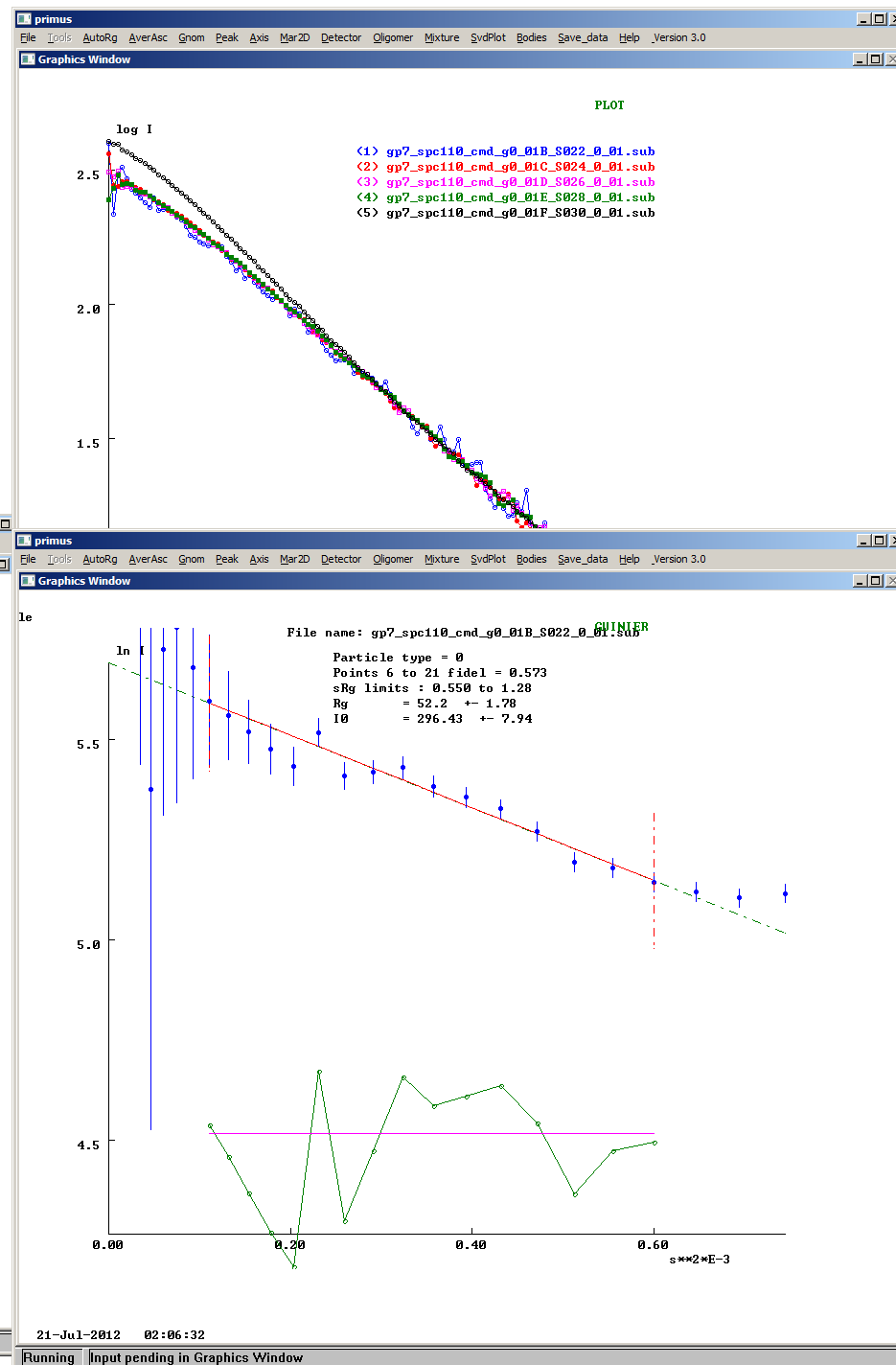
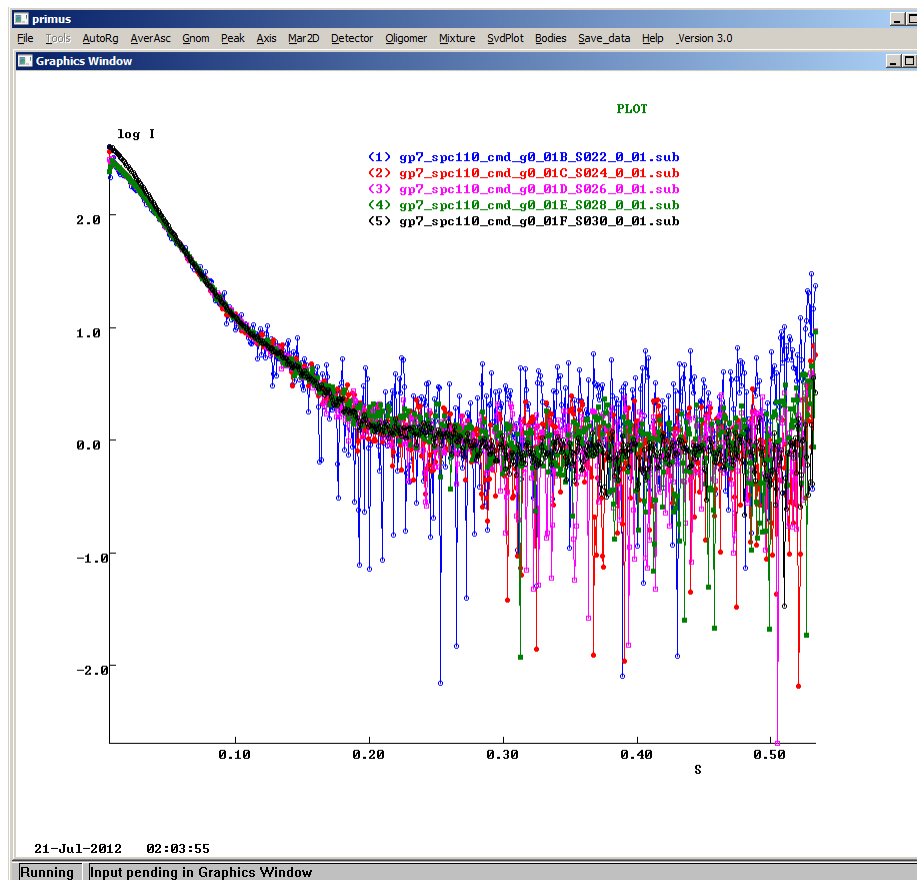
