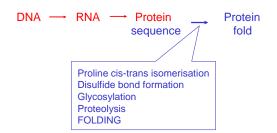


Lecture notes at

people.cryst.bbk.ac.uk/~ubcg16z/hsplec.html

Central Dogma



MOLECULAR CHAPERONES: Definition

A large group of unrelated protein families whose role is to stabilize unfolded proteins, unfold them for translocation across membranes or for degradation, and/ or to assist in their correct folding and assembly.

- Molecular chaperones interact with unfolded or partially folded protein subunits, e.g. nascent chains emerging from the ribosome, or extended chains being translocated across subcellular membranes.
- They stabilize non-native conformation and facilitate correct folding of protein subunits.
- They do not interact with native proteins, nor do they form part of the
- Some chaperones are non-specific, and interact with a wide variety of the specific tarriets. polypeptide chains, but others are restricted to specific targets.
- They often couple ATP binding/hydrolysis to the folding process.
- They often couple ATP binding/nydroiysis to the rouning p.
 Essential for viability, their expression is often increased by cellular

Main role: They prevent inappropriate association or aggregation of exposed hydrophobic surfaces and direct their substrates into productive folding, transport or degradation pathways.

Examples of molecular chaperones

Heat shock proteins: hsp104, 90, 70, 60 and small hsps, including homologues of lens α -crystallin.

Catalysts of folding: Protein disulfide isomerase, Peptidyl prolyl cis-trans isomerase

Nucleoplasmin: nucleosome assembly

Prosequences: subtilisin, α -lytic protease (intramolecular

chaperones)

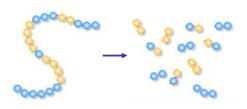


Unfolded or misfolded proteins

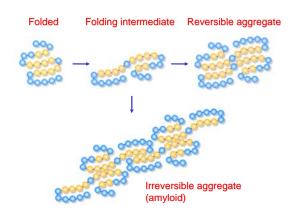
Aggregation-prone Protease-sensitive Bind chaperones Non functional



Globular soluble protein Stable and soluble Protease resistant No chaperone binding Functional



Unfolded protein chains are prone to proteolysis



FAMILIES OF MOLECULAR CHAPERONES

Small heat shock proteins (hsp25) [holders]

•protect against cellular stress •prevent aggregation in the lens (cataract) Hsp60 system (cpn60, GroEL) ATPase [(un)folders]

•protein folding

Hsp70 system (DnaK, BiP) ATPase [(un)folders]

•stabilization of extended chains •membrane translocation

•regulation of the heat shock response

Hsp90 [holder]

•binding and stabilization/regulation of steroid receptors, protein kinases

•Buffer for genetic variation? Hsp100 (Clp) ATPase [unfolder]

•thermotolerance, proteolysis, resolubilization of aggregates

Calnexin, calreticulin

•glycoprotein maturation in the ER

•quality control
Folding catalysts: PDI, PPI [folders]

Prosequences: alpha-lytic protease, subtilisin (intramolecular chaperones)

Molecular chaperones



ER chaperones

Disulfide, prolyl isomerases;

oligosaccharide processing

Small heat shock proteins Sponges for denatured protein



Hsp70 Folding/unfolding Translocation/ disaggregation



folding/refolding

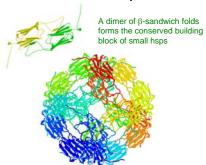


Hsp90 Stabilize steroid receptors/kinases; Buffer genetic variation?



Hsp100 Clp ATPases Unfolding/ disaggregation

Small heat shock proteins

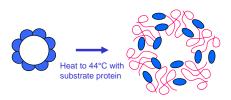


Crystal structure of sHsp from Methanococcus jannaschi (Kim et al, 1998)

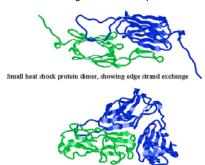
Small Hsp function

- Superfamily includes the eye lens protein α -crystallin
- Protective role in suppressing protein aggregation in vivo and in vitro
- Bind and stabilise denatured protein under conditions of cellular stress, ageing and degenerative disease
- · Do not appear to have unfolding and refolding activity
- High capacity for protein binding: up to 2 denatured proteins per subunit

Formation of substrate complexes



Immunoglobulin fold chaperones



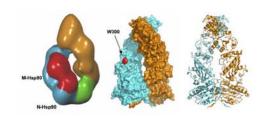
Chaperone papD (blue) complexed with papK (green), subunit of the bacterial pilus, showing edge strand donation. In the assembled pilus, each papK subunit donates an edge strand to its neighbour.

HSP70 FAMILY

Location	Chaperone	Roles
Prokaryotic cytosol	DnaK cofactors DnaJ, GrpE	Stabilizes newly synthesised polypeptides and preserves folding competence; reactivates heat-denatured proteins; contro heat-shock response
Eukaryotic cytosol	SSA1, SSB1(yeast) Hsc/hsp70, hsp40 (mammalian)	Protein transport across organelle membranes; binds nascent polypeptides; dissociates clathrin from coated vesicles; promotes lysosomal degradation of cytosoli proteins
ER	KAR2, BiP/Grp78	Protein translocation into ER
Mitochondria/ Chloroplasts	SSC1 ctHsp70	Protein translocation into mitochondria; Insertion of light-harvesting complex into thylakoid membrane

Bound peptide Substrate-binding domain Both domains, Jiang et al, 2005

Asymmetric complex of Hsp90 dimer, cofactor and substrate protein



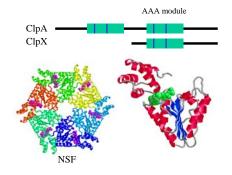
Hsp90-cdc37-cdk4 (kinase) Vaughan et al, 2006

