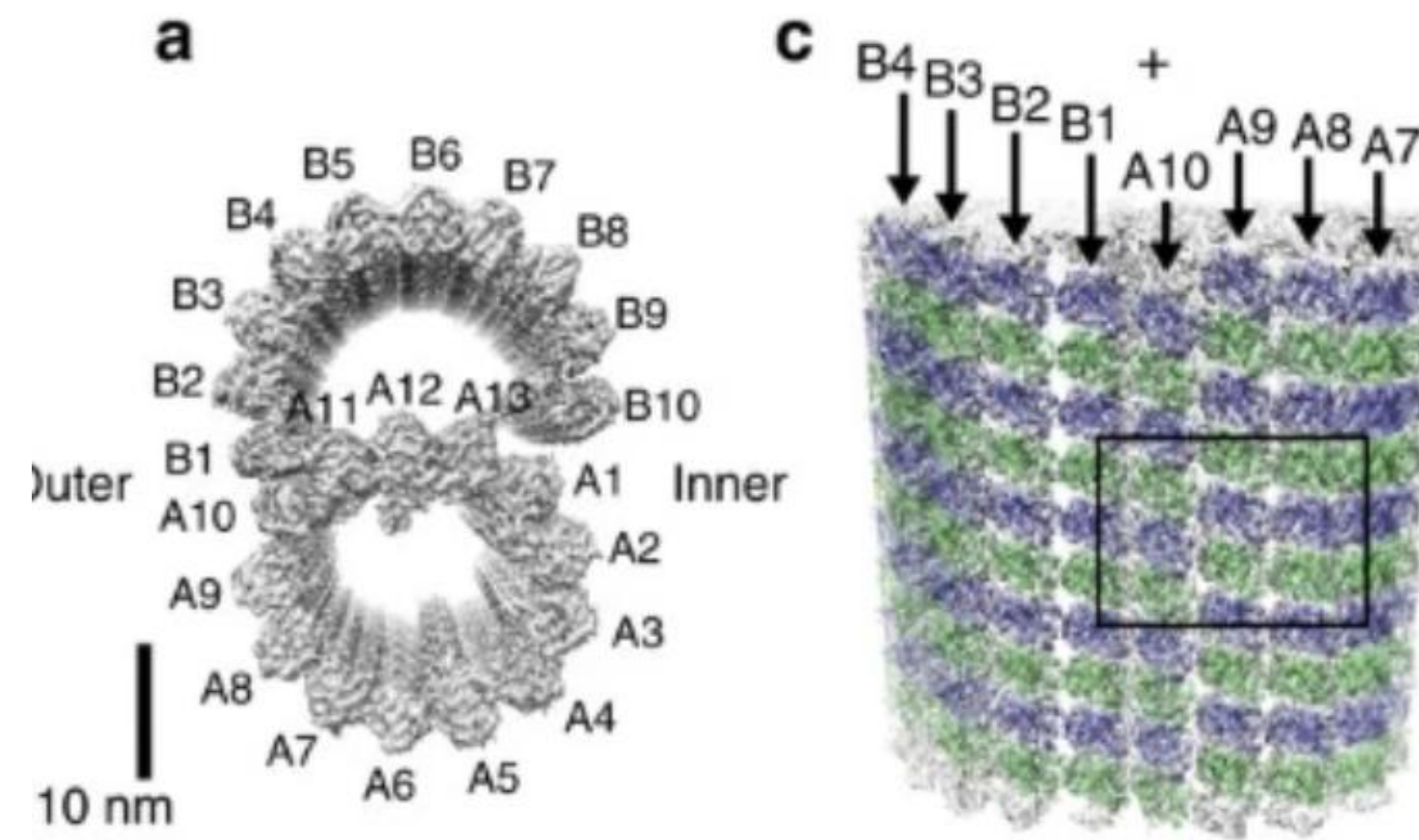


- Major structures missing:
- Nexin-dynein regulatory complex
 - Inner dynein arms
 - Radial spokes

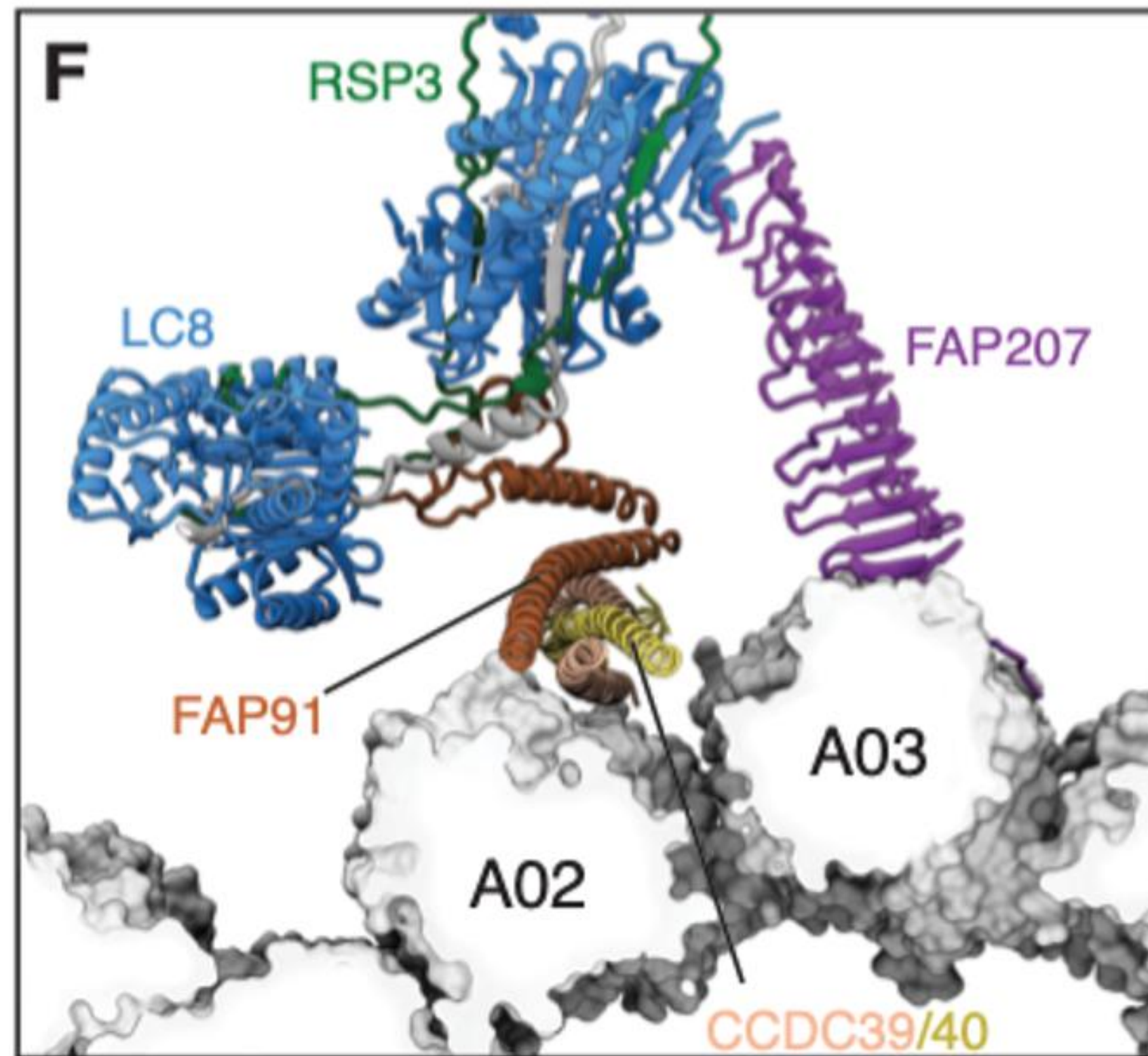
Brody et al., 2025



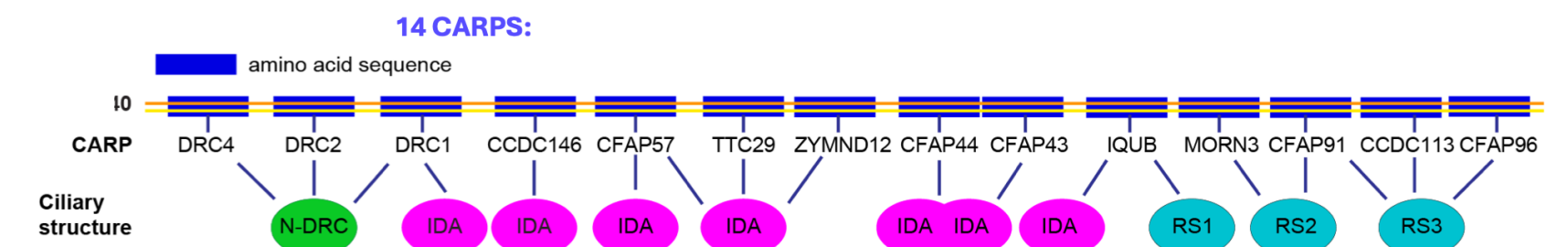
Finding addresses for ciliary proteins



CCDC39/CCDC40 heterodimer



CARPS: Cilia Address Recognition Proteins attached to CCDC39/40 heterodimer



- Major structures missing:
- Nexin-dynein regulatory complex
 - Inner dynein arms
 - Radial spokes

