**Supplementary Table 1**

**Residues built in the Mrp model.**

All side-chains are assigned, there are no UNK residues.

|  |  |  |  |
| --- | --- | --- | --- |
| Subunit | Number of residues in sequence | Residues built | Missing fragments |
| MrpA | 821 | 29-816 | N- and C-terminus |
| MrpB | 140 | 3-140 | N-terminus |
| MrpC | 110 | 1-107 | C-terminus |
| MrpD | 490 | 1-489 | C-terminus |
| MrpE | 158 | 1-158 | none |
| MrpF | 91 | 2-89 | N- and C-terminus |
| MrpG | 119 | 8-111 | N- and C-terminus |

**Supplementary Table 2**

**Homologous counterparts among Mrp (*Anoxybacillus flavithermus* WK1), complex I (*Thermus thermophilus*) and MBH (*Pyrococcus furiosus*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Proposed Mrp Module** | **Mrp complex** | **MBH** | **Module of MBH** | **Complex I** | **Module of CI** |
|  | - | - |  | Nqo1 | N-module |
|  | - | - |  | Nqo2 | N-module |
|  | - | - |  | Nqo3 | N-module |
|  | - | MbhL | MA hydrogenase  | Nqo4 | Q-module |
|  | - | MbhK | MA hydrogenase  | Nqo5 | Q-module |
|  | - | MbhN | MA hydrogenase  | Nqo9 | Q-module |
|  | - | MbhJ | MA hydrogenase  | Nqo6 | Q-module |
|  | - | MbhM | MA hydrogenase  | Nqo8 | P-module |
|  | - | MbhI N-terminal |  | Nqo7 N-terminal | P-module |
|  | - | MbhI C-terminal |  | Nqo12 C-terminal |  |
| Proton translocation | MrpA TM1-TM16  | - |  | Nqo12 TM1-TM16 | P-module |
| Sodium translocation | MrpA TM17-TM19 | MbhD | Proton translocation? | Nqo10 | P-module |
| Sodium translocation | MrpA TM20 – TM21 | MbhE | Proton translocation? | Nqo10 | P-module |
| Sodium translocation | MrpB | MbhF | Sodium translocation | - |  |
| Sodium translocation | MrpC | MbhG | Proton translocation? | Nqo11 | P-module |
| Proton translocation | MrpD | MbhH | Proton translocation | Nqo13/14 | P-module |
| Sodium translocation | MrpE | MbhA | Sodium translocation | - |  |
| Sodium translocation | MrpF | MbhB | Sodium translocation | - |  |
| Sodium translocation | MrpG | MbhC | Sodium translocation | - |  |

In complex I, N-module represents NADH-oxidising module, Q-module is a connecting module where quinone is reduced and P-module is a proton-pumping membrane module. For MBH, we propose to re-assign the role of MbhDEG subunits to sodium translocation, similarly to Mrp. MA hydrogenase stands for membrane-anchored hydrogenase module.

**Supplementary Table 3**

**Summary of impact of mutations on expression level of Mrp subunits, growth in high salt, antiport activity in everted membrane vesicles, Km values for Na+ and assembly of the mutant, as well as of structural environment of the mutated residue.**

a Mutated residue as it was published in the respective reference and the same mutated residue *in italics* according to our own alignment (if different from published reference) using the UNIPROT accession codes B7GL84 for MrpA, B7GL83 for MrpB, B7GL82 for MrpC, B7GL98 for MrpD, B7GL97 for MrpE, B7GL96 for MrpF, B7GIG3 for MrpG from *Anoxybacillus flavithermus* WK1, Q9RGZ5 for MrpA, Q9RGZ4 for MrpB, Q9RGZ3 for MrpC, Q9RGZ2 for MrpD, Q9RGZ1 for MrpE, Q9RGZ0 for MrpF, Q9RGY9 for MrpG from *Bacillus pseudofirmus* OF4, Q9K2S2 for MrpA, O05259 for MrpB, O05260 for MrpC, O05229 for MrpD, Q7WY60 for MrpE, O05228 for MrpF, O05227 for MrpG from *Bacillus subtilis*. For Mrp1 from *Corynebacterium glutamicum* the sequences from EnsemblBacteria CAF18840 for Mrp1A, CAF18839 for Mrp1C, CAF18838 for Mrp1D, CAF18837 for Mrp1E, CAF18836 for Mrp1F and CAF18835 for Mrp1G were used.