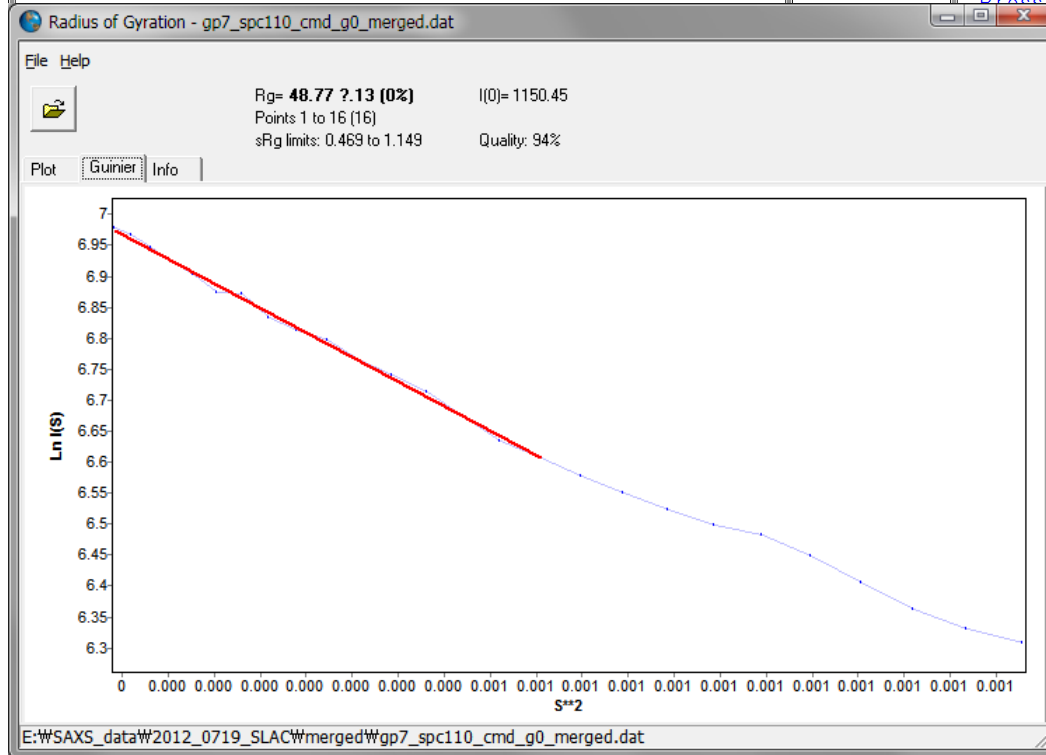
