

ISA Workshop – Amyloidosis from Bench to Bedside and Back Again

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Selective cellular vulnerability and resilience in amyloidosis

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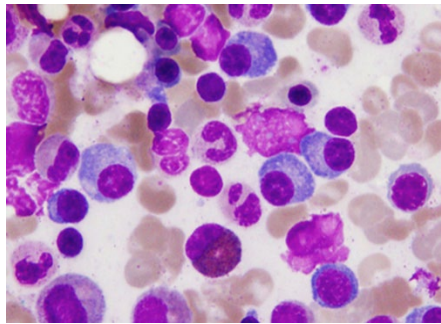
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Table 1. Amyloid fibril proteins and their precursors in human^a.

Fibril protein	Precursor protein	Systemic or localised	Acquired or hereditary	Target organs
AL	Immunoglobulin light chain	S, L	A, H	All organs, usually except CNS
AH	Immunoglobulin heavy chain	S, L	A	All organs except CNS
AA	(Apo) Serum amyloid A	S	A, H	All organs except CNS
ATTR	Transthyretin, wild type	S*	A	Heart mainly in males, lung, ligaments, tenosynovium
	Transthyretin, variants	S	H	PNS, ANS, heart, eye, kidneys, leptomeninges
Aβ2M	β2-microglobulin, wild type	S	A	Musculoskeletal system
	β2-microglobulin, variants	S	H	ANS, tongue, heart
AApoAI	Apolipoprotein A I, variants	S	H	Heart, liver, kidney, PNS, testis, larynx (C terminal variants), skin (C terminal variants)
AApoAII	Apolipoprotein A II, variants	S	H	Kidney
AApoAIV	Apolipoprotein A IV, wild type	S	A	Kidney medulla, heart, gastrointestinal
AApoAIV	Apolipoprotein A IV, variant	S	H	Heart, kidney
AApoCII	Apolipoprotein C II, variants	S	H	Kidney
AApoCIII	Apolipoprotein C III, variants	S	H	Kidney
AGel	Gelsolin, variants	S	H	Kidney PNS, cornea
ALys	Lysozyme, variants	S	H	Kidney
ALECT2	Leukocyte chemotactic factor-2	S	A	Kidney, primarily
AFib	Fibrinogen α, variants	S	H	Kidney, primarily
ACys	Cystatin C, variants	S	H	PNS, skin
ABri	ABriPP, variants	S	H	CNS

AL amyloidosis



λ LC in $\sim 78\%$

Dangerous, small clone¹
Median BMPC infiltrate: 10%

Kinetically/
thermodynamically
unstable LC²⁻⁴

endoproteases, metal ions
shear forces, cell
interactions

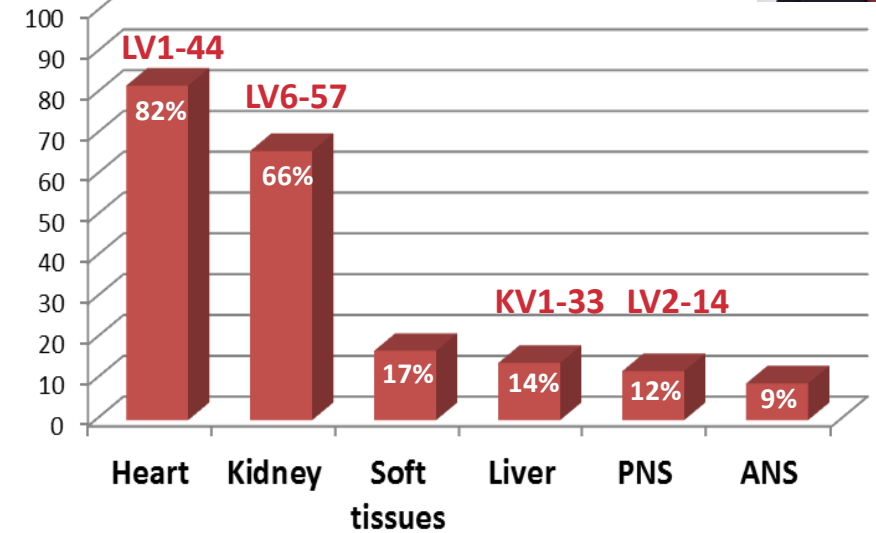
Oligomers

SAP,
GAGs

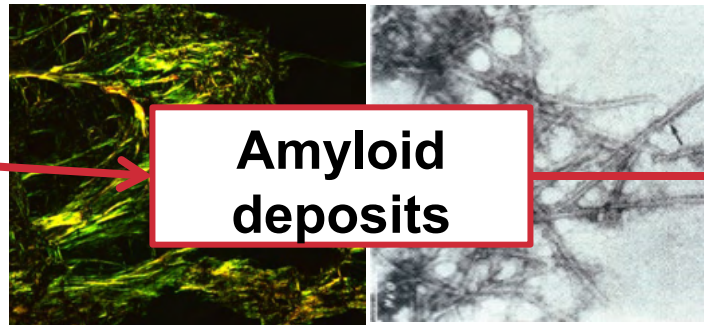


Toxicity

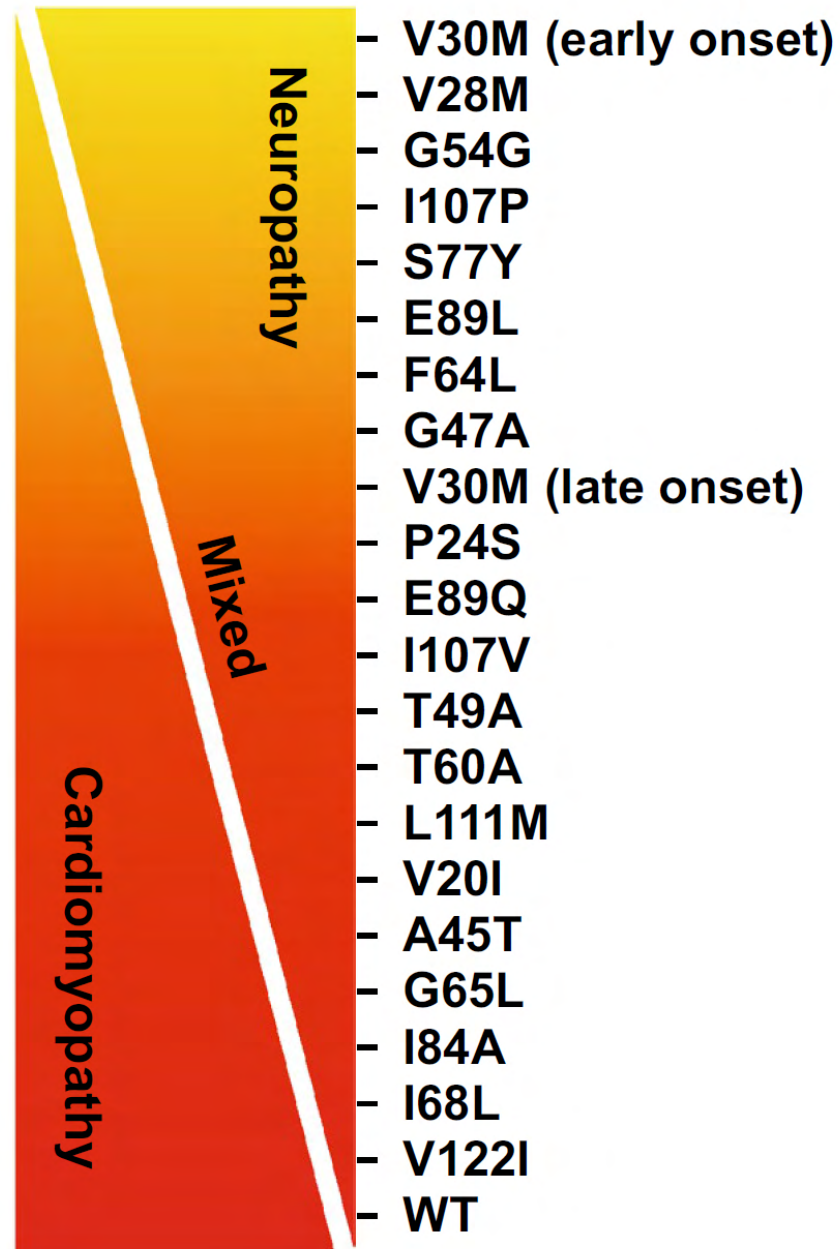
Amyloid
deposits



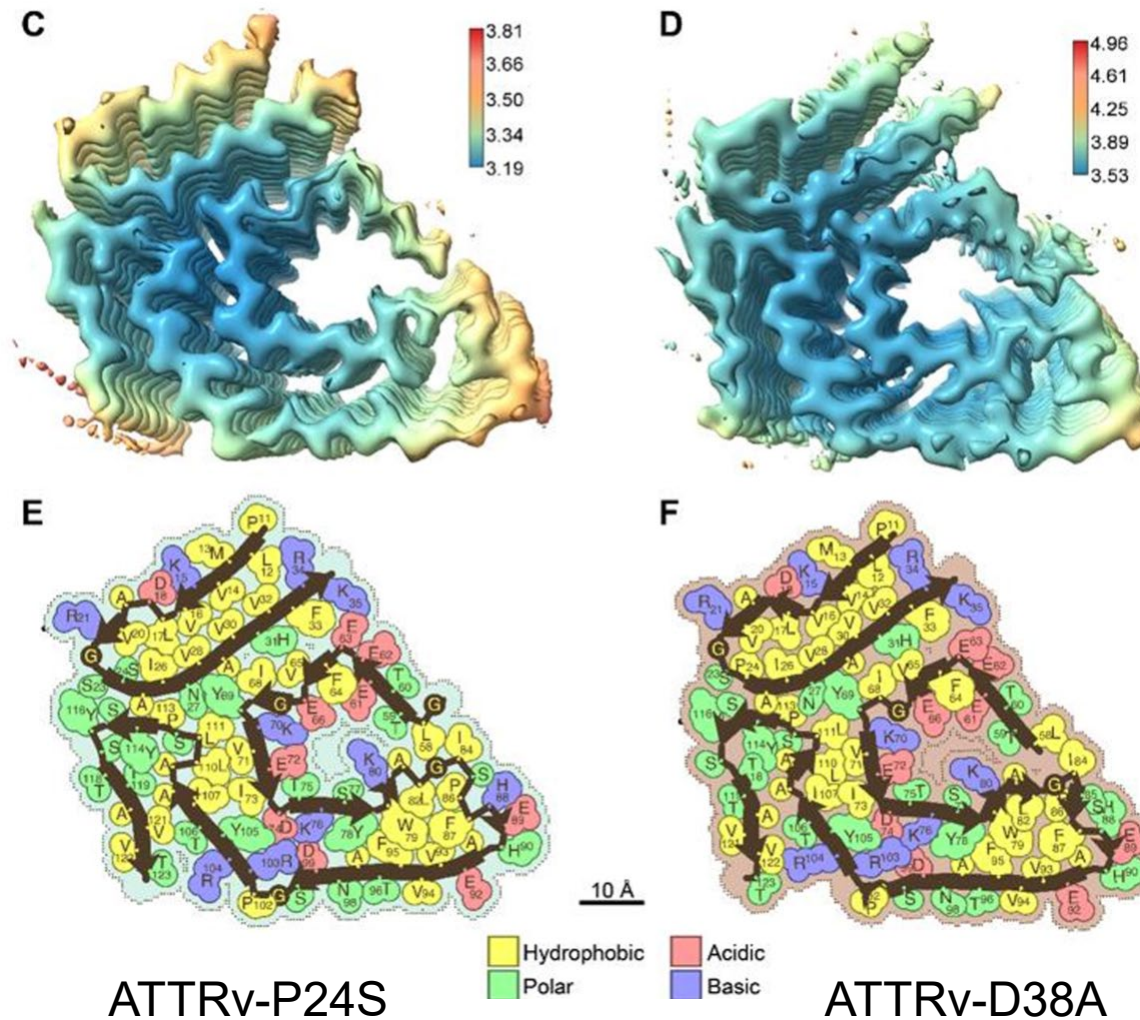
Comenzo et al, *Blood* 2001
Perfetti et al, *Blood* 2012
Kourelis et al, *Blood* 2017



