

Supplemental Data for BamA is required for autotransporter secretion

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Table S1: Lipid compositions of YadA-M systems [62, 63]

Lipid	Upper or Lower	Number of Lipids
Y. pestis LPS (Type B)	Upper	34
DGPE	Lower	1
DGPG	Lower	1
DLIPE	Lower	1
DLPE	Lower	1
DMPA	Lower	1
DMPE	Lower	5
DMPG	Lower	3
DOPE	Lower	2
DOPG	Lower	1
DPPA	Lower	2
DPPE	Lower	20
DPPG	Lower	12
DPPS	Lower	1
DSPA	Lower	2
DSPE	Lower	19
DSPG	Lower	12
DSPS	Lower	1
DYPA	Lower	1
DYPE	Lower	7
DYPG	Lower	4
PMPE	Lower	5
SLPG	Lower	1

Table S2: Lipid compositions of EspP systems [64, 65]

Lipid	Upper or Lower	Number of Lipids
E. coli LPS (Type K12)	Upper	42
DPPE	Lower	90
PVPG	Lower	24
PVCL2	Lower	6

Table S3: Simulations for BamA-EspP barrel structure

Structure	Source	System Size	Runs
BamA-LinkSt	BamA barrel (PDB ID: 5L0O) [72] and EspP passenger domain from linker-stretched model	179K atoms	302 ns, 303 ns, 309 ns