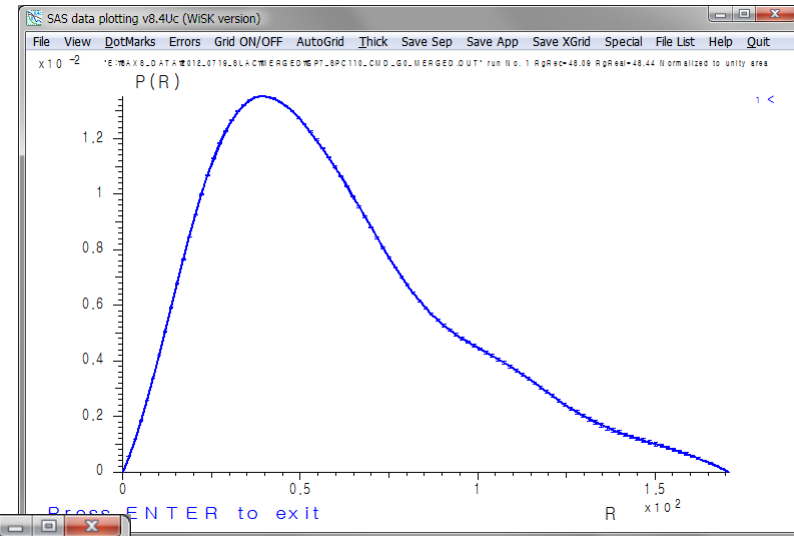
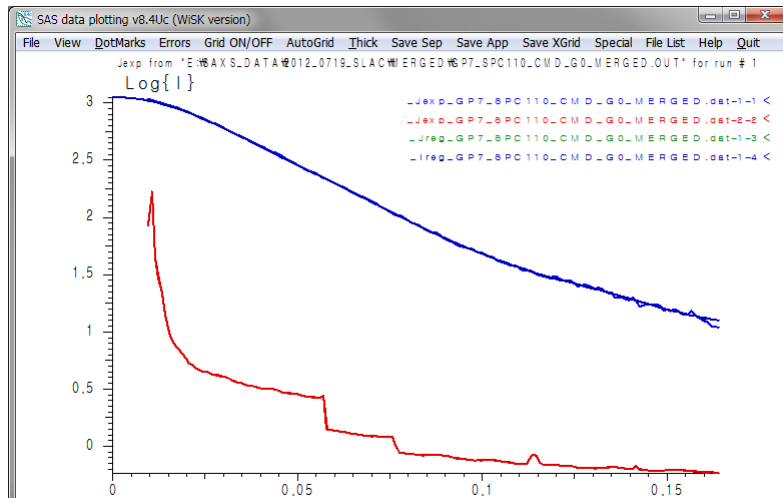


