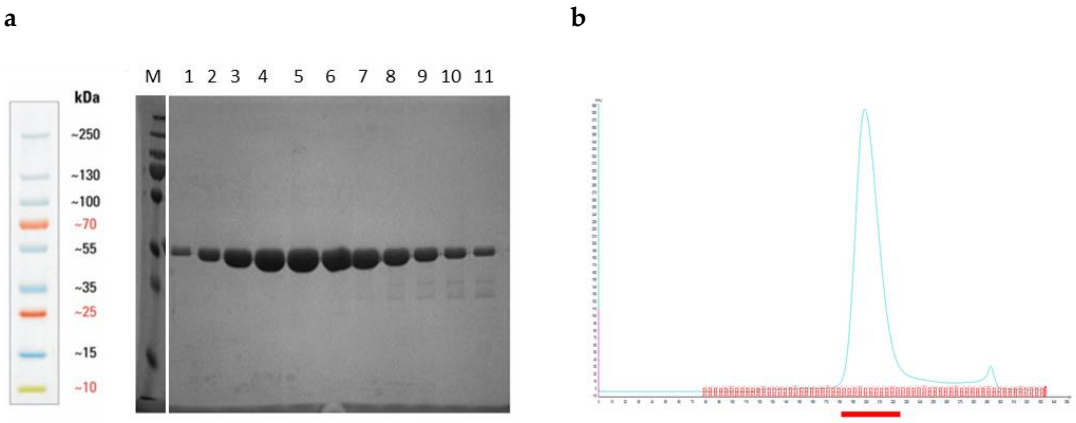
CLUSTAL O(1.2.4) multiple sequence alignment

```
EL11_EPI51560.1         MSKRGIDVSVWQGDIDFNAVKASGVEFVIIRAGYGIGHKDKWFEQNYRKAKTTGLDVGAY 60
EL3_WP_065189629.1      MSKKGIDVSVWQGDIDFNSVKASGVEFVIIRAGYGIGHKDKWFEENYRKAKTAGLDVGSY 60
EL10_WP_064340486.1     MSKRGIDVSVWQGDIDFNAVKASGVEFVIIRAGYGIGHKDKWFEENYRKAKTVGLDVGAY 60
EL12_WP_048730021.1     MSKKGIDVSVWQGDIDFNAVKASGVEFVIIRAGYGIGHKDKWFEENYRKAKTAGLDVGSY 60
EL8_EPI52092.1          MSKKGIDVSEWQGDIDFNAVKASGVEFVIIRAGYGIGCKDKWFEQNYRKAKTAGLDVGAY 60
EL5_EPI54247.1          MSKKGIDVSEWQGDIDFNAVKASGVEFVIIRAGYGIGCKDKWFEQNYRKAKTAGLDVGAY 60
EL7_WP_004104952.1      MSKKGIDVSEWQGDIDFNAVKASGVEFVIIRAGYGIGCKDKWFEQNYRKAKTAGLDVGAY 60
EL4_WP_004111234.1      MSKKGIDVSEWQGDIDFNAVKASGVEFVIIRAGYGIGCKDKWFEQNYRKAKTCGLDVGAY 60
EL6_EIK79883.1          MSKKGIDVSVWQGDIDFNAVKASGVEFVIIRAGYGIGCKDKWFEQNYRKAKTCGLDVGAY 60
EL1_AEF31373.1          MSKKGIDVSEWQGDIDFNAVKASGVEFVIIRAGYGIGCKDKWFEQNYRKAKTAGLDVGAY 60
EL9_WP_004118369.1      MSKKGIDVSEWQGDIDFNAVKASGVEFVIIRAGYGIGCKDKWFEQNYRKAKTCGLDVGAY 60
EL2_WP_065189413.1      MSKRGIDVSEWQGDIDFNAVKASGVEFVIIRAGYGIGCKDKWFEQNYRKAKTCGLDVGAY 60
EL13_WP_076002731.1     MSKKGIDVSVWQGDIDFNAVKASGVEFVIIRAGYGIECKDKWFEQNYRKAKTAGLDVGAY 60
EL14_WP_076002856.1     MSKKGIDVSVWQGDIDFNAVKASGVEFVIIRAGYGIGCKDKWFEQNYRKAKTCGLDVGAY 60
                        ***:***** ********:*****************  ******:******* *****:*

EL11_EPI51560.1         WYSYASSAGEAAEEAQSCVNILSGKSFEYPVYFDLEEKSQLNRGRDFCDSLITSFCNKLE 120
EL3_WP_065189629.1      WYSYASSAGEASEEAQSCVNILSGKSFEYPIYFDLEEKSQLNRGRDFCDSLITSFCNKLE 120
EL10_WP_064340486.1     WYSYASSAGEASEEAQSCVNILSGKSFEYPVYFDLEEKSQLNRGRDFCDSLITSFCNKLE 120
EL12_WP_048730021.1     WYSYASSAGEVALEAQSCVNILSGKSFEYPVYFDLEEKSQLNRGRDFCDSLITSFCNKLE 120
EL8_EPI52092.1          WYSYANSSSEAAEEAQSCVNMLSGKSFEYPVYFDLEEKSQLNRGRAFCDSLITSFCSKLE 120
EL5_EPI54247.1          WYSYANSSSEAAEEAQSCANMLSGKSFEYPVYFDLEEKSQLNRGRAFCDSLITGFCSKLE 120
EL7_WP_004104952.1      WYSYANSASEAAEEAQSCANMLSGKSFEYPVYFDLEEKSQLNRGRAFCDSLITSFCSKLE 120
EL4_WP_004111234.1      WYSYANSGFEAAEEAQSCVNMLSGKSFEYPVYFDLEEKSQLNRGRAFCDSLITSFCSKLE 120