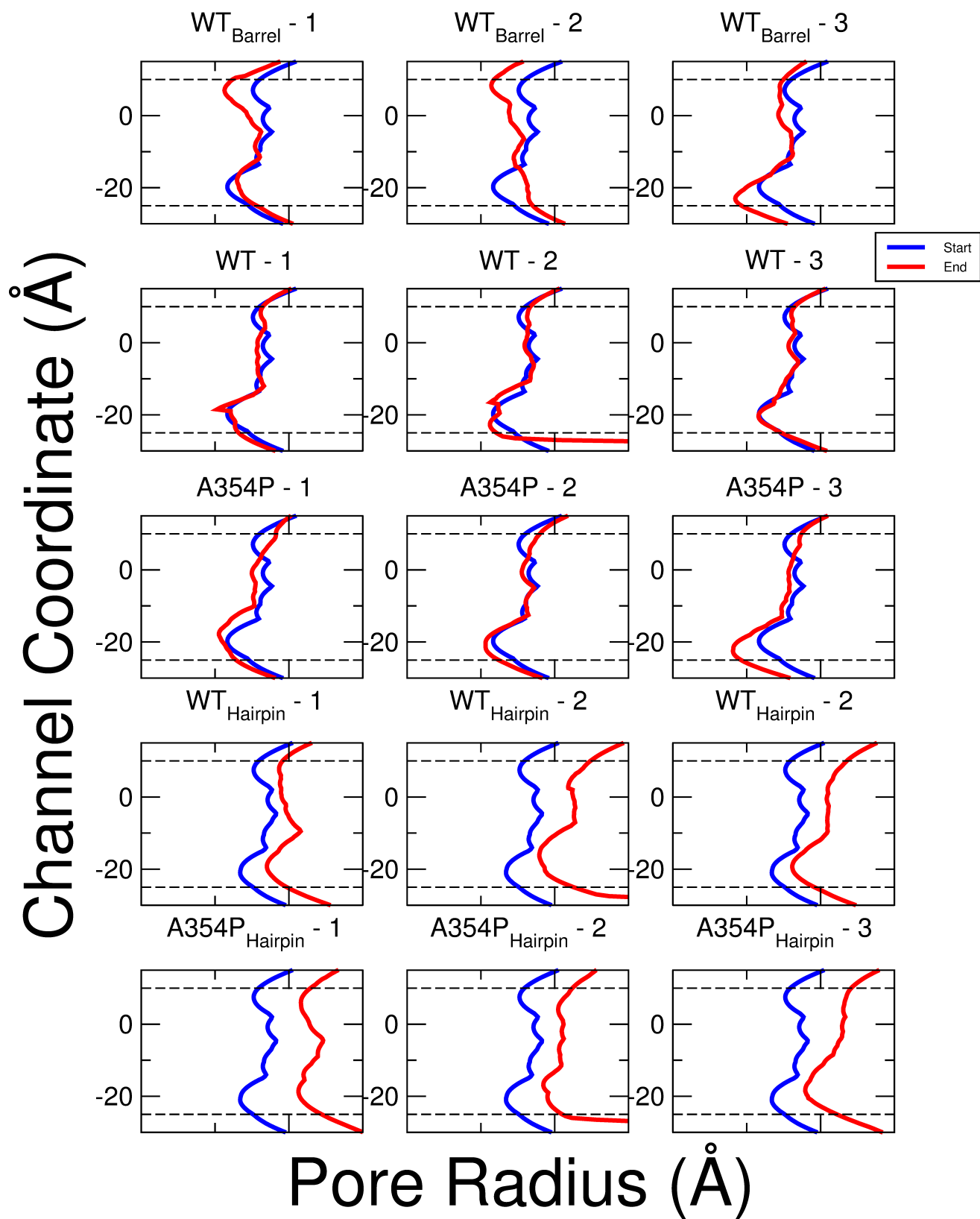


Figure S1: Pore size analysis results of different YadA-M variants

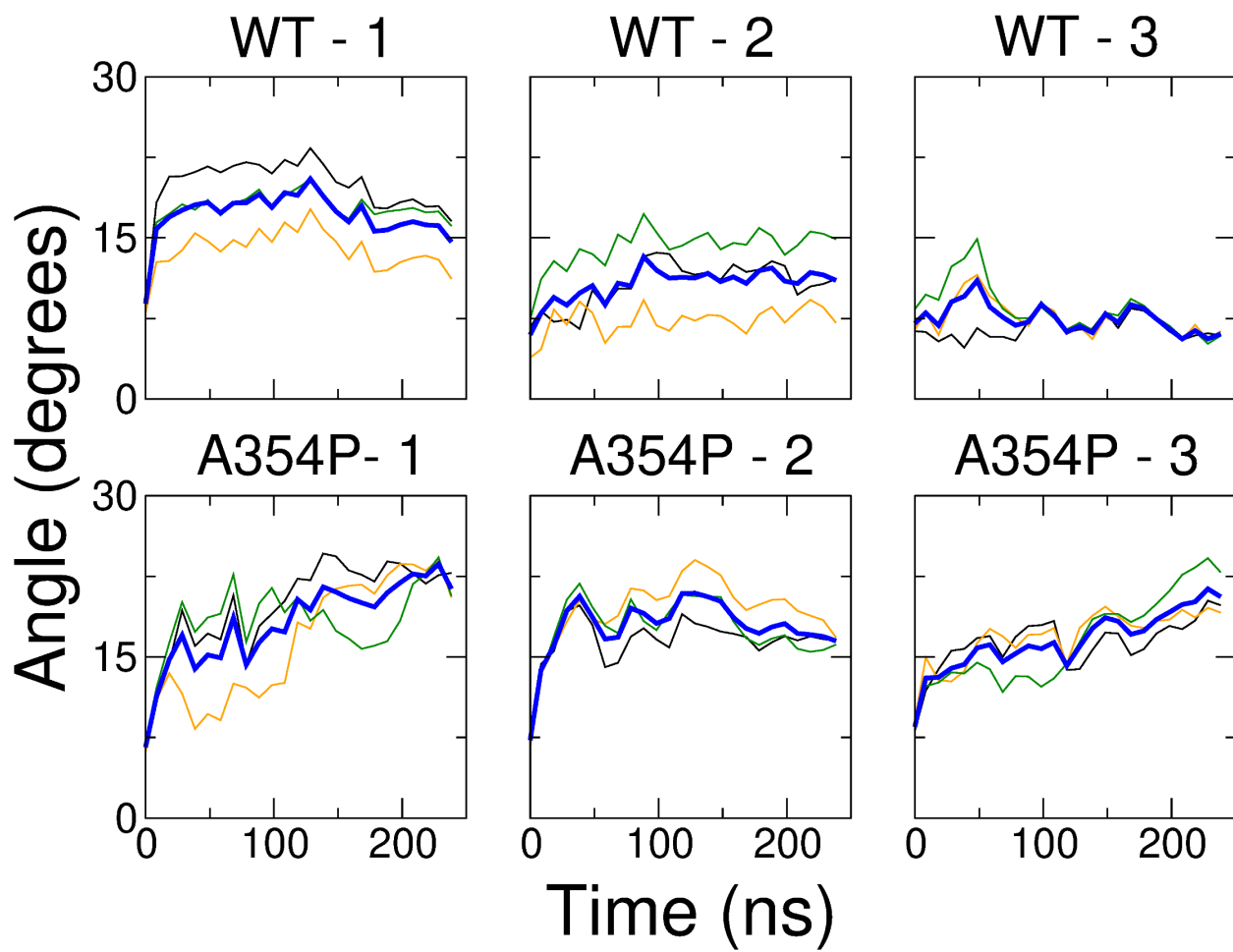


Figure S2: Relative angles formed between the principal axes of each helix pair. The black, green, and orange lines represent the relative angles of each helix and the blue line represent the average. The data shown are running averages taken over 10 ns.