b Ratio of the lowest expressed Mrp subunit compared with the positive control which has a value of 1. For references 4 and 6, the protein bands were visually compared with the control band.

c Percent dequenching in everted membrane vesicles as compared with the positive control at pH 8.0 or pH 8.5 and Km values for Na+.

d The “+” indicates a growth of KNabc cells in LBK medium containing 400-600 mM NaCl. The percentage values are the means of growth of KNabc cells in LBK medium containing 600 mM NaCl as compared with the control.

e The presence of the Mrp monomer, dimer and MrpA-D subcomplex is indicated as “✓”.

f Expression, antiport activity and growth in NaCl were tested in the antiporter-deficient KNabc *E. coli* strain and/or in *Bacillus subtilis.*

g “Top” means towards the cytoplasm and “bottom” towards the periplasm.

**Abbreviations:**

BS… *Bacillus subtilis*

BP…*Bacillus pseudofirmus* OF4

CG*…Corynebacterium glutamicum*

**Categories:**

1. Effects on monomer/dimer/sub complex
2. Reduced EMV activity
3. Reduced growth in NaCl
4. Normal
5. Km for Na+ at least 2.5 fold increase

\* The asterisk indicates a contradiction between the antiport activity and the growth in NaCl. Usually the growth in NaCl is a more reliable indicator of antiport activity.

Controls from different references

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Reference | Bacterial species | Control | Expressionb | Effect |
| Antiport activityc | Growth in NaCld | Assemblyof the mutante |
| 1 | Bacillus pseudofirmus OF4 | TFCHS7 | 1 | 100%Km 0.096 | + | D✓ | M✓ | A-D✓ |
| 2 | Bacillus pseudofirmus OF4 | TFCHS7 | 1 | NormalKm 0.079 | NA | D✓ | M✓ | A-D✓ |
| 3 | Bacillus pseudofirmus OF4 | TFCHS7 | 1 | 100%Km 0.079 | + | D✓ | M✓ | A-D✓ |
| 4 | Bacillus subtilis | pTY11 | 100% | 100% | 100% | NA |
| 5 | Corynebacterium glutamicum | Original mrp1 | NA | NA | + | NA |
| 6 | Bacillus subtilisBacillus subtilis  | pTY11Δstrains | 100%KNabcf100%BSf | 100%KNabcf100%BSf | 100%KNabcf100%BSf | NANA |