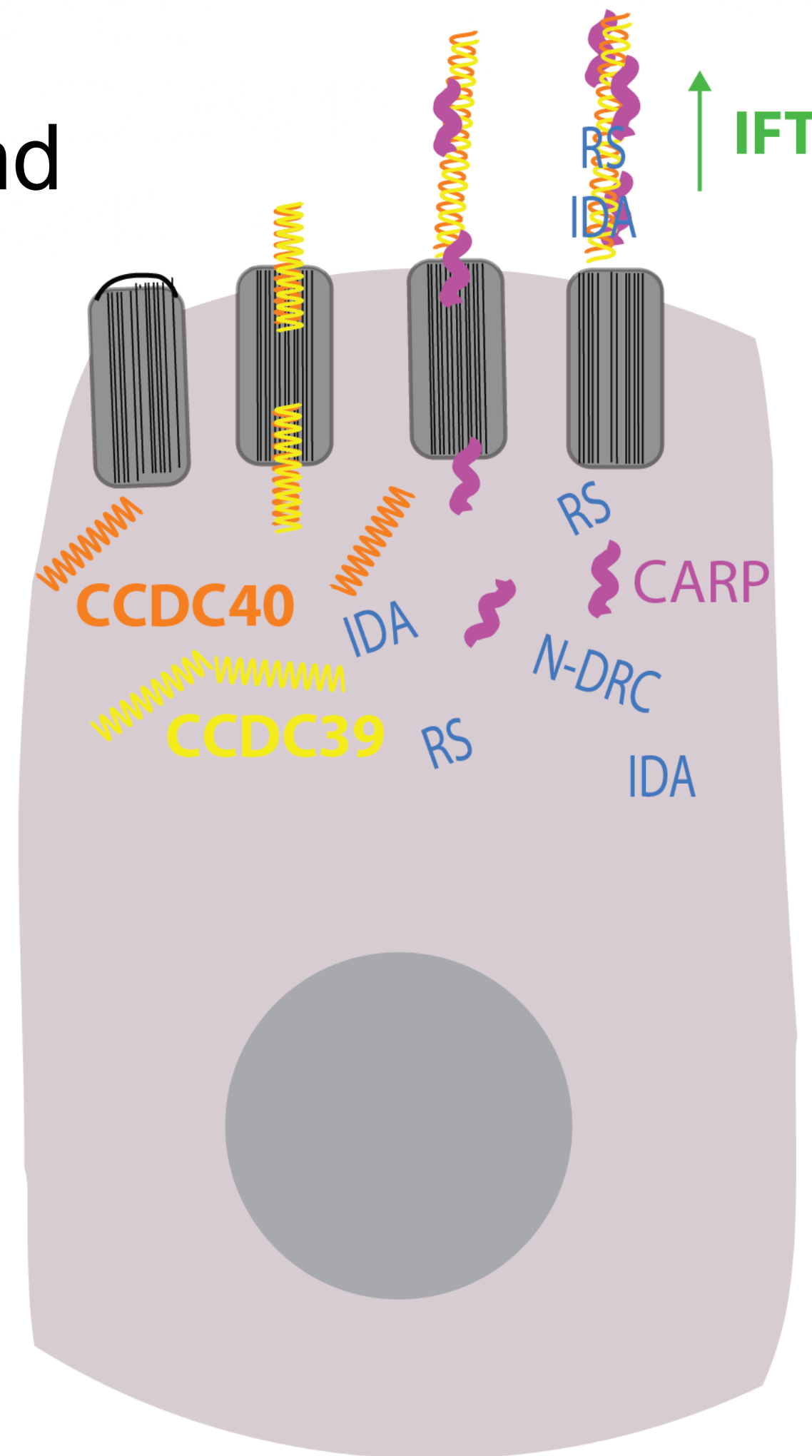
Brody et al., 2025

Timing of events during cilia assembly

3. Complexes enter and dock

2. CARPs enter and bind CCDC39/40 heterodimer

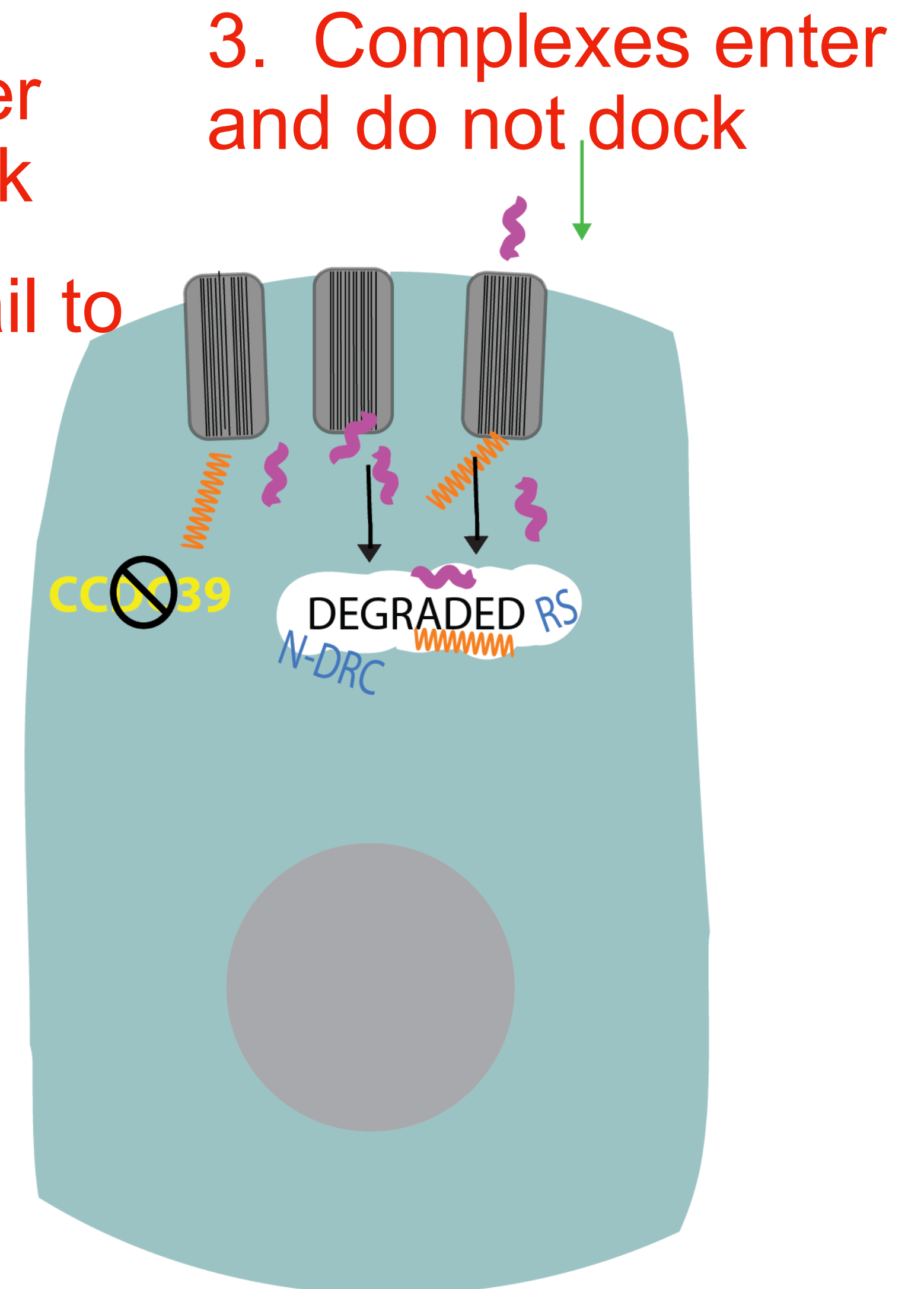
1. CCDC39/40 enter



Control cells

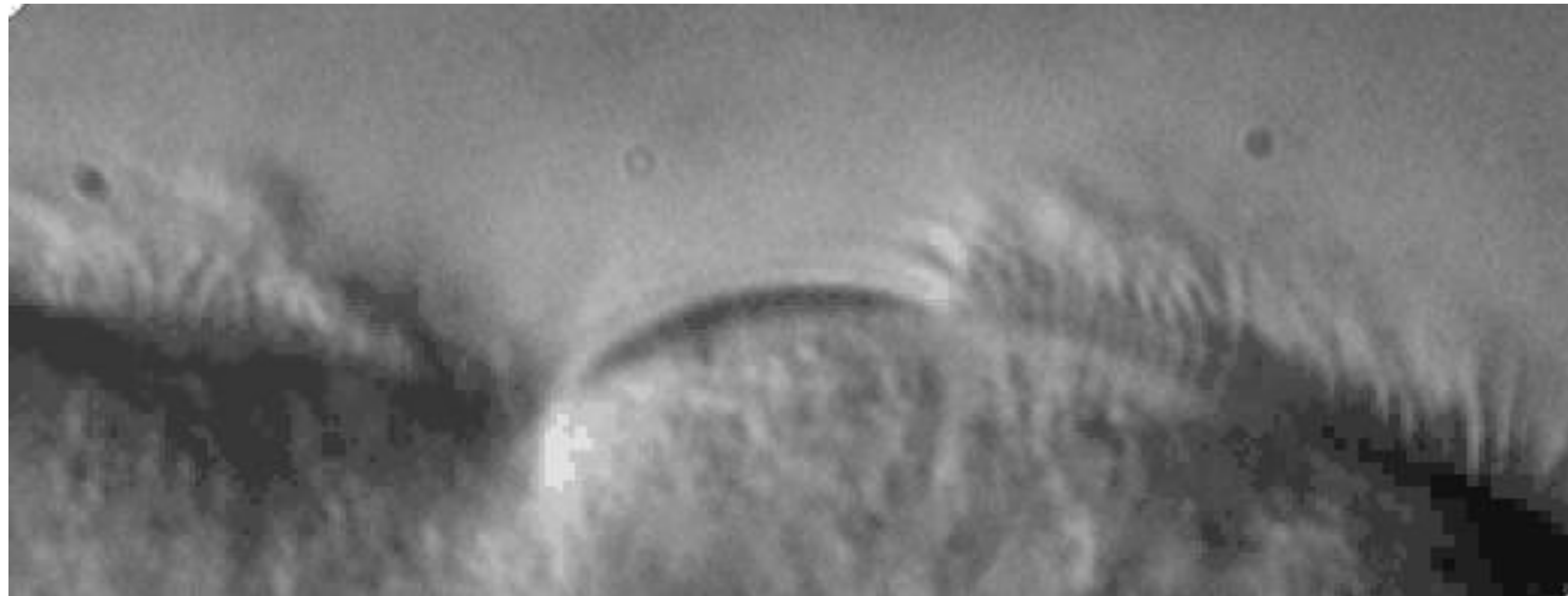
2. CARPs enter but do not dock

1. CCDC39/40 fail to enter



Variant cells

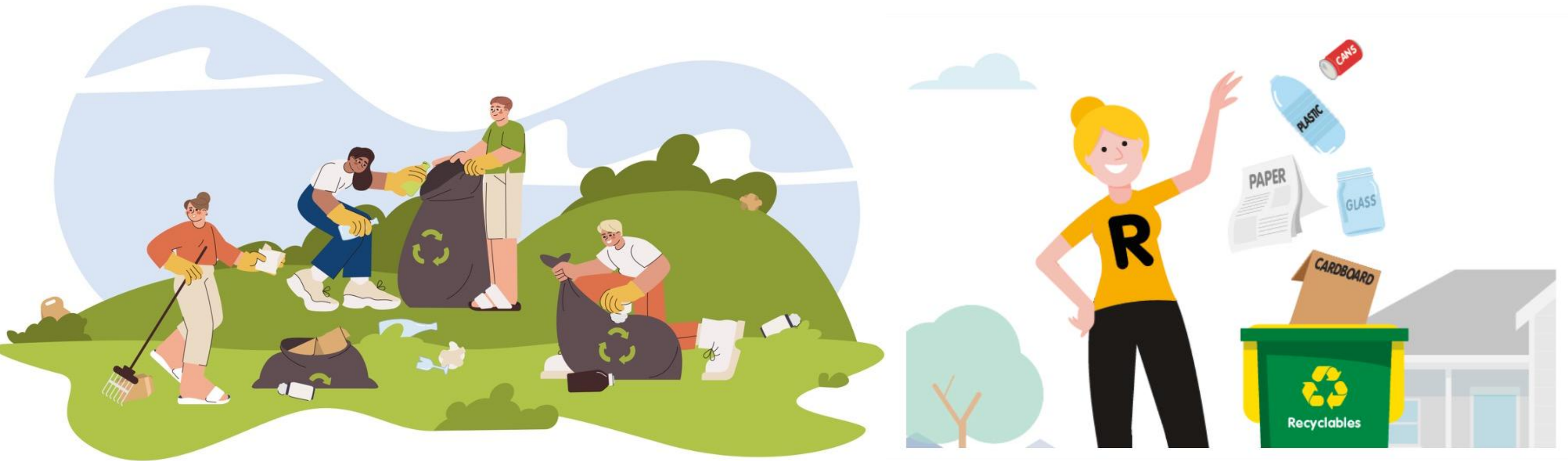