EL6_EIK79883.1          WYSYANSGFEAAEEAQSCVNMLSGKSFEYPVYFDLEEKSQLNRGRAFCDSLITSFCSKLE 120
EL1_AEF31373.1          WYSYANSGFEAAEEAQSLMNMLSGKSFEYPVYFDLEEKSQLNRGRAFCDSLITSFCNKLE 120
EL9_WP_004118369.1      WYSYANSGFEAAEEAQSCVNMLSGKSFEYPVYFDLEEKSQLNRGRVFCDSLITSFCNKLE 120
EL2_WP_065189413.1      WYSYANSGFEAAEEAQSCVNMLSGKSFEYPVYFDLEEKSQLNRGRAFCDSLITGFCNKLE 120
EL13_WP_076002731.1     WYSYANSGFEAAEEAQSCVNMLSGKSFEYPVYFDLEEKSQLNRGRAFCDSLITSFCNKLE 120
EL14_WP_076002856.1     WYSYANSGFEAAEEAQSCVNMLSGKSFEYPVYFDLEEKSQLNRGRAFCDSLITSFCNKLE 120
                        *****.*. *.: ****  *:*********:************** *******.**.***

EL11_EPI51560.1         TYGYYAGFYTSLSVANNLVSSHVRDRYALWIAQWNTHCDYQGSYGLWQYSSSGSVDGIAG 180
EL3_WP_065189629.1      ACGYYAGFYTSLSVANNLVSSHVRDRYALWIAQWNTHCSYQGSYGLWQYSSSGSVNGIAG 180
EL10_WP_064340486.1     ACGYYAGFYTSLSVANNLVSSHVRDRYALWIAQWNTHCSYQGSYGLWQYSSSGSVNGIAG 180
EL12_WP_048730021.1     ACGYYAGFYTSLSVANNLVSSHVRDRYALWIAQWNTHCSYQGSYGLWQYSSSGSVNGIAG 180
EL8_EPI52092.1          TYGYYAGFYTSLSTANNLVSSHVRNRYALWIAQWNTHCSYQGSYGLWQYSSNGSVPGVAG 180
EL5_EPI54247.1          ACGYYAGFYTSLSTANNLVSAHVRNRYALWIAQWNTHCSYQGSYGLWQYSSNGSVPGVAG 180
EL7_WP_004104952.1      TYGYYAGFYTSLSTANNLVSSHVRNRYALWIAQWNTHCSYQGSYGLWQYSSSGSVPGVAG 180
EL4_WP_004111234.1      TYGYYAGFYTSLSVVNNLVSAHVRDRYALWIAQWNTHCSYQGSYGLWQYSSSGSVPGVAG 180
EL6_EIK79883.1          SCGYYAGFYTSLSTANNLVSAHVRNRYALWIAQWNTHCDYQGSYGLWQYSSSGSVPGVAG 180
EL1_AEF31373.1          ACGYYAGFYTSLSTANNLVSAHVRNRYALWIAQWNTHCNYQGSYGLWQYSSNGSVPGVAG 180
EL9_WP_004118369.1      ACGYYAGFYTSLSTANNLVSSHVRNRYALWIAQWNTHCDYQGSYGLWQYSSSGSVPGVAG 180
EL2_WP_065189413.1      SCGYYAGFYTSLSTANNLVSAHVRNRYALWIAQWNTHCSYQGSYGLWQYSSSGSVPGVAG 180
EL13_WP_076002731.1     SCGYYAGFYTSLSTANNLVPAHVRNRYALWIAQWNTHCDYQGSYGLWQYSSSGSVPGVAG 180
EL14_WP_076002856.1     ACGYYAGFYTSLSTANNLVSAHVRNRYALWIAQWNTHCSYQGSYGLWQYSSSGSVPGVAG 180
                        : ***********..**** :***:*************.************.*** *:**

EL11_EPI51560.1         RVDMDYTYVDYPSVIKKAGLNGYKNGGSYTAPQTSSIDEVAREVINGDWGNGNERKNRLT 240
EL3_WP_065189629.1      RVDMDYAYVDYPSVIKNAGLNGYQNGGSYTAPQTSSIDEVAREVINGDWGNGNDRKNRLI 240