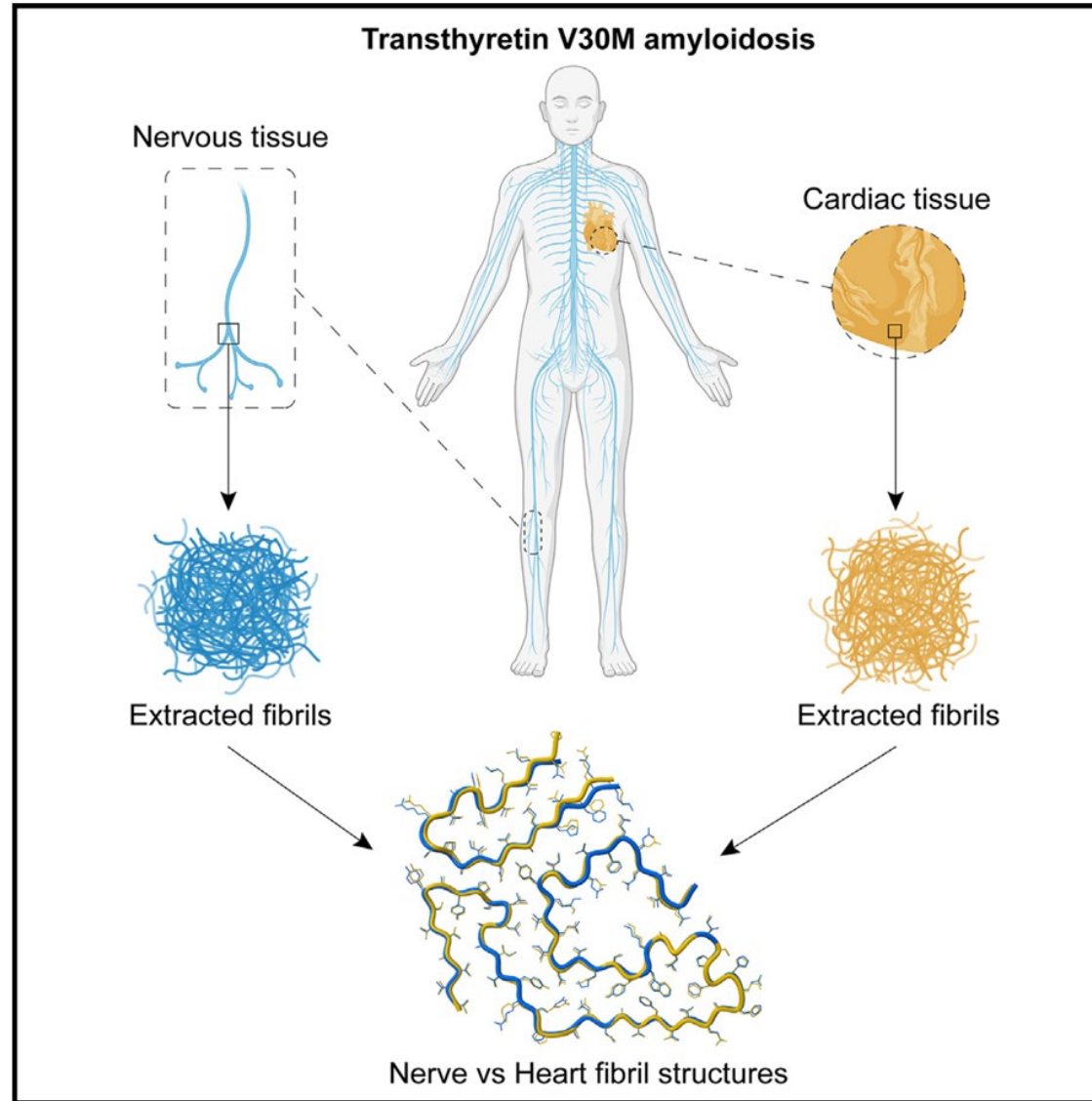
Genotype–phenotype correlations in ATTR amyloidosis



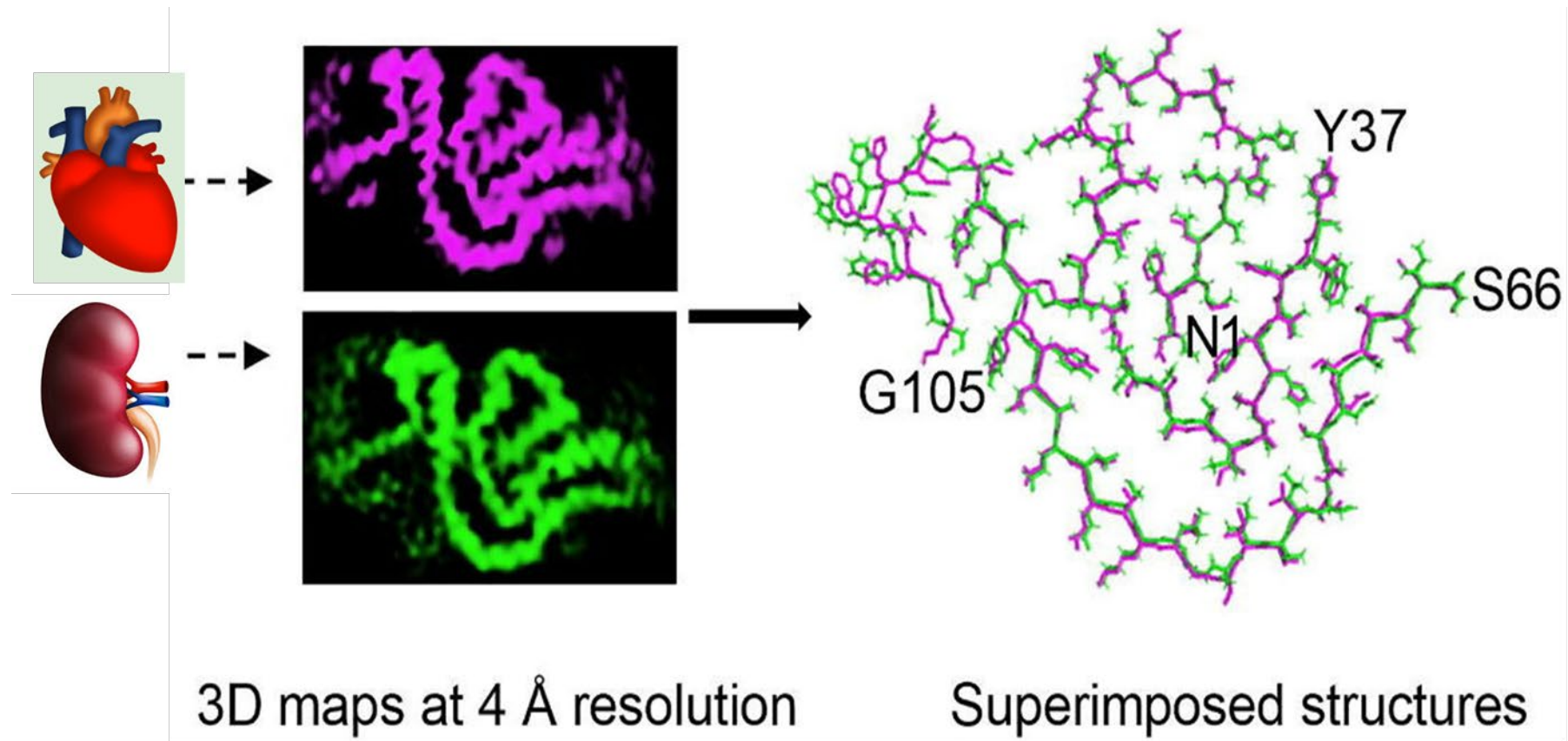
A Shared Amyloid Architecture in Cardiac Fibrils from Three Neuropathy-Associated ATTR Variants



ATTRv-V30M amyloid fibrils from heart and nerves exhibit structural homogeneity



In AL amyloidosis a common fibril structure is present across organs in the same patient



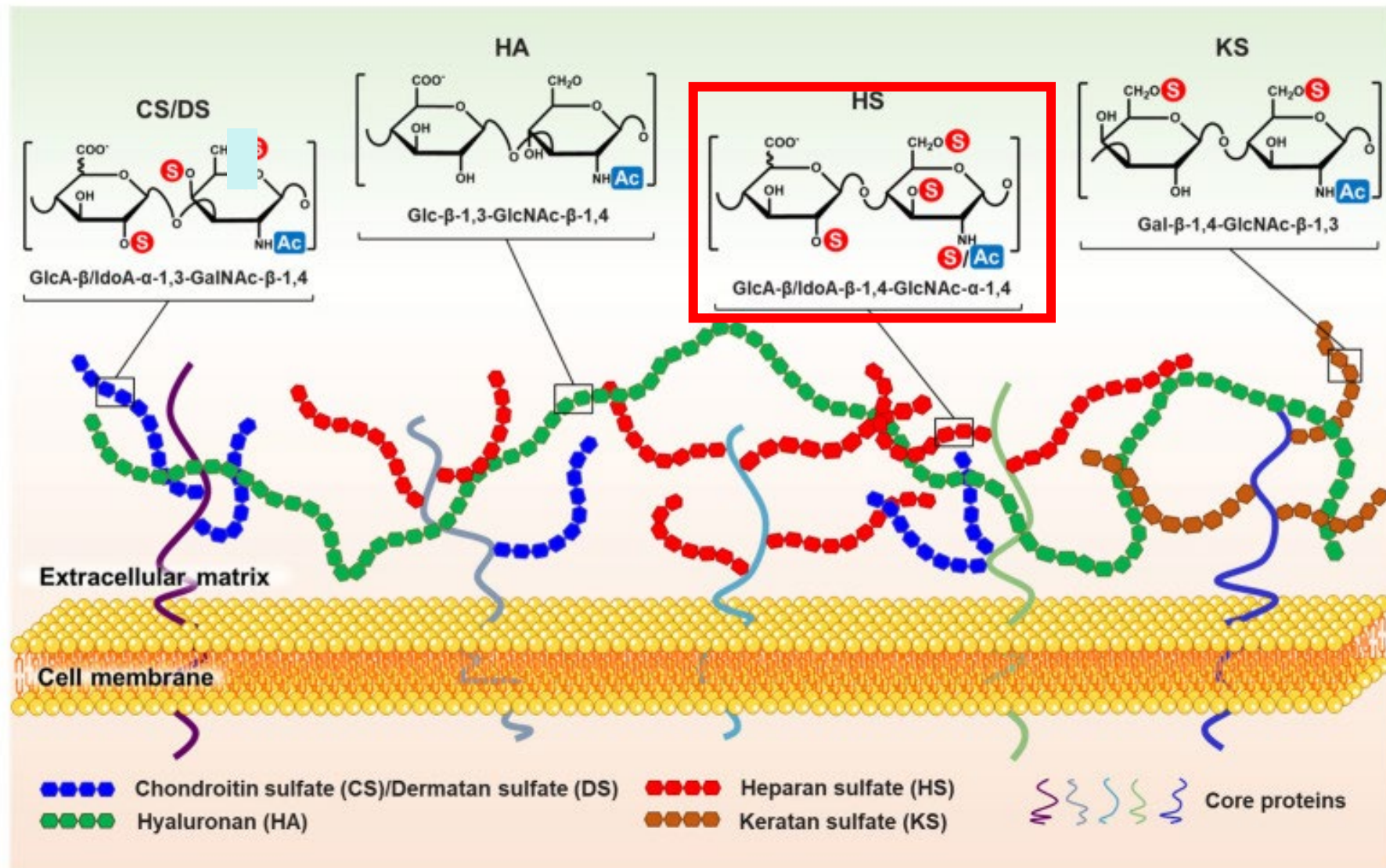
Extracted fibrils from the **kidney** of an AL patient whose **cardiac** fibril structure had been solved previously, and showed the renal fibril is **virtually identical** to the cardiac fibril—supporting a common fold across organs within the same patient.

