

Supplementary Information

Key determinants of VDAC-hexokinase I complex assembly revealed by a minimal vesicle-based interaction assay

Authors: Milena Wessing^{1,2}, Isabelle Watrinet^{2,3}, Michael Timme^{1,2}, Britta Fiedler^{1,2}, Manel N. Melo⁴, Jacob Piehler^{2,3}, Joost C. M. Holthuis^{1,2}

Affiliations:

¹Division of Molecular Cell Biology, Department of Biology/Chemistry, Osnabrück University, 49076 Osnabrück, Germany.

²Center for Cellular Nanoanalytics, Osnabrück University, 49076 Osnabrück, Germany.

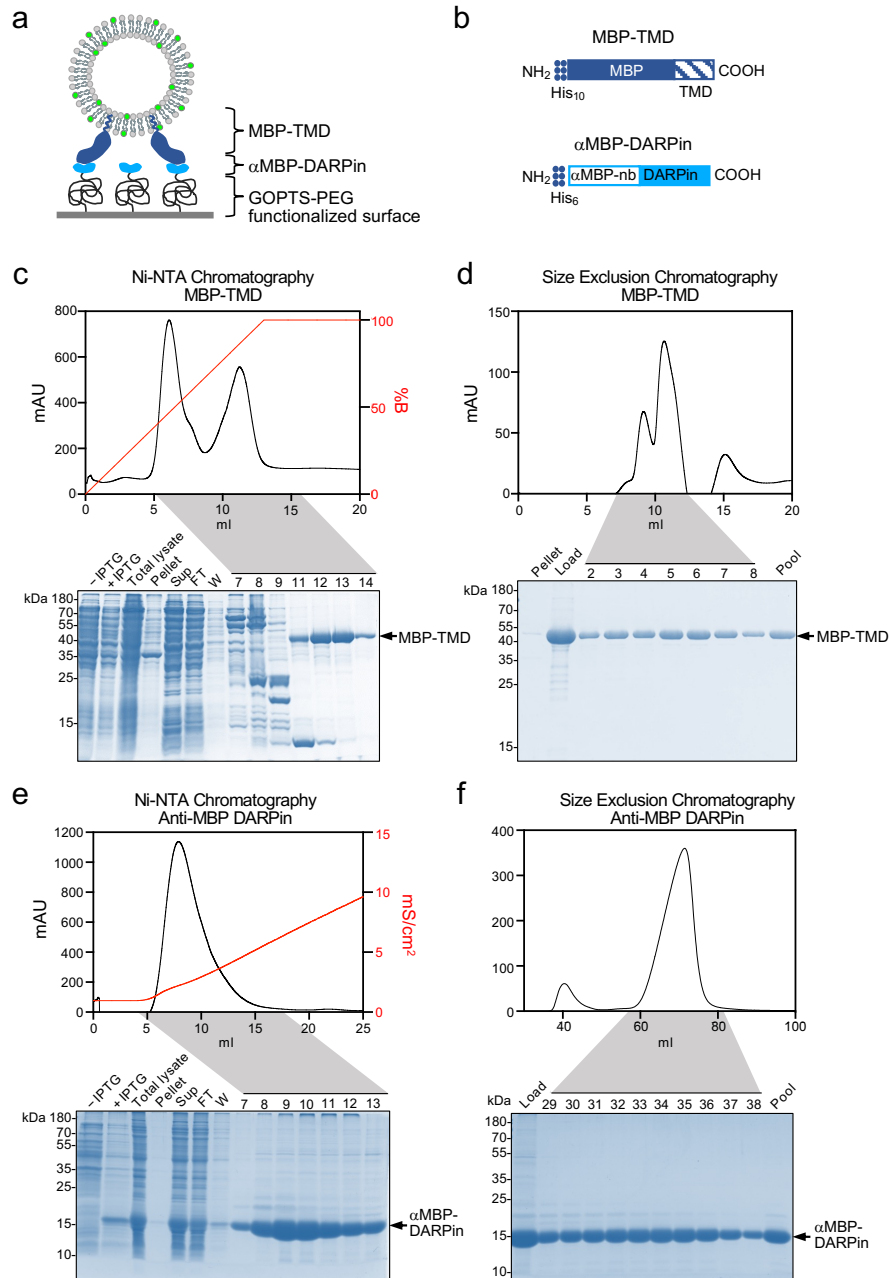
³Division of Biophysics, Department of Biology/Chemistry, Osnabrück University, 49076 Osnabrück, Germany.

⁴Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa, Av. da República, 2780-157 Oeiras, Portugal.