## 2012/07/19 raw SAXS Results

- 0% glycerol (No significant dependence on glycerol)
- concentrations of 0.5, 1.0, 1.5, 2.0, 5 mg/ml



- merged SAXS data from multiple concentrations



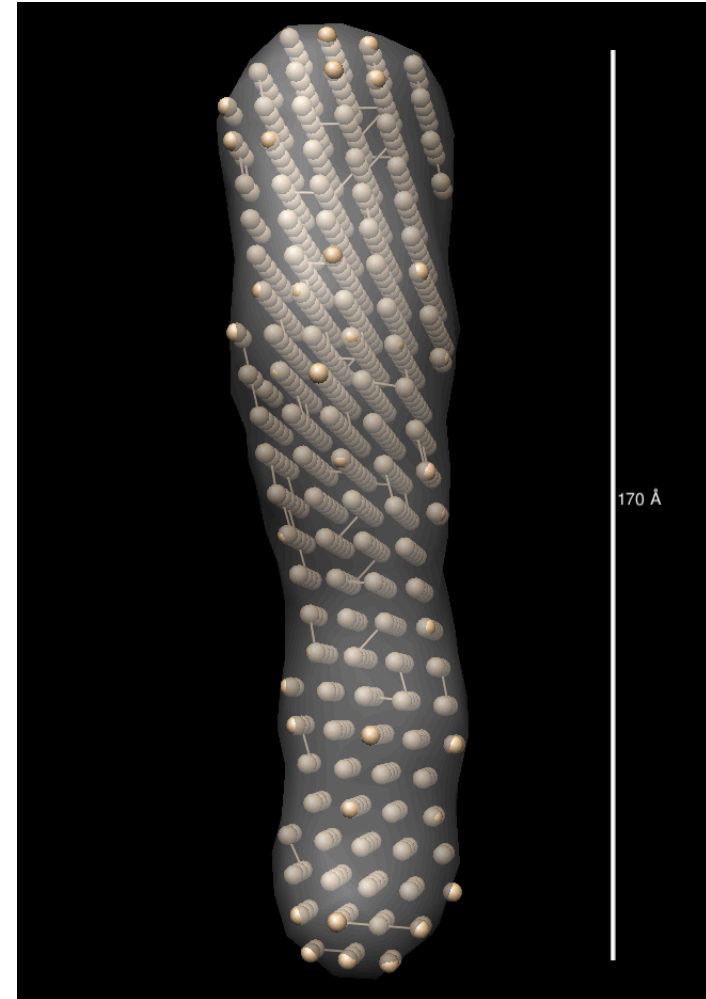
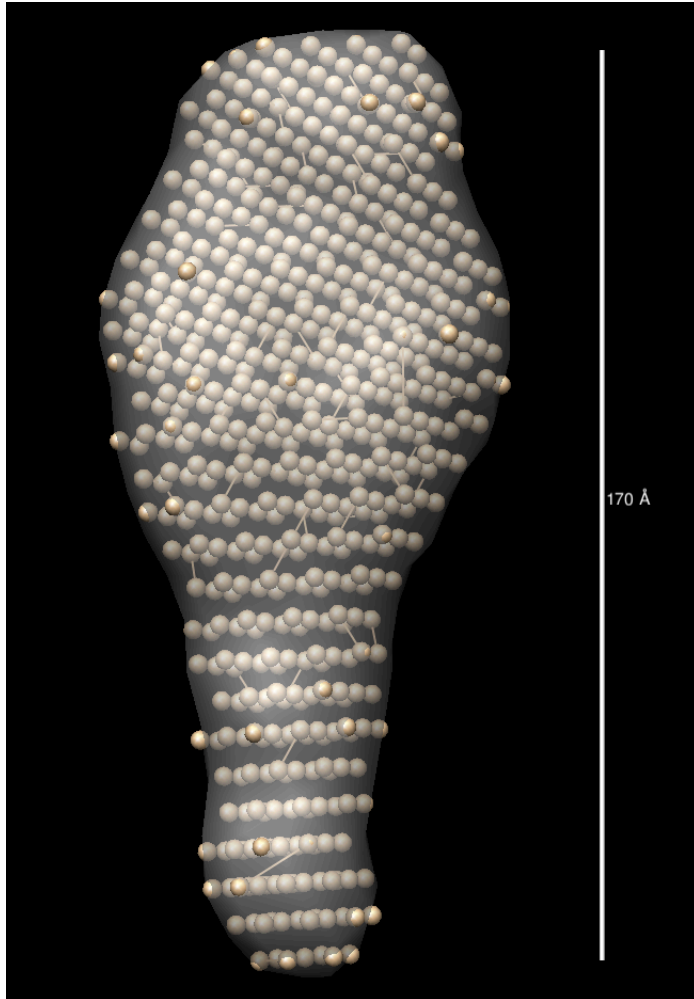
D\_max = 170 Angstrom