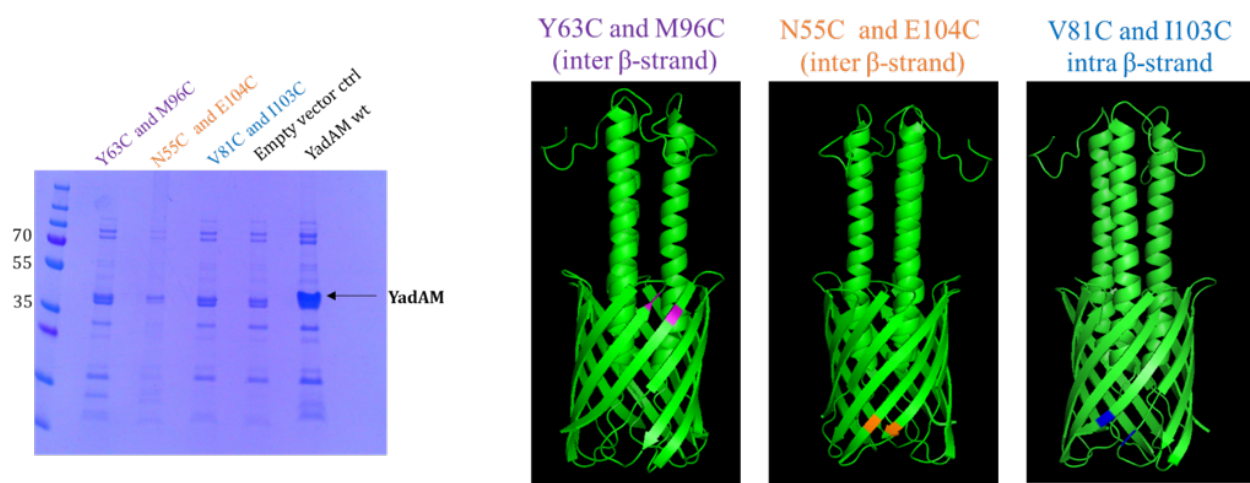


Figure S3: Expression tests for YadAM double-cysteine mutants in a $\Delta ompFdegP$ deficient strain. YadA-M wt, double-cysteine variants, and an empty vector control were expressed and purified in the OM as described previously [70], with the addition of 10 mM TCEP to the growth medium. The OM samples were run on a 4-20% Tris-glycine gradient gel (NOVEX WedgeWell) without heating.