Interactions of the amyloid protein with the extracellular matrix

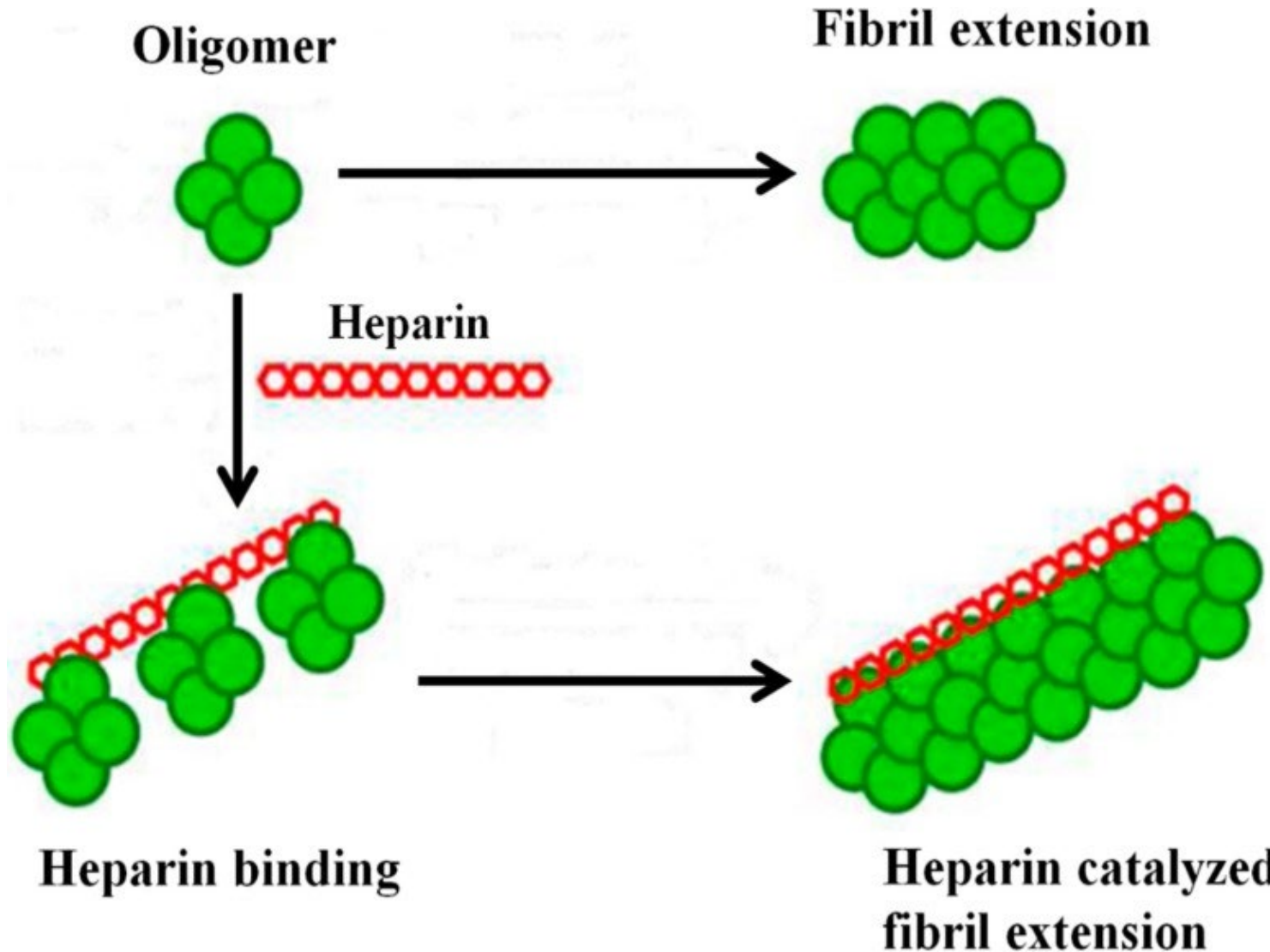


- Glycosoaminoglycans
- Collagens
- Endoproteases (shear forces)

Distribution and structures (repeating disaccharide units) of GAGs in the extracellular matrix



Polyanionic heparin works as scaffold in enhancing aggregation by aligning the peptide molecules in the correct orientation and with the appropriate periodicity

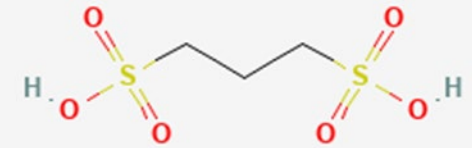


Amyloid seeding is strongly influenced by **which HSPGs are present**, **how their HS chains are sulfated**, and **whether local disease signals remodel them**. This creates **organ- and microdomain-specific “permissive matrices”** that capture seeds, enable cell entry, and stabilize nascent fibrils

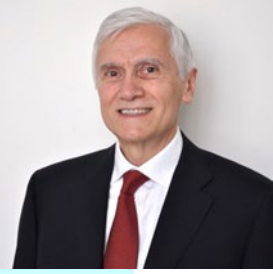
GAGs modulate amyloid formation across proteins



- **A β (Alzheimer's amyloid- β)** McLaurin et al., *FASEB J* 1999
- **Tau** Zhu et al, *J Biol Chem* 2009
- **α -Synuclein** Tao et al, *Nat Commun* 2022
- **Prions** Warner et al, *J Biol Chem* 2002
- **Serum Amyloid A** Kisilevsky, *J Clin Invest* 1988
- **Transthyretin** Noborn et al, *PNAS* 2011
- **β 2-Microglobulin** So et al, *Protein Sci* 2017
- **Immunoglobulin light chains** Blancas-Mejía et al., *J Biol Chem* 2014

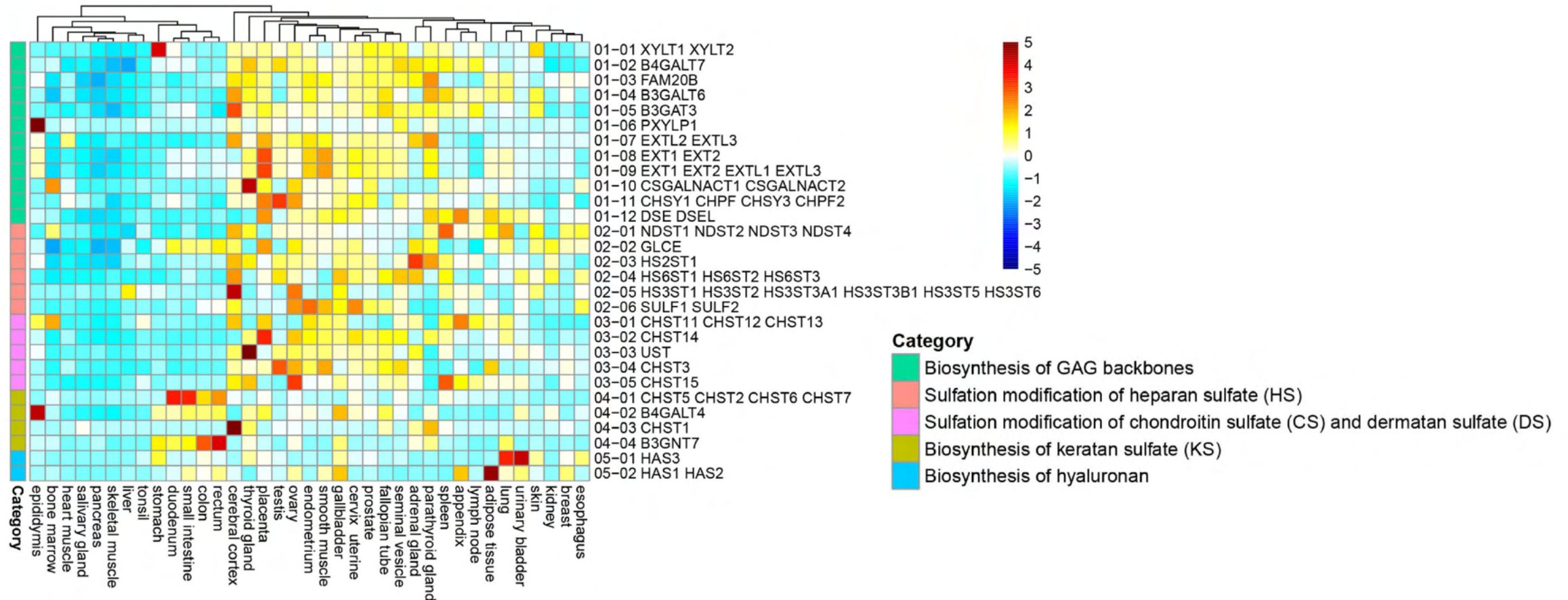


Eprodinate

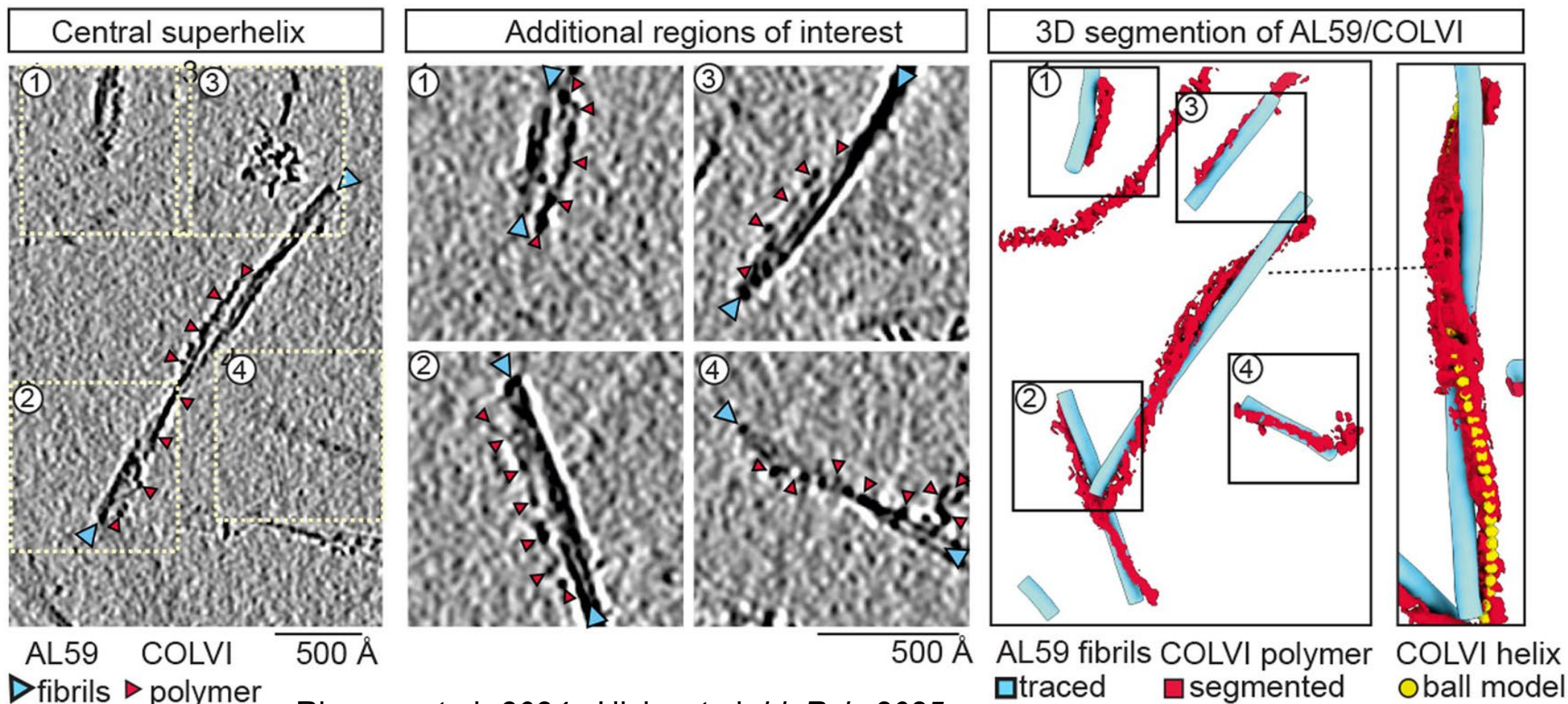


Glycosaminoglycans display notable heterogeneity in their distribution, composition (e.g., chain length, disaccharide units), sulfation patterns and attachment to proteoglycans across human organs.