EL10_WP_064340486.1     RVDMDYAYVDYPSVIKNAGLNGYKNGGSYTAPQISSIDEVAREVINGDWGNGNERKQRLT 240
EL12_WP_048730021.1     RVDMDYAYVDYPSVIKNAGLNGYQNGGSYTAPQTSSIDEVAREVINGDWGNGIERKNRLT 240
EL8_EPI52092.1          RVDMDYAYVDYPSIIKNAGLNGYKNGGSYTAPQTSSIDDVAREVINGAWGNGNERKQRLT 240
EL5_EPI54247.1          RVDMDYAYKDYPSIIKNAGLNGCKNGGSDQAARTSSIDEVAREVINGAWGNGNERKQRLT 240
EL7_WP_004104952.1      RVDMDYAYKDYPSIIKNAGLNGCKNGGSDQAARTSSIDEVAREVINGAWGNGNERKQRLT 240
EL4_WP_004111234.1      RVDMDYAYVDYPSIIKNVGLNGCKNGGSDQATRTSSIDEVAREVINGAWGNGNERKQRLT 240
EL6_EIK79883.1          RVDMDYAYKNYPSIIKNAGLNGCKNGGSNQAARTSSIDDVAREVINGAWGNGNERKQRLT 240
EL1_AEF31373.1          RVDMDYAYVDYPSIIKNAGLNGCKNGGSDQAARTSSIDEVAREVINGAWGNGSTRKQRLT 240
EL9_WP_004118369.1      RVDMDYAYVDYPSIIKNAGLNGCKNGGSDQAARTSSIDEVAREVINGAWGNGSTRKQRLT 240
EL2_WP_065189413.1      RVDMDYAYVDYPSIIKNVGLNGCKNGGSDQAARTSSIDEVAREVINGAWGNGNERKQRLT 240
EL13_WP_076002731.1     RVDMDYAYVDYPSIIKNAGLNGYKNGESHQATRTTSIDEVAREVINGAWGNGNERKQRLT 240
EL14_WP_076002856.1     RVDMDYAYVDYPSIIKNAGLNGYKNGESHQATRTTSIDEVAREVINGAWGNGNERKQRLT 240
                        ******:* :***:**:.**** :** *  * : :***:******** ****  **:**
```

```
EL11_EPI51560.1          SAGYDYTSVQNKVNELLGVKAYRKSVDELAREVIRGTWGNGSTRKQRLTQAGYDYDAVQK 300
EL3_WP_065189629.1       SAGYDYASVQNKVNELLGVKAYRKSVDELAREVIRGTWGNGSMRKHRLTQAGYDYDAVQK 300
EL10_WP_064340486.1      SAGYDYASVQNKVNELLGVKAYRKSVDELAREVIRGTWGNGSTRKQRLTQAGYDYNAVQK 300
EL12_WP_048730021.1      SAGYDYTSVQNKVNELLGVKAYRKSVDELAREVIRGTWGNGKTRKQRLTQAGYDYNAVQK 300
EL8_EPI52092.1           QAGYDYTSVQNKVNKLLGVKACRKSVDELAREVIRGTWGNGNERKNRLTQAGYDYDTVQK 300
EL5_EPI54247.1           QAGYDYTSVQNKVNKLLGVKACRKSVDELAREVIRGTWGNGNERKNRLTQAGYDYDTVQK 300
EL7_WP_004104952.1       QAGYDYTSVQNKVNKLLGVKACRKSVDELAREVIRGTWGNGNERKNRLTQAGYDYDTVQK 300
EL4_WP_004111234.1       SAGYDYASVQNKVNKLLGVKAYRKSVDELAREVIRGTWGNGNERKQRLAQAGYDYDTVQK 300
EL6_EIK79883.1           QAGYDYASVAK---------------------------------------------- 251
EL1_AEF31373.1           SAGYDYASVQNKVNELLGVKACRKSVDELAREVIRGAWGNGSTRKQRLAQAGYDYDTVQK 300
EL9_WP_004118369.1       SAGYDYASVAK---------------------------------------------- 251
