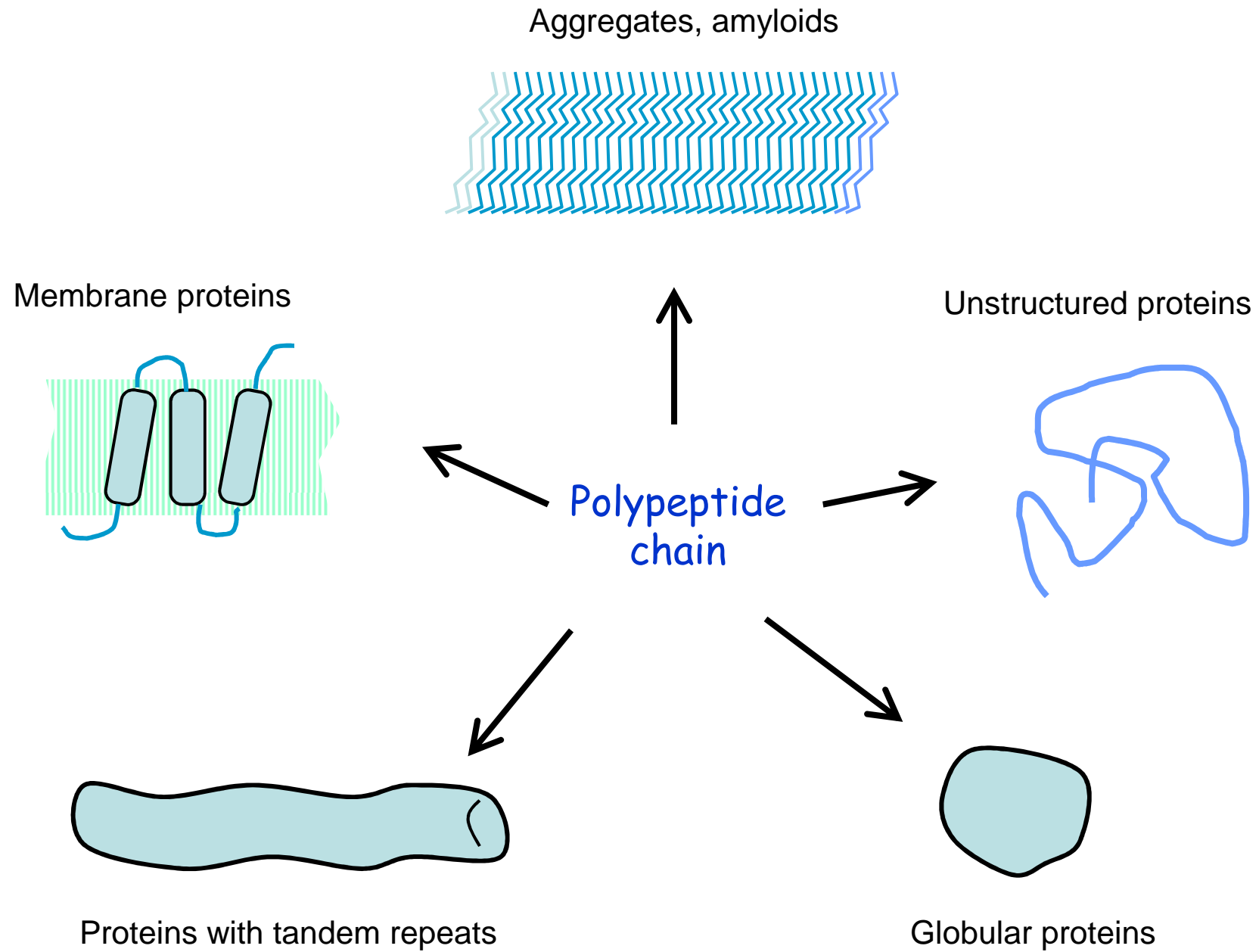


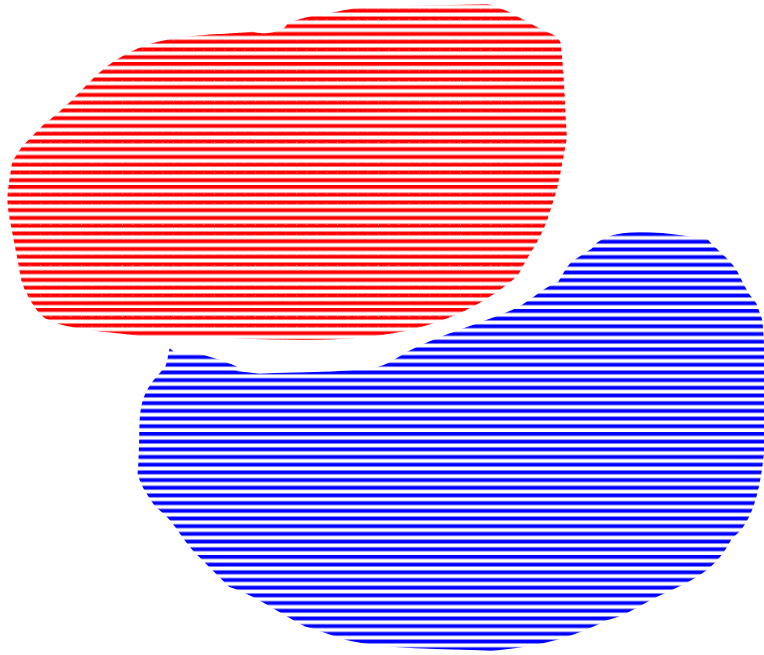
Structural Folds of Amyloid Fibrils

Andrey Kajava

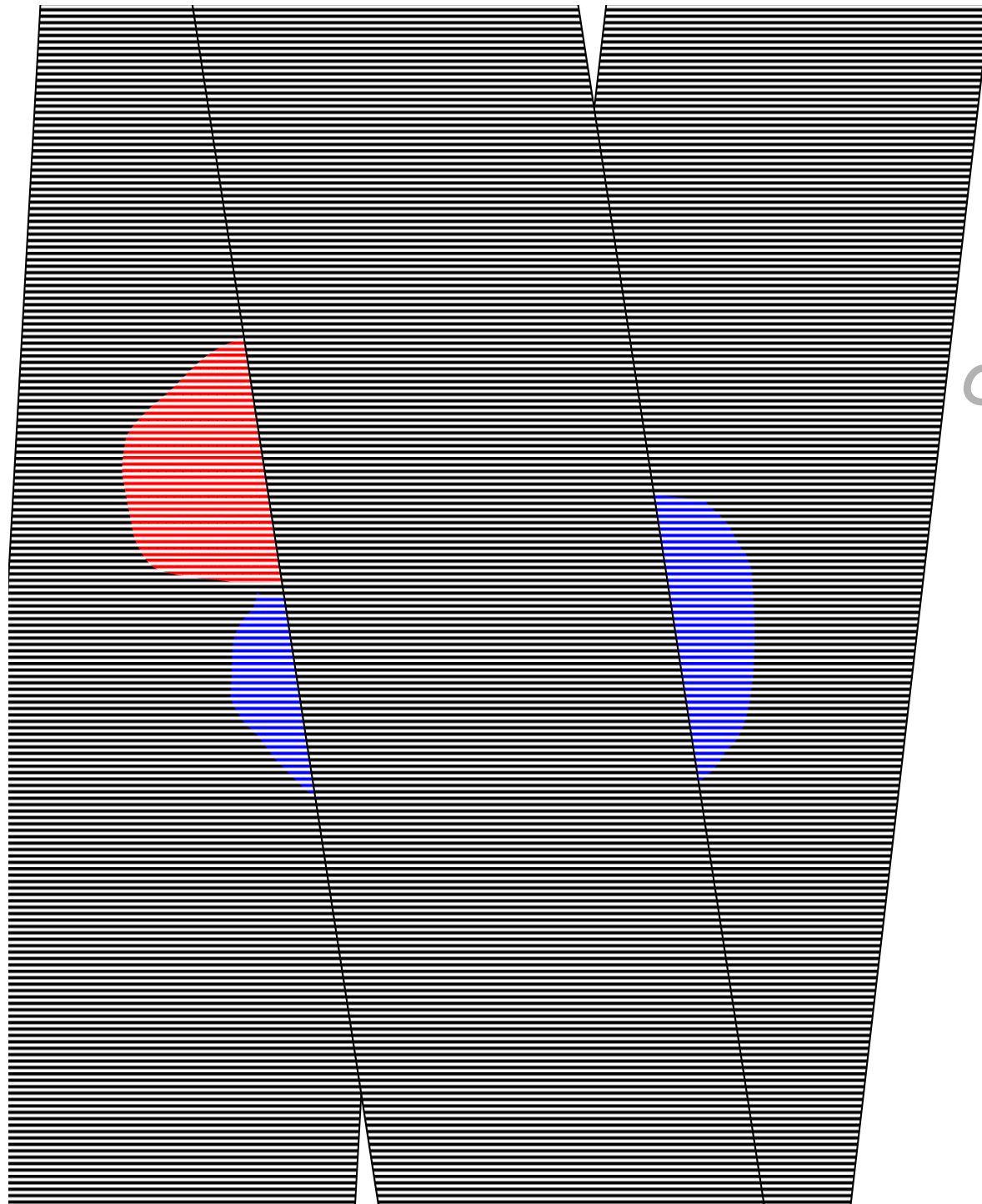
Group of Structural Bioinformatics and Molecular Modelling
Centre de Recherches de Biochimie Macromoléculaire, CNRS
Montpellier, France



Structure of Amyloid Fibrils

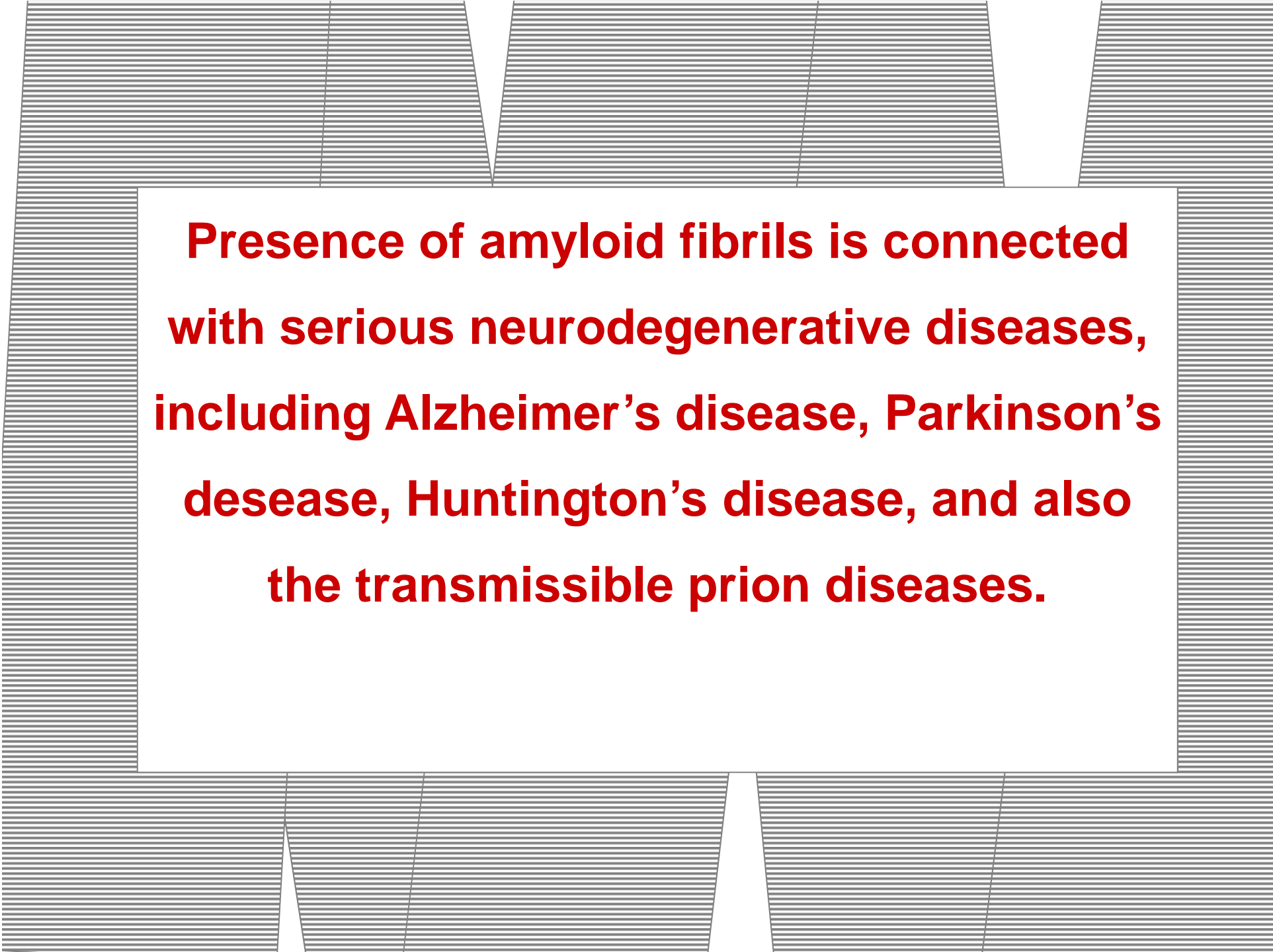


Limited size
and
Optimal stability
of
Protein
Structures



Limited size
and
Optimal stability
of
Proteins
Structures

**Stable structures
of
Unlimited size**



Presence of amyloid fibrils is connected with serious neurodegenerative diseases, including Alzheimer's disease, Parkinson's disease, Huntington's disease, and also the transmissible prion diseases.

Destroy neuronal tissues
in the human **brain**

Span over **many years**



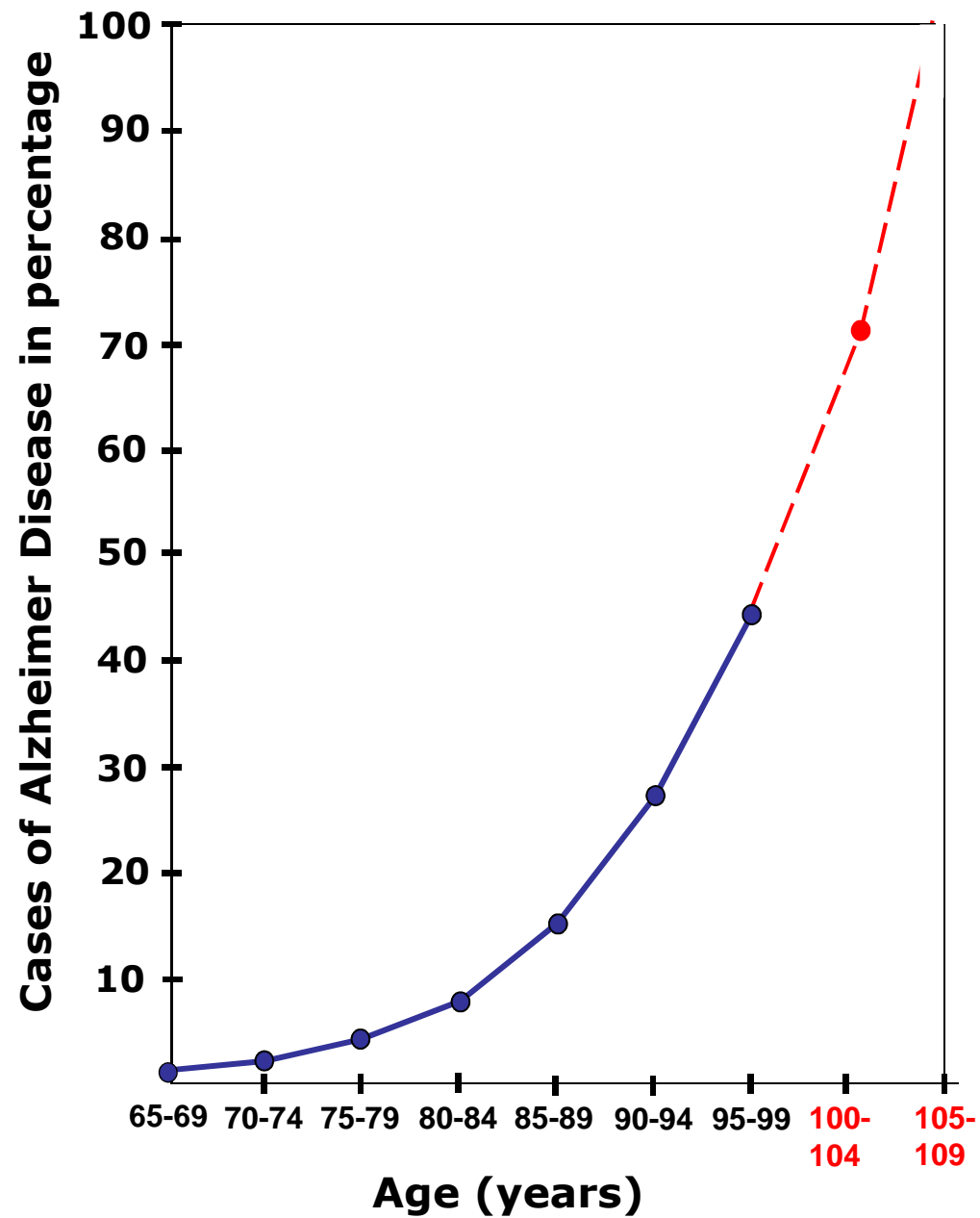
Intense care

In France

Patients ~ 2% of population

Cost for each citizen ~ **350 euros** annually in 2005

Represents **0.6%** of GDP in 2005; **0.8%** in 2020; **1.8%** in 2040



● Nussbaum and Ellis
N. Engl. J. Med. 2003; 348:1356-1364

● Approximation

The 3D structure of amyloid fibrils?