Why do patients with *CCDC39* and *CCDC40* variants show more severe disease than PCD patients with variants in other genes?



Disease is caused by more than just loss of ciliary movement

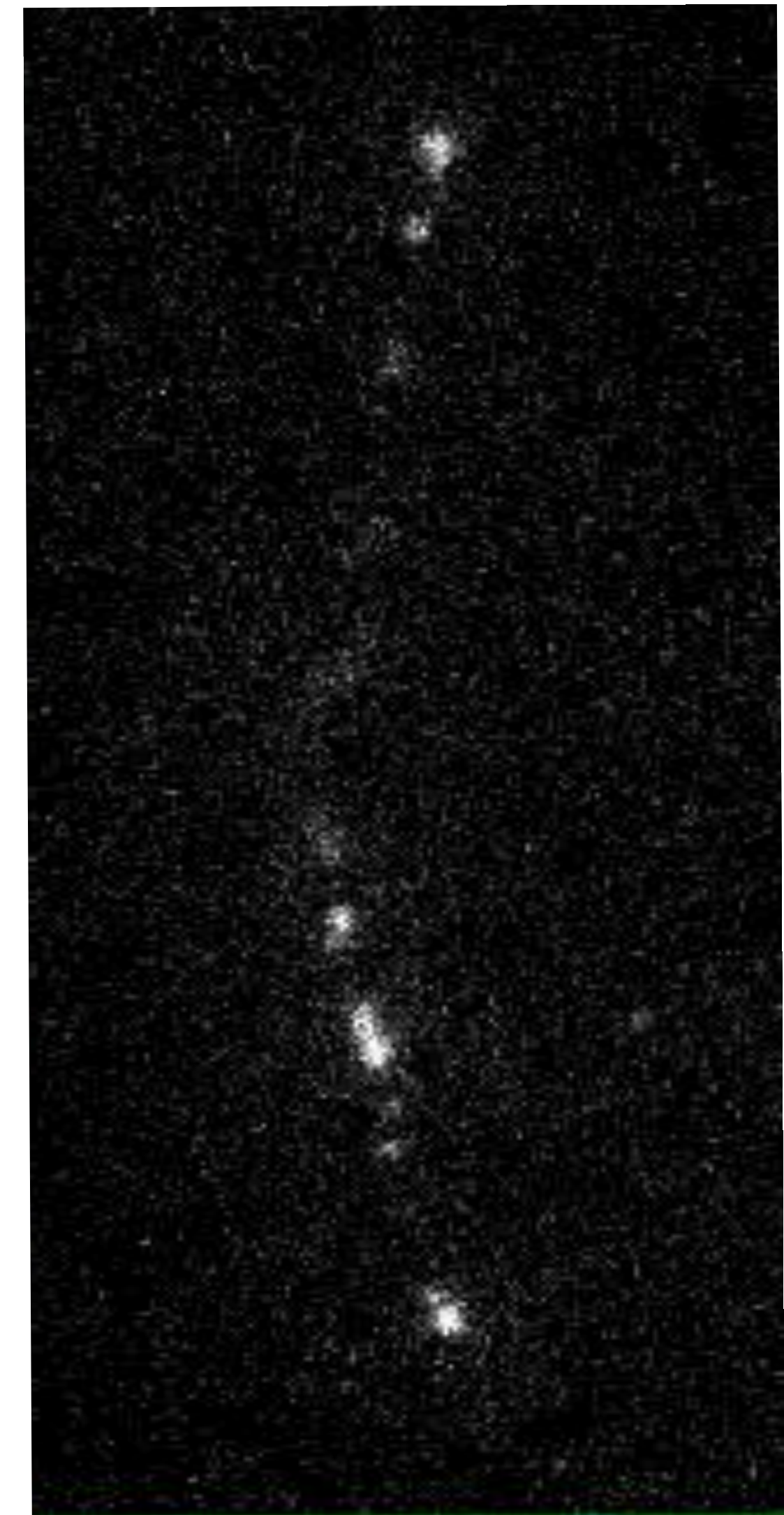
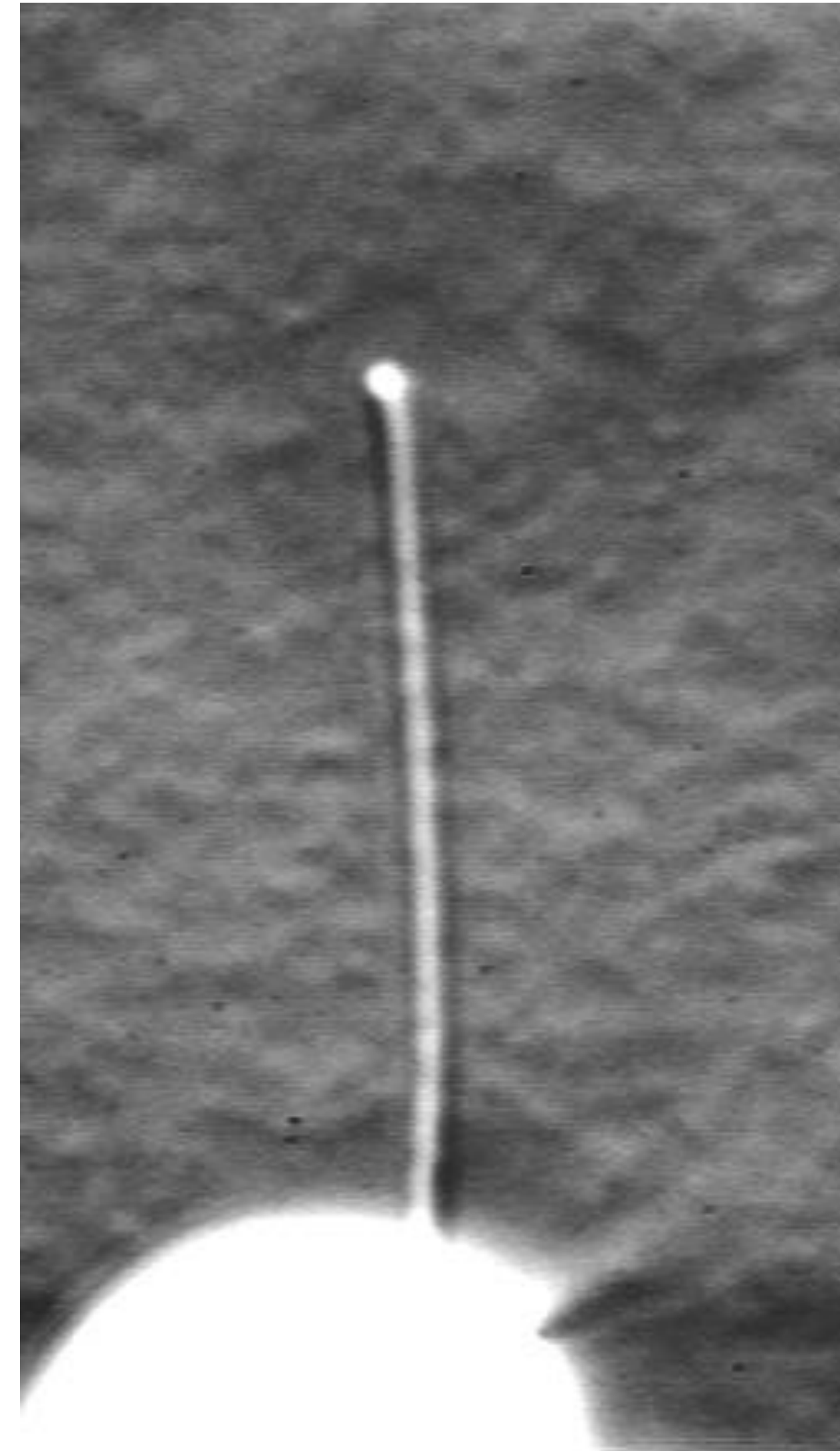
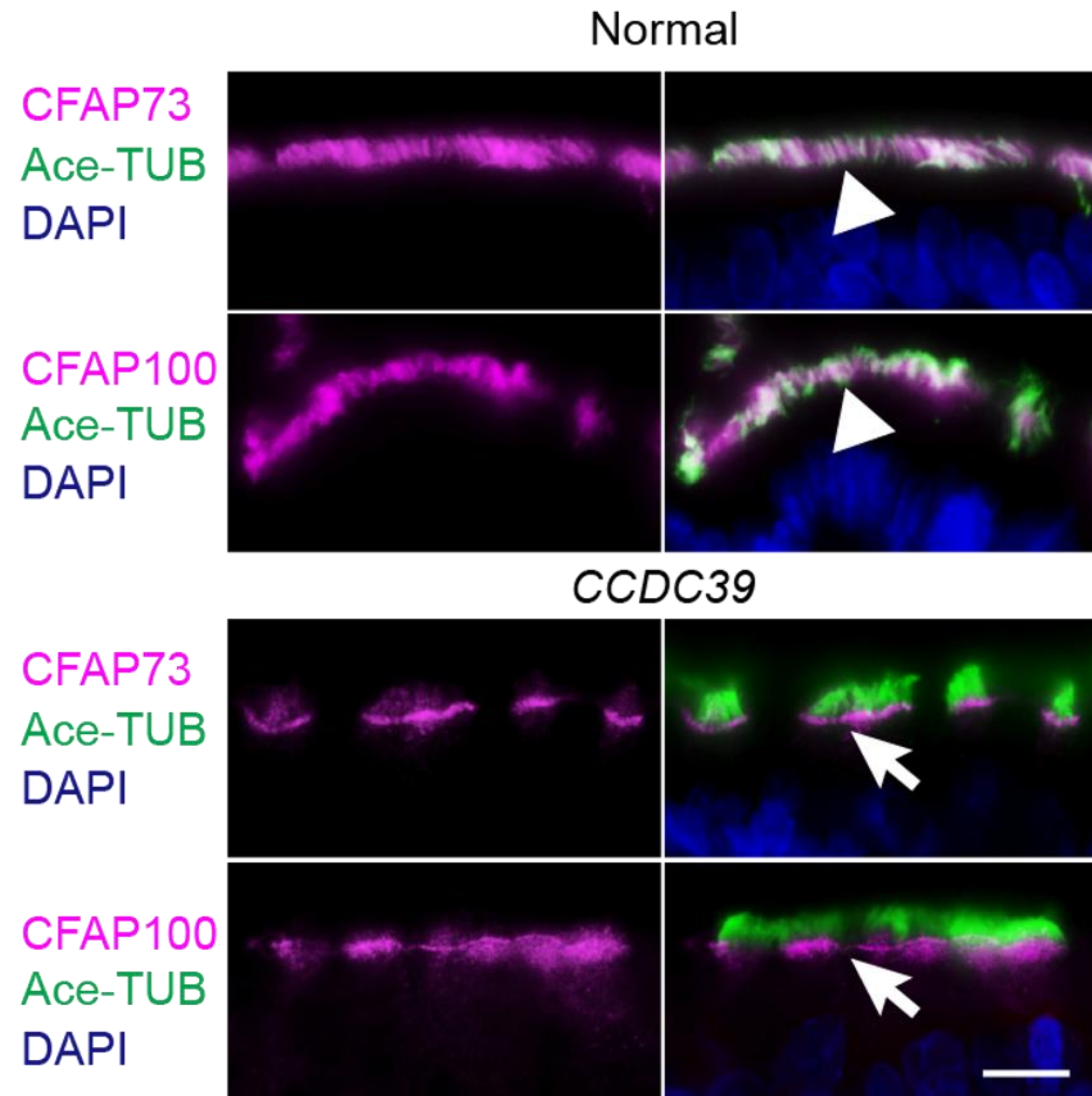
Why do patients with *CCDC39* and *CCDC40* variants show more severe disease?