This PDF file includes:

Supplementary Figs. 1 to 4

Supplementary Table 1



Supplementary Figure 1 | Purification of MBP-TMD and αMBP-DARPin.

(a) Cartoon of vesicle containing maltose binding protein fused to a transmembrane domain (MBP-TMD) captured on a glass coverslip decorated with αMBP-DARPin via crosslinking to GOPTS-PEG-NHS maleimide.

(b) Schematic outline of the MBP-TMD and αMBP-DARPin proteins used for capturing vesicles to glass surface as in (a).

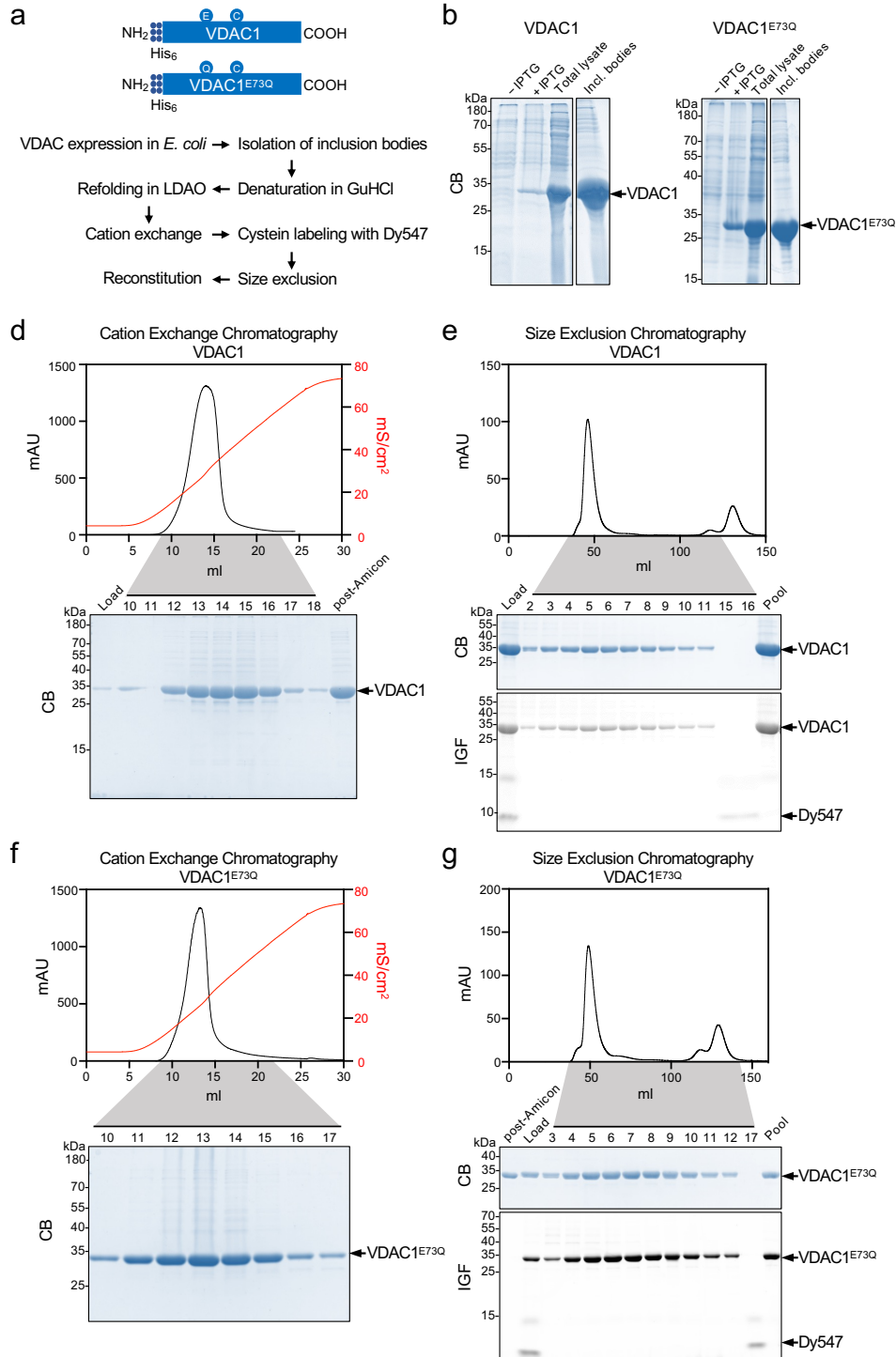
(c) Ni-NTA chromatography of MBP-TMD upon its IPTG-induced expression in *E. coli*. After binding to the Ni-NTA matrix, MBP-TMD was released using a linear imidazole gradient. Expression, release from

bacterial lysates, and Ni-NTA chromatography of MBP-TMD was monitored by SDS-PAGE and CB staining. Sup, supernatant; FT, flow through.

