The N-terminus of a-Subunit Isoforms is Involved in Signaling between V-ATPase and Cytohesin-2*S

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SUPPLEMENTAL DATA

SUPPLEMENTAL LEGENDS

Table S1. Synthesis of V-ATPase a1-, a2-, a3- and a4-subunit isoforms derived peptides coupled with PEG or TAT sequence to render them soluble and cell permeable. Peptides were further coupled at the N-terminus with either: i) biotin (in blue), ii) fluorescein isothiocyanate (FITC)(in green), iii) 5-carboxy-fluorescein (Fluor)(in green) or 5-carboxy-teramethyl rhodamine (CTMR)(in red). After testing all peptides for their solubility and cell permeability in our experiments following peptides: i) Biotin-a2N$_{1-17}$-TAT; ii) FITC-a2N$_{1-17}$-TAT; iii) FITC-a1N$_{1-17}$-TAT; iv) FITC-a3N$_{1-17}$-TAT; v) FITC-a4N$_{1-17}$-TAT as well as FITC-TAT as control were used.

Table S2. Structural statistics of the peptide a2N$_{1-17}$.

Movie S1. Arf1/Sec7/a2N$_{1-17}$ complex.mov

Movie S2. Arf6/Sec7/a2N$_{1-17}$ complex.mov

Table S1

Peptide Synthesis #1:	*PEG* - **a2N$_{1-17}$**	*PEG* - **MGSLFRSESMCLAQLFL**
Peptides labeling #1:	Biotin - *PEG* - **a2N$_{1-17}$**	Biotin - *PEG* - **MGSLFRSESMCLAQLFL**
	Fluor - *PEG* - **a2N$_{1-17}$**	Fluor - *PEG* - **MGSLFRSESMCLAQLFL**
Peptide Synthesis #2:	**a2N$_{1-17}$** - *PEG*	**MGSLFRSESMCLAQLFL** - *PEG*
Peptides labeling #2:	Biotin - **a2N$_{1-17}$** - *PEG*	Biotin - **MGSLFRSESMCLAQLFL** - *PEG*
	Fluor - **a2N$_{1-17}$** - *PEG*	Fluor - **MGSLFRSESMCLAQLFL** - *PEG*
Peptide Synthesis #3:	*TAT* - **a2N$_{1-17}$**	*YGRKKRRQRRR***MGSLFRSESMCLAQLFL**
Peptides labeling #3:	Biotin - *TAT* - **a2N$_{1-17}$**	Biotin - *YGRKKRRQRRR***MGSLFRSESMCLAQLFL**
	Fluor - *TAT* - **a2N$_{1-17}$**	Fluor - *YGRKKRRQRRR***MGSLFRSESMCLAQLFL**
Peptide Synthesis #4:	**a2N$_{1-17}$** - *TAT*	**MGSLFRSESMCLAQLFL***YGRKKRRQRRR*
Peptides labeling #4:	Biotin - **a2N$_{1-17}$** - *TAT*	Biotin - **MGSLFRSESMCLAQLFL***YGRKKRRQRRR*
	Fluor - **a2N$_{1-17}$** - *TAT*	Fluor - **MGSLFRSESMCLAQLFL***YGRKKRRQRRR*
	FITC - **a2N$_{1-17}$** - *TAT*	FITC - **MGSLFRSESMCLAQLFL***YGRKKRRQRRR*
	CTMR - **a2N$_{1-17}$** - *TAT*	CTMR - **MGSLFRSESMCLAQLFL***YGRKKRRQRRR*
Peptide Synthesis #5:	*TAT*	*YGRKKRRQRRR*
Peptides labeling #5:	FITC - *TAT*	FITC - *YGRKKRRQRRR*
	CTMR - *TAT*	CTMR - *YGRKKRRQRRR*
Peptide Synthesis #6:	**a1N$_{1-17}$** - *TAT*	**MGELFRSEEMTLAQLFL***YGRKKRRQRRR*
	a3N$_{1-17}$ - *TAT*	**MGSMFRSEEVALVQLLL***YGRKKRRQRRR*
	a4N$_{1-17}$ - *TAT*	**MASVFRSEEMCLSQVFL***YGRKKRRQRRR*
Peptides labeling #6:	FITC - **a1N$_{1-17}$** - *TAT*	FITC - **MGELFRSEEMTLAQLFL***YGRKKRRQRRR*
	FITC - **a3N$_{1-17}$** - *TAT*	FITC - **MGSMFRSEEVALVQLLL***YGRKKRRQRRR*
	FITC - **a4N$_{1-17}$** - *TAT*	FITC - **MASVFRSEEMCLSQVFL***YGRKKRRQRRR*

Table S2

Structural statistics of the peptide a2N$_{1\text{-}17}$

Distance restraints	
Total	233
Intraresidue (i – j = 0)	77
Sequential (|i-j| = 1)	81
Medium-range (2 ≤ |i–j| ≤ 4)	75
Long-range (|*i*–*j*| ≥ 5)	0
Average number of violations	
Distance violations > 0.5 Å	0
Ramachandran plot[2] (%)	
Residues in most favoured regions	78.2
Residues in additionally allowed regions	21.8
Residues in generously allowed regions	0
Residues in disallowed regions	0
Average RMSD to Mean (Å)	
Residues 11-19, Backbone (C^{α}, C′, and N)	0.311
rmsd heavy atoms	1.355