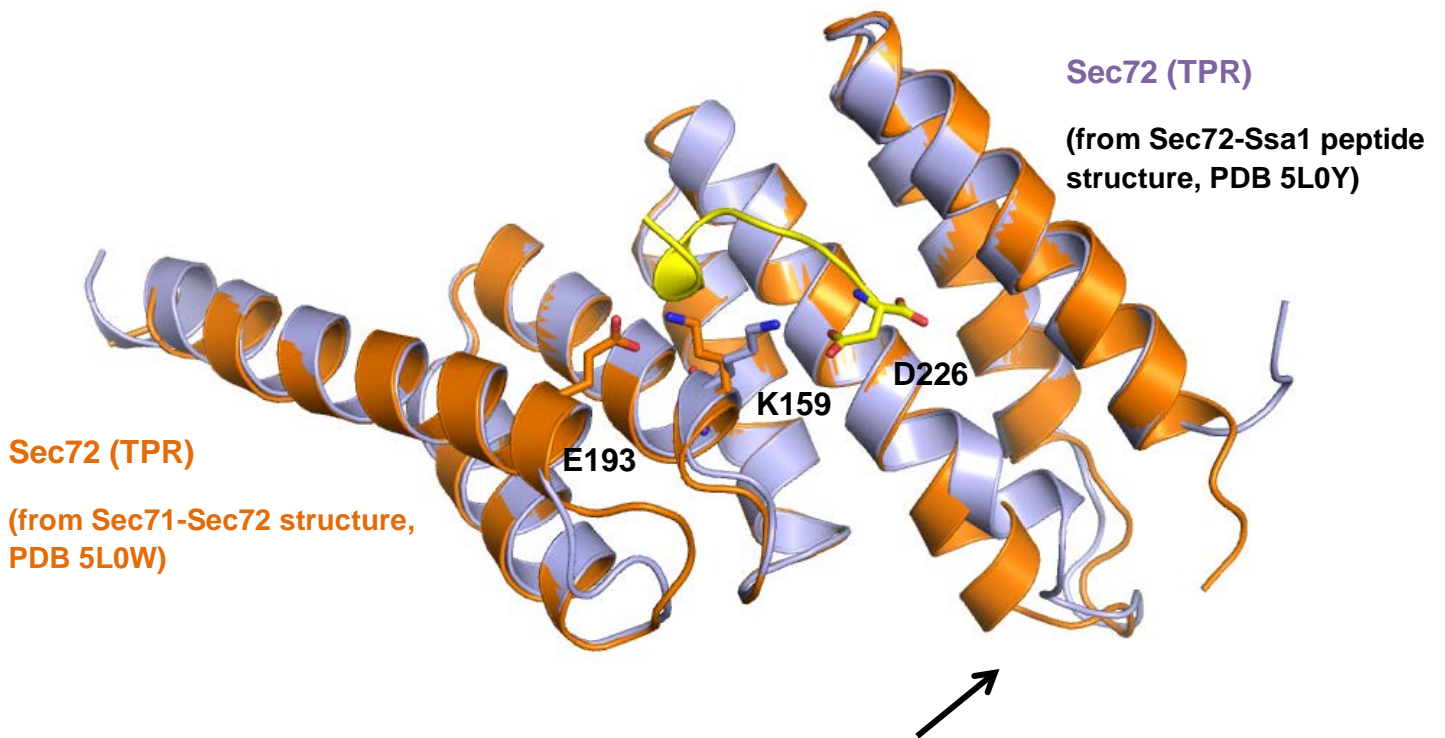
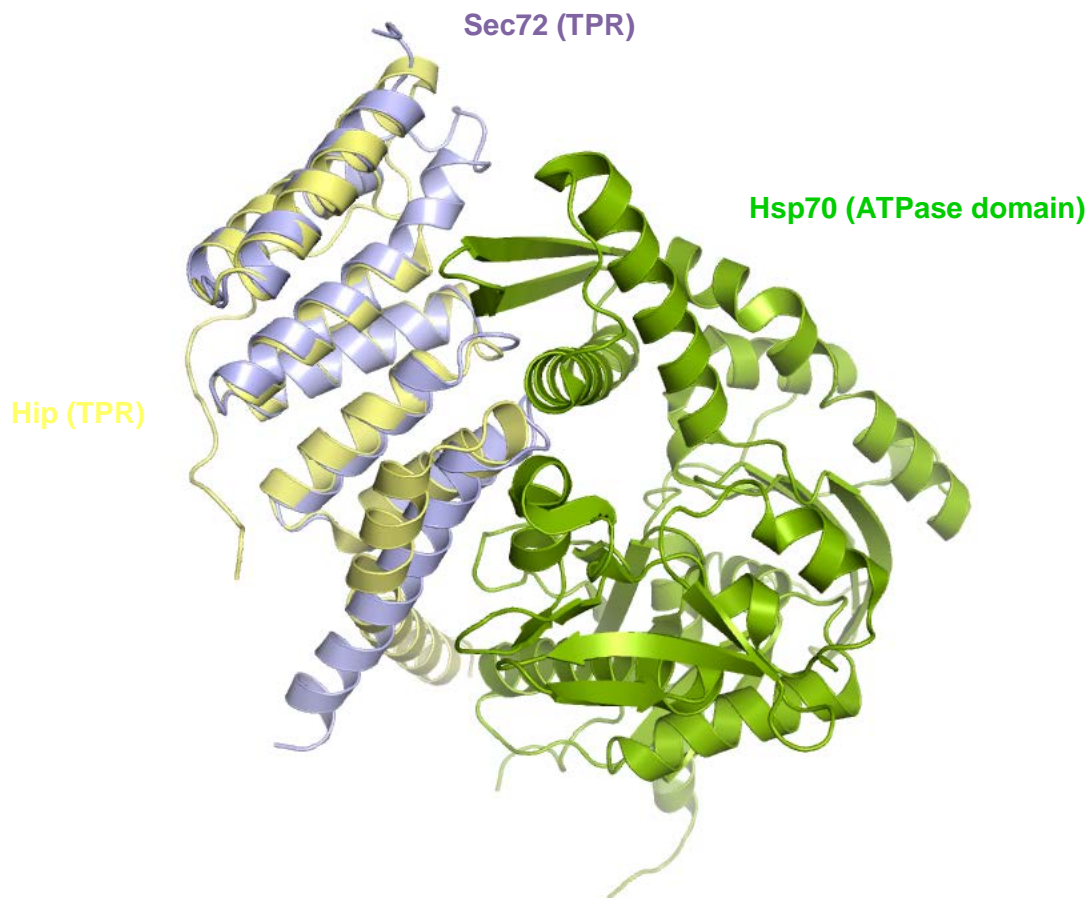