Expression profiles of GAG-related genes in human tissues.



Helical superstructures between amyloid and collagen in cardiac fibrils from a patient with AL amyloidosis



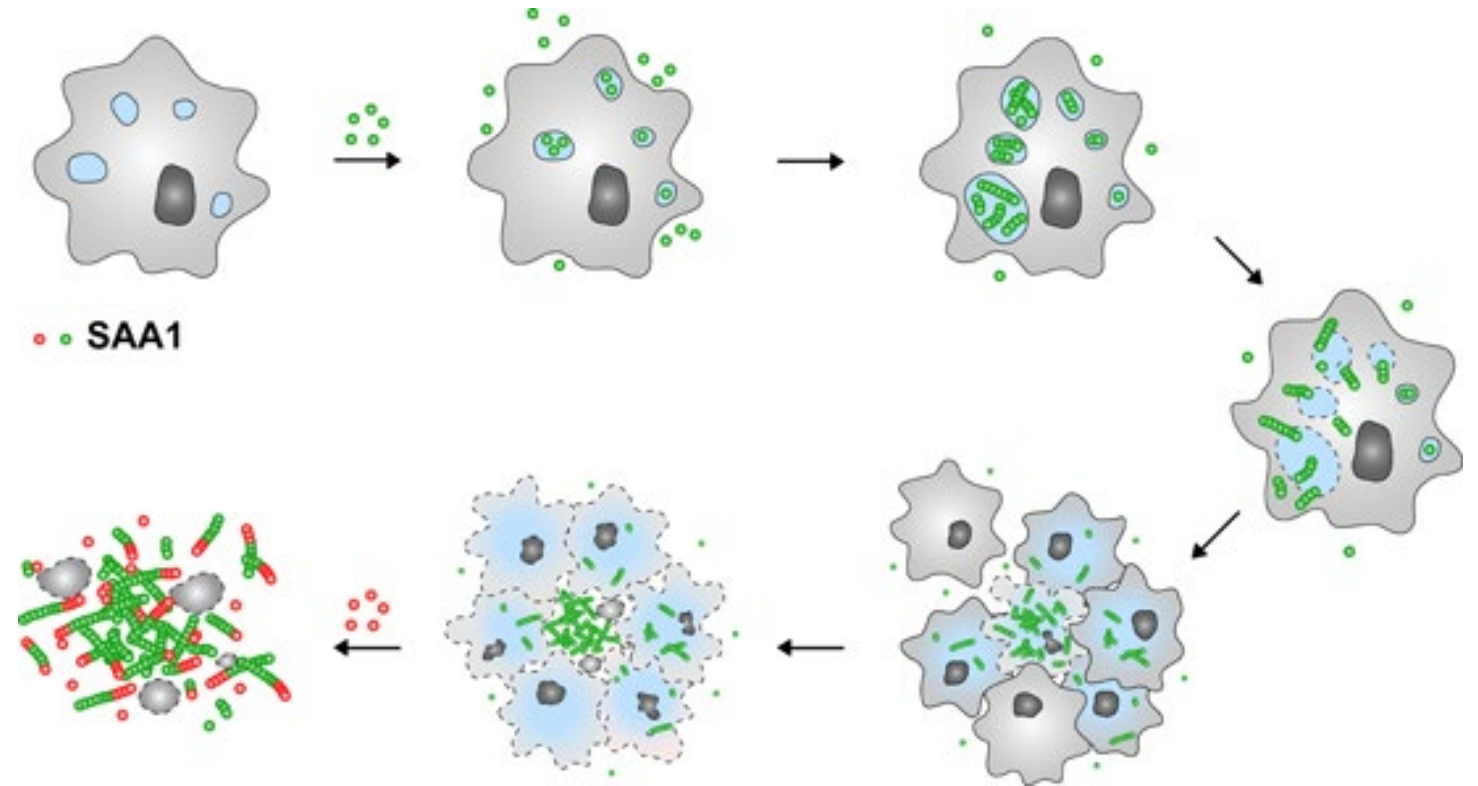


The role of amyloid protein-cell interaction in tissue vulnerability

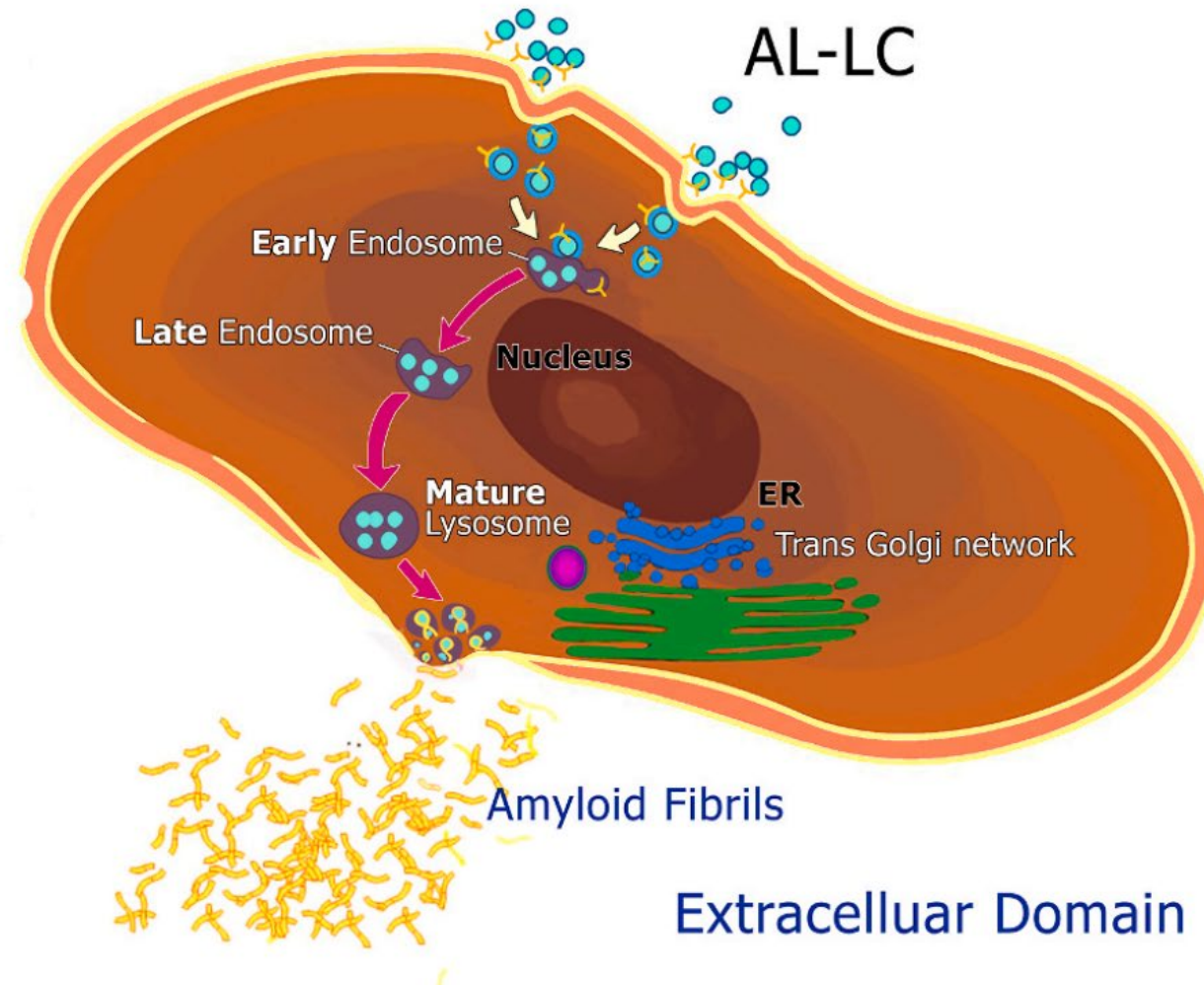
Cellular mechanism of fibril formation from serum amyloid A1 protein



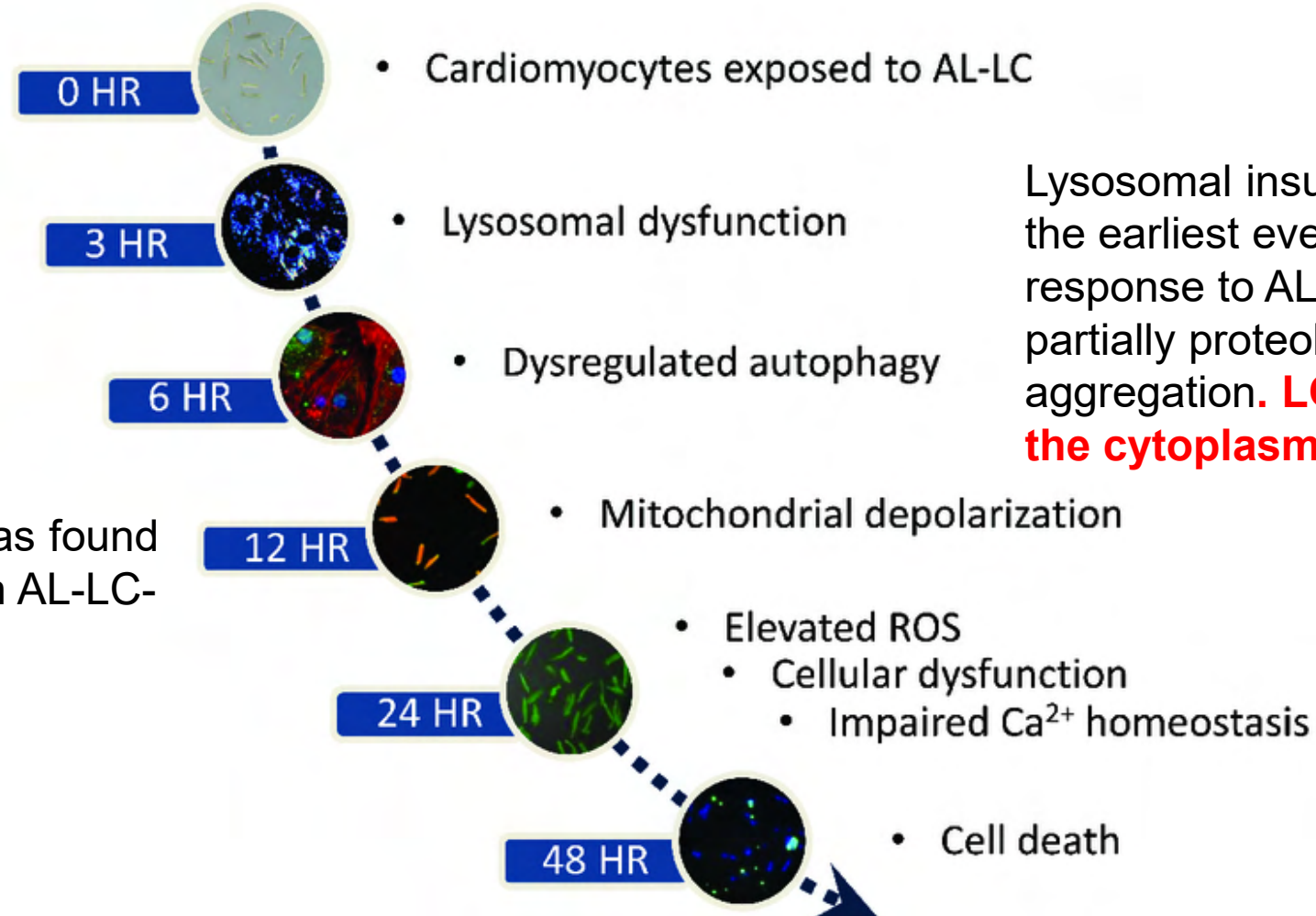
- SAA1 is taken up by cells via clathrin-dependent endocytosis.
- Internalized SAA1 can be directed to the lysosomes.
- FRET demonstrates the formation of intracellular SAA1 aggregates.
- SAA1 aggregation induces lysosomal leakage and cellular death.