**MrpA**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Residue in *A. flavi-thermus* | Homologousresidue, species, mutationa | Expressionb | Effect | Amino acid locationg | Cate-gory | Refe-rence |
| Antiport activityc | Growth in NaCld | Assemblyof the mutante |
| D104 | D50N*D77N*BSD50N*D77N*BS | ~100%~50%BS | 12%56%BS | >100%65%BS | NANABS | Link between βH element and TM8 | 2\*2/3 | 46 |
| D104 | D77A*D78A*BPD50A*D77A*BS | >0.8~90% | 99%0% | +71% | D✓NA | M✓NA | A-D✓NA | 42\* | 14 |
| D104 | D77E*D78A*BPD50E*D77E*BSD50E*D77E*BS | >0.77~100%~10%BS | 84%21%40%BS | +79%45%BS | D✓NANA | M✓NANA | A-D✓NANA | 42\*2/3 | 146 |
| D157 | D103A*D130A*BS | ~20% | 38% | 0% | NA | Link between TM5 and βH element  | 2/3 | 4 |
| D157 | D103E*D130E*BSD103E*D130E*BS | ~50%~50%BS | 0%64%BS | 0%61%BS | NANA | 2/32/3 | 46 |
| D157 | D103N*D130N*BSD103N*D130N*BS | ~100%~50%BS | 62%76%BS | 5%24%BS | NANA | 3\*3\* | 46 |
| Y163 | Y136A*Y137A*BP | >1 | 100% | + | D✓ | M✓ | A-D✓ | Near GluTMH5, interface to MrpD | 4 | 3 |
| E167 | E113D*E140D*BSE113D*E140D*BS | ~80%~50 %BS | 45%60%BS | 7%1%BS | NANA | GluTMH5 | 33\* | 46 |
| E167 | E113Q*E140Q*BSE113Q*E140Q*BS | ~80%~50%BS | 0%20%BS | 0%0%BS | NANA | 2/32/3 | 46 |
| E167 | E140A*E141A*BPE113A*E140A*BS | >0.19~70% | 6%12% | -0% | D✓NA | M✓NA | A-DXNA | 12/3 | 34 |
| K248 | K223A*K224A**BP* | >0.11 | 0% | - | DX | M✓ | A-D✓ | LysTMH7 | 1 | 3 |
| Y255 | H230K*H231A*BPH230KCG | >0.79NA | 65%Km 0.25 mMNA | ±± | D✓NA | M✓NA | A-D✓NA | Interaction between TMH7 and HL helix | 53 | 35 |
| Y255 | H230A*H231A*BP | 0.89 | >100% | + | D✓ | M✓ | A-D✓ | 4 | 3 |
| W257 | W232A*H233A*BP | >0.84 | 86% | + | D✓ | M✓ | A-D✓ | Upper part of TM7 | 4 | 3 |
| Y283 | Y258A*Y259A*BP | >1 | 92% | + | D✓ | M✓ | A-D✓ | Lower part of TM8 | 4 | 3 |
| R287 | R262A*R263A*BP | >0.87 | 96% | + | D✓ | M✓ | A-D✓ | Salt bridge to D104 | 4 | 1 |
| Q320 | Q295A*Q296A*BP | >0.5 | 91% | + | D✓ | M✓ | A-D✓ | Loop between TM9-TM10 | 4 | 1 |
| K324 | K299A*K300A*BP | >0.5 | 5% | - | D✓ | M✓ | A-D✓ | Top of TM10,Possible exit point for H+ | 2/3 | 3 |
| K324 | K299HCG | NA | NA | - | NA | 3 | 5 |
| G336 | G311A*G312A*BP | >0.83 | 97% | + | D✓ | M✓ | A-D✓ | Middle of TM10 | 4 | 1 |
| H369 | H345A*H346A*BP | >0.94 | 90%Km 0.092 mM | + | D✓ | M✓ | A-D✓ | Middle of TM11, part of H+ entry cluster | 4 | 3 |
| F381 | F357A*F358A*BP | >0.96 | 93% | + | D✓ | M✓ | A-D✓ | Top of TM11 | 4 | 1 |
| G416 | G392ABP | >0.98 | 100% | + | D✓ | M✓ | A-D✓ | Upper part of TM12 | 4 | 3 |
| G416 | G392R*G393R*BP | >0.18 | 3% | - | DX | M✓ | A-D✓ | 1 | 3 |
| G416 | G378TCG | NA | NA | + | NA | 4 | 5 |
| F429 | F405A*F406A*BP | >0.9 | 100% | + | D✓ | M✓ | A-D✓ | TM12, next to the break | 4 | 3 |
| H547 | H499KCG | NA | NA | + | NA | Loop between TM14 and TM15 | 4 | 5 |
| F690 | F671A*F672A*BP | >0.97 | 79% | + | D✓ | M✓ | A-D✓ | TM18, next to MrpC | 4 | 1 |
| P696 | P677G*P678G*BP | >0.91 | 84% | + | D✓ | MX | A-D✓ | TM19; periplasmic surface | 1 | 1 |
| T701 | T683ABP | >0.7 | 87% | + | D✓ | M✓ | A-D✓ | TM19, next to MrpC | 4 | 1 |
| E706 | E687A*T688A*BPE657A*E684A*BS | >0.48~100% | 0.7%0% | -0% | D✓NA | M✓NA | A-D✓NA | TM19, next to MrpC,5 Å from bound K+ | 2/32/3 | 14 |
| E706 | E657D*E684D**BS*E657D*E684D**BS* | ~100%~70%BS | 93%100%BS | >100%89%BS | NANA | 44 | 46 |
| E706 | E657Q*E684Q**BS*E657Q*E684Q*BS | ~100%~70%BS | 2%48%BS | 5%0%BS | NANA | 2/32/3 | 46 |
| H719 | H700A*H701A*BP | >0.9 | 19%Km 0.30 mM | + | D✓ | M✓ | A-D✓ | Loop between TM19 & TM20, coordinates headgroup of lipid bound in Na+ cavity | 5 | 3 |
| H719 | H700K*H701A*BP | >1 | 56%Km 0.43 mM | + | D✓ | M✓ | A-D✓ | 5 | 3 |
| H719 | H700W*H701A*BP | >1 | 63%Km 0.37 mM | + | D✓ | M✓ | A-D✓ | 5 | 3 |
| P721 | P702G*P703A*BP | 0.45 | 34%Km 0.326 mM | + | D✓ | M✓ | A-D✓ | Loop between TM19 & TM20 | 5 | 1 |
| R789 | R773A*R774A*BP | >0.18 | 1% | - | NA | Loop before TM21; salt bridge to D128*d* | 2/3 | 1 |
| D792 | D743A*D770A*BS | ~30% | 0% | 0% | NA | Periplasmic end of TM21; exit of Na+ pathway | 2/3 | 4 |
| D792 | D743E*D770E*BSD743E*D770E*BS | ~100%~100%BS | >100%>100%BS | 90%90%BS | NANA | 44 | 46 |
| D792 | D743N*D770N*BSD743N*D770N*BS | ~100%~90%BS | 0%16%BS | 0%0%BS | NANA | 2/32/3 | 46 |
| E796 | E747D*E774D*BSE747D*E774D*BS | ~100%~100%BS | 0%36%BS | 10%2%BS | NANA | TM21, facing MrpC;Part of Na+ pathway | 2/32/3 | 46 |
| E796 | E747Q*E774Q*BSE747Q*E774Q*BS | ~100%~20%BS | 0%4%BS | 0%0%BS | NANA | 2/32/3 | 46 |
| E796 | E780A*E781A*BPE747A*E774A*BS | >0.46~100% | 0%0% | -0% | D✓NA | M✓NA | A-D✓NA | 2/32/3 | 14 |