Motility independent phenotype

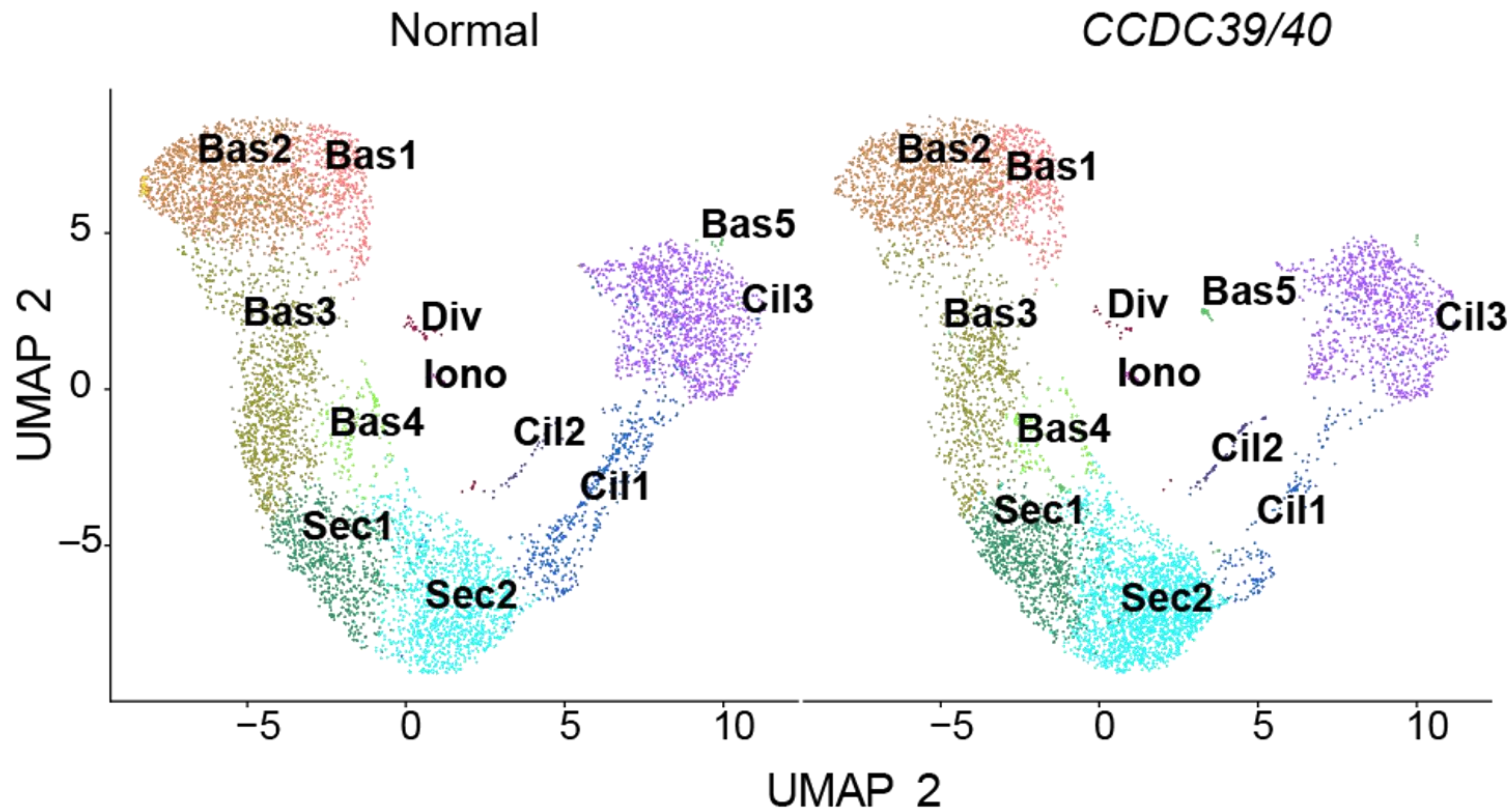


Cleaning and recycling up the "trash"