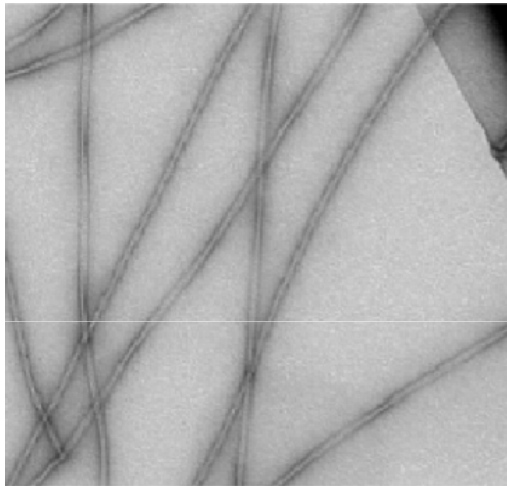
Incomplete structural information from
electron-microscopy, X-ray fiber diffraction,
solid-state NMR etc



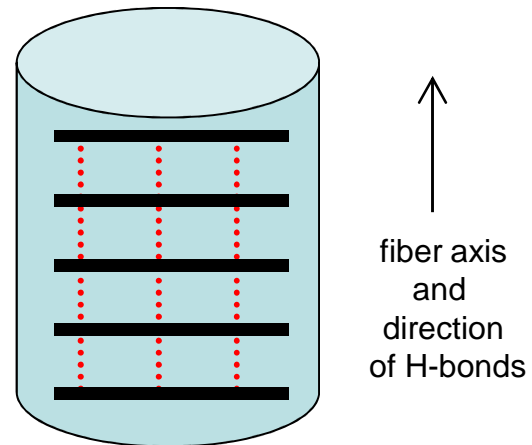
Structural model

COMMON FEATURES OF AMYLOID FIBRILS

From EM
straight, unbranched fibrils
4 to 15 nm in diameter

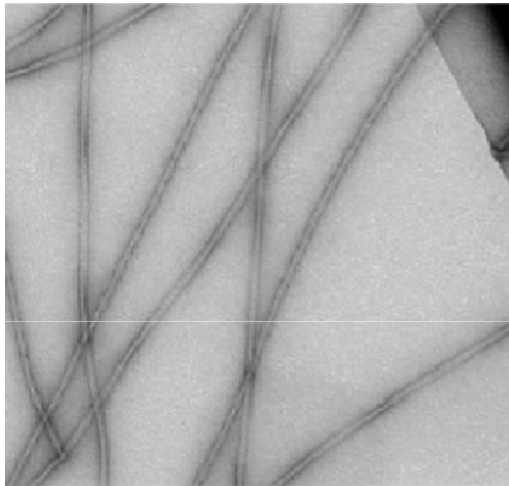


From X-ray diffraction
« cross-beta » structures

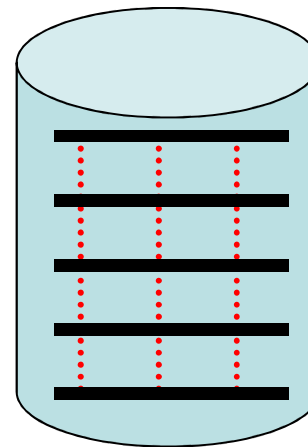


COMMON FEATURES OF AMYLOID FIBRILS

From EM
straight, unbranched fibrils
4 to 15 nm in diameter

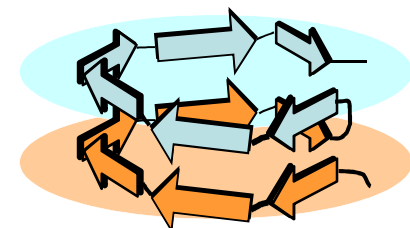
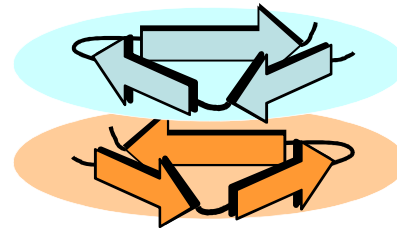
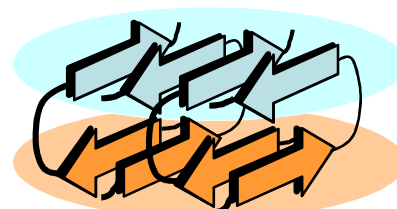
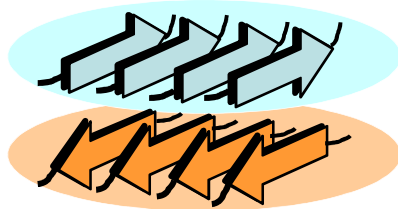


From X-ray diffraction
« cross-beta » structures

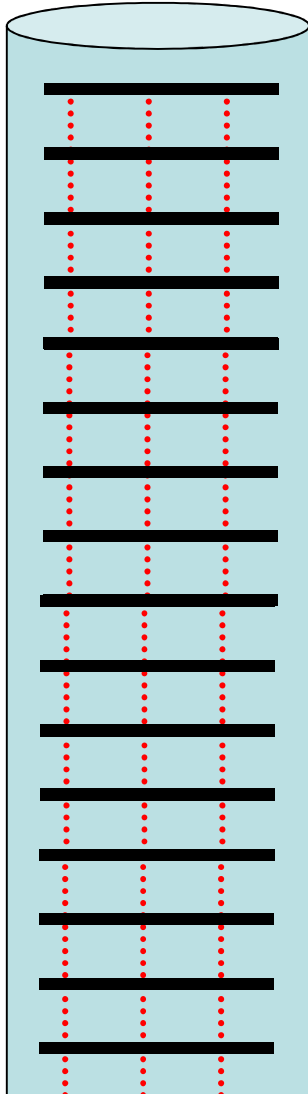


↑
fiber axis
and
direction
of H-bonds

?

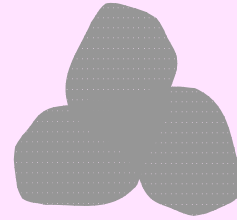


**EM and
X-ray fiber diffraction**
(*diameter, twist,
coiling, cross-beta
structures*)



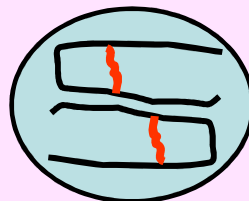
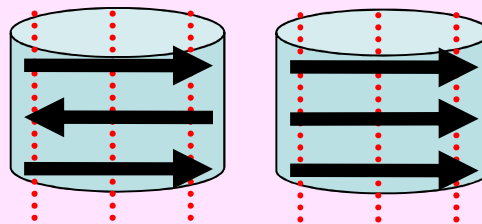
NEW METHODS

✓ Cryo-EM

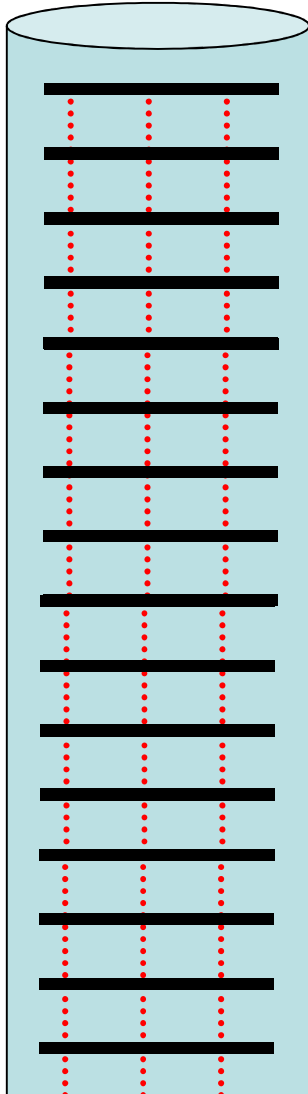


✓ STEM (number of peptides
in fibril cross-section)

✓ ssNMR,
EPR spectroscopy

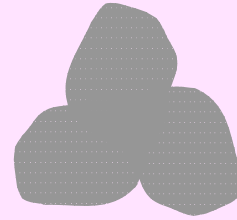


**EM and
X-ray fiber diffraction**
(diameter, twist,
coiling, cross-beta
structures)



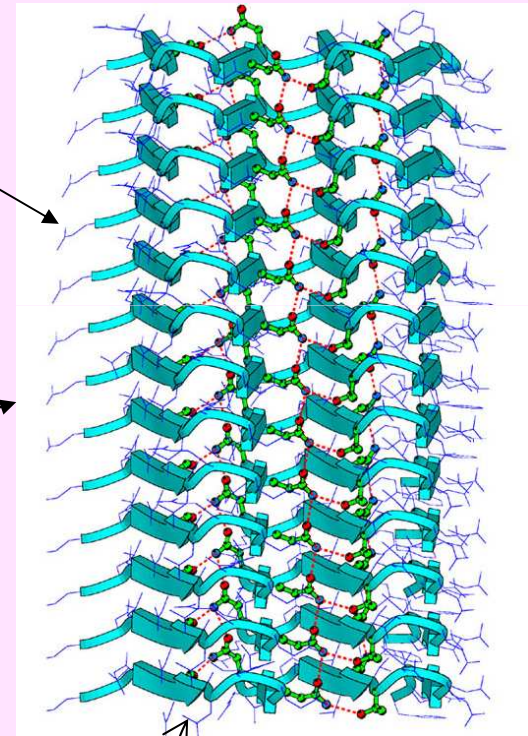
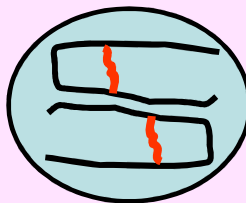
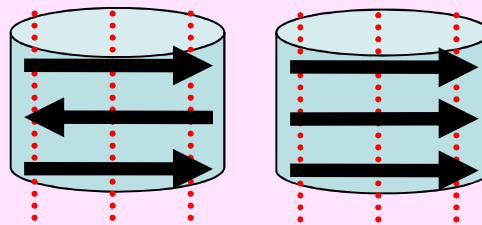
NEW METHODS

✓ Cryo-EM



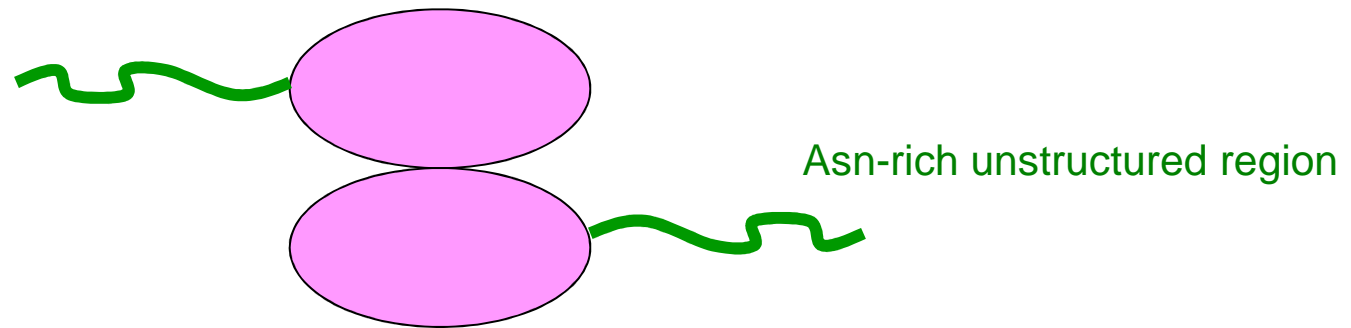
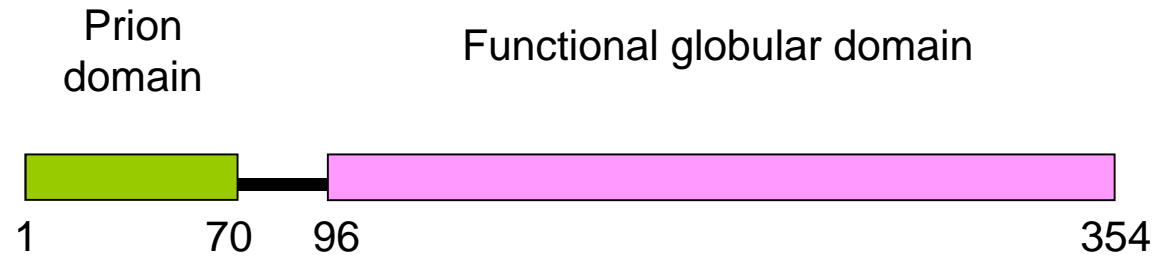
✓ STEM (number of peptides
in fibril cross-section)

✓ ssNMR,
EPR spectroscopy



Yeast prion filaments
formed by Ure2p

Yeast prion filaments formed by Ure2p



Homodimer, interacts with GATA transcription factor Gln3p

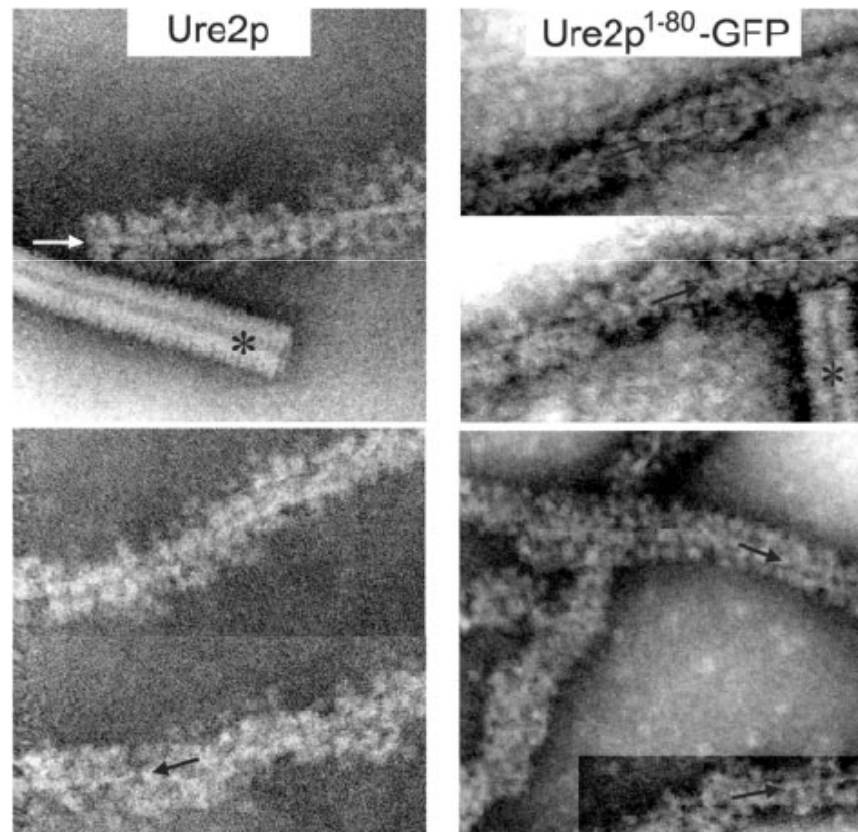
Architecture of Ure2p Prion Filaments

THE N-TERMINAL DOMAINS FORM A CENTRAL CORE FIBER*[§]