(d) MBP-TMD affinity-purified by Ni-NTA chromatography was loaded onto a size exclusion column. Peak fractions were analyzed by SDS-PAGE and CB staining.

(e) Ni-NTA chromatography of α MBP-DARPin upon its IPTG-induced expression in *E. coli*. After binding to the Ni-NTA matrix, α MBP-DARPin was released using a linear imidazole gradient. Expression, release from bacterial lysates, and Ni-NTA chromatography of α MBP-DARPin was monitored by SDS-PAGE and CB staining.

(f) α MBP-DARPin affinity purified by Ni-NTA chromatography was loaded onto a size exclusion column. Peak fractions were analyzed by SDS-PAGE and CB staining.



Supplementary Figure 2 | Purification and cysteine labelling of VDAC1 and VDAC1^{E73Q}

(a) Schematic outline of the production, purification and cysteine-labeling of recombinant human VDAC1 using an IPTG-inducible bacterial expression construct encoding single cysteine VDAC1 (C127S, A134C, C232S) or its HKI binding-deficient variant VDAC1^{E73Q} (E73Q, C127S, A134C, C232S) tagged with a *N*-terminal His-tag.

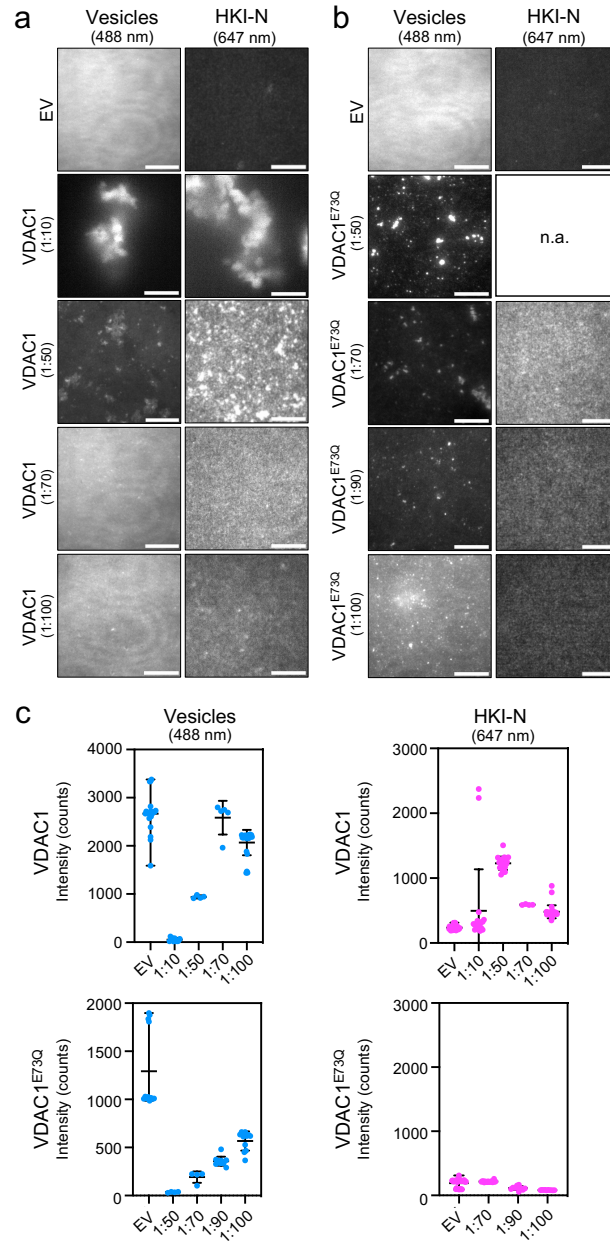
(b) Inclusion bodies isolated from *E. coli* following IPTG-induced expression of VDAC1 or VDAC1^{E73Q} were analyzed by SDS-PAGE and CB staining.

(c) VDAC1 solubilized from inclusion bodies was refolded, loaded onto a cation exchange column and released using a linear salt gradient. Cation exchange chromatography of VDAC1 was monitored by SDS-PAGE and CB staining. Peak fractions were pooled and concentrated using an Amicon filter (post Amicon).

(d) VDAC1 purified by cation exchange chromatography was cysteine-labeled with DY-547P1 and loaded onto a size exclusion column. Peak fractions were analyzed by SDS-PAGE, CB staining and in-gel-fluorescence (IGF) analysis.