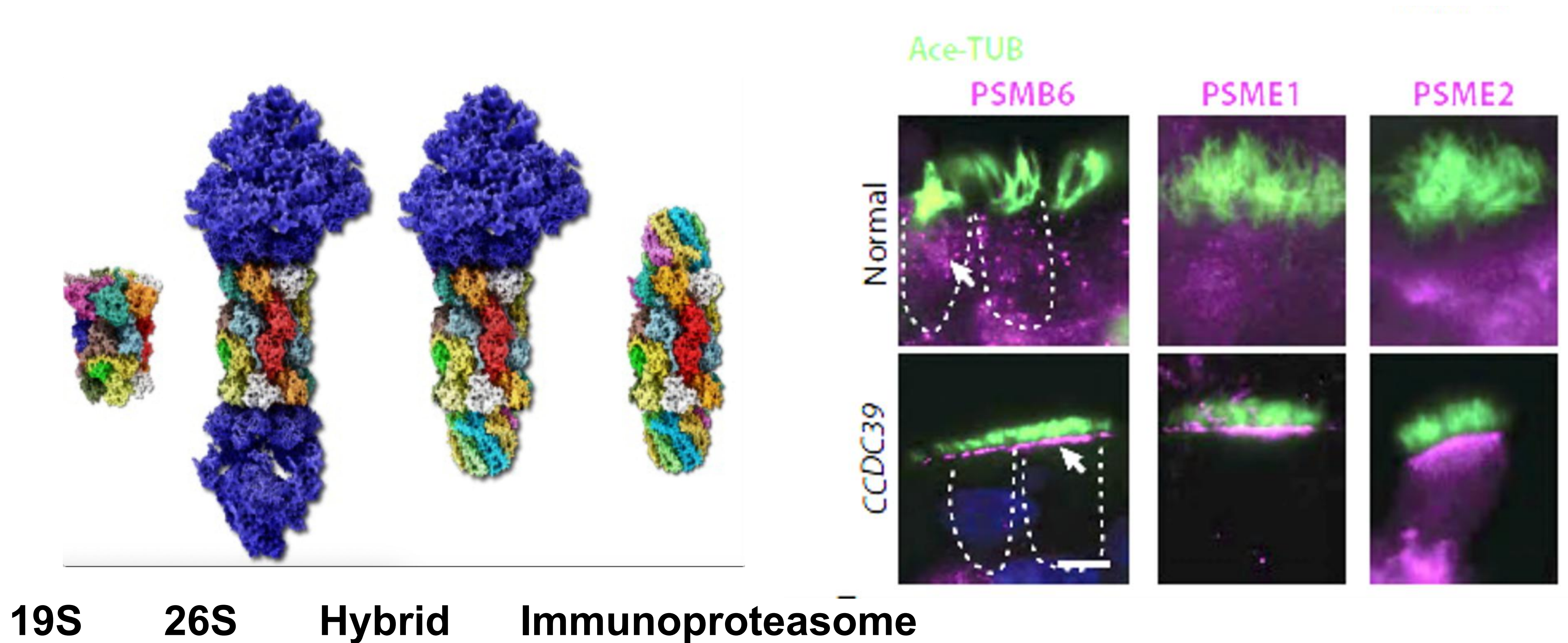
Motility independent phenotype: Cleaning and recycling up the "trash"



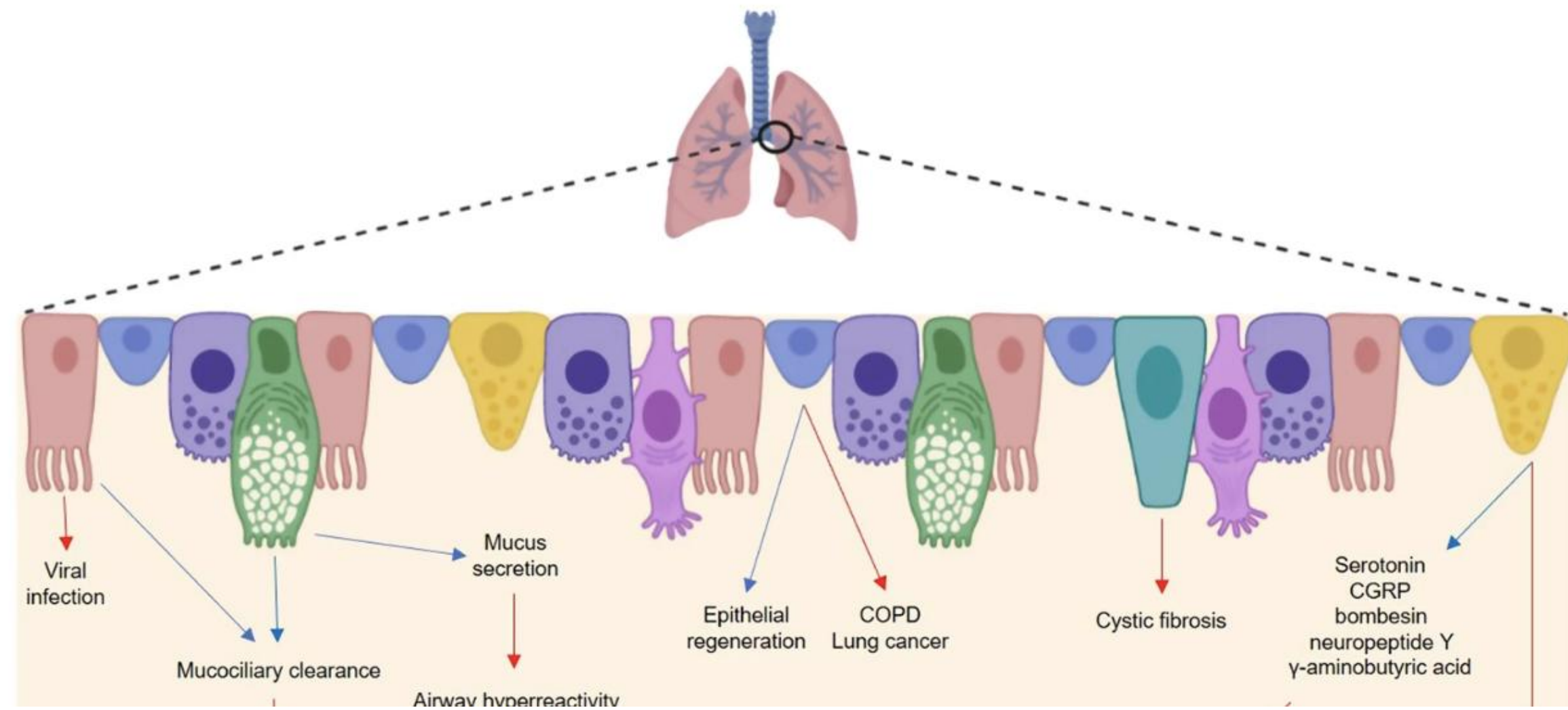
Motility independent phenotype: Cleaning and recycling up the "trash"



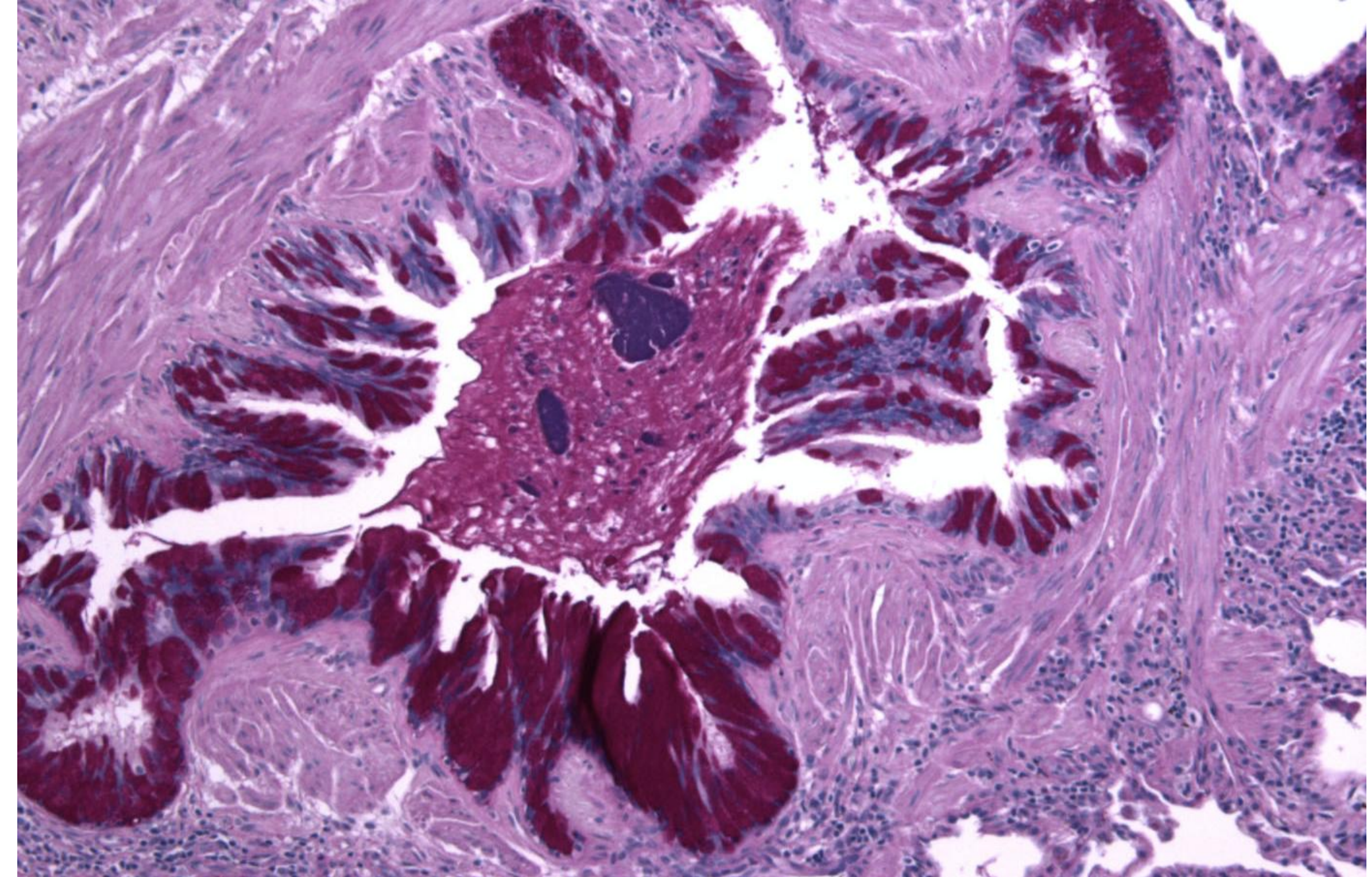
The immunoproteasome is turned up in the disease cells



Why do patients with *CCDC39* and *CCDC40* variants show more severe disease?