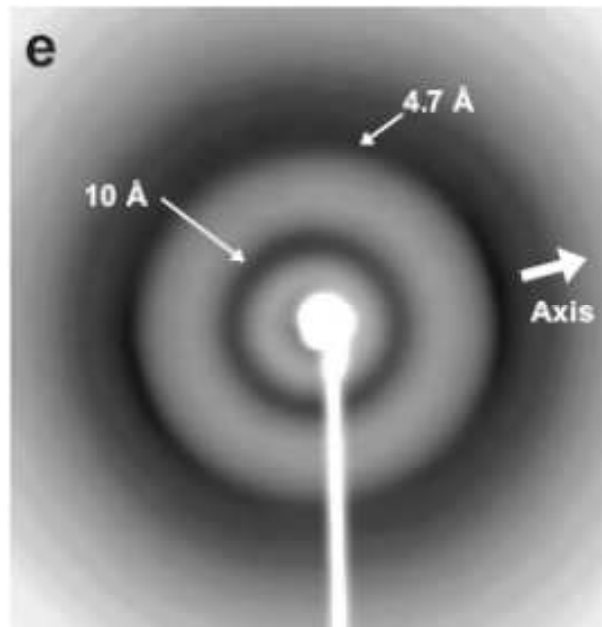
Received for publication, June 6, 2003, and in revised form, August 6, 2003
Published, JBC Papers in Press, August 12, 2003, DOI 10.1074/jbc.M306004200

Ulrich Baxa^{‡‡}, Kimberly L. Taylor^{§1}, Joseph S. Wall^{||}, Martha N. Simon^{||}, Naiqian Cheng[‡],
Reed B. Wickner[§], and Alasdair C. Steven^{* **}

Diameter of core
fiber is about 4 nm

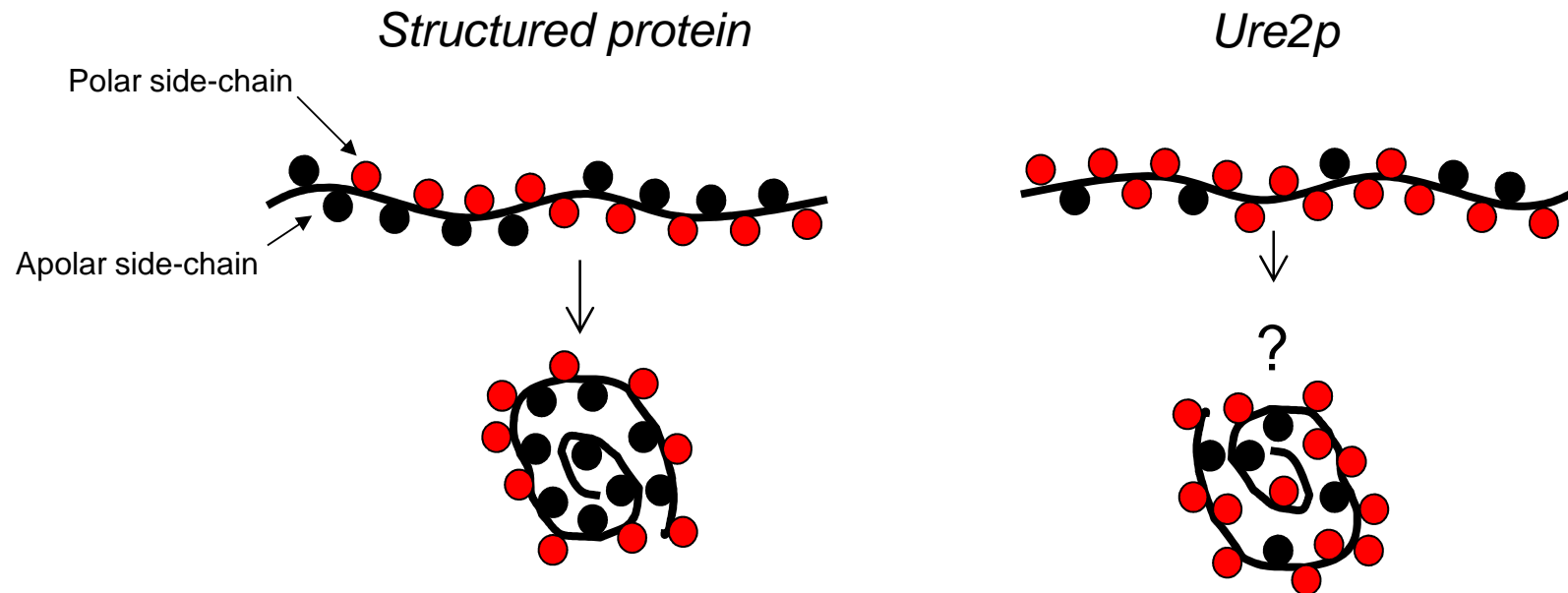


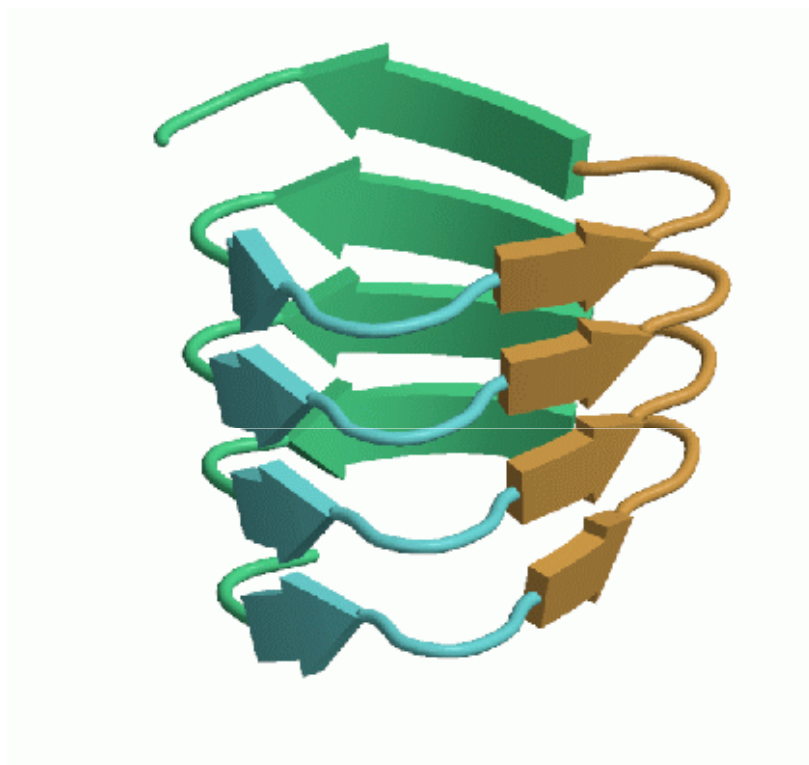
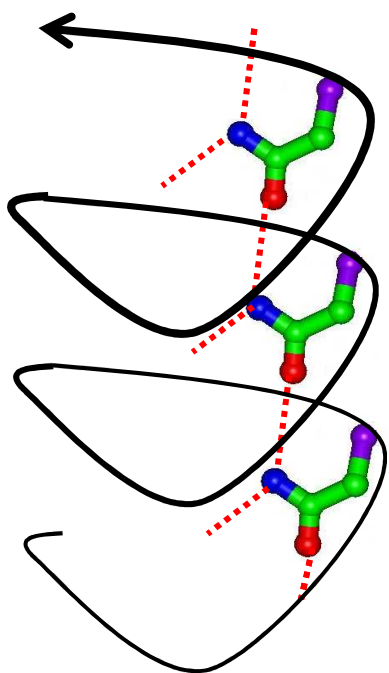
Ure2p core fibril has cross-beta structure



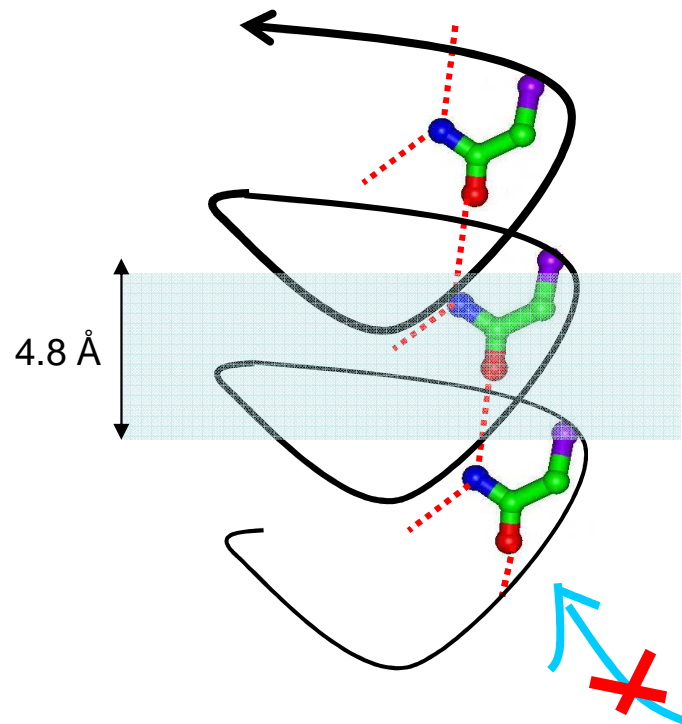
X-ray and electron fiber diffraction
(Baxa *et al.*, *J. Struct. Biol.* 2005)

Ure2p prion domain has Asn-rich amino acid sequence



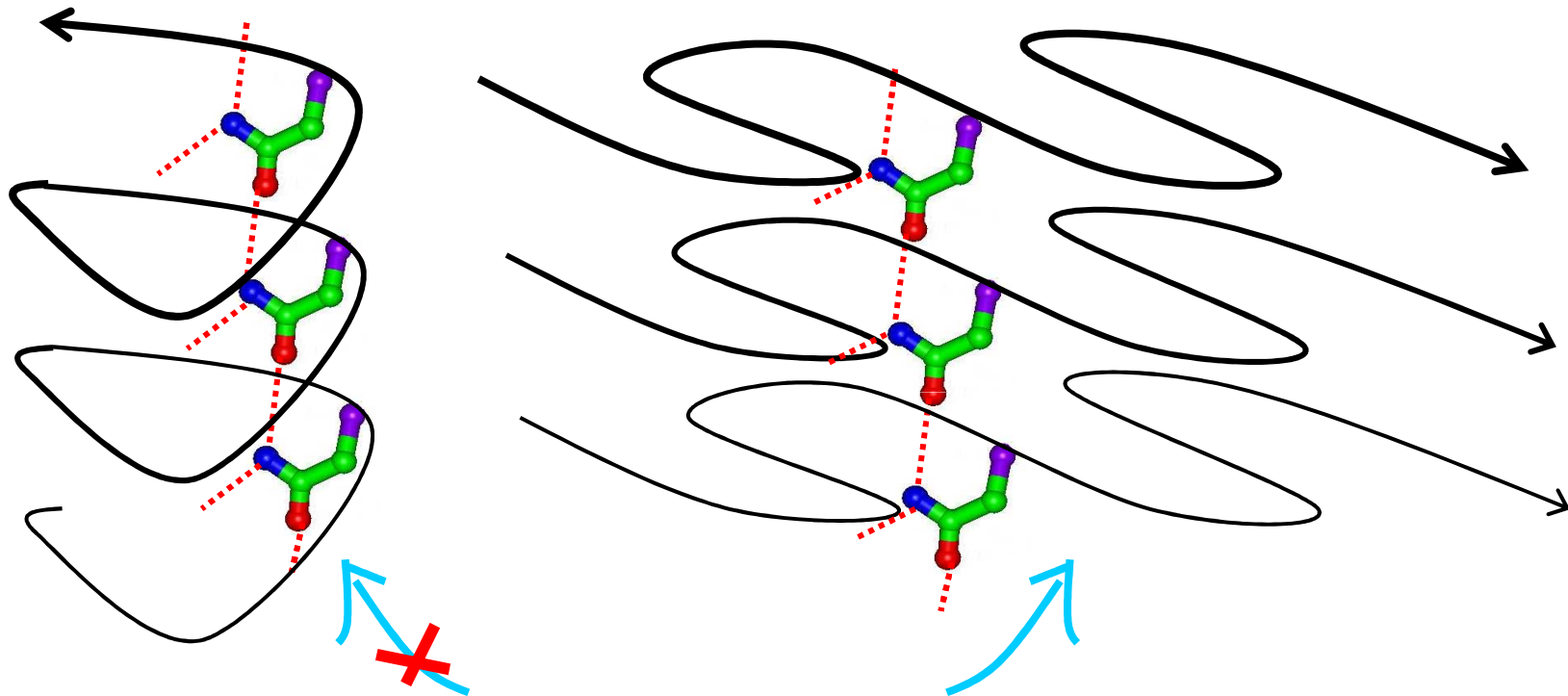


Structural fold for Ure2p prion domain

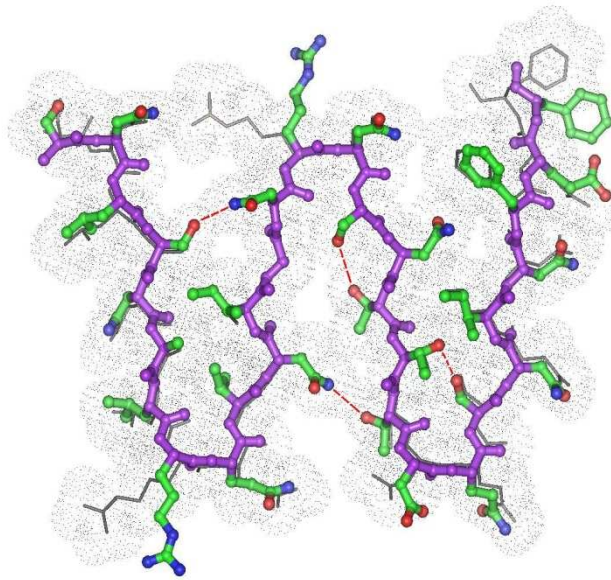


- ✓ One peptide per one beta-layer, according to scanning transmission EM
(Baxa *et al.*, (2003) *JBC*, 278, 43717)
- ✓ Parallel and in-register beta-structure according to solid state NMR
(Chan and Tycko, (2005) *Biochemistry* 44, 10669)

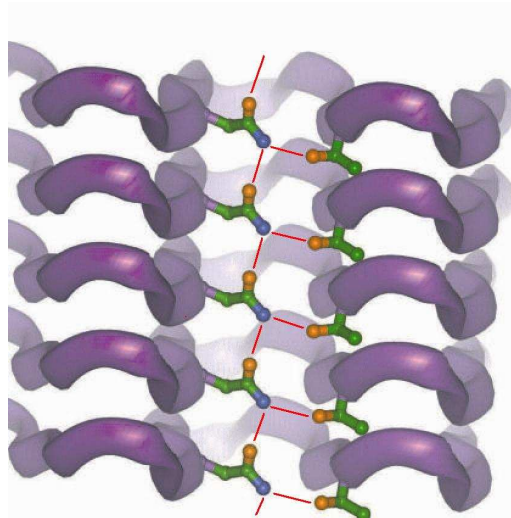
Structural fold for Ure2p prion domain



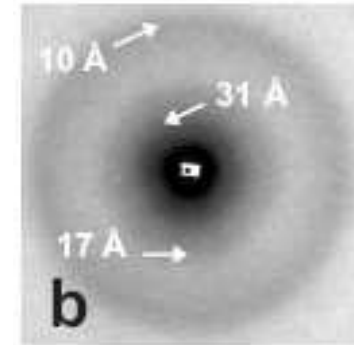
- ✓ One peptide per one beta-layer, according to scanning transmission EM
(Baxa *et al.*, (2003) *JBC*, 278, 43717)
- ✓ Parallel and in-register beta-structure according to solid state NMR
(Chan and Tycko, (2005) *Biochemistry* 44, 10669)