SUPPLEMENTARY FIGURE S1.



Supplementary Figure S1 : Structure of the Sec72 TPR domains with and without bound Ssa peptide. Superposition of the structures of the TPR domains of the Sec71/Sec72 complex (orange) and the fusion to a Ssa peptide (light blue). The arrow points to a difference between the two structures, which is caused by crystal contacts. Lys159 has a different position in the two structures. The linker between the C-terminus of Sec72 and the Ssa peptide is invisible in the density map and thus likely unstructured.

SUPPLEMENTARY FIGURE S2.



Supplementary Figure S2: Sec72 TPR domain bound to the ATPase domain of Hsp70 modeled after a Hip-ATPase structure. The structure of the TPR domain of Sec72 (light blue) was aligned with the TPR domain of Hip (yellow) in a structure of a complex with the Hsp70 ATPase domain (green; PDB 4J8F).

SUPPLEMENTARY TABLE 1.

Table 1. Data collection and refinement statistics

	Sec71/Sec72 SeMet		TPR-peptide
Data collection			
Space group	P 6 ₅ 2 2		P 2 ₁ 2 ₁ 2
Cell dimensions			
<i>a</i> , <i>b</i> , <i>c</i> (Å)	108.6, 108.6, 271.2		76.5, 118.5, 164.0
α , β , γ (°)	90.0, 90.0, 120.0		90.0, 90.0, 90.0
Wavelength (Å)	0.9792		1.033
	Crystal 1	Crystal 2	
Resolution	46.74 – 3.02(3.13 – 3.02)	46.77 – 3.07(3.18–3.07)	164.05 – 2.87(2.973 – 2.87)
<i>R</i> _{meas}	0.145(1.75)	0.136(1.72)	0.064(0.595)
<i>I</i> / σ <i>I</i>	17 (1.8)	19 (1.8)	16.0 (2.10)
Completeness (%)	99.8(99)	99.5(99)	99.34 (99.65)
Redundancy	9.4(9.1)	9.5(9.6)	2.0(2.0)
<i>CC</i> _{1/2}	0.99(0.76)	0.99(0.70)	0.99(0.66)
Refinement			
Resolution (Å)	20.1 - 3.04		96.08 - 2.87
No. reflections	18882		34691
<i>R</i> _{work} / <i>R</i> _{free}	0.223/0.250		0.236/0.284
No. atoms	2962		9720
Protein	2962		9720
Ligand/ion			
Water			
<i>B</i> -factors			
Protein	90.00		79.00
Ligand/ion			
Water			
R.m.s. deviations			
Bond lengths (Å)	0.005		0.008
Bond angles (°)	0.91		1.07

*Values in parentheses are for highest-resolution shell.