Light chain-amyloidogenesis by mesangial cells involves active participation of lysosomes



Lysosomal dysfunction and impaired autophagy underlie the pathogenesis of amyloidogenic light chain-mediated cardiotoxicity



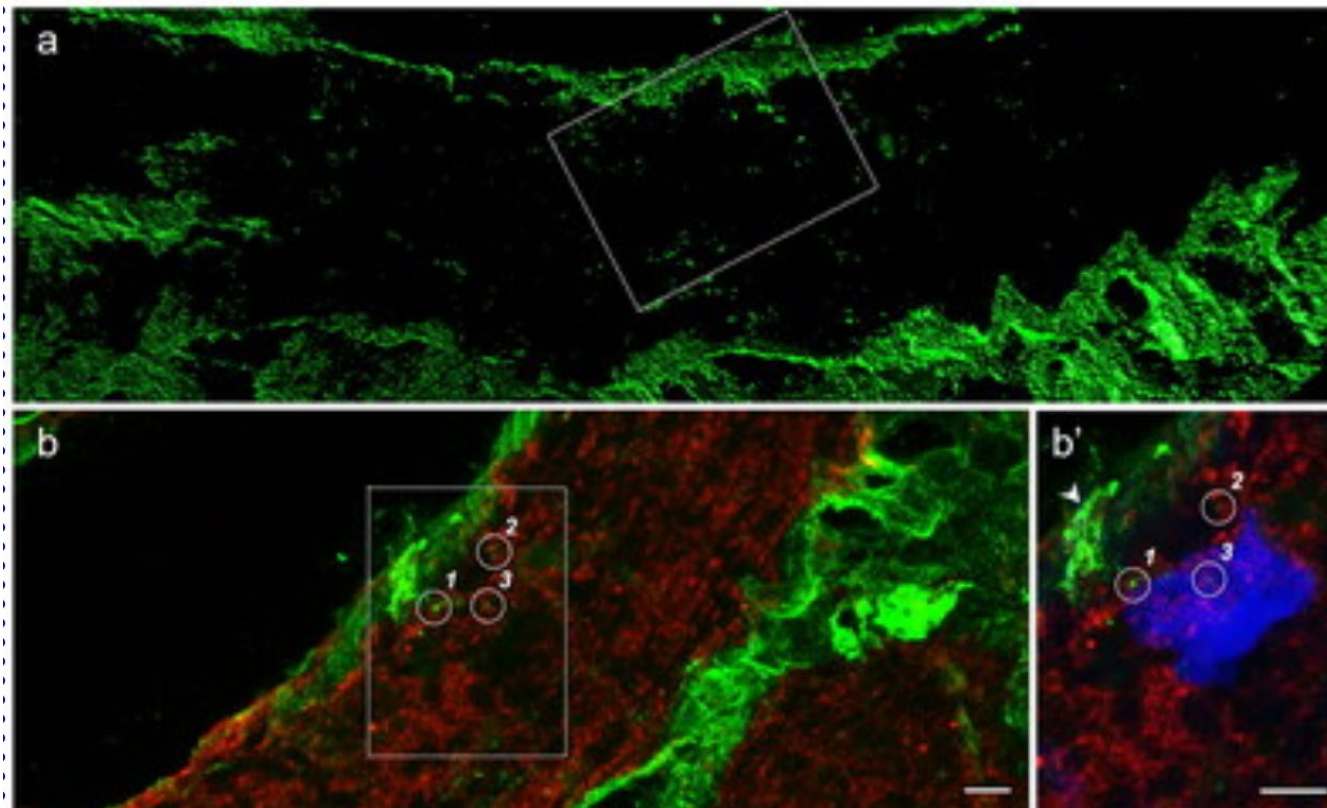
Lysosomal insufficiency is among the earliest events that occur in response to AL-LC. They are partially proteolyzed favoring their aggregation. **LC are released into the cytoplasm.**

Mitochondrial dysfunction was found to be closely associated with AL-LC-induced pathology.

Internalisation of immunoglobulin light chains by cardiomyocytes in AL amyloidosis



We show, for the first time **directly in patient tissue**, the presence of LCs inside cardiomyocytes, and report their proximity to nuclei and to caveolin-3-rich areas. Our observations point to **macropinocytosis as a probable mechanism of LC uptake**.

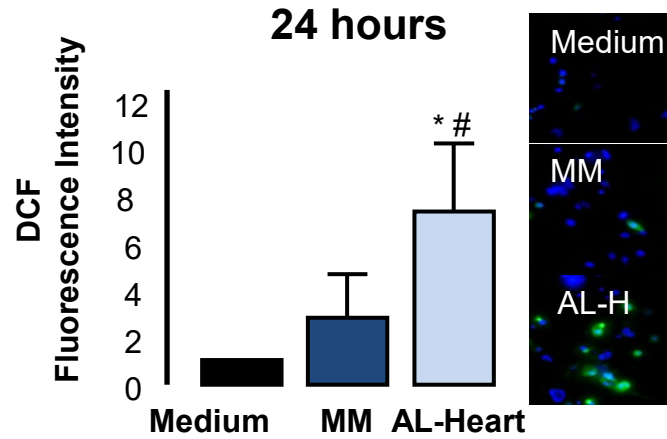


Bezard et al, *Amyloid* 2024

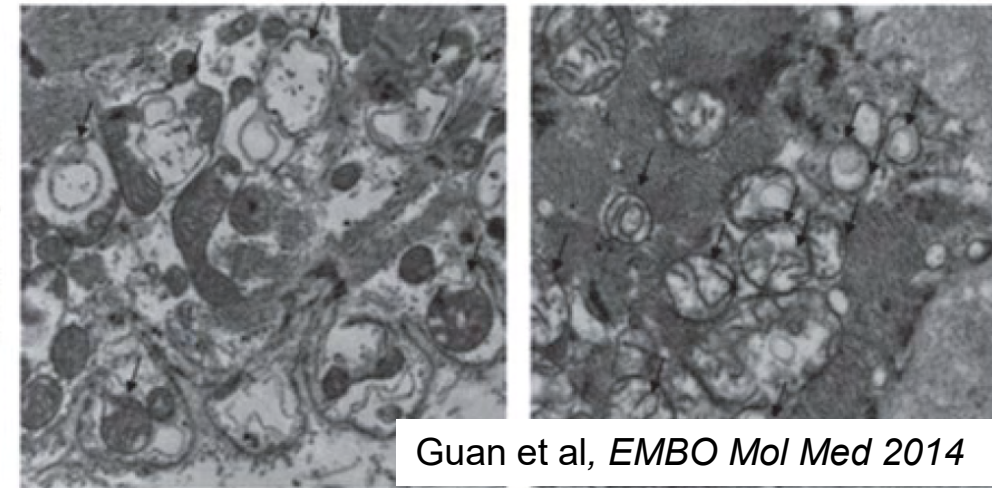
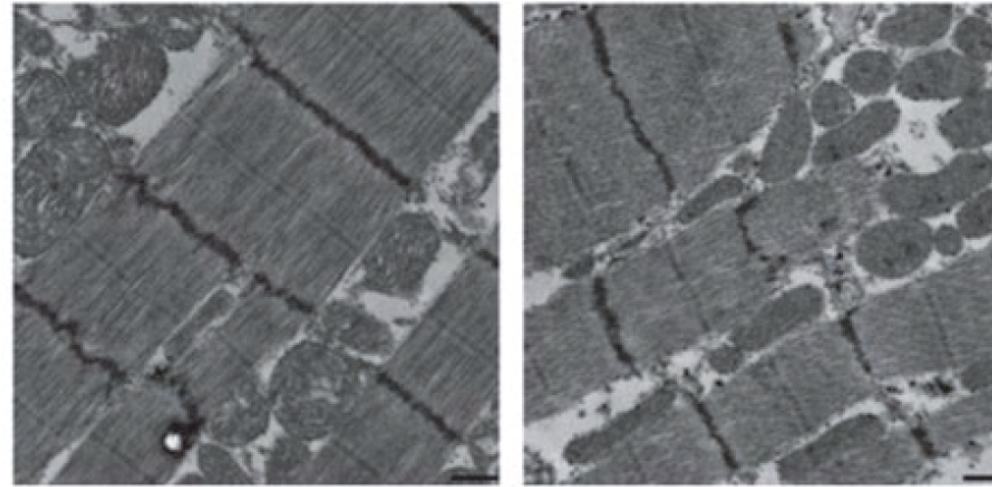
In cardiac cell cultures: Monis et al, *Am J Pathol* 2006; Sikkink et al, *Cell Death Dis* 2010

AL LCs impair mitochondrial function and survival in human cardiac cells

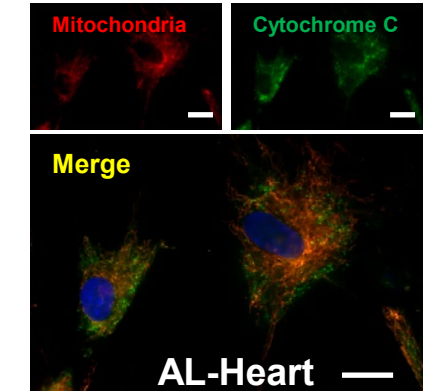
ROS increase driven by metals



Cardiotropic LCs interact with mitochondrial proteins



Apoptotic signals

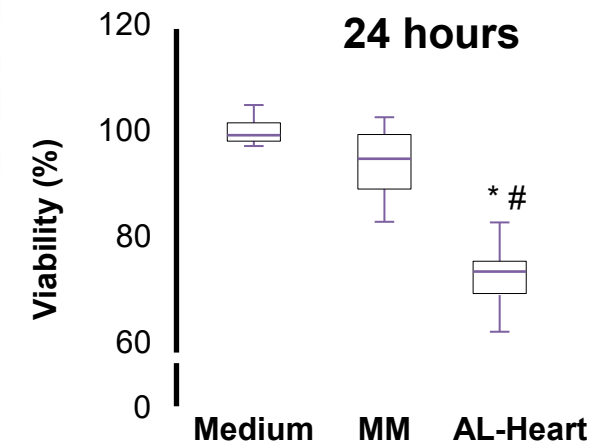
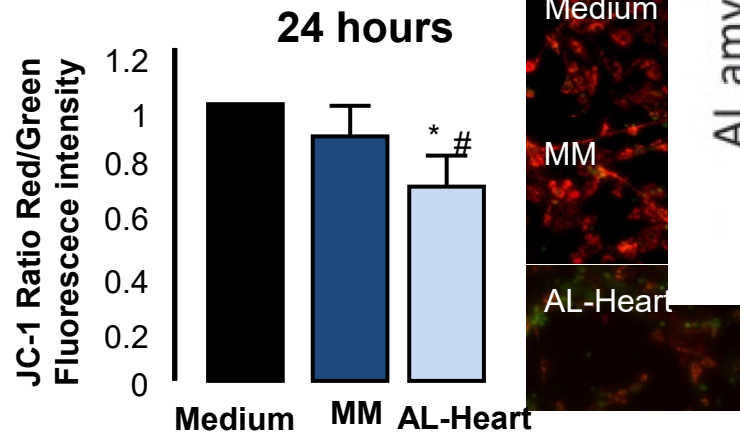