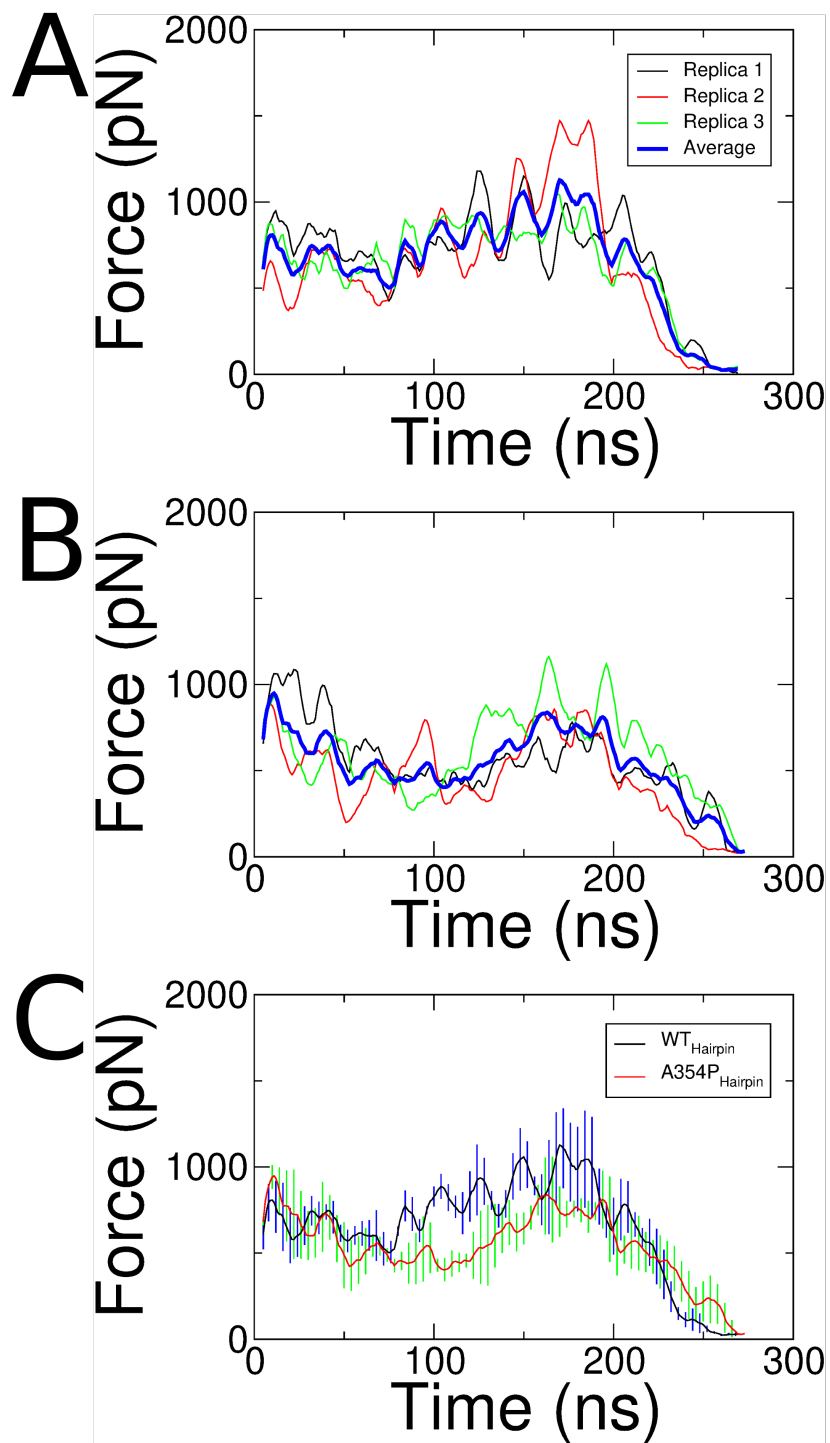


Figure S4: Force vs. time for SMD simulations of A) WT_{hairpin} and B) A354P_{hairpin}, and C) comparison of the average force vs. time for SMD simulations of secretion for the two YadA variants. The simulations were run at a constant velocity of 1 Å/ns. The error bars for C) are shown in blue for WT_{hairpin} and green for A354P_{hairpin}.