**MrpB**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Residue in *A. flavi-thermus* | Homologous residue, species, mutationa | Expressionb | Effect | Amino acid locationg | Cate-gory | Refe-rence |
| Antiport activityc | Growth in NaCld | Assemblyof the mutante |
| H31 | H34ABP | >0.9 | >100%Km 0.092 | + | D✓ | M✓ | A-D✓ | Loop between TM1 & TM2; periplasmic surface | 4 | 3 |
| P34 | P37GBP | >1 | 83%Km 0.057 mM | + | D✓ | MX | A-D✓ | Loop between TM1 & TM2; periplasmic surface | 1 | 3 |
| F38 | F41ABP | >1 | 83%Km 0.14 mM | - | D✓ | M✓ | A-D✓ | TM2 next to MrpA | 3\* | 3 |
| D118 | D121ABS | ~100%KNabc | 0%KNabc | 0%KNabc | NA | Periplasmic end ofTM2, interacts with N782*a* | 2/3 | 6 |
| D121EBSD121EBS | ~90%KNabc~100%BS | 18%KNabc80%BS | 84%KNabc91%BS | NANA | 2\*4 | 66 |
| D121NBSD121NBS | ~70 %KNabc~100%BS | 10%KNabc0%BS | 0%KNabc91%BS | NANA | 2/32\* | 66 |

**MrpC**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Residue in *A. flavi-thermus* | Homologous residue, species, mutationa | Expressionb | Effect | Amino acid locationg | Cate-gory | Refe-rence |
| Antiport activityc | Growth in NaCld | AssemblyOf the mutante |
| Q70 | Q70ABP | 0.85 | 77%Km 0.068 mM | + | D✓ | MX | A-D✓ | Bottom of TM3, interacts with MrpA | 1 | 3 |
| T75 | T75ABP | >0.86 | 88%Km 0.11 mM | - | D✓ | M✓ | A-D✓ | TM3; interface with MrpD/A, part of Na+ exit pathway | 3\* | 3 |
| I77 | I76FCG | NA | NA | - | NA | Middle of TM3, part of cavity where K+ ion is bound. | 3 | 5 |
| G82 | G82PBP | >0.43 | 81%Km 0.083 mM | + | D✓ | M✓ | A-D✓ | TM3, next to C-terminus of MrpA | 4 | 3 |
| G82 | G82IBP | >0.7 | 55%Km 0.12 mM | + | D✓ | M✓ | A-D✓ | 2 | 3 |