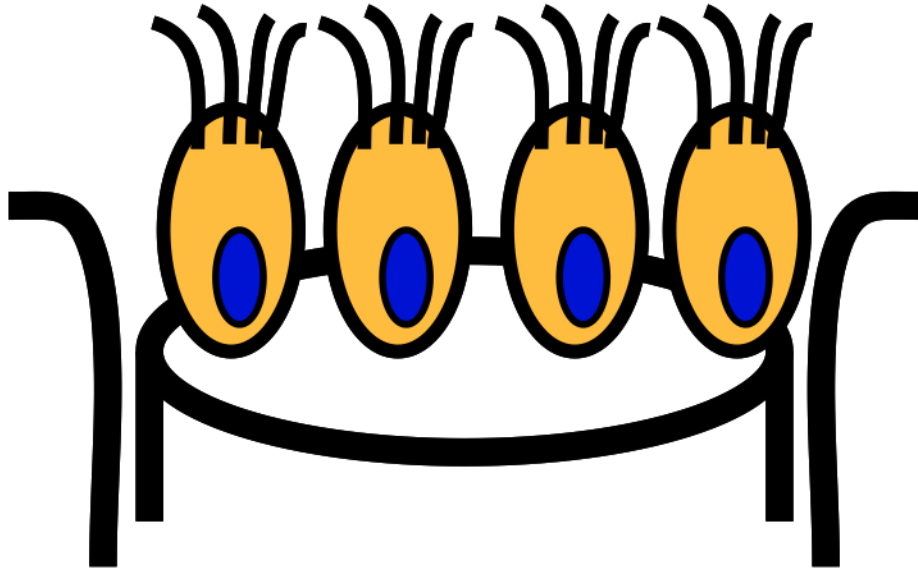


Davis and Wypych, 2021

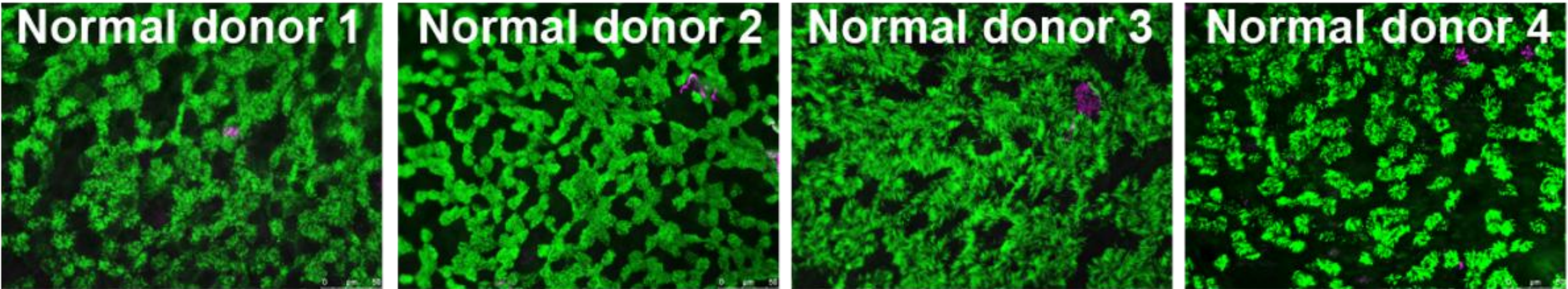


Change the cell fate of the multiciliated cells to secretory cells

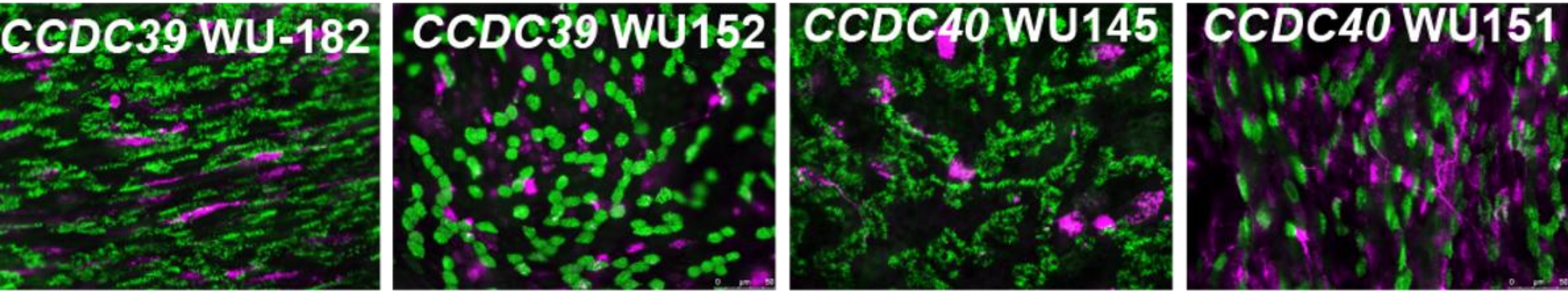
Motility independent phenotype: Transdifferentiation of multiciliated cells



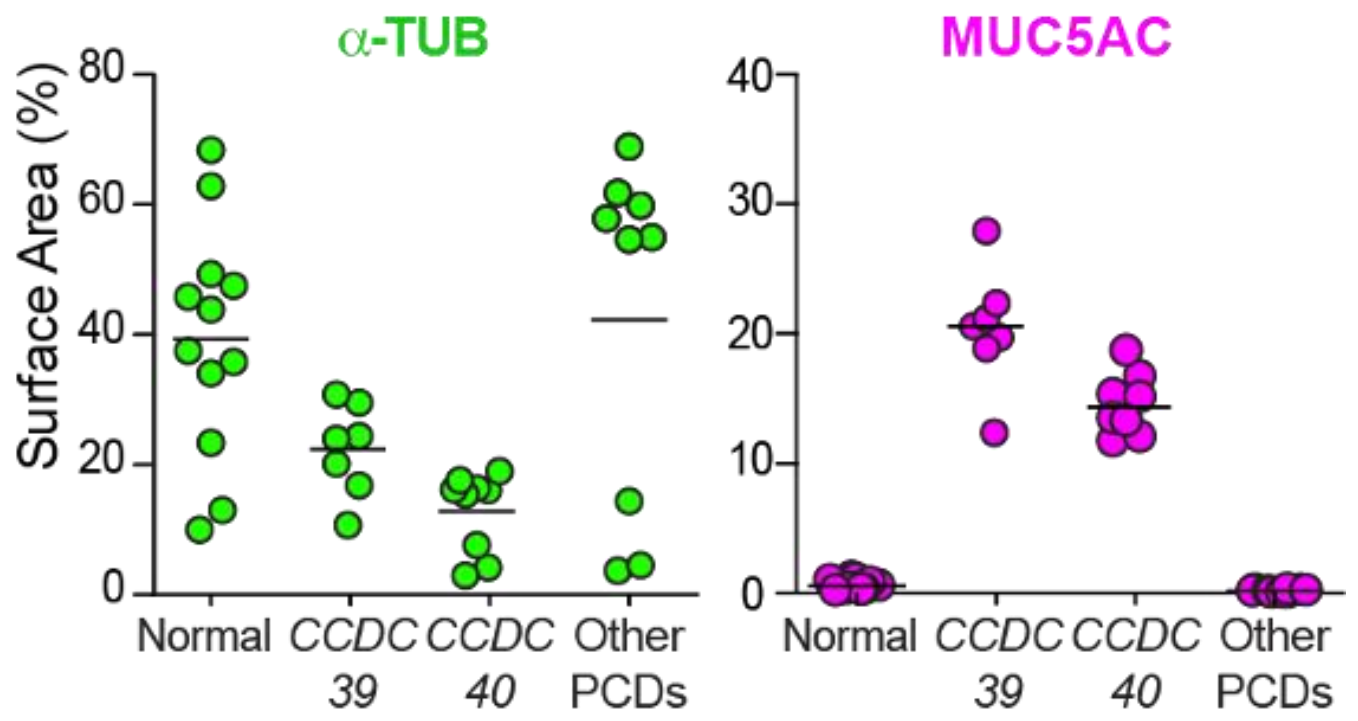
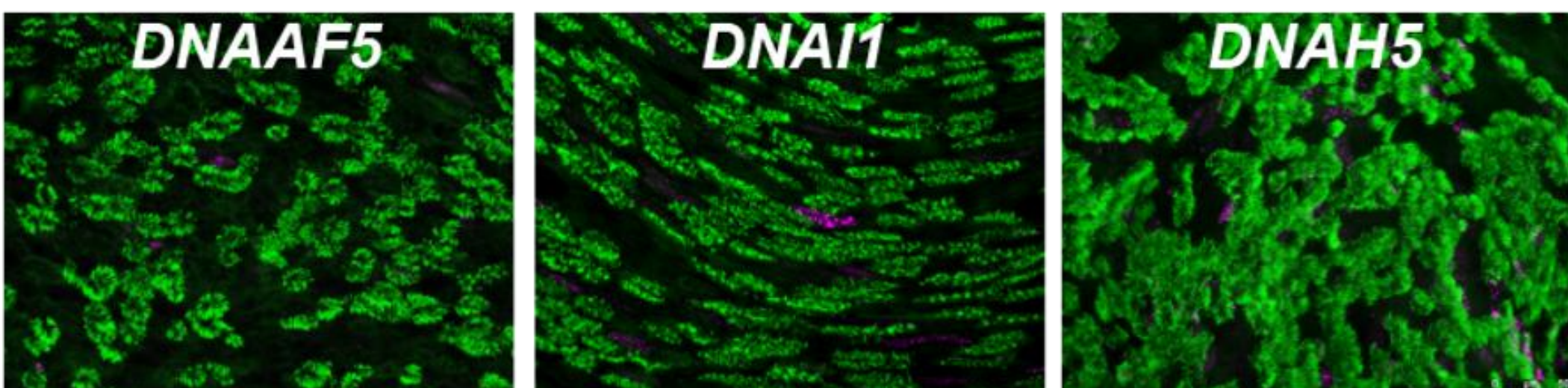
Normal