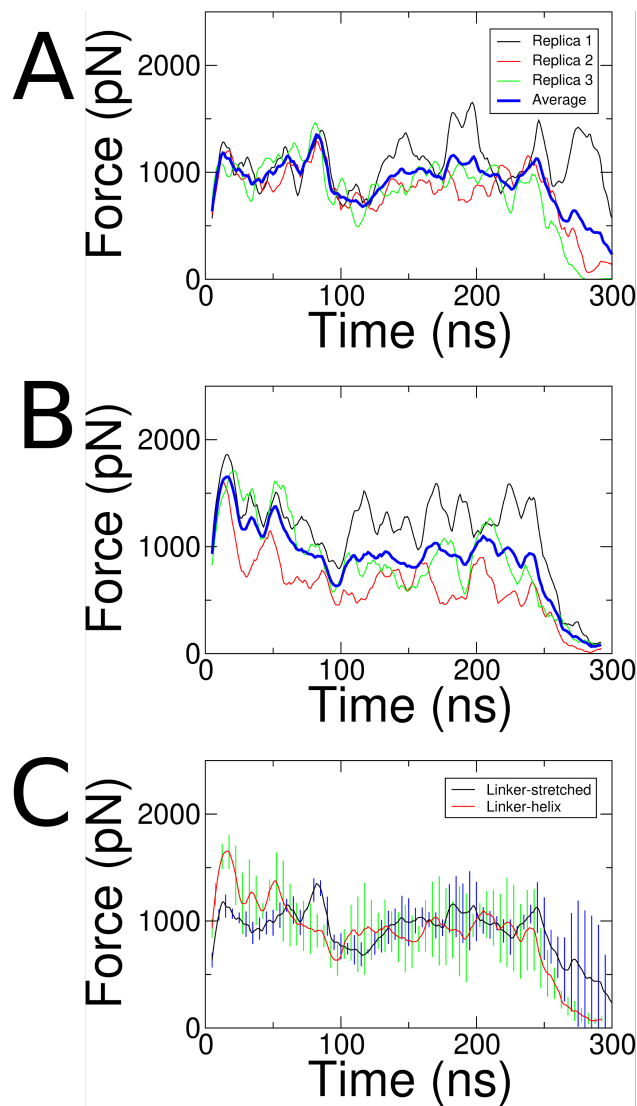


Figure S5: Force vs. time for SMD simulations of secretion using A) linker-stretched and B) linker-helix models, and C) comparison of the average force vs. time for SMD simulations of secretion for the two EspP variants. The simulations were run at a constant velocity of 1 Å/ns. The error bars for C) are shown in blue for linker-stretched and in green for linker-helix, respectively.

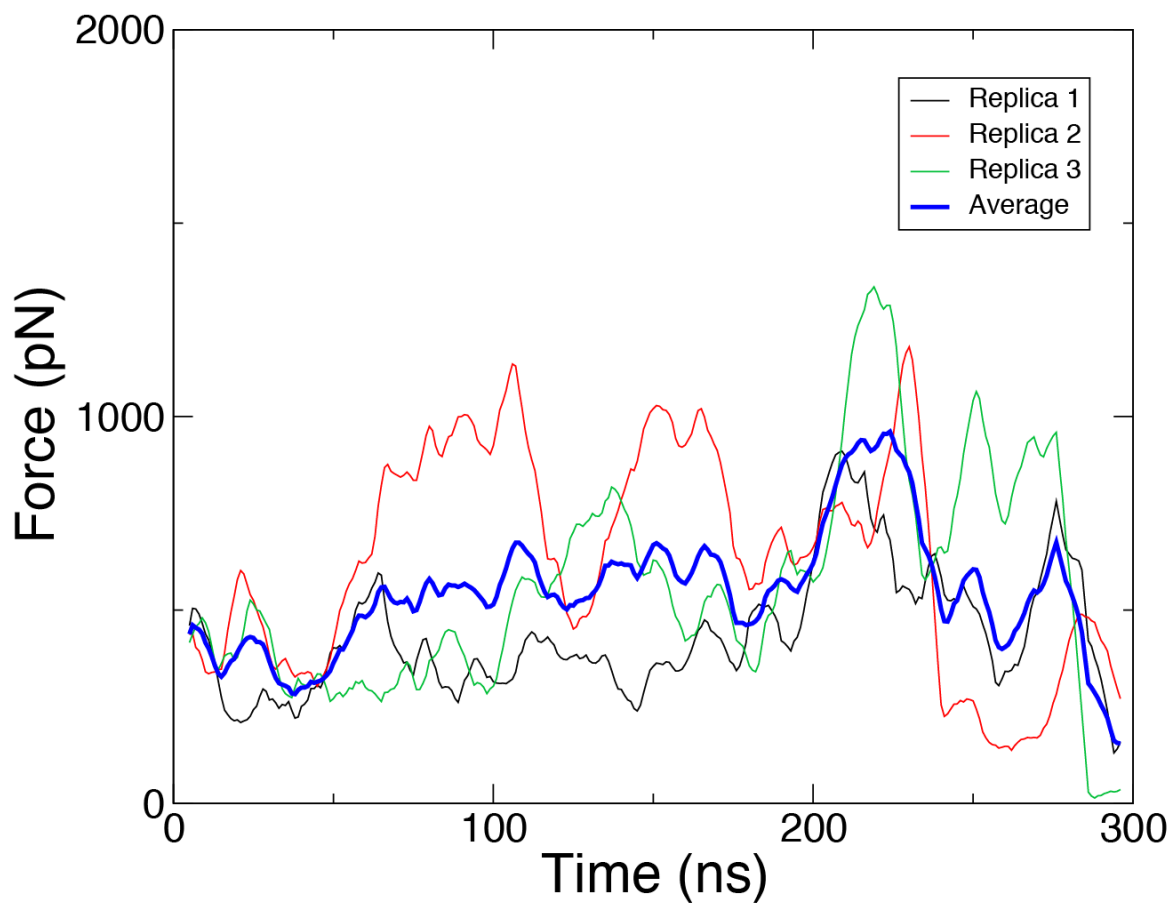


Figure S6: Force vs. time for SMD simulations of BamA structures with EspP passenger domain. The simulations were run at a constant velocity of 1 Å/ns.