**MrpD**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Residue in *A. flavi-thermus* | Homologous residue, species, mutationa | Expressionb | Effect | Amino acid locationg | Cate-gory | Refe-rence |
| Antiport activityc | Growth in NaCld | Assemblyof the mutante |
| D75 | D75EBPD75EBSD75EBS | >0.5~50 %KNabc~100%BS | 69%Km 0.056 mM9%KNabc87%BS | +0% KNabc>100%BS | D✓NANA | M✓NANA | A-D✓NANA | Link between βH element and TM8 | 22/34 | 166 |
| D75 | D75ABPD75ABS | >0.06~50%KNabc | 9%9%KNabc | -0%KNabc | DXNA | MXNA | A-DXNA | 12/3 | 16 |
| D75 | D75NBSD75NBS | ~80 %KNabc~100%BS | 15%KNabc97%BS | 0%KNabc99%BS | NANA | 2/34 | 66 |
| D128 | D128EBSD128EBS | ~100 %KNabc~100 %BS | 13%KNabc81%BS | >100%KNabc>100%BS | NANA | Link between TM5 and βH element | 2\*4 | 66 |
| D128 | D128ABS | >50 %KNabc | 4%KNabc | 8%KNabc | NA | 2/3 | 6 |
| D128 | D128NBSD128NBS | ~100 %KNabc~100%BS | 15%KNabc100%BS | 89%KNabc74%BS | NANA | 2\*4 | 66 |
| F135 | F135ABP | >0.9 | 97% | + | D✓ | M✓ | A-D✓ | TM5; next to C-term. of MrpA | 4 | 3 |
| F136 | F136ABP | >0.94 | 75% | + | D✓ | M✓ | A-D✓ | TM5; next to GluTMH5 | 4 | 3 |
| F136 | F136TBP | >1 | 79% | + | D✓ | M✓ | A-D✓ | 4 | 3 |
| F136 | F136EBP | >1 | 78% | + | D✓ | M✓ | A-D✓ | 4 | 3 |
| F136 | F136GBP | >1 | 37%Km 0.31 mM | - | D✓ | M✓ | A-D✓ | 5 | 3 |
| E137 | E137ABPE137ABS | >0.26NAKNabc | 0%2%KNabc | -0%KNabc | DXNA | M✓NA | A-DXNA | GluTMH5;Na+ coupling | 2/32/3 | 36 |
| E137 | E137DBPE137DBSE137DBS | >0.84~100%KNabc100%BS | 92%Km 0.22 mM53%KNabc48%BS | ->100%KNabc80%BS | D✓NANA | M✓NANA | A-D✓NANA | 52\*2\* | 366 |
| E137 | E137QBPE137QBSE137QBS | NA~100 %KNabc~50%BS | NA0%KNabc0%BS | -0%KNabc0%BS | NANANA | 32/32/3 | 366 |
| K219 | K219ABP | >0.95 | 0.% | - | D✓ | M✓ | A-D✓ | LysTMH7 | 2/3 | 3 |
| W228 | W228ABP | >0.96 | 86%Km 0.063 mM | + | D✓ | M✓ | A-D✓ | Loop of TM7 | 4 | 3 |
| R258 | R258ABP | >0.01 | 30%Km 0.064 mM | - | DX | MX | A-DX | TM8;Salt bridge to D75 | 2/3 | 1 |
| G309 | G309ABP | >0.5 | 88% | + | D✓ | M✓ | A-D✓ | Middle part of TM10 | 4 | 1 |
| F341 | F341ABP | >0.5 | 64%Km 0.463 mM | - | D✓ | M✓ | A-D✓ | Part of the block between cytoplasm and LysTM8 | 5 | 1 |

**MrpE**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Residue in *A. flavi-thermus* | Homologous residue, species, mutationa | Expressionb | Effect | Amino acid locationg  | Cate-gory | Refe-rence |
| Antiport activityc | Growth in NaCld | Assemblyof the mutante | A | A |
| Q4 | Q4ABP | NA | Normal | NA | NA | Start of TM1 | 