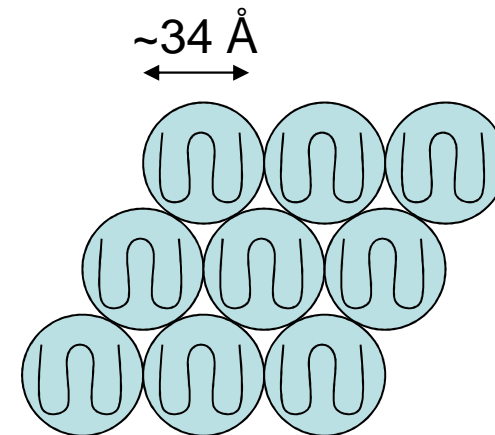
Axial projection
Ure2p (10-39)



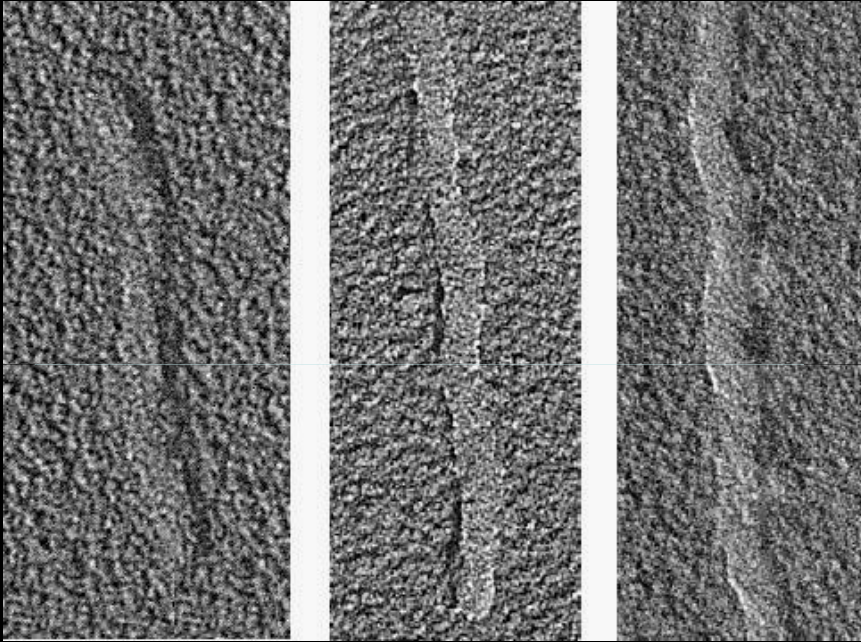
Radial projection



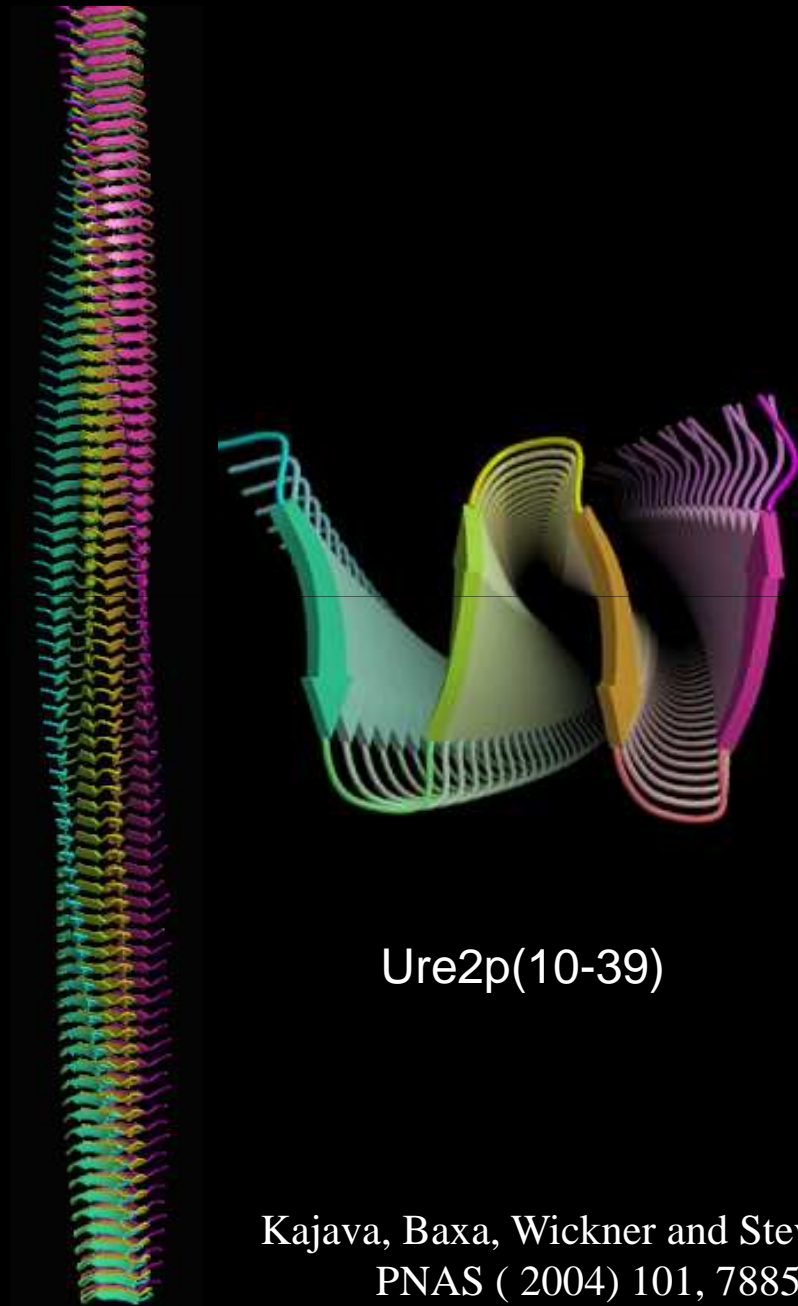
(Adapted from Baxa et al.,
J. Struct. Biol. 2005)



Left-handed twist of fibrils

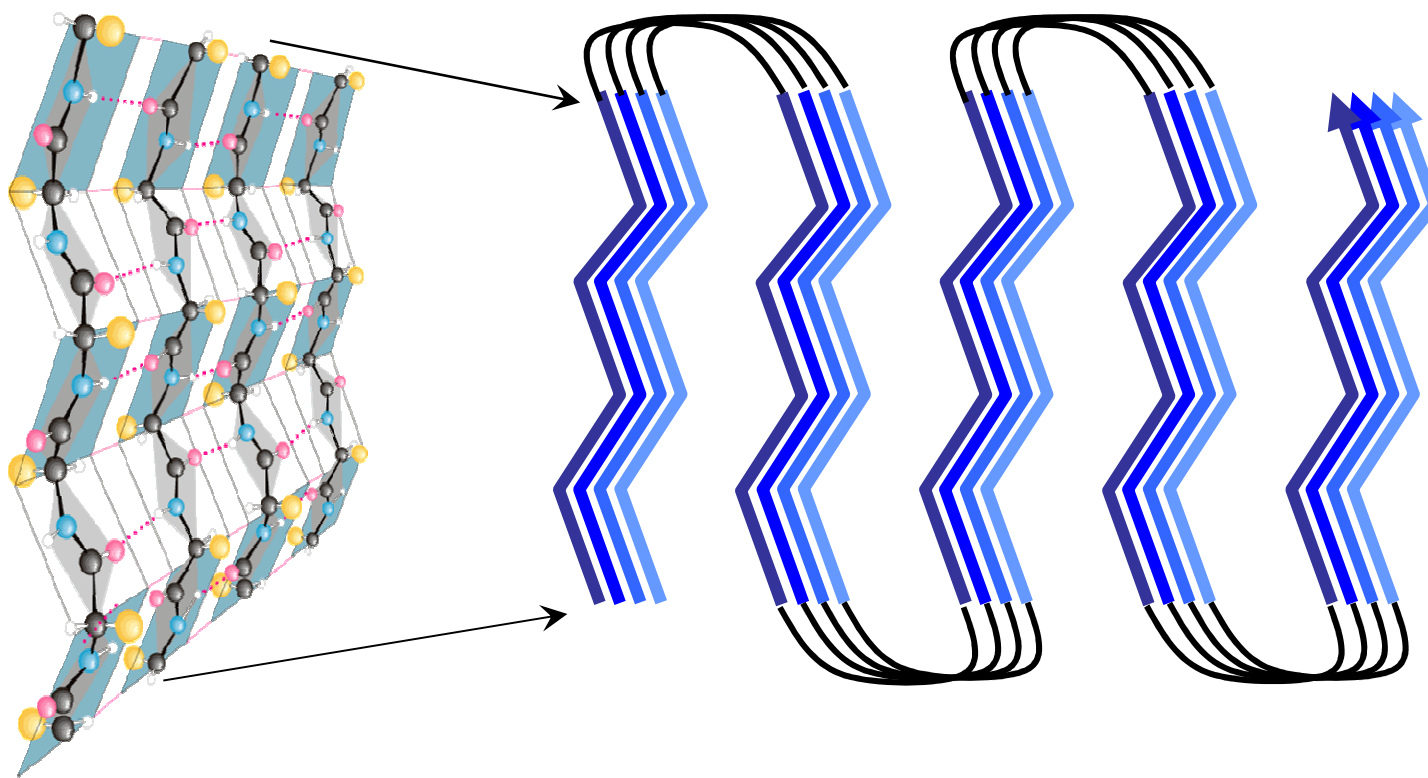


Unidirectional shadowing
of Ure2p(10-80)-GFP



Ure2p(10-39)

Kajava, Baxa, Wickner and Steven
PNAS (2004) 101, 7885.



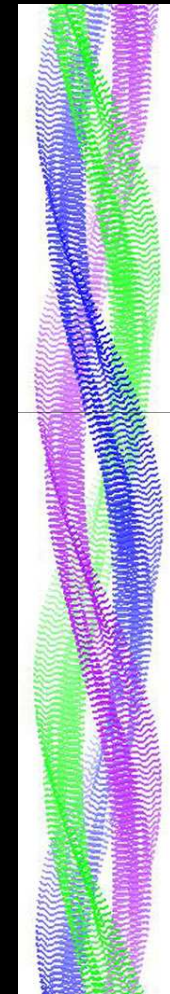
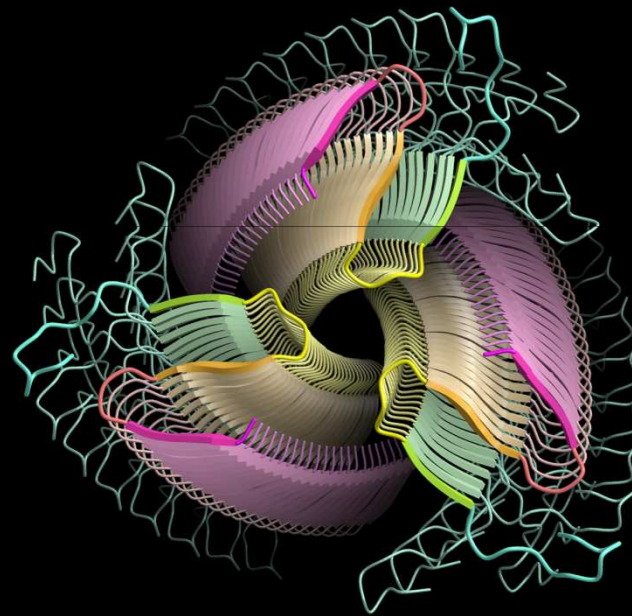
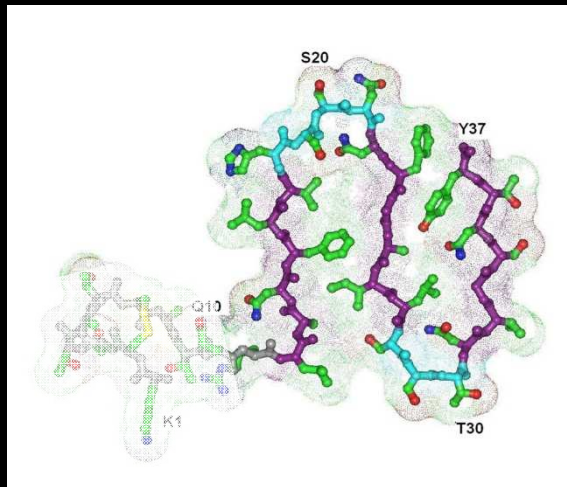
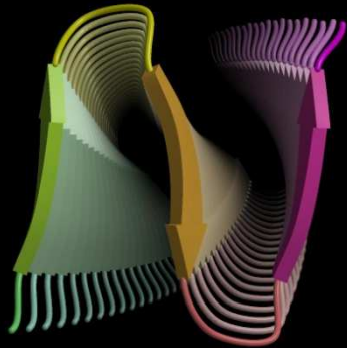
Canonical pleated β -structure

Superpleated β -structure

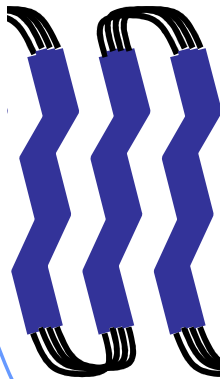
Amyloid Fibrils of Human Amylin

Human amylin is the major component of pancreatic amyloid deposits found in ~ 90% of persons with non-insulin-dependent (type 2) diabetes mellitus.