Radius of Gyration = 48.77 Angstrom

## 2012/07/19 SAXS Results

- Ab initio shapes generated from merged SAXS data

- the “Beads model” and its density map (no symmetry applied)



D\_max = 170 Angstrom  
Radius of Gyration = 48.77 Angstrom

## Gp7 – Spc110 (778-944) – Cmd1

Blue: Gp7

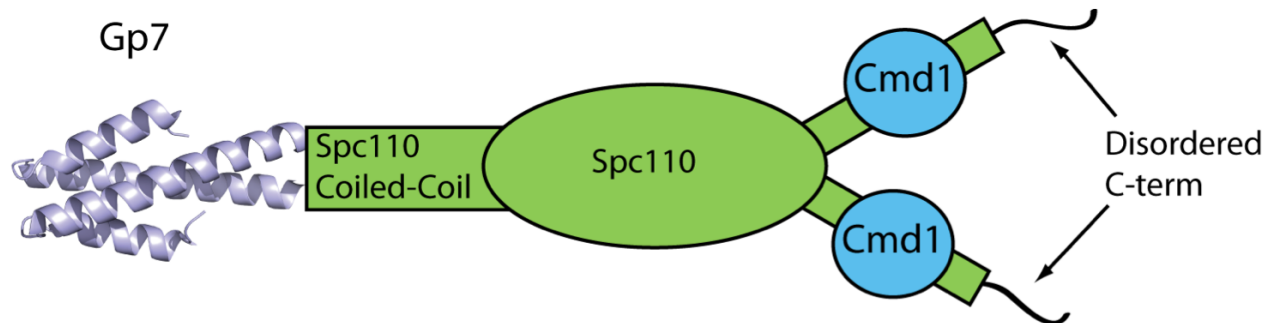
Green: Spc110

Coiled-coil is underlined

Cmd1 binding site in bold

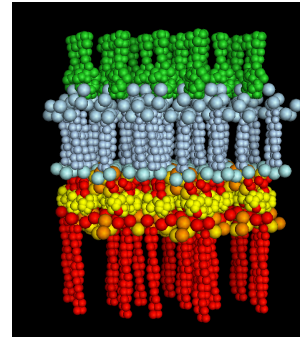
GGSGPLKPEEHEDILNKLLDPELAQSERTEALQQLRVNYGSFVSEYNDLQEENRRLEERLI  
LNERRKDNDSTMQLNDIISYYKLKYHSEVRHNNDLKVINDYLNKVLALGTRRLRLDTRKG  
EHSLNISLPDDDELDRDYNSHVYTRYHDYEPYPLRFNLNRRGPYFERRLSFKT**VALLVLA**  
**CVRMKRIA****FYRRSDDNRLRLRDRIESS**SGRISW

Here is a cartoon of how we think Gp7-Spc110 is structured:



The known structure of Gp7 combined with the structural information we have on the C-terminus of Spc110 should allow us to determine the overall shape of the central Spc110 domain.