Cytochrome C release



Cell loss

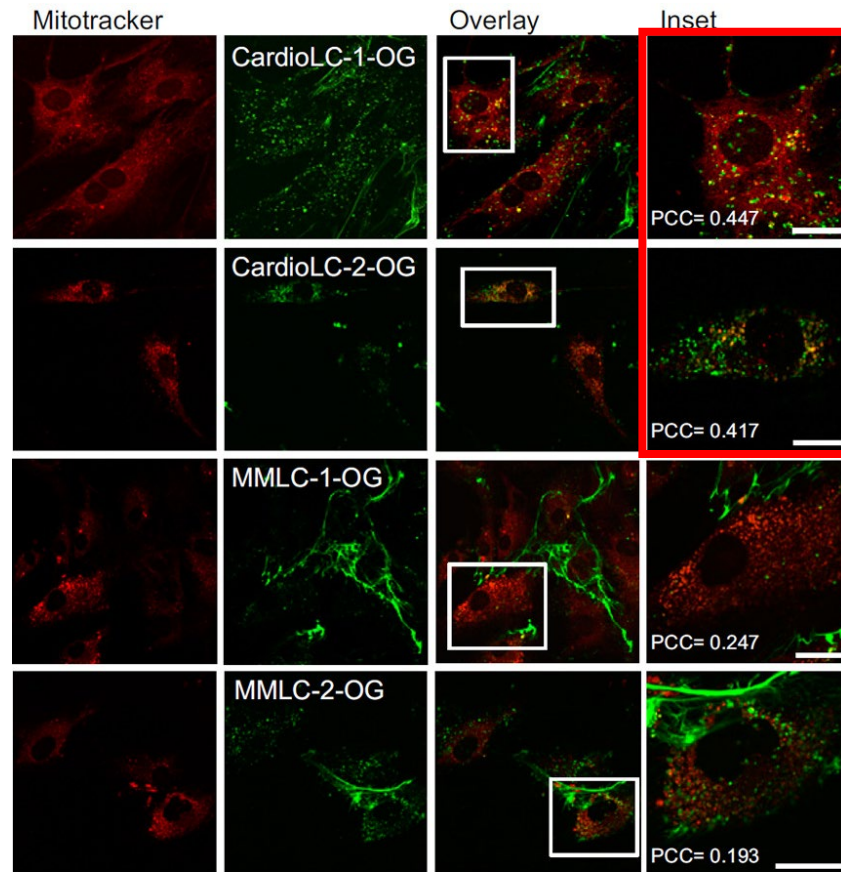
Loss of transmembrane potential



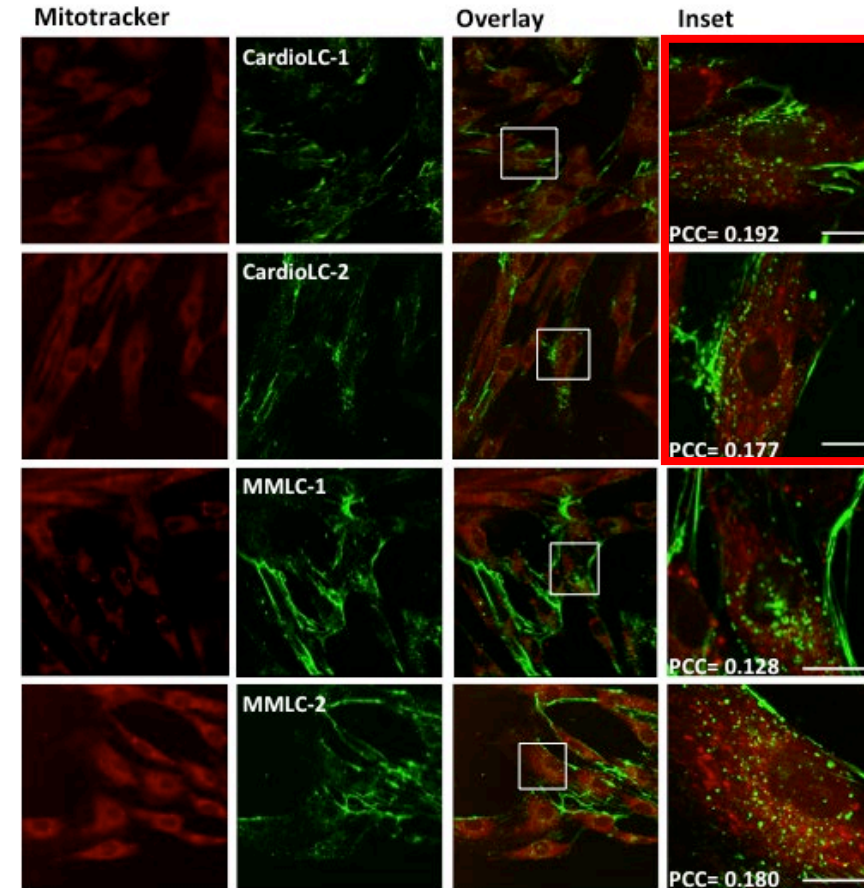
Cardiotoxic LC colocalize with mitochondria in human cardiac fibroblasts but not in dermal fibroblasts



Cardiac fibroblasts



Dermal fibroblasts

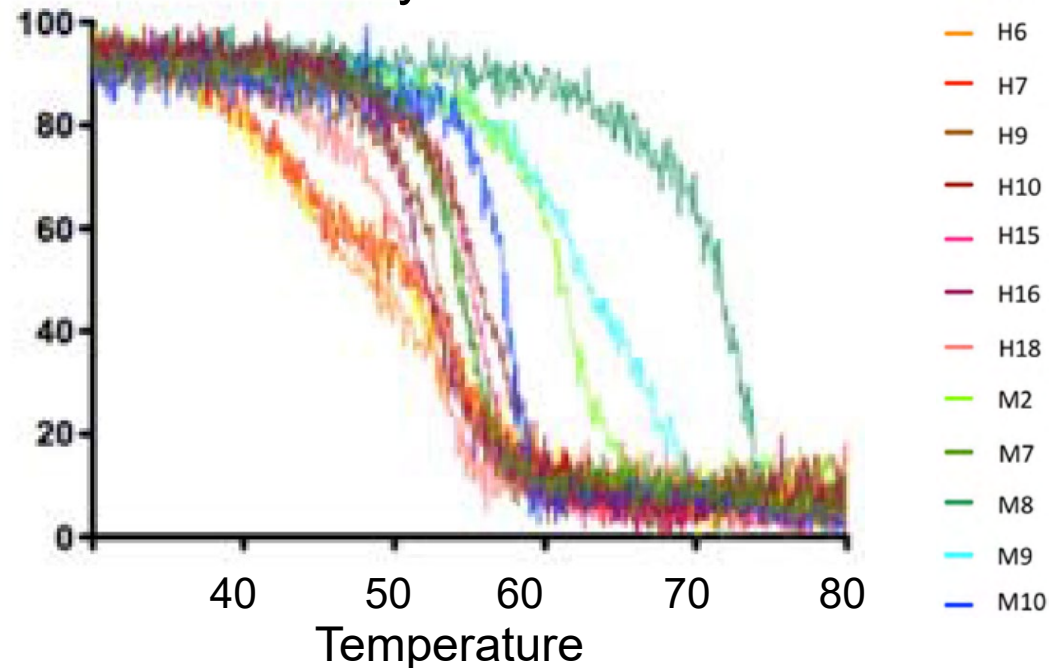


No colocalizations between mitochondria, OPA1 or ACOX1 and all tested LCs in dermal fibroblasts

Low fold stability and high protein dynamics correlate with amyloidogenic LCs

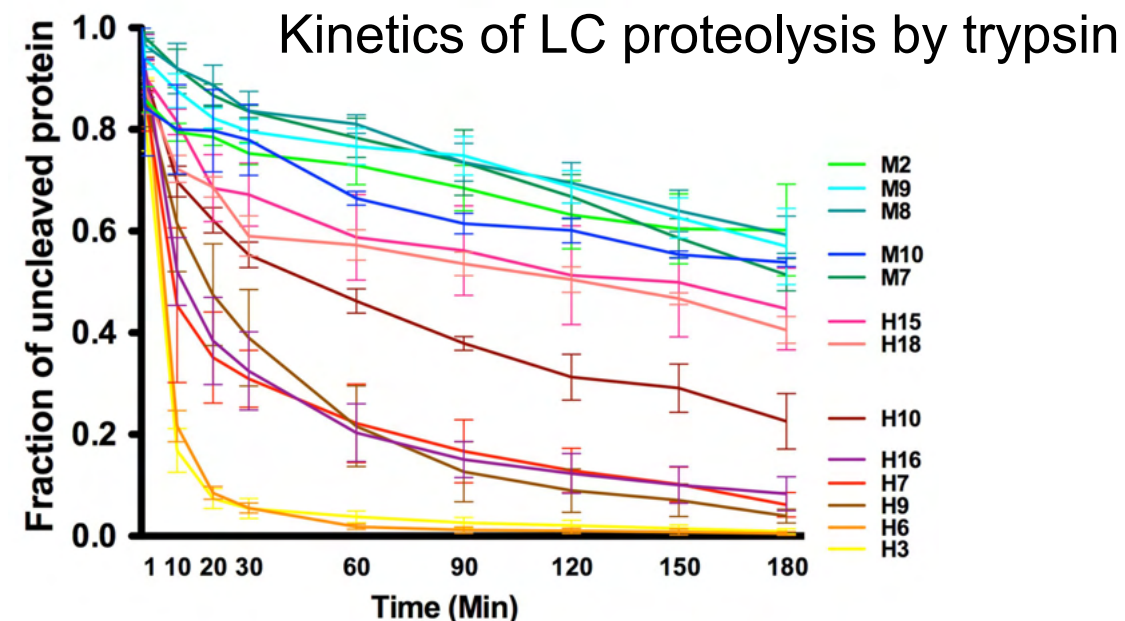
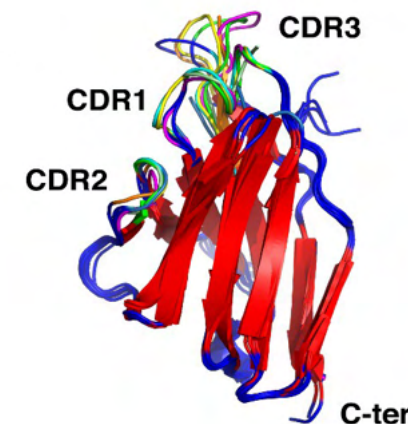


Thermal stability of H and M LCs



- **low fold stability**
 - **high protein dynamics**
- correlate with amyloidogenic LCs,
while hydrophobicity and structural rearrangements
are not relevant

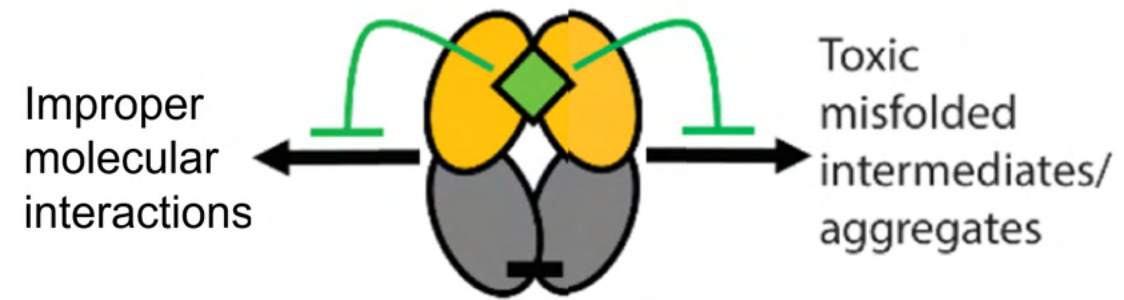
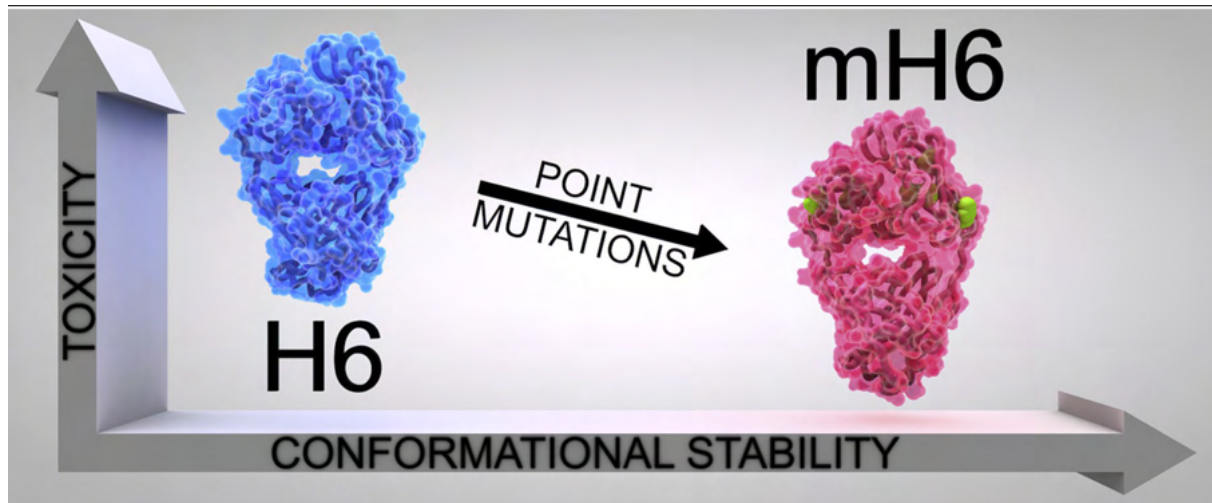
Crystal structure of 8 amyloidogenic
cardiotoxic LCs (H), and 5 non amyloid LCs (M)



Light chain instability is linked to cardiotoxicity



We rationally engineered the amino acid sequence of the highly cardiotoxic LC H6 by introducing three residue mutations (V47L, T70N, and G75T), designed to reduce the dynamics of its native state.