STEM + EM + X-ray fiber diff + EPR



Applicability of the superpleated β -structure to other amyloids



Poly(Q) tracts (**Huntingtin disease**)

α -synuclein (**Parkinson's disease**)

(Der-Sarkissian et al., 2003, JBC, 278, 37530)

Tau protein (**Alzheimer's disease**)

(Margittai and Langen, 2004, PNAS, 101, 10278)

Prion domains of yeast proteins Sup35

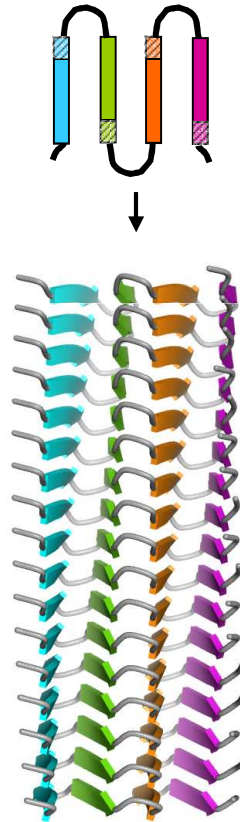
(Shewmaker et al., PNAS. 2006103(52):19754)

Protofilaments of disease-related amyloid fibrils

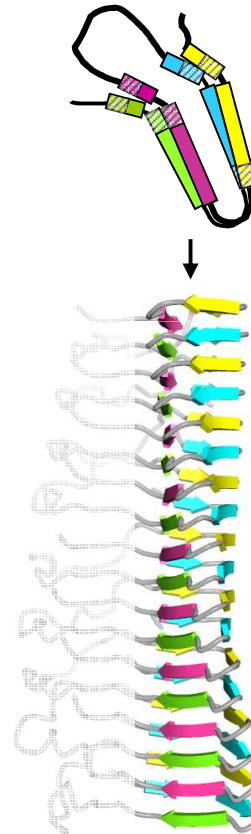
Type 1
Stack of β -arches
(β -amyloid)



Type 2
Superpleated β -structure
(Ure2p, Sup35p, α -synuclein)



Type 3
Stack of β -solenoids
(HET-s prion)

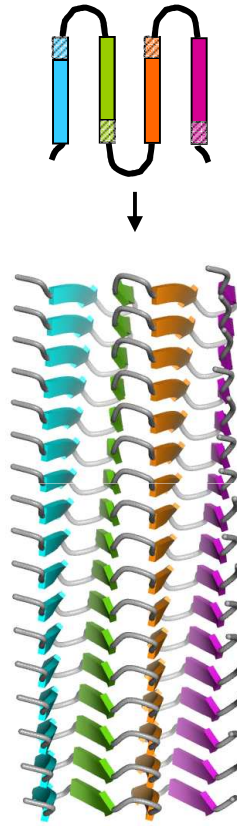


Protofilaments of disease-related amyloid fibrils

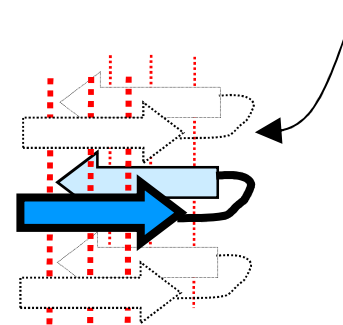
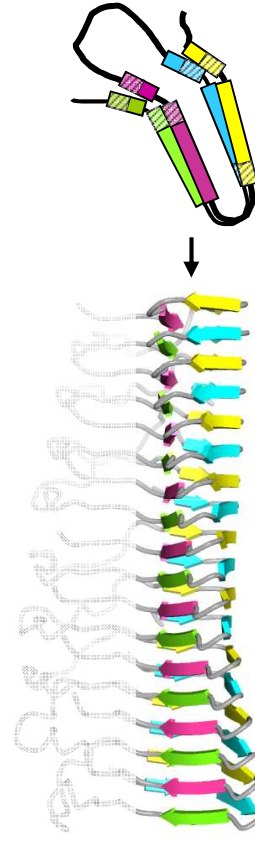
Type 1
Stack of β -arches
(β -amyloid)



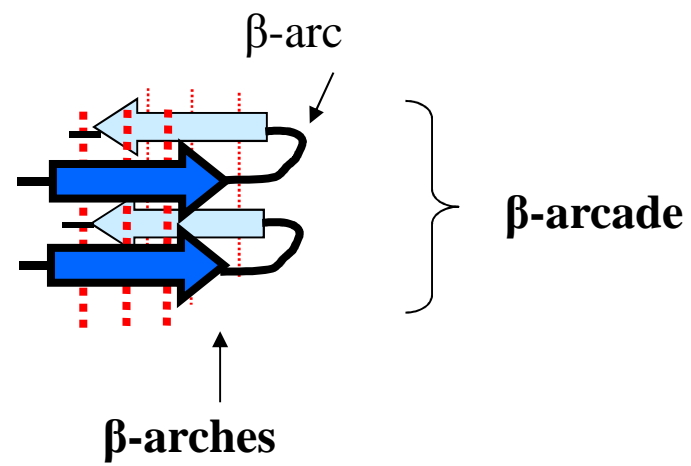
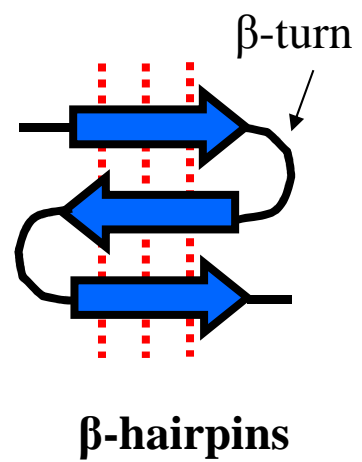
Type 2
Superpleated β -structure
(Ure2p, Sup35p, α -synuclein)



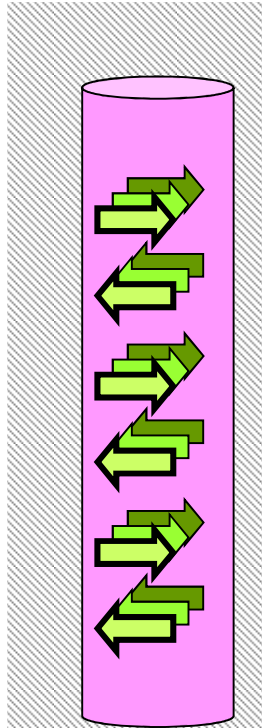
Type 3
Stack of β -solenoids
(HET-s prion)



Kajava, Baxa and Steven
(2010) *FASEB J.* 24:1311

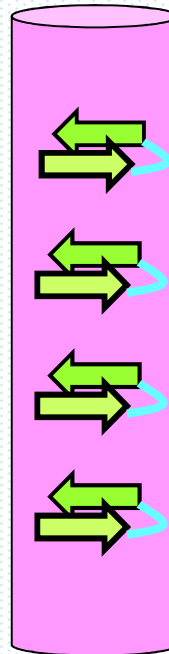


Predominantly
antiparallel
beta-structure



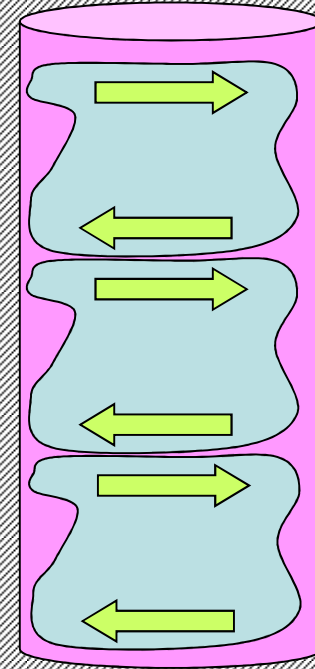
10

Predominantly
parallel
beta-structure



50

Globular domains

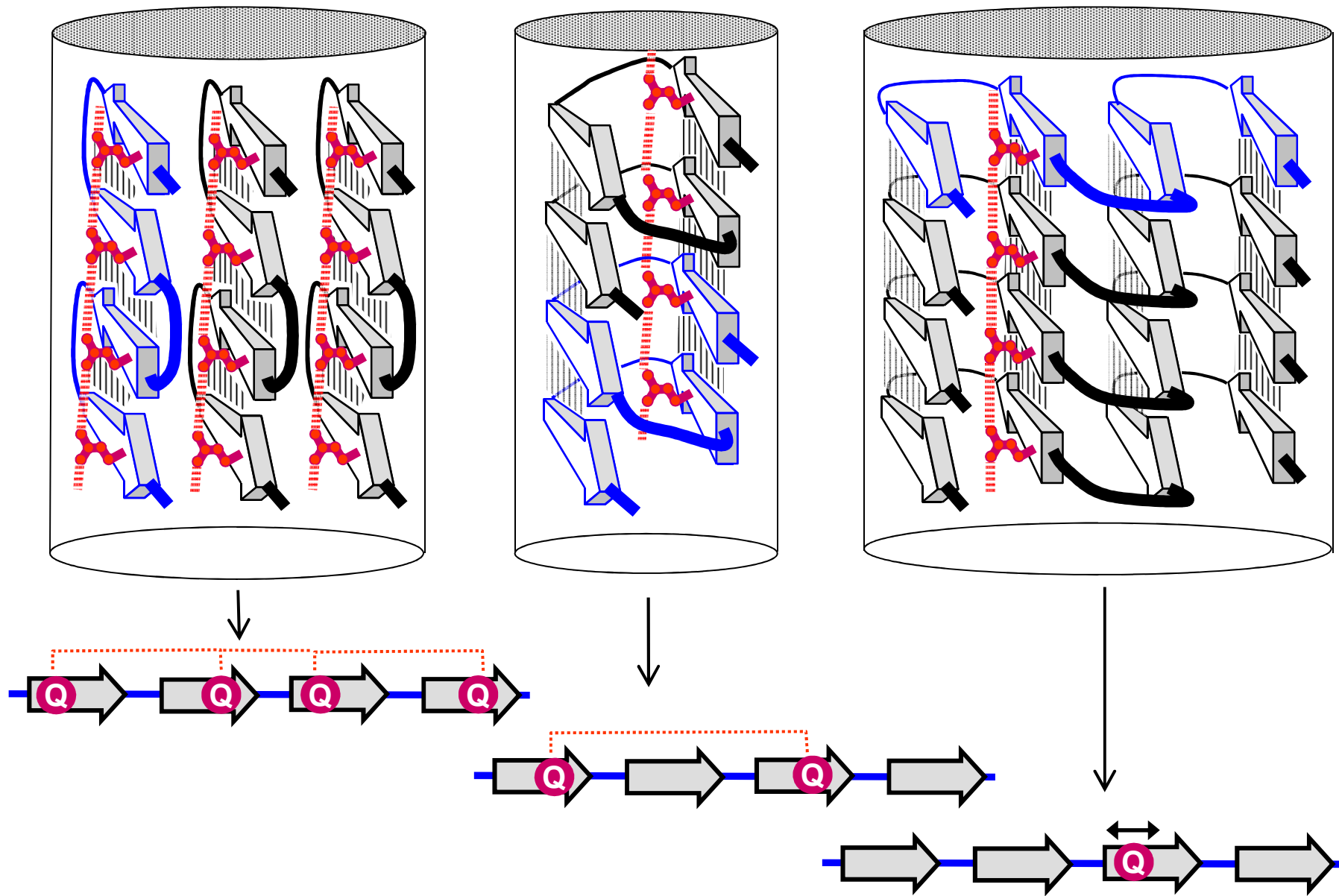


100

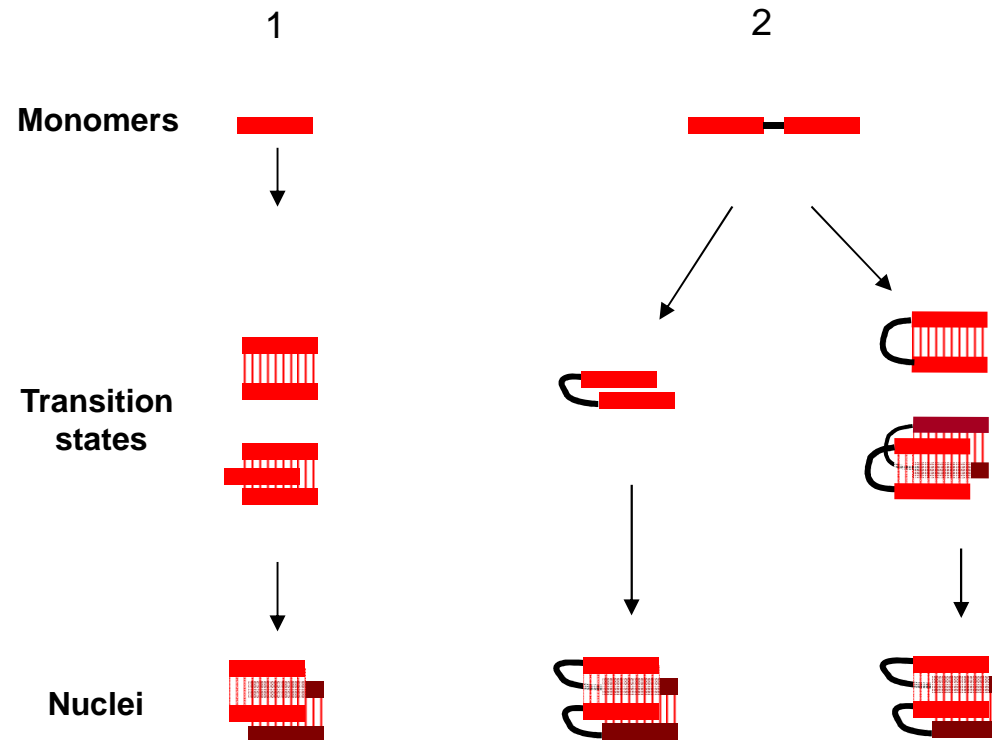
Number of residues in peptide

Only *in vitro*!

Kajava, Baxa and Steven
(2010) *FASEB J.* 24:1311



Beta-arches may provide the best nuclei for fibrillogenesis

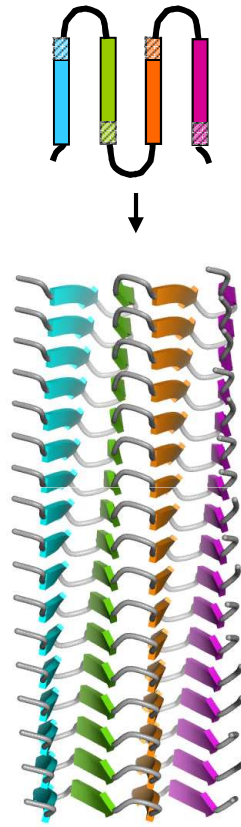


Protofilaments of amyloid fibrils

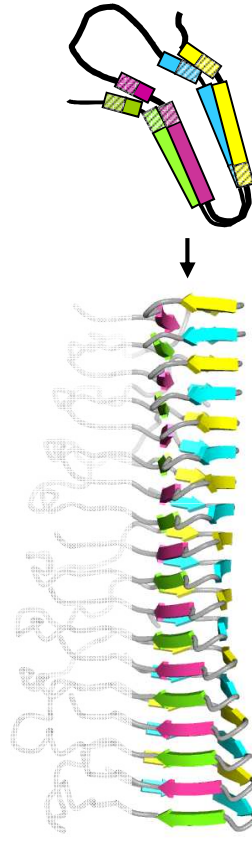
Type 1
Stack of β -arches
(β -amyloid)



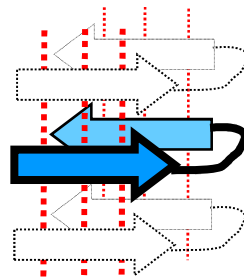
Type 2
Superpleated β -structure
(Ure2p, Sup35p, α -synuclein)



Type 3
Stack of β -solenoids
(HET-s prion)

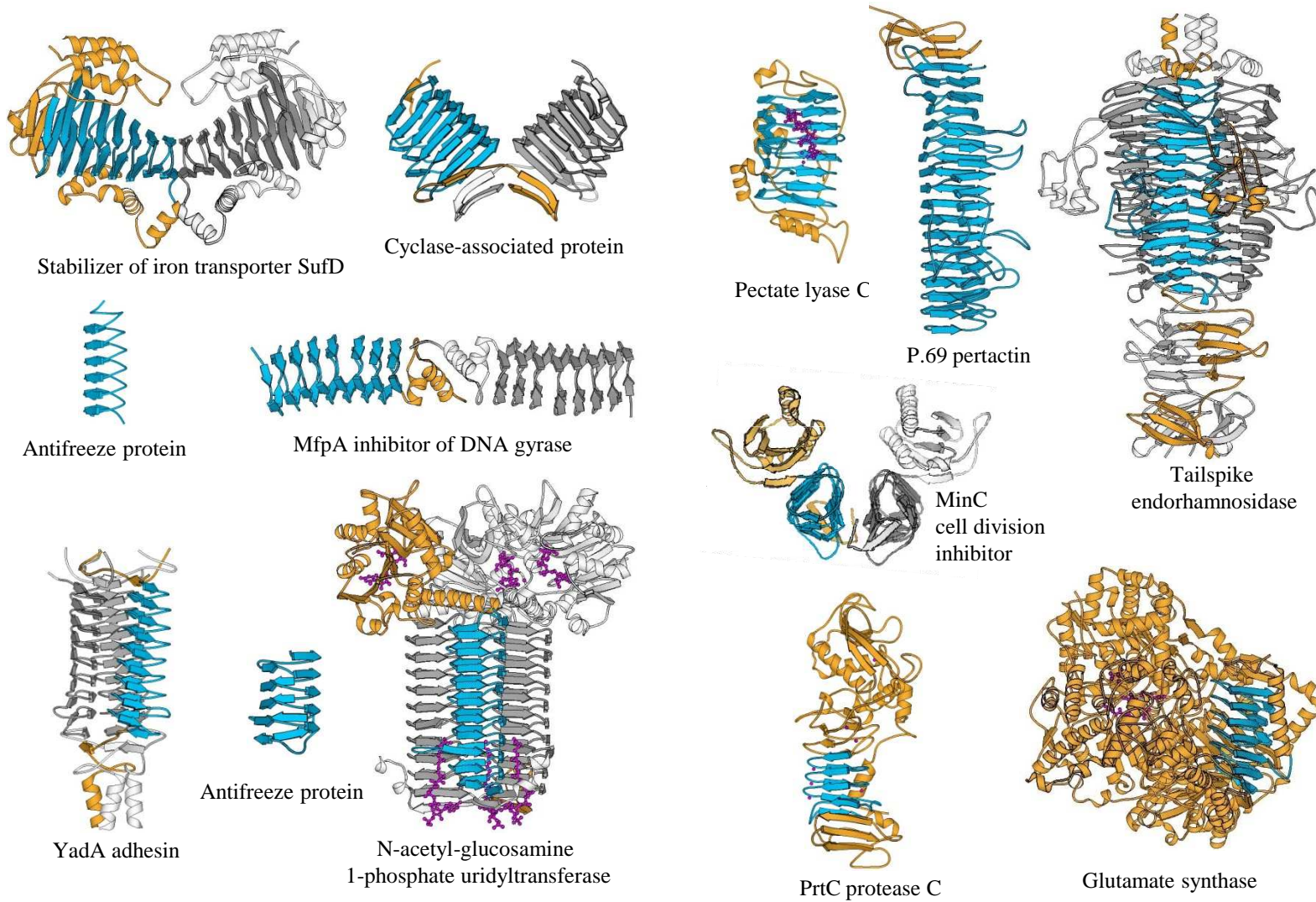


β -solenoids
(~50 structures of
non-homologous proteins)