Modeling of Spc110 (679-944) – Cmd1  
in the context of CP and IL2 from FRET,  
Cryo-EM, tomography and yeast two-hybrid  
data.



1. **RED blobs** – SPC 110 model (dimeric units)

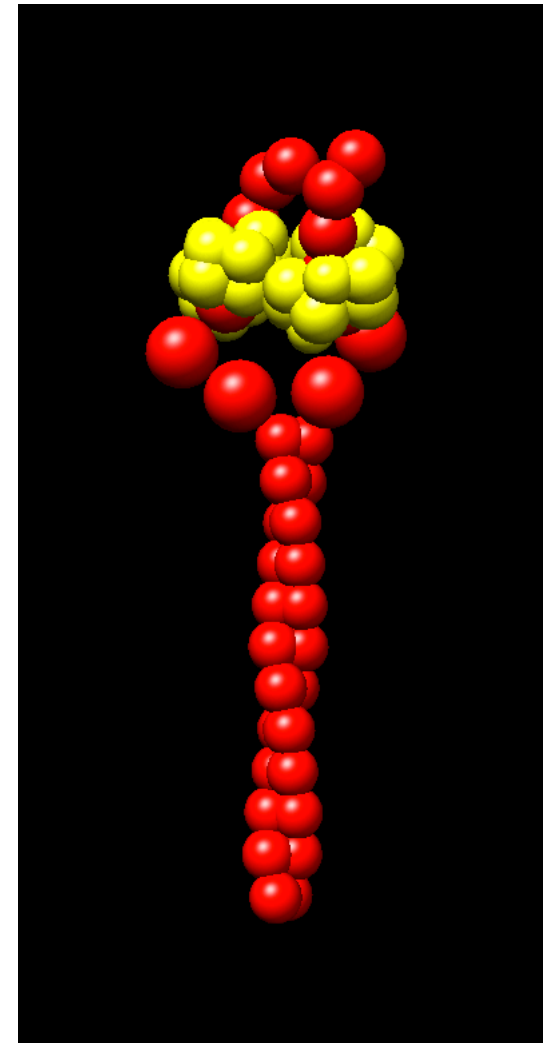
Small RED blobs (679-798, bottom) : 10 residues per unit  
- coiled / coiled region

Big RED blobs (799-895): 50 residues per unit  
- structured region, but we don't know the details