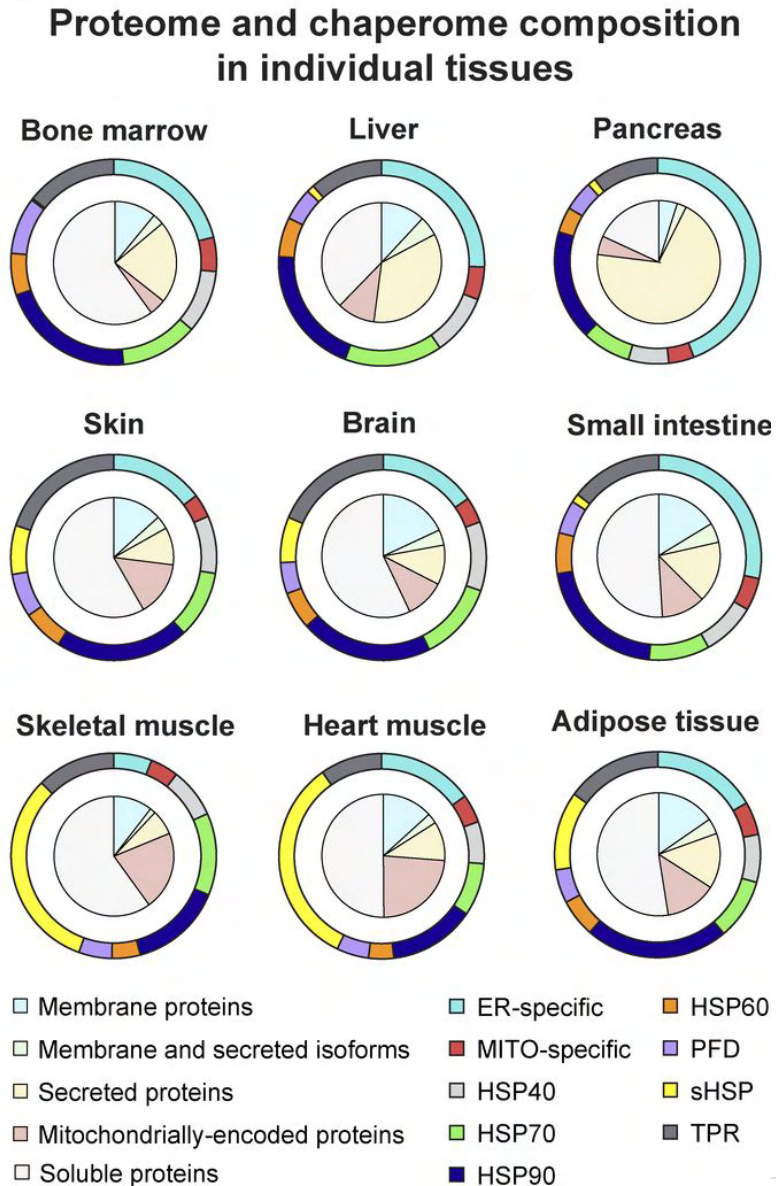
These findings support the ongoing development of a new class of drugs: LC stabilizers

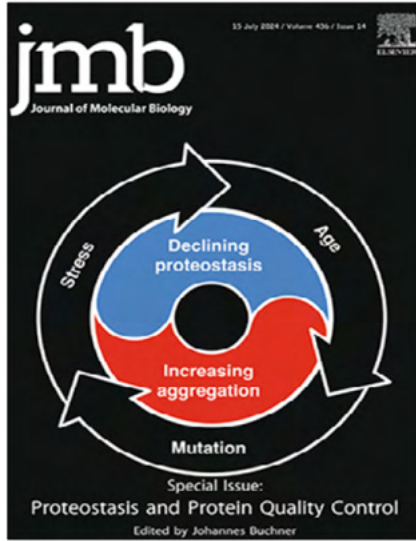
The stabilized LC, restored the cardiac cells viability, ATP production, pumping rate of *C. elegans*, and reduced oxidative stress



The proteostatic capacity, the cell's ability to preserve protein homeostasis by balancing protein synthesis, folding, and clearance, varies in different tissues/organs and may underlie tissue vulnerability and resilience in amyloidosis

Shaping proteostasis at the cellular, tissue, and organismal level



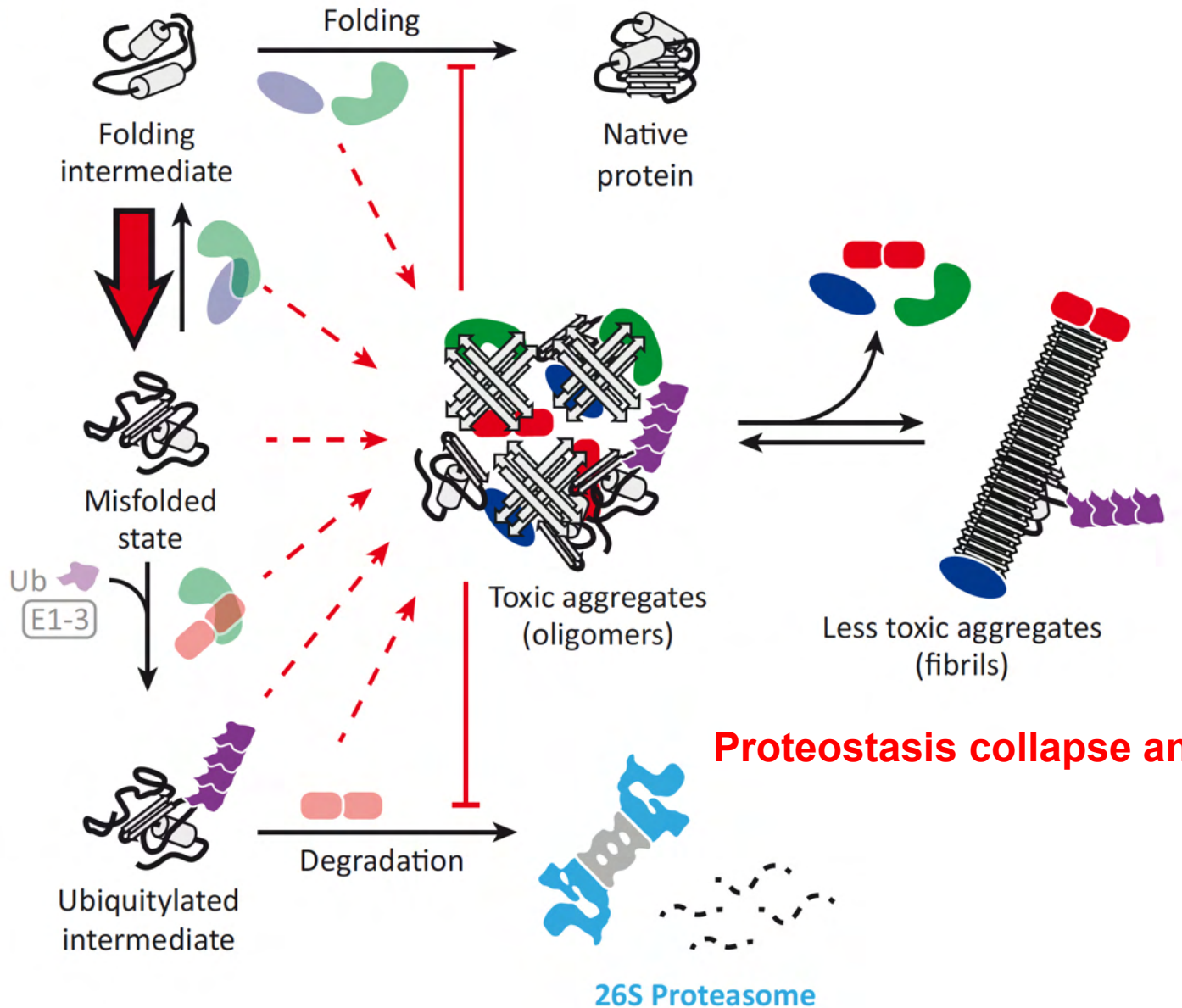


Interplay of Proteostasis Capacity and Protein Aggregation: Implications for Cellular Function and Disease

Mark S. Hipp ^{1,2,3,*} and **F. Ulrich Hartl** ^{4,5,6,*} 2024



When the intracellular protein aggregates overwhelm the proteostasis capacity, cytotoxic protein aggregates accumulate and place an excessive burden on the proteostasis network's ability to maintain proteome integrity. This initiates a feed-forward loop, wherein the generation of misfolded and aggregated proteins ultimately leads to proteostasis collapse and cellular demise.