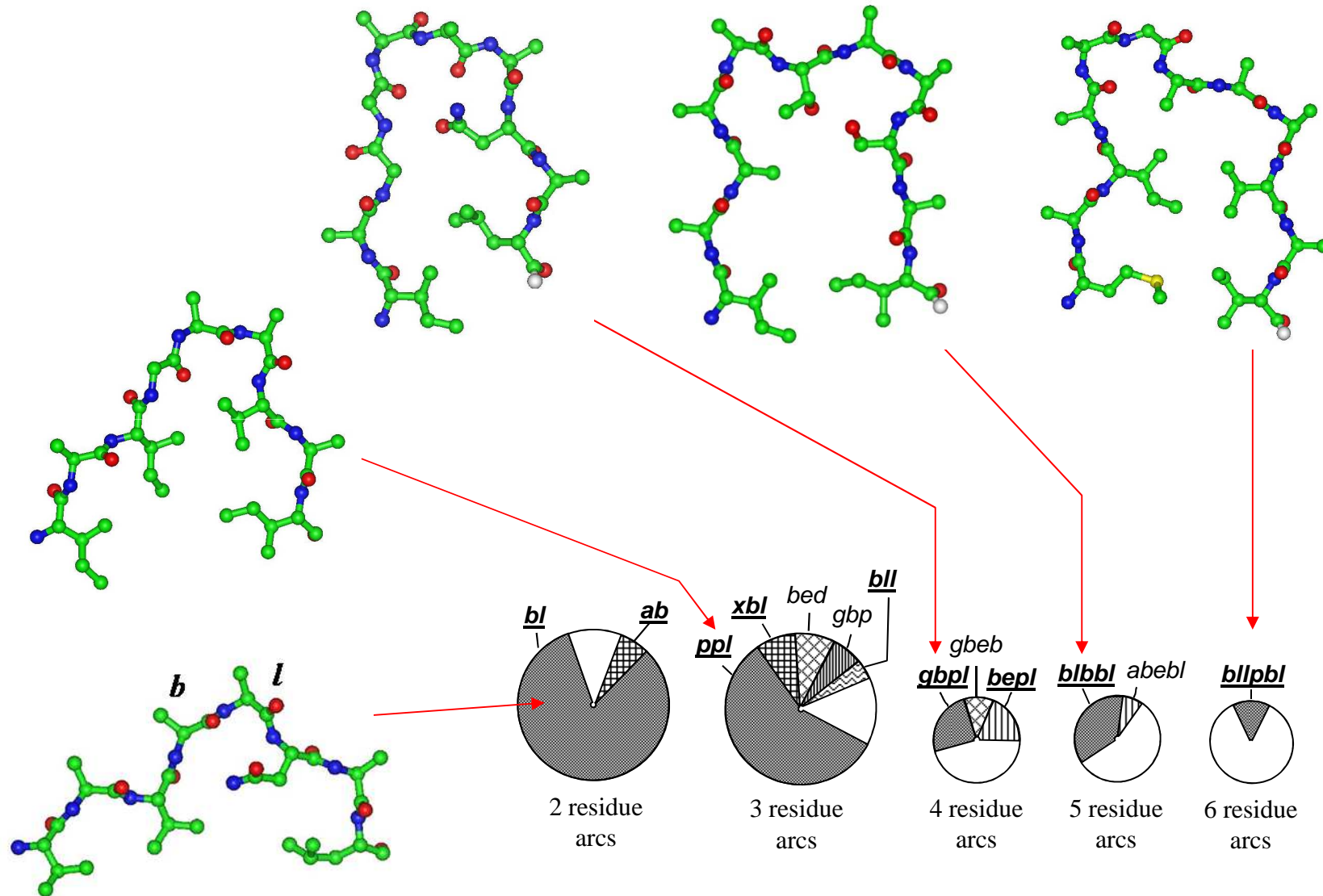


Kajava, Baxa and Steven (2009) *FASEB J* (in press)

Known β -solenoids

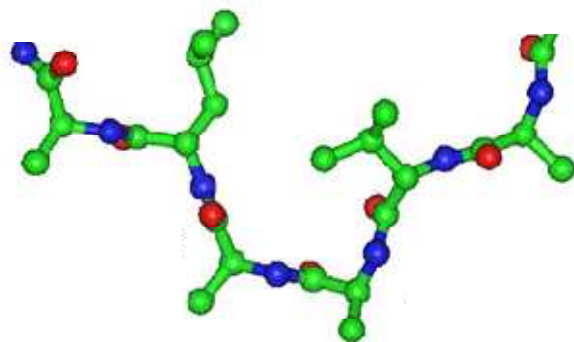


Standard conformations of β -arches

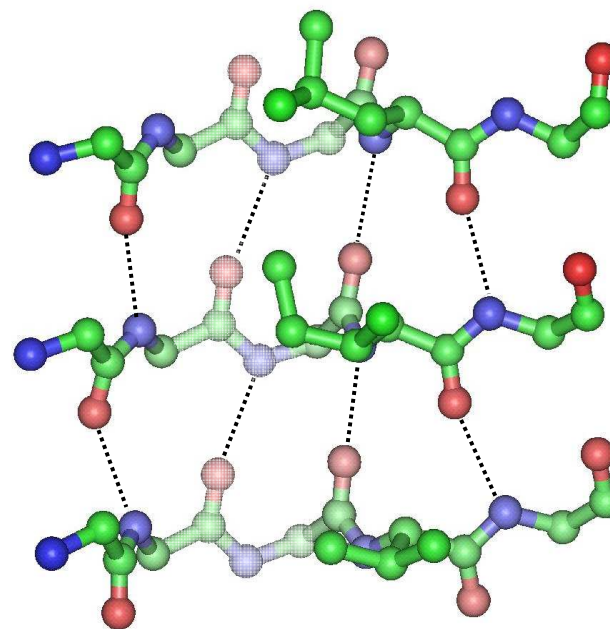


Standard conformations of beta-arches in beta-solenoid proteins
 Hennetin, Julien, Steven and Kajava (2006) J.Mol.Biol., 358, 1094

Standard conformations of β -arches

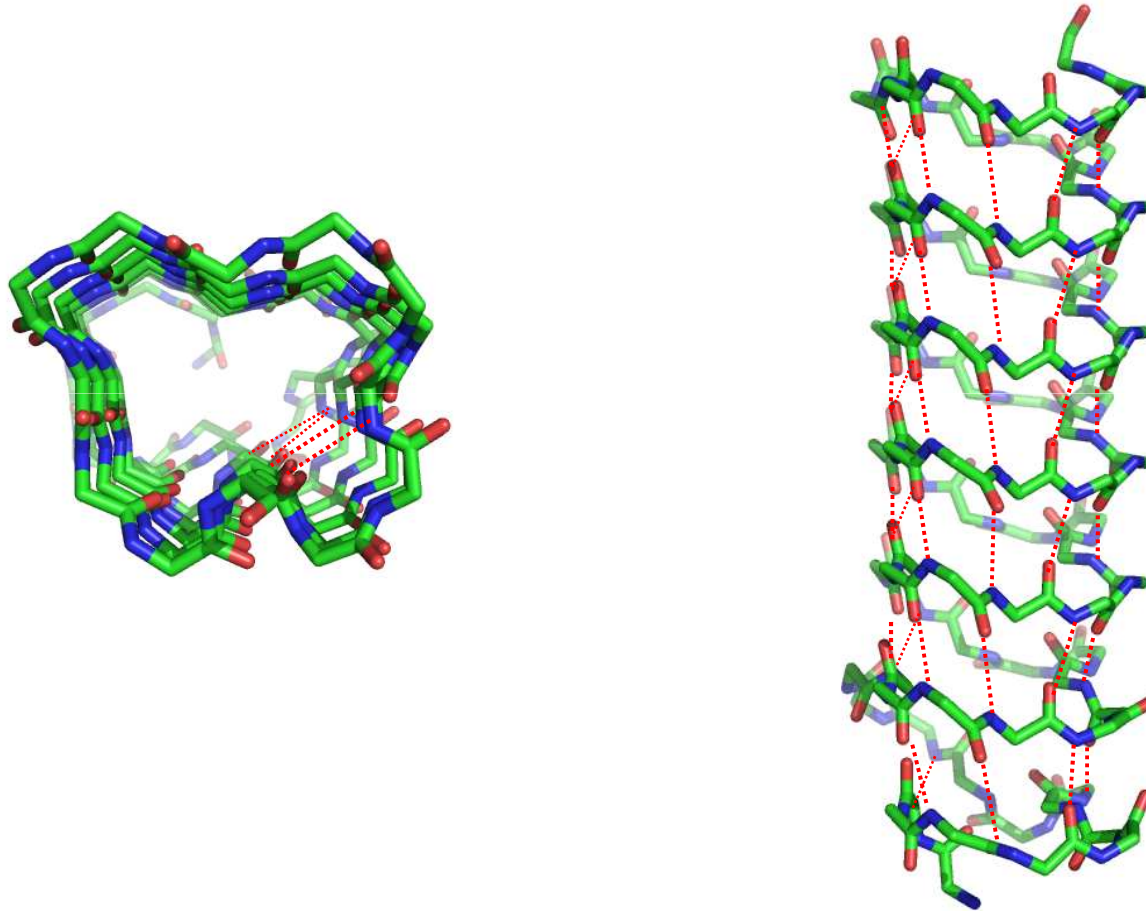


Axial projection
of beta-arch



Lateral projection of
beta-arch stack

CRYSTAL STRUCTURE OF ANTIFREEZE PROTEIN
FROM THE BEETLE, *TENEBRIO MOLITOR*

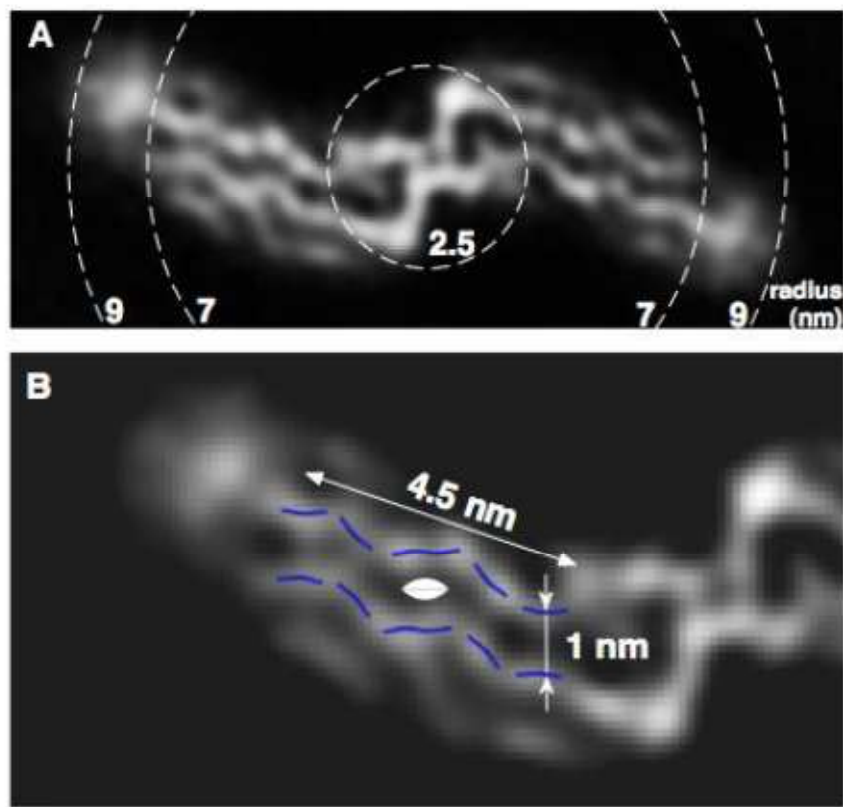


Liou, Y.C., Tocilj, A., Davies, P.L., Jia, Z. (2000) Nature **406**: 322-324

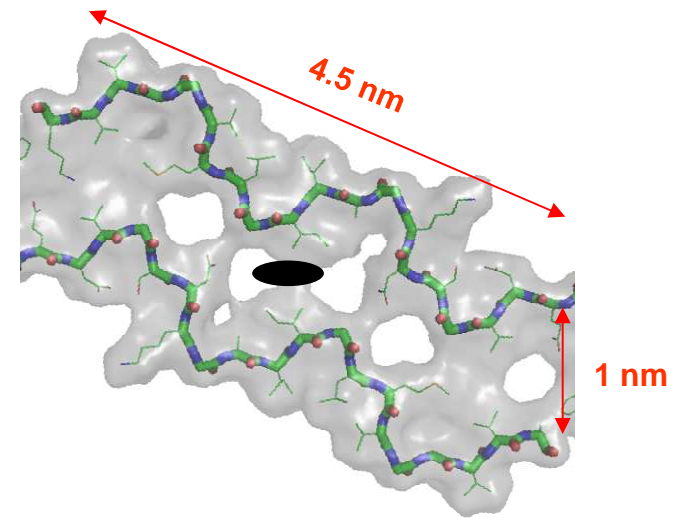
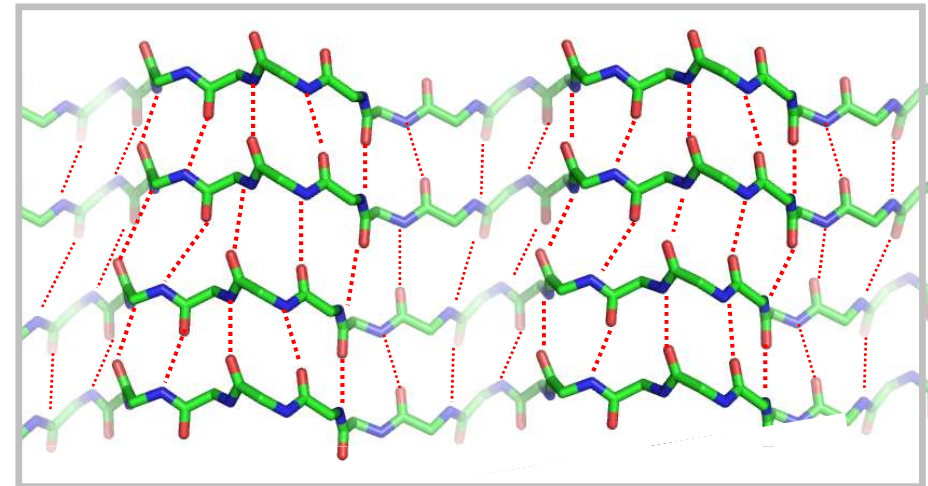
Corrugated paired beta-sheet

Paired beta-sheet structure of an A β (1-40) amyloid fibril revealed by electron microscopy.