Small RED blobs (896-944, top): 10 residues per unit

2. **YELLOW blobs**

calmodulin : 10 residues per unit  
bound to SPC 110 structured region



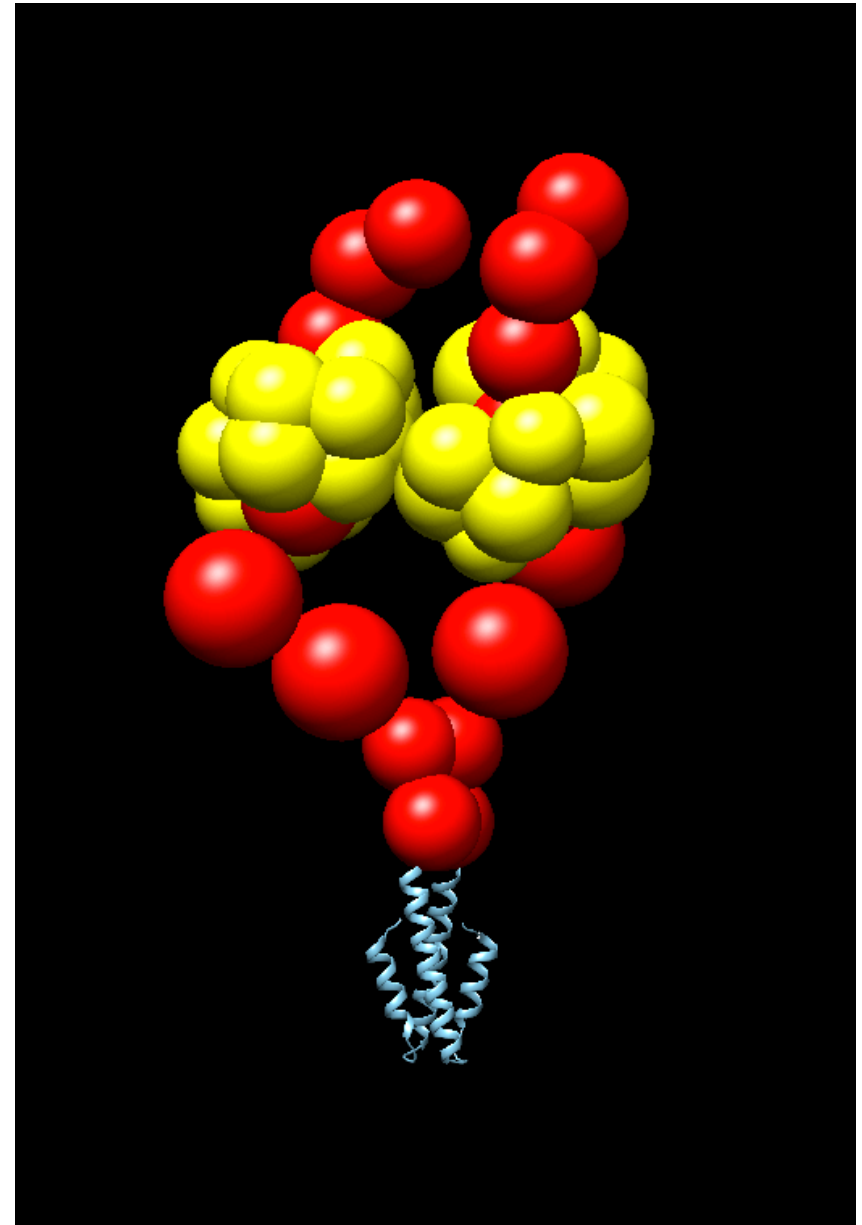
Homology model of one calmodulin bound to Spc110 from 4DS7  
dimeric structure.