(e) Cation exchange chromatography of VDAC1^{E73Q} performed as in (c).

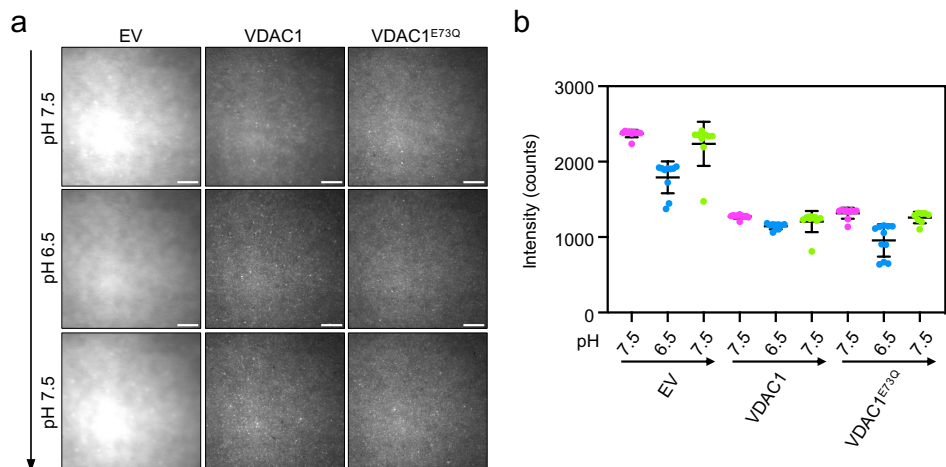
(f) Size exclusion chromatography of Dy-547P1-labelled VDAC1^{E73Q} performed as in (d).



Supplementary Figure 3 | Protein-lipid ratio optimization for reconstitution of MBP-TMD and VDAC1 in proteoliposomes.

(a, b) Vesicles containing MBP-TMD in combination with VDAC1 or VDAC1^{E73Q} were prepared using molar protein:lipid reconstitution ratios of 1:500 for MBP-TMD and the indicated ratios for VDAC1 and VDAC1^{E73Q} in eggPC:DHPE-OG488 (99.5:0.5). Vesicles were captured on α MBP-DARPin-decorated coverslips, incubated with 200nM HK-N⁶⁴⁷ and analyzed for OG488 and HK-N⁶⁴⁷ fluorescence using TIRF microscopy.

(c) Intensity plots of OG488 (*blue*) and HK-N⁶⁴⁷ (*magenta*) fluorescence on the surface of coverslips as in (a, b). Data shown are intensities measured in 4-12 different areas on the surface of one cover slip per condition and representative of three independent experiments.



Supplementary Figure 4 | Mild acidification does not affect binding of VDAC-containing vesicles to αMBP-DARPin-decorated coverslips.

(a) Vesicles prepared by (co)-reconstitution of MBP-TMD, VDAC1 and/or VDAC1^{E73Q} at molar protein:lipid reconstitution ratios of 1:500 (MBP-TMD), 1:50 (VDAC1) and 1:100 (VDAC1^{E73Q}) in eggPC:DHPE-OG488 (99.5:0.5) were captured on αMBP-DARPin-decorated coverslips in pH 7.5 buffer. After 5 min, OG488 fluorescence levels were measured by TIRF microscopy. Incubation was then continued in pH 6.5 buffer for 5 min before measuring OG488 fluorescence levels again. This procedure was then repeated once more in pH 7.5 buffer.

(b) Intensity plots of OG488 fluorescence on the surface of coverslips treated as in (a). Data shown are intensities measured in 5-10 different areas on the surface of one cover slip per condition and representative of three independent experiments.

Supplementary Table 1. Primers used for cloning and site-directed mutagenesis.

Primer name	Primer sequence (5'-3')
pColdI-hVDAC1 F	ATCATATCGAAGGTAGGCACGCTGTGCCACCCAC
pColdI-hVDAC1 R	GCTTTTAAGCAGAGATTACCTATTTATGCTTGAAATTCCAGTCCTAGA CCAAG
hVDAC1-E73Q F	ATGGACTGAGTACGGCCTGACGTTTACACAGAAATGGAATACCGAC
hVDAC1-E73Q R	GTCGGTATTCCATTTCTGTGTAAACGTCAGGCC
hVDAC1 A134C F	TTTCGACATTTGCGGGCCTTCCATCCGGGG
hVDAC1 A134C R	TCCATGTCGCTGCCCAGG