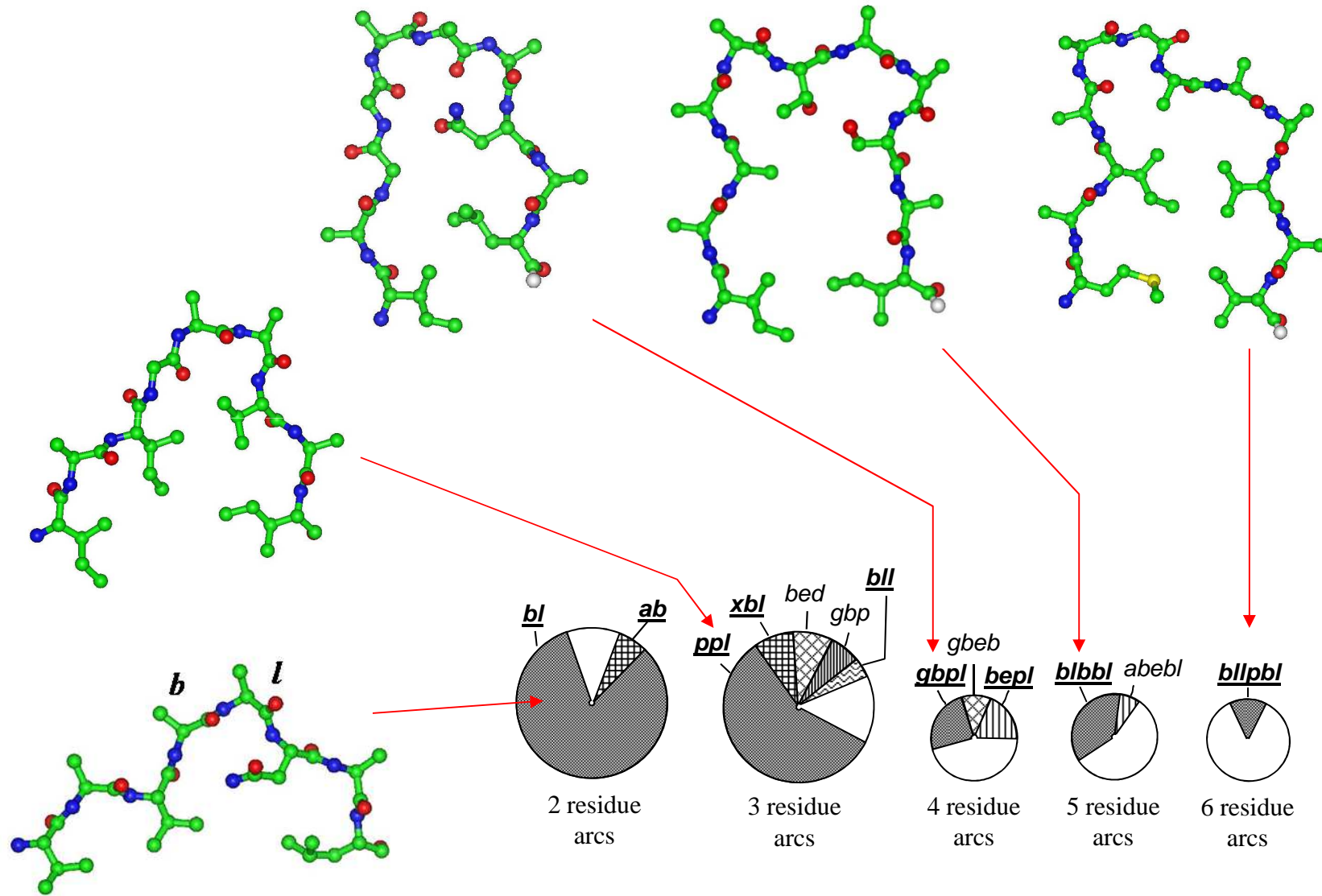
Sachse, Fändrich, Grigorieff, *PNAS*, 2008, 105:7462



Molecular model

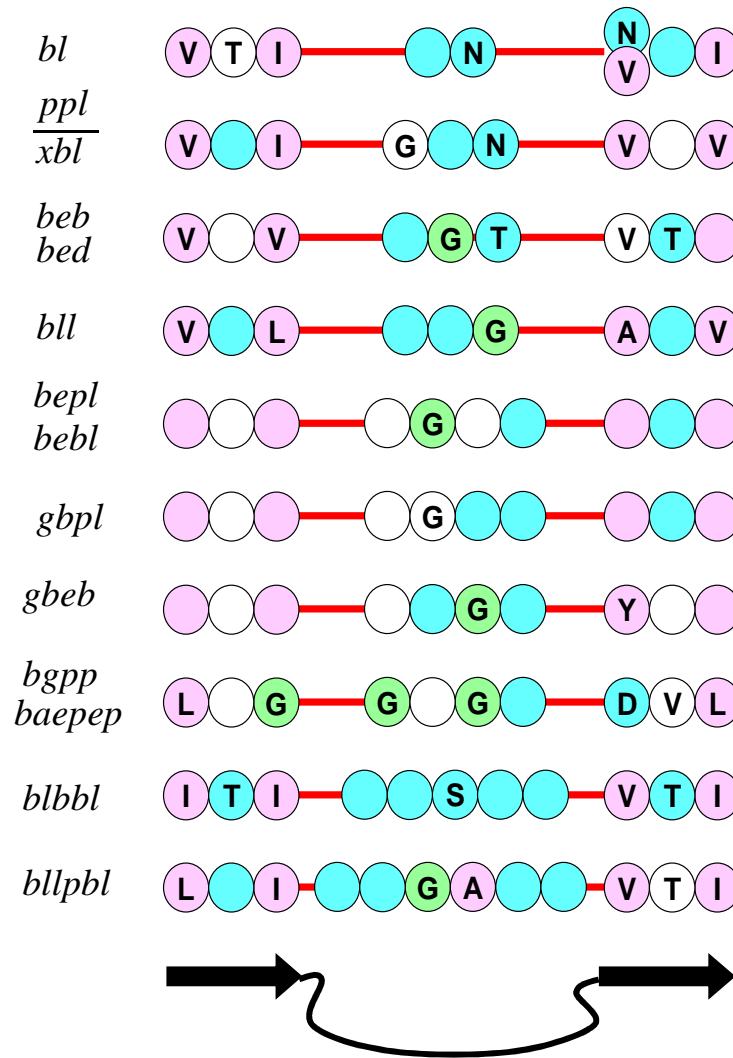


Standard conformations of β -arches

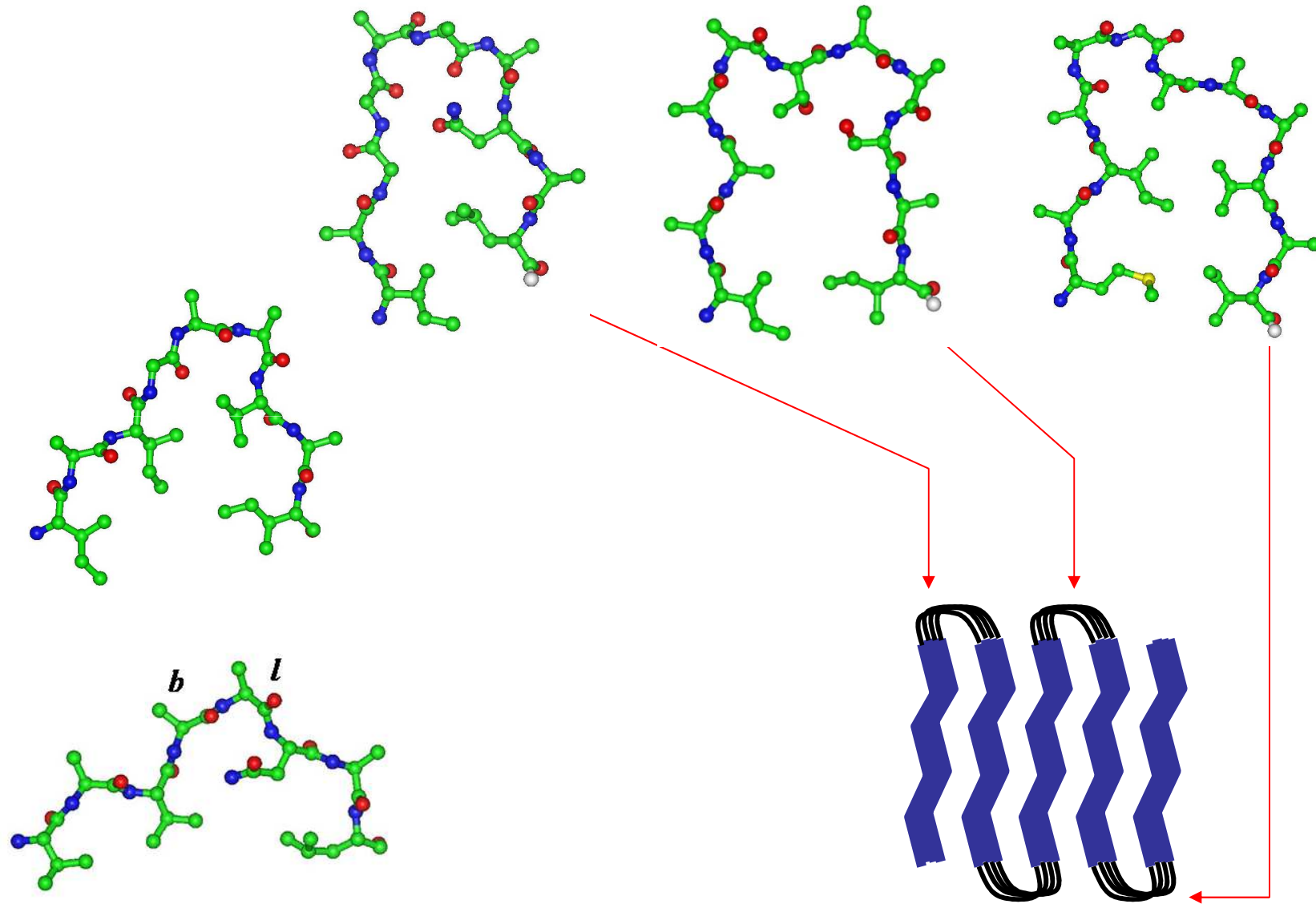


Standard conformations of beta-arches in beta-solenoid proteins
 Hennetin, Julien, Steven and Kajava (2006) J.Mol.Biol., 358, 1094

Standard conformations of β -arches



Prediction of amyloidogenicity of proteins



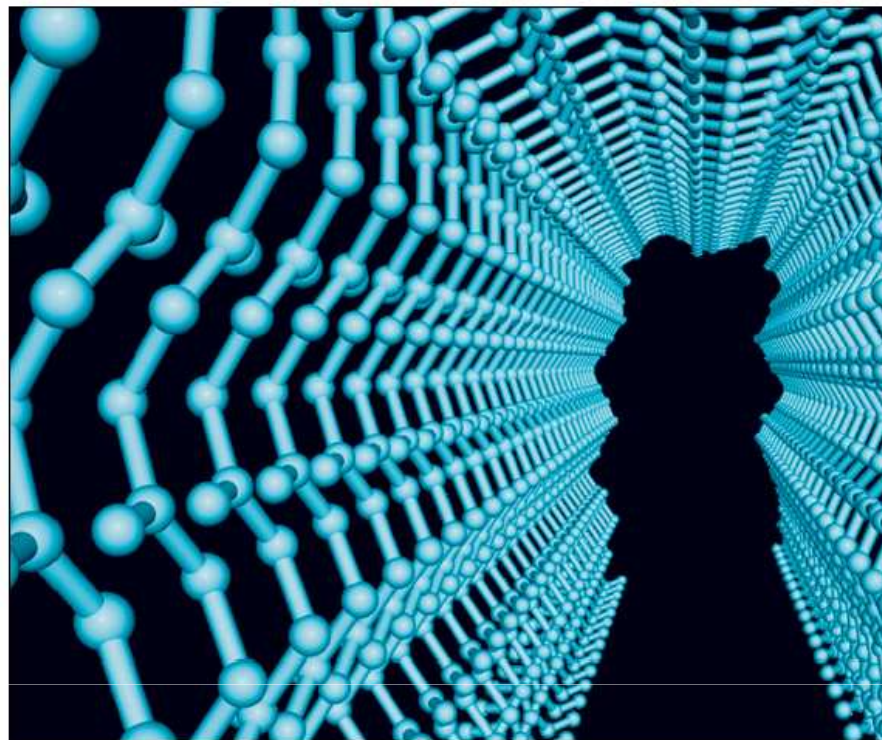
CONCLUSIONS

Stack of β -arches is a common arrangement of disease-related amyloid fibrils.

This can be explained by capacity of β -arch stacks

- (1) to be stabilized not only by apolar residues but also by polar residues,
- (2) to be the most efficient nuclei for amyloidogenesis

Known β -arcs have preferred conformations and sequence motifs. We identified them. This information can be used for prediction and modeling of amyloid fibrils.



ФИНИШ ПОД БЕЛКОВОЙ АРКАДОЙ?

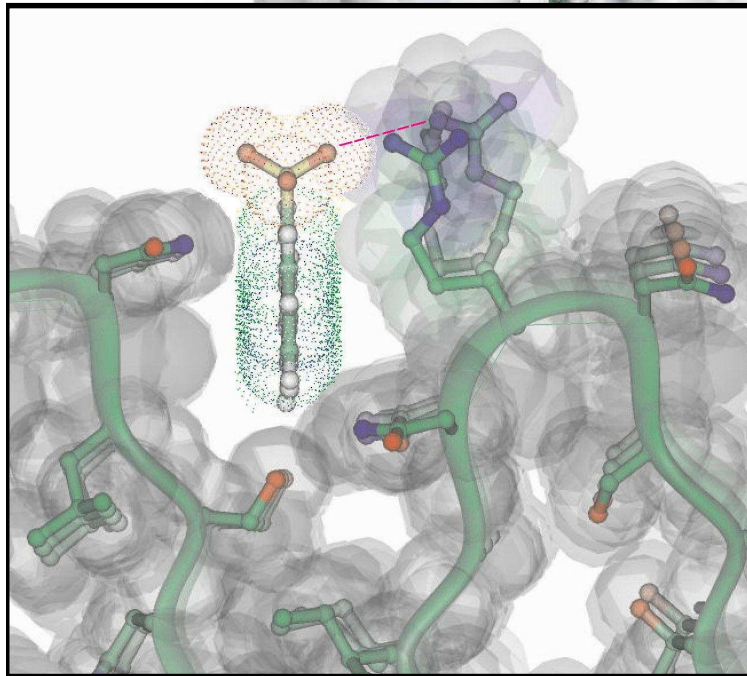
Человечество находится в постоянном поиске лекарств, медицинских технологий и рецептов образа жизни, которые бы позволили ему жить дольше. И успехи бесспорны: в течение последнего полувека средняя продолжительность жизни в экономически развитых странах возростала каждые пять лет на один год. Сегодня люди, живущие 80 лет и более, уже не редкость. Однако, чем дольше мы живём, тем отчётливей вырисовывается очередное серьёзное препятствие на нашем пути к дальнейшему увеличению продолжительности жизни. Это нейродегенеративные заболевания: болезни Альцгеймера, Паркинсона, синдром Хантингтона и другие, ведущие к старческому слабоумию. На сегодняшний день эти болезни неизлечимы и заканчиваются постепенным угасанием психических функций и неминуемой смертью. Рост случаев нейродегенеративных заболеваний по мере старения впечатляет. Среди доживших до семидесяти такими болезнями страдает не более чем каждый тридцатый, а среди девяностолетних это уже чуть ли не каждый третий.