Patient

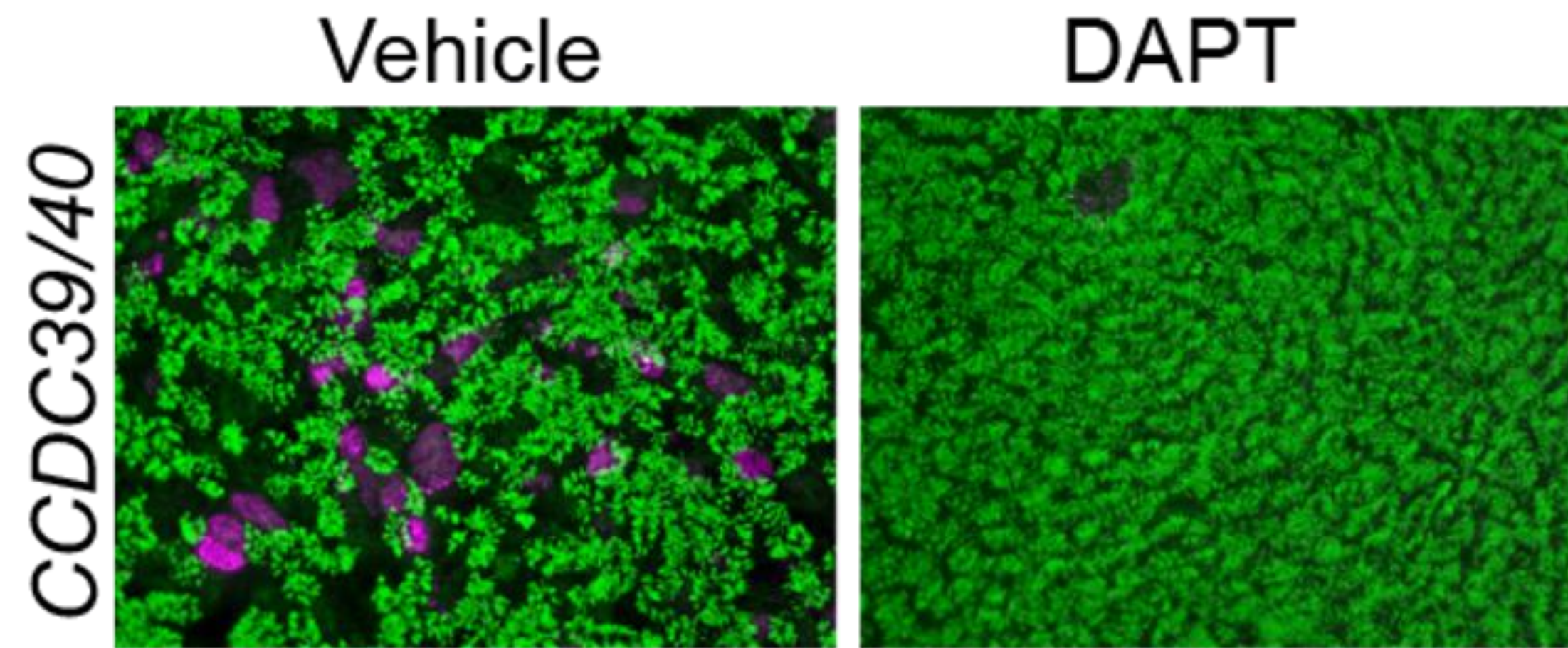
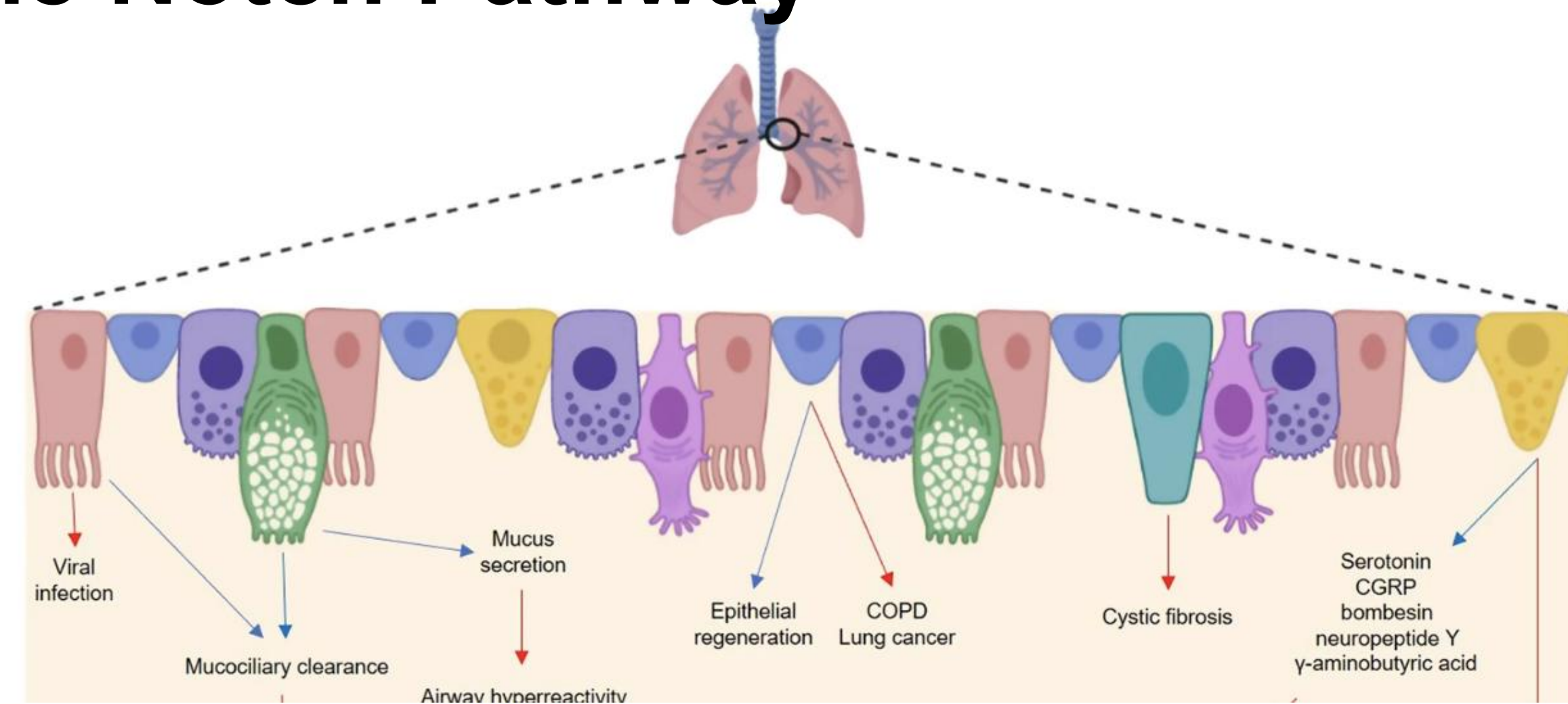
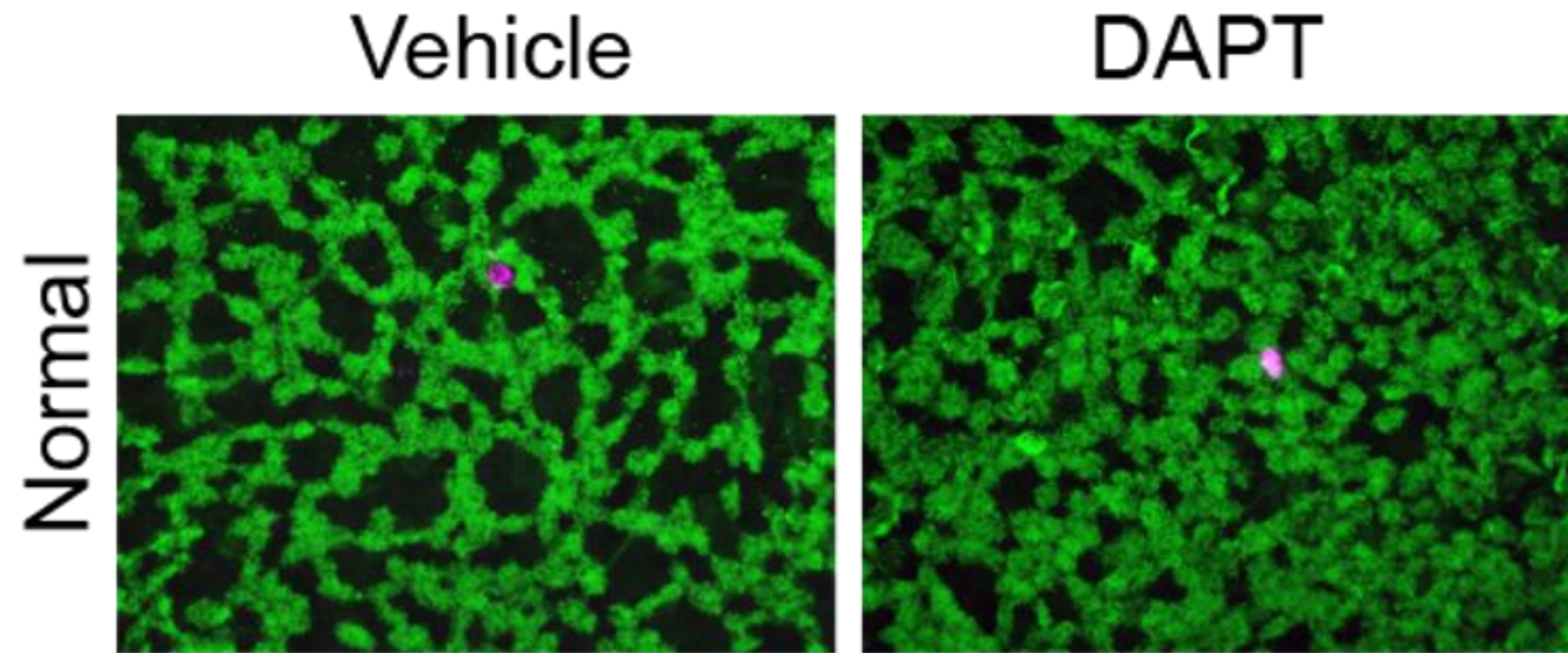