Proteostasis network impairment by aggregate formation





The proteostasis network and its decline in ageing

Mark S. Hipp , Prasad Kasturi and F. Ulrich Hartl *

Nat Rev Mol Cell Biol 2019

Aged / Declining capacity

Basal ER stress; PERK→eIF2α/ATF4/CHOP bias; IRE1α/XBP1s & ATF6 programs wane

Chaperone/co-chaperone insufficiency; ERAD, proteasome & autophagy flux fall

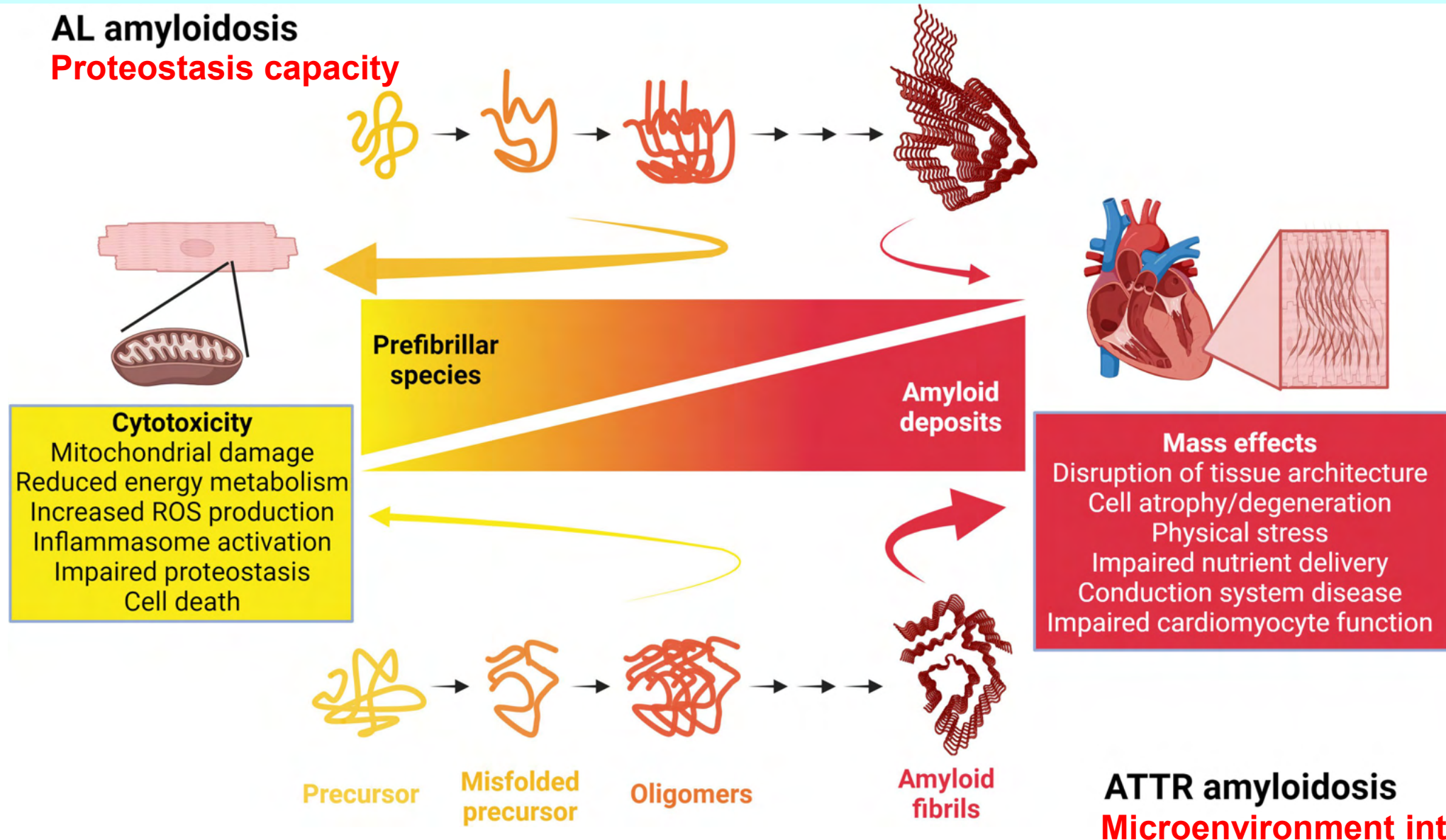
Secretory QC slippage → amyloidogenic intermediates escape ER

Extracellular chaperone capacity declines

Net result: increased misfolded/aggregated species, organ vulnerability



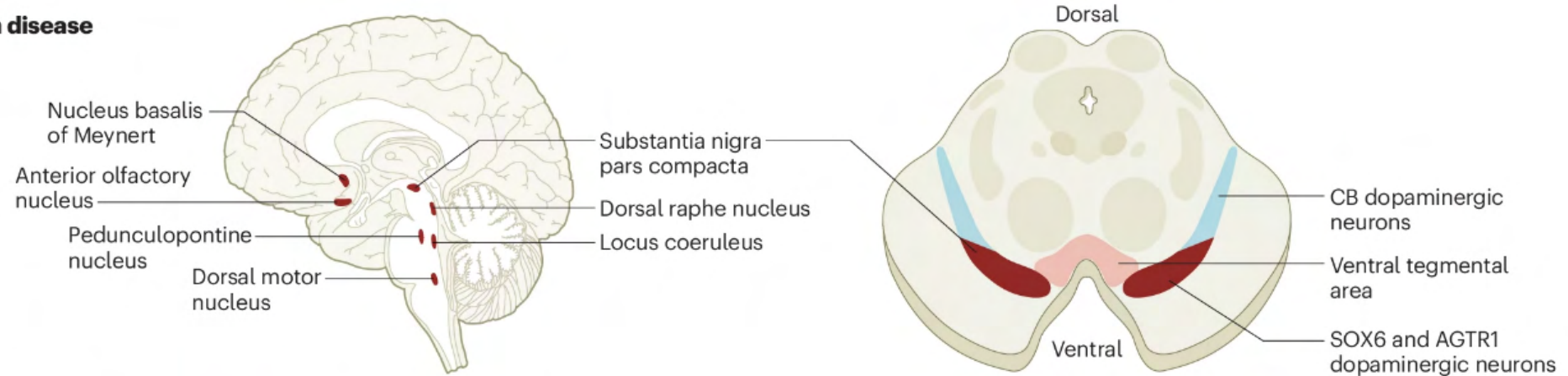
Proteostasis capacity and microenvironment interactions play a different role in various amyloidosis types



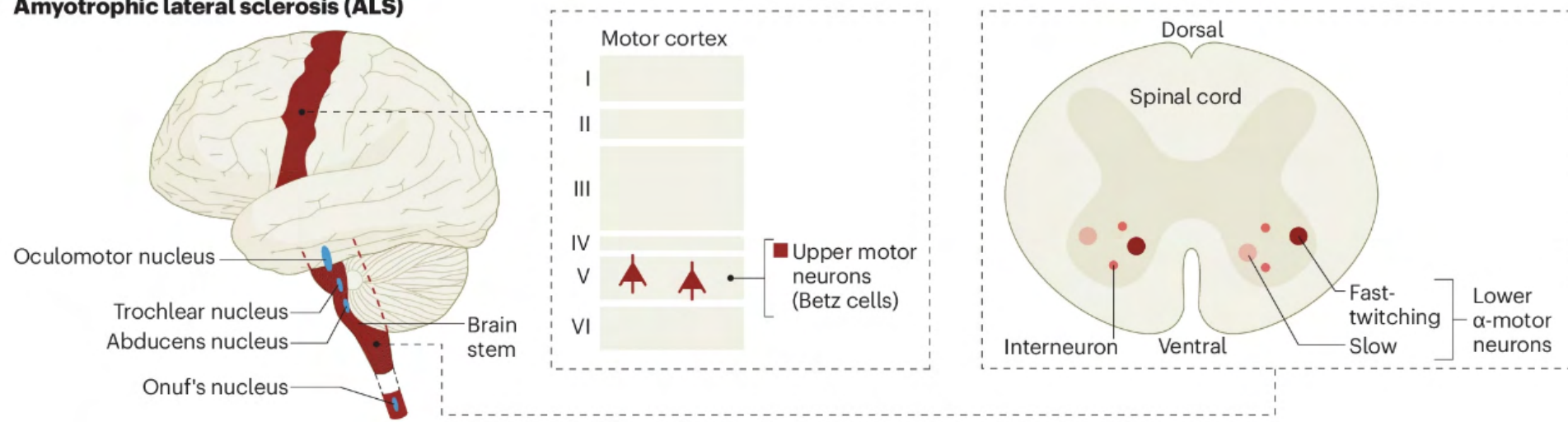
Selective vulnerability is a hallmark of neurodegenerative diseases



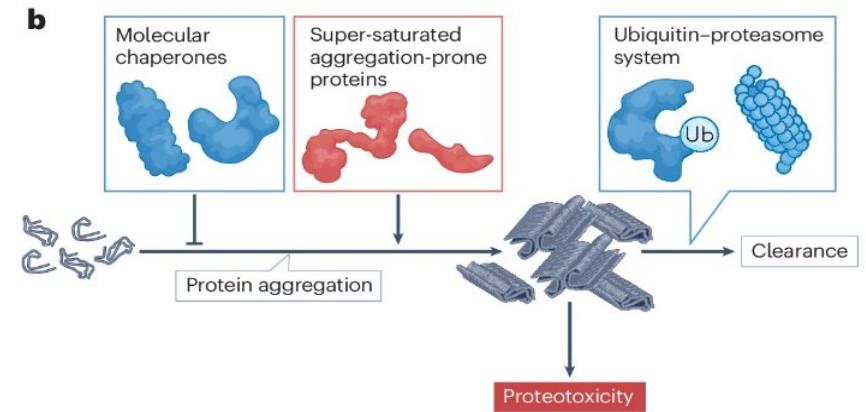
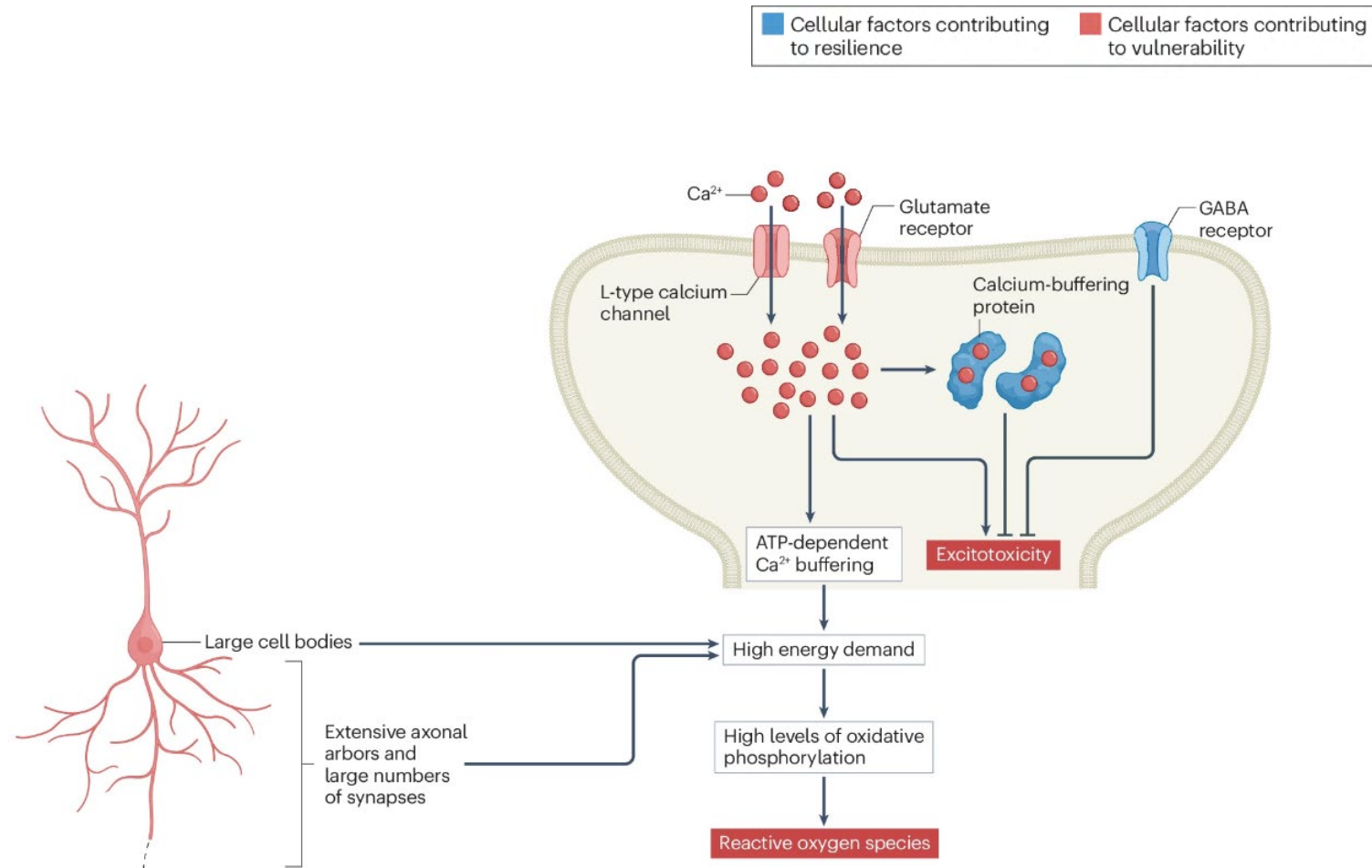
b Parkinson disease



c Amyotrophic lateral sclerosis (ALS)



Cell-autonomous mechanisms of selective vulnerability





Microenvironment + proteostasis capacity gate organ
vulnerability and resilience

Further research is required to elucidate the underlying
molecular mechanisms

These factors represent actionable targets for improving
the management of both systemic and localized
amyloidosis

THANK YOU!