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Молекулярные механизмы нейродегенеративных заболеваний до конца не выяснены и остаются объектом жарких дискуссий. Очевидно одно — мозговые ткани всех пациентов, страдающих такого рода бо-

лезнями, содержат нерастворимые отложения (белковые «бляшки»). Белки — основные молекулы живых организмов, представляющие собой цепочки из соединённых пептидными связями аминокислот. Существует 20

Potential impact of the results



More precise models



Structure-based design
of inhibitors of fibrillogenesis

Better prediction
of amyloidogenicity
of proteins



Patient-oriented risk prediction
to develop age-related,
neurodegenerative
and other diseases

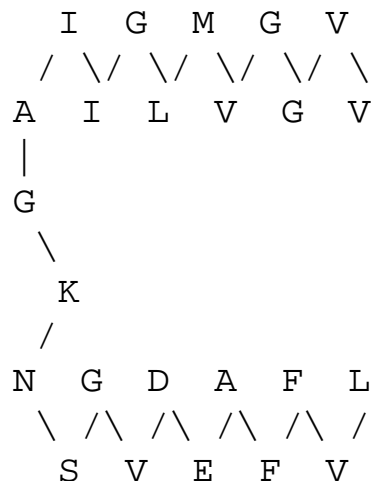
*Computer program for identification of
regions that can form beta-arcades
and prediction of their 3D structure*



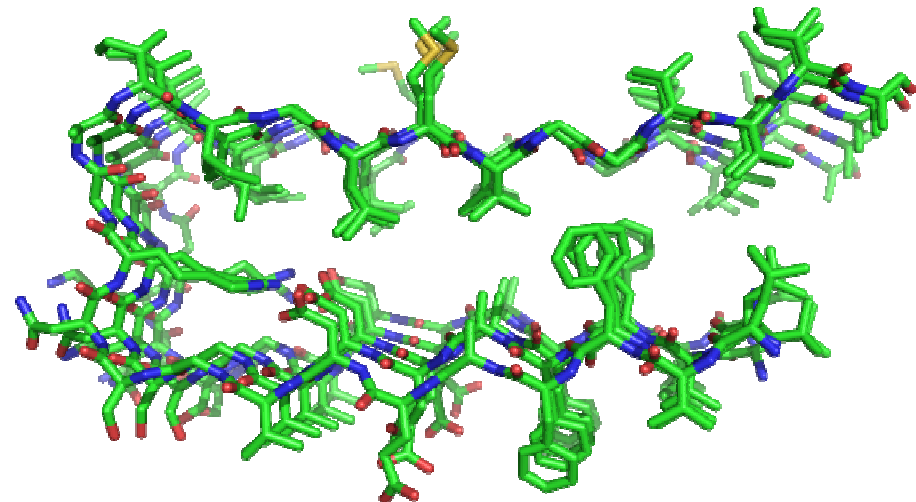
It correctly predicts 3D structures available in PDB : 2LMN, 2BEG, 2LQN -
different forms of Abeta, 2E8D - beta2-microglobulin, 2NNT Human CA150

and explains the increase of amyloidogenicity in Abeta mutants linked to FAD.

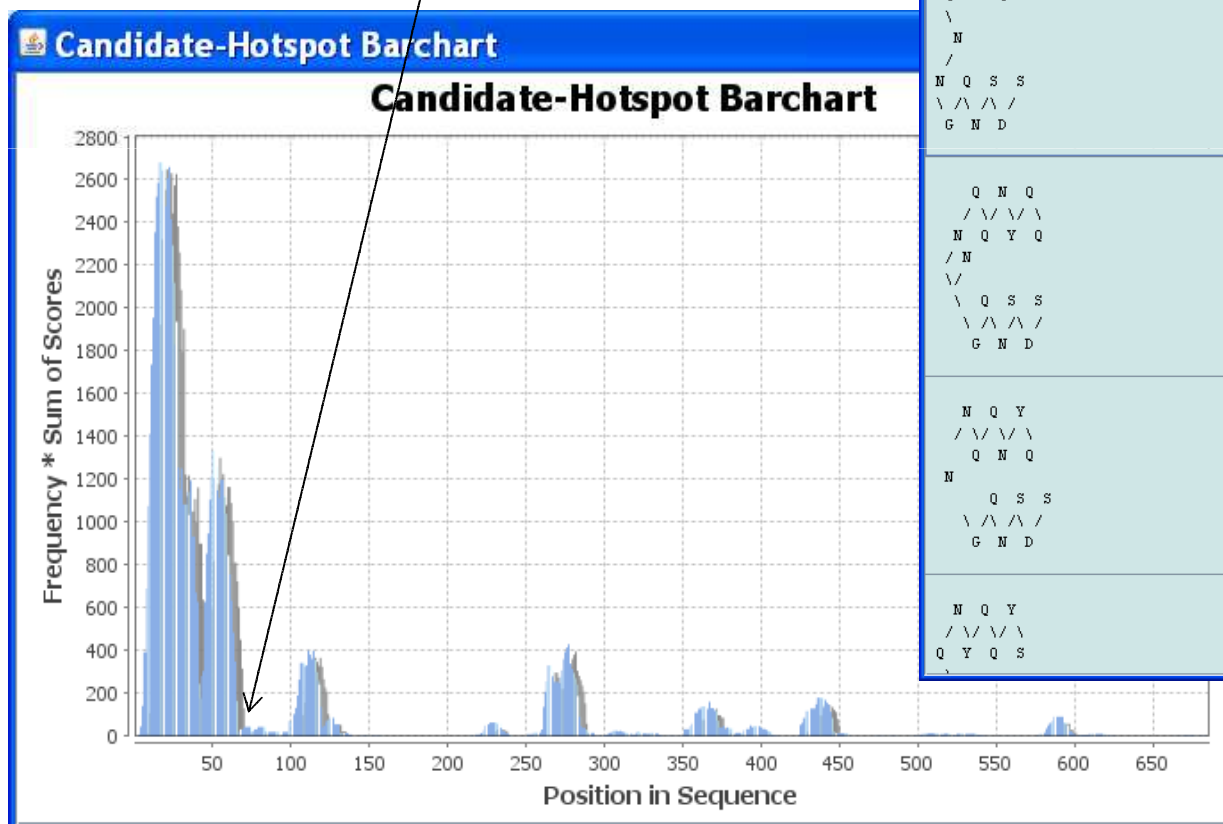
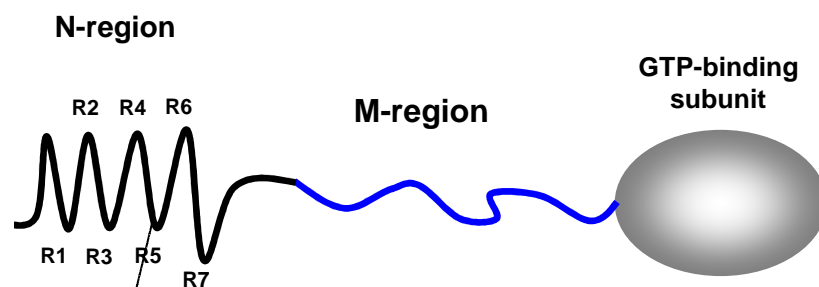
**Prediction of the 3D Structure
of Alzheimer's Abeta(1-42) fibrils**



**Known structure
PDB code 2BEG**



Sup35



| Table of Candidates | | | | | |
|--|--------|-------|--------------|----------|-----|
| Diagram | Number | Score | Conformation | Position | cUP |
| <pre> Q Y Q / \ / \ Q N Q Y \ N / N Q S S \ / \ / G N D </pre> | 01 | 0.366 | BLBBL | 02-17 | 0 |
| <pre> Q N Q / \ / \ N Q Y Q / N \ / \ Q S S \ / \ / G N D </pre> | 02 | 0.359 | GBPL | 02-16 | 0 |
| <pre> N Q Y / \ / \ Q N Q N Q S S \ / \ / G N D </pre> | 03 | 0.351 | PPL | 02-15 | 0 |
| <pre> N Q Y / \ / \ Q Y Q S \ </pre> | 04 | 0.264 | BLLPBL | 02-18 | 0 |

Ure2p

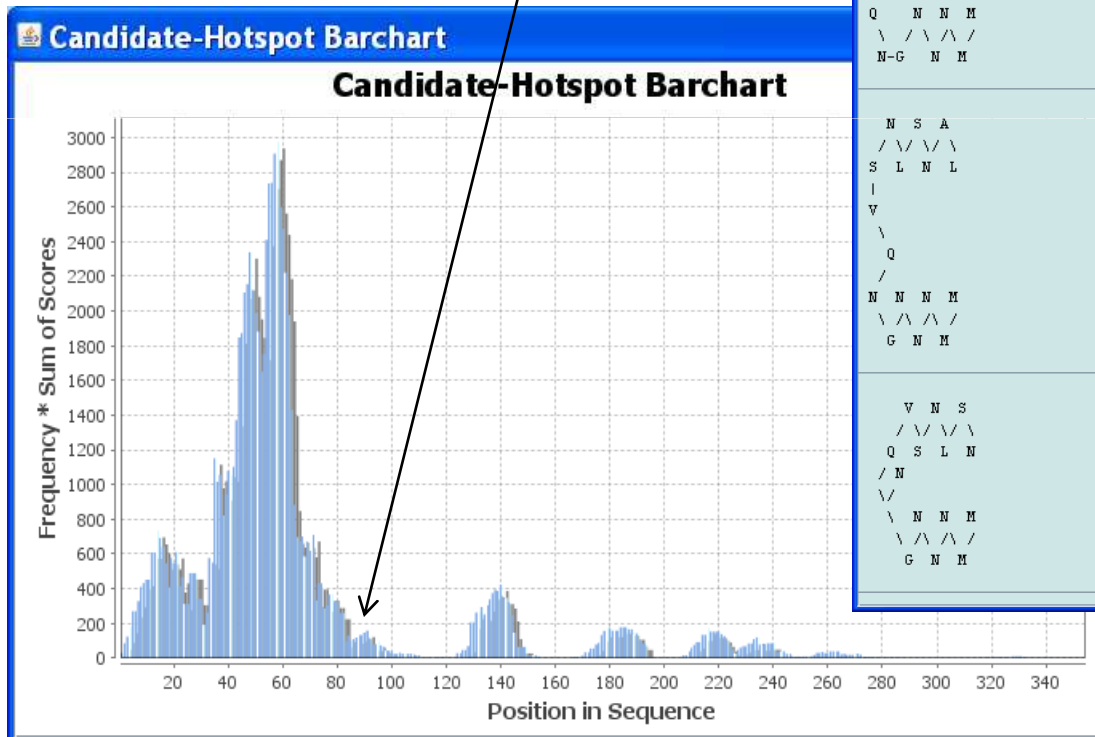
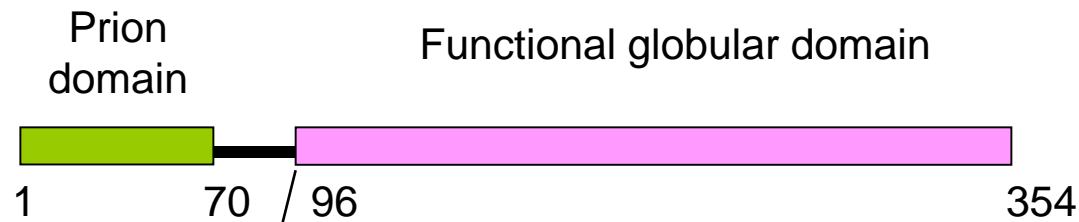


Table of Candidates

| Diagram | Number | Score | Conformation | Position | cUP | nUP |
|--|--------|-------|--------------|----------|-----|-----|
| <pre> N S A / \ / \ S L N L \ V / Q N N M \ / \ / N-G N M </pre> | 01 | 0.767 | BLLPBL | 01-17 | 0 | 0 |
| <pre> N S A / \ / \ S L N L V \ Q / M N N M \ / \ / G N M </pre> | 02 | 0.767 | BLPPPX | 01-17 | 0 | 0 |
| <pre> V N S / \ / \ Q S L N / M \ / \ N N M \ / \ / G N M </pre> | 03 | 0.724 | GBPL | 01-15 | 0 | 0 |

Where do beta-arcades lead?

Drug design?

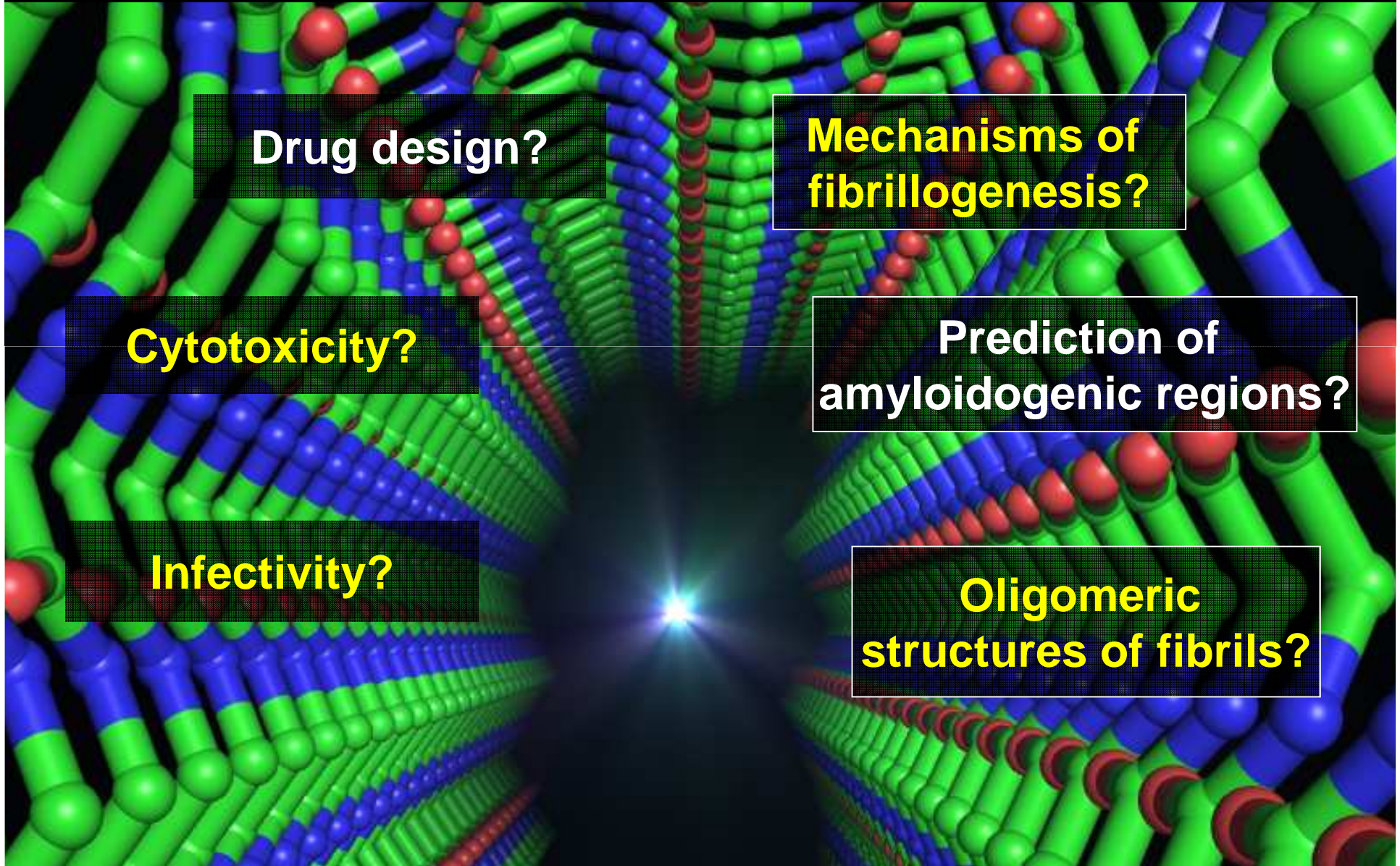
Mechanisms of
fibrillogenesis?

Cytotoxicity?

Prediction of
amyloidogenic regions?

Infectivity?

Oligomeric
structures of fibrils?





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