Patient



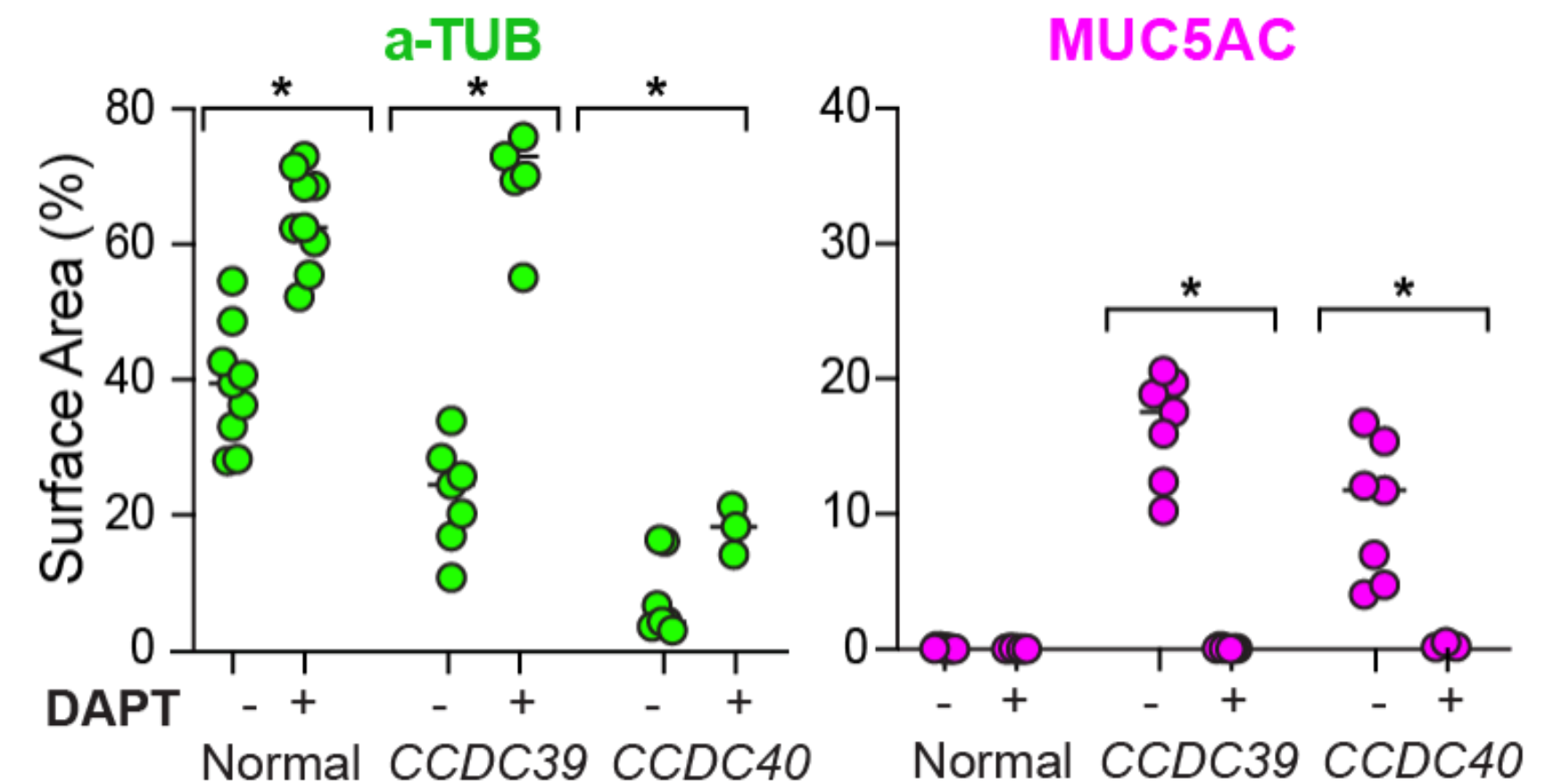
■ Cilia ■ Mucus

Motility independent phenotype: Transdifferentiation of multiciliated cells via misregulation of the Notch Pathway

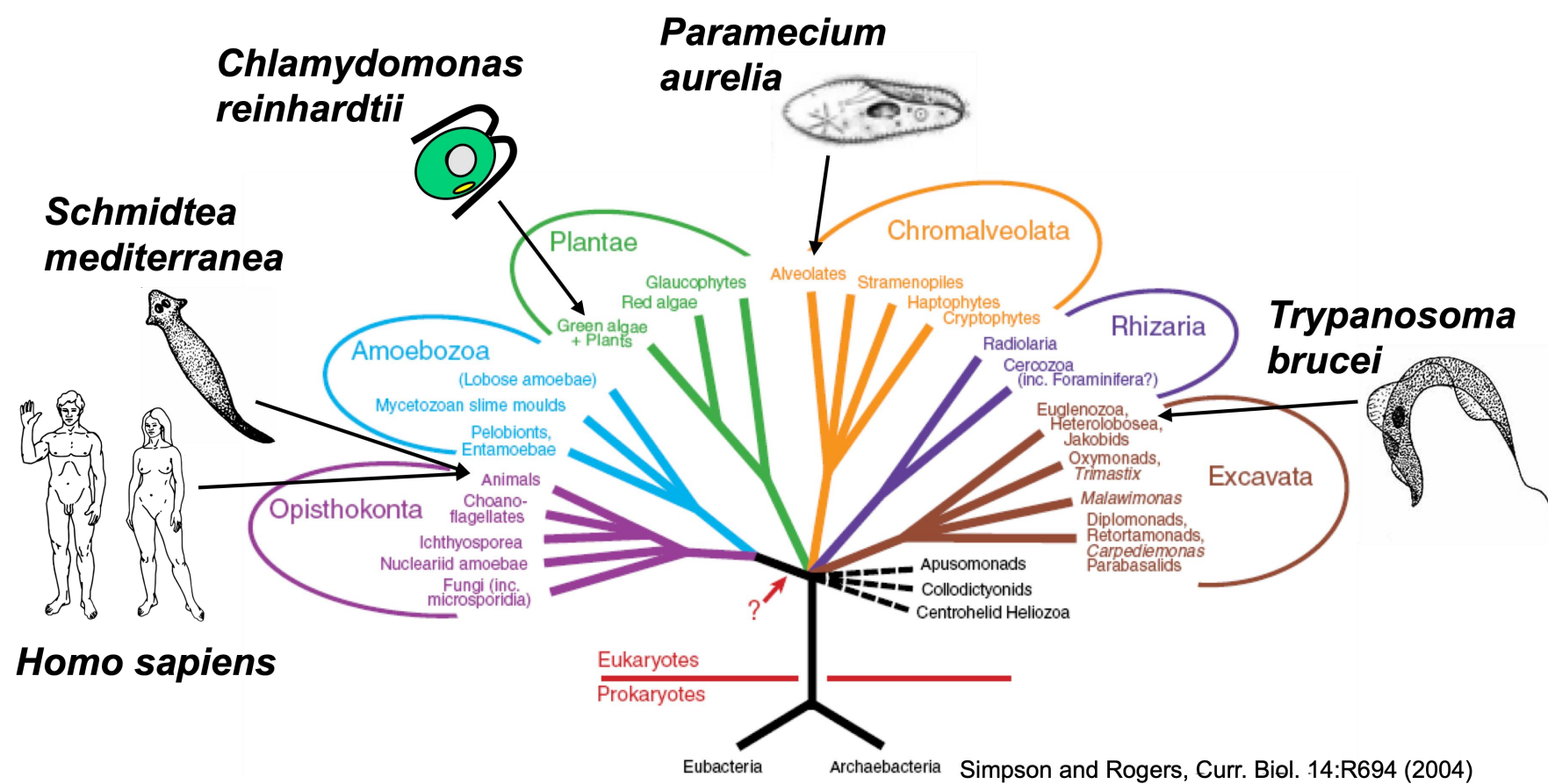


■ Cilia ■ Mucus

Davis and Wypych, 2021



Take home messages



Evolution provides a wealth of information about key genes involved in human disease

Motile organisms provide fast and easy functional assays and therapeutic assays

Human variation and diseases provide additional functional tests and new phenotypes