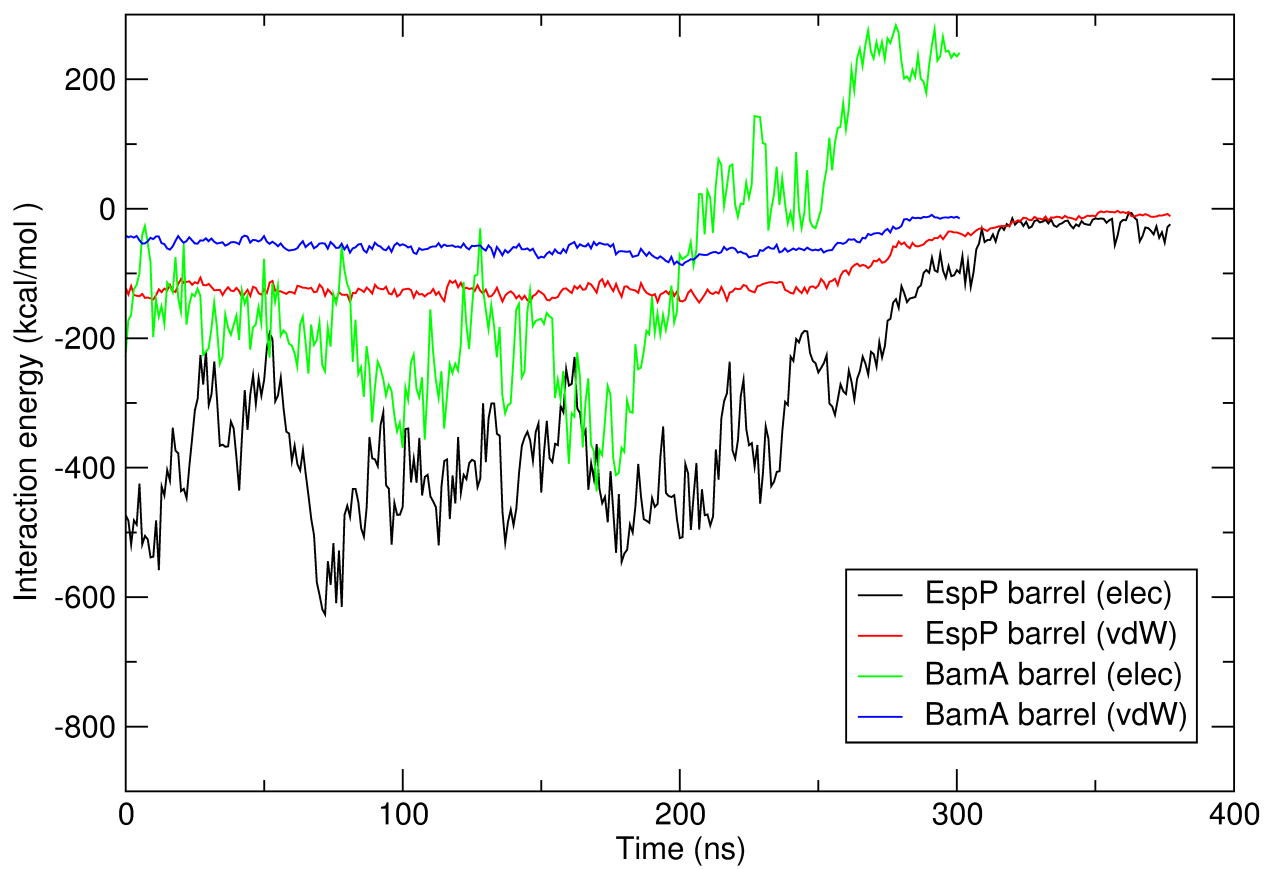


Figure S7: Interaction energy from SMD simulations of EspP structures