## Modeling of GP7 - Spc110 (778-944) - Cmd1

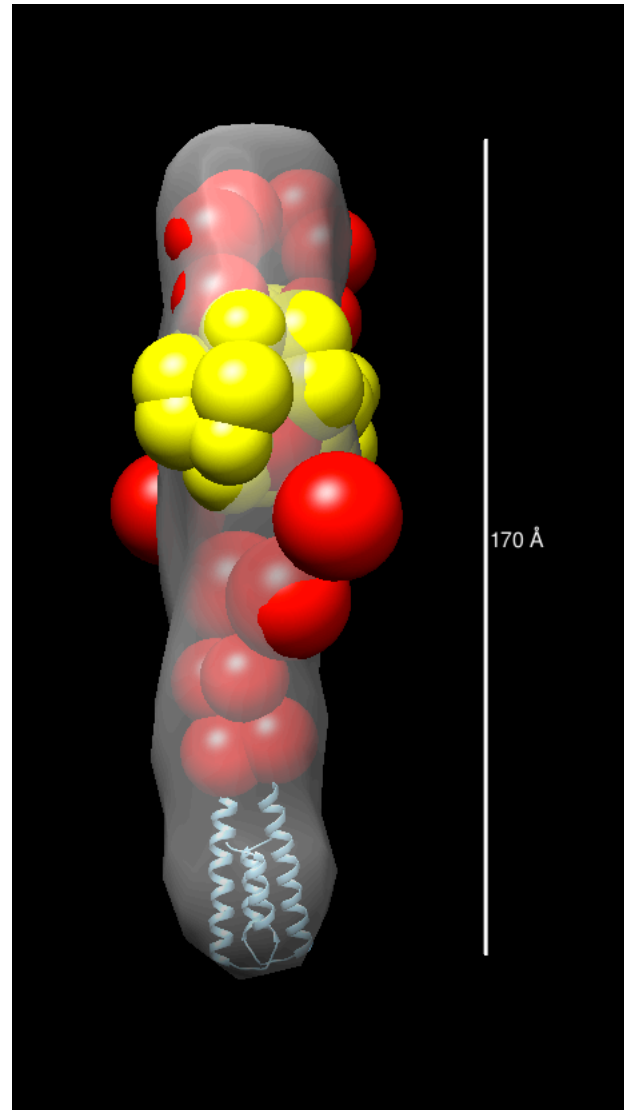
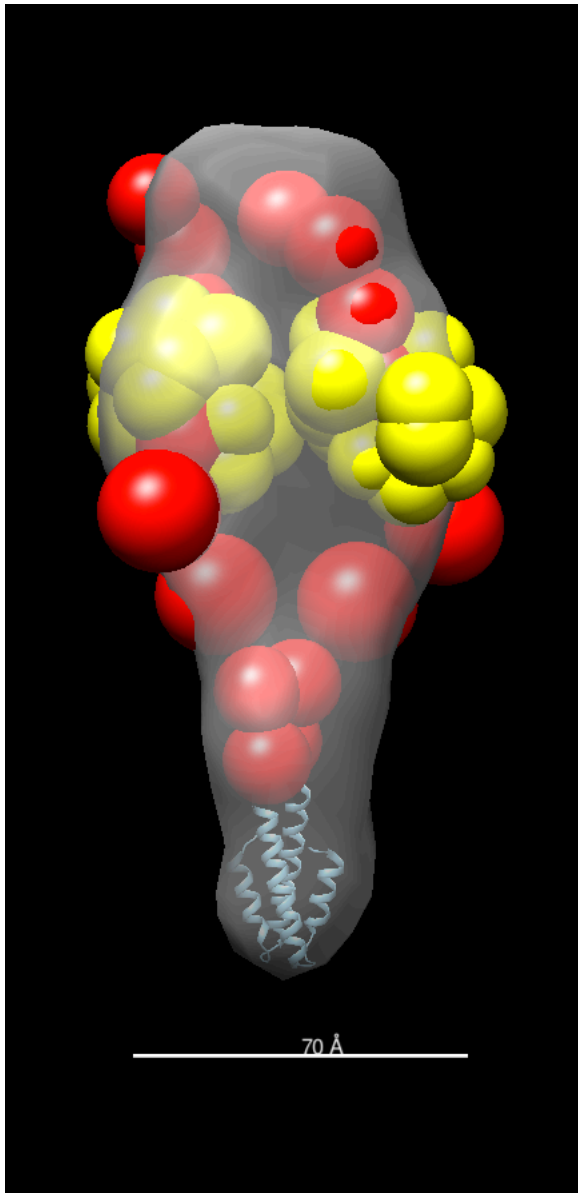
GP7 – used PDB 1NO4 (residue 1 – 46), CYAN

Spc110 (778-944), from IMP model on the previous page, RED

Cmd1 - from IMP model on the previous page  
YELLOW



## Modeling of GP7 - Spc110 (778-944) - Cmd1, with SAXS ab initio shape (envelope)



GP7 – used PDB 1NO4  
(residue 1 – 46), **CYAN**

Spc110 (778-944), from  
IMP model on the  
previous page, **RED**

Cmd1 - from IMP model on  
the previous page, **YELLOW**

GRAY envelope –  
overlapped SAXS Ab initio  
shape, **GRAY**