EL2_WP_065189413.1       SAGYDYASVQNKVNELLGVKACRKSVDEIAREVIRGTWGNGSTRKQRLTQAGYDYDTVQK 300
EL13_WP_076002731.1      QAGYDYASVQNKVNELLGVKACRKSVDELAREVIRGTWGNGNERKNRLTSAGYDYDTVQK 300
EL14_WP_076002856.1      SAGYDYASVQNKVNELLGVKACRKSVDELAREVIRGAWGNGSTRKQRLTSAGYDYDTVQK 300
                         .*****:** :

EL11_EPI51560.1          RVNELL       306
EL3_WP_065189629.1       RVNELL       306
EL10_WP_064340486.1      RVNELL       306
EL12_WP_048730021.1      RVNELL       306
EL8_EPI52092.1           RVNELL       306
EL5_EPI54247.1           RVNELL       306
EL7_WP_004104952.1       RVNELL       306
EL4_WP_004111234.1       RVNELL       306
EL6_EIK79883.1           ------       251
EL1_AEF31373.1           RVNELL       306
EL9_WP_004118369.1       ------       251
EL2_WP_065189413.1       RVNELL       306
EL13_WP_076002731.1      RVNELL       306
EL14_WP_076002856.1      RVNELL       306
```

Supplementary Figure 1: Wild-type endolysins (EL1-EL14) encoded on prophage-like regions of *Gardnerella* genomes. A multiple sequence alignment was performed by Clustal Omega analysis (https://www.ebi.ac.uk/Tools/msa/clustalo/). The protein accession numbers are given after each endolysin name (e.g. EL1_AEF31373.1). The yellow background indicates the EAD (H-domain), the linker sequence is highlighted in grey, and the cell wall binding domain (B-domain) in blue. The domain regions were predicted by Interpro (https://www.ebi.ac.uk/interpro/).



Supplementary Figure 2. (a) PM-477 endolysin protein was recombinantly expressed and purified via Ni-NTA chromatography (FPLC). Fractions obtained from the final size exclusion chromatography (FPLC) were analyzed for purity by SDS-PAGE and Coomassie blue staining. MWM was used to confirm the expected protein size (left). Fractions 1-11 were pooled and used for further experiments. (b) FPLC chromatograph of PM-477 purification on a Superdex 75 column resulting in a defined peak from 182 mL to 222 mL. Red bar represents the fractions 1-11 that were pooled and concentrated to a final volume with a concentration of 0.616 mg/mL (determined by A280 measurement).