Hsp90 dimer Ali et al, 2006

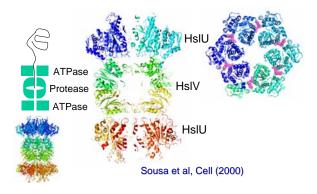
AAA Proteins

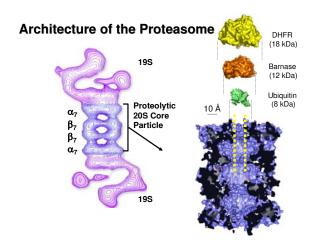
- A large and diverse family of ATPases associated with unfolding, unwinding, assembly and disassembly of protein and nucleic acid complexes (ATPases Associated with various cellular Activities)
- Includes the Hsp100/Clp family of chaperones/ proteases, components in DNA replication, recombination and restriction, the NSF protein in vesicle fusion, dynein motor proteins and many others
- Hsp100 proteins can totally unfold their substrate proteins, in order to deliver them to associated proteases, or they can dissolve large aggregates, in cooperation with the Hsp70 system

AAA ATPases



Hsp100 chaperone-protease complexes





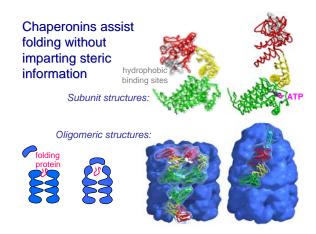
CHAPERONINS

Group I

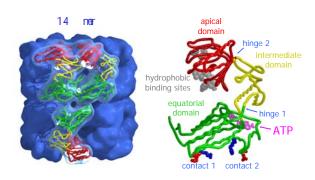
- GroEL/Hsp60 14 x 60 kD subunits
- GroES/Hsp10 7 x 10 kD subunits
- found in eubacteria, mitochondria, chloroplasts
- very abundant and non-specific, will interact with most non-native proteins

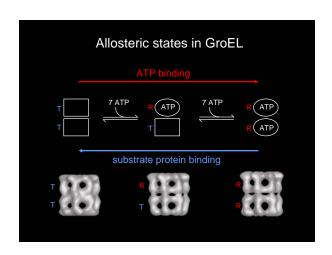
Group II

- 16 or 18 x 55 kD subunits
- TF55 & thermosome in archaea
- TCP-1 in eukaryotic cytosol, >8 related gene products
- TCP-1 not very abundant, folds actin, tubulin, transducin, WD-40 domain proteins

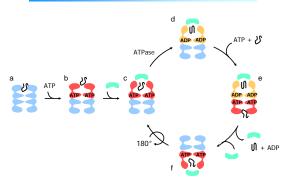


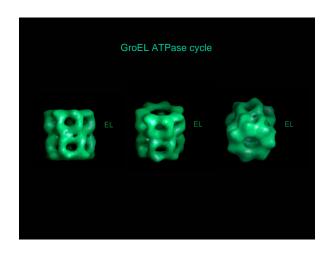
E. coli GroEL



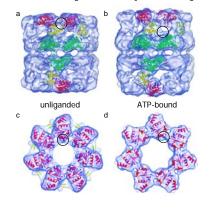


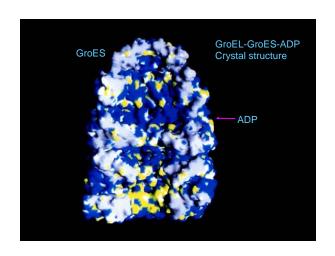
The chaperonin functional cycle



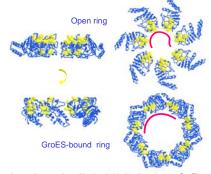


Conformational changes induced by ATP binding to GroEL

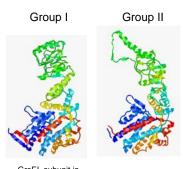




Apical domain movements in GroEL



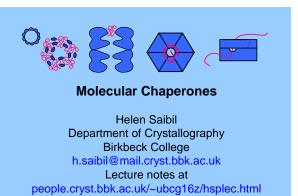
Rotation and separation of hydrophobic binding sites on GroEL could unfold a substrate protein bound to several sites (Shtilerman et al, 1999).



GroEL subunit in GroES-bound conformation

Thermosome subunit in closed conformation

GroEL QDES Thermosome
Group I Group II (conformation with both ends closed)



Molecular Chaperones: References

Reviews

Hartl, FU (1996) Molecular chaperones in cellular protein folding. Nature 381, 571-580.

Bukau & Horwich (1998) The Hsp70 and Hsp60 chaperone machines. Cell 92, 351-366.

Sigler, PB, Xu, Z, Rye, H, Burston, SG, Fenton, WA & Horwich, AL (1998) Structure and function in GroEL-mediated protein folding. Ann. Rev. Biochem. 67, 581-608.

Saibil, H. (2000) Molecular chaperones: containers and surfaces for folding, stabilising or unfolding proteins. Current Opinion in Struct. Biol. 10, 251-258.

Saibil, H & Ranson, N. (2002) The chaperonin molecular machine, Trends in Biochem. Sci. 27, 627-632 .

Bukau, B, Weissman, J, Horwich A (2006) Molecular chaperones and protein quality control. Cell 125, 443-451.

Research papers & additional references on lecture notes web site: people.cryst.bbk.ac.uk/~ubcg16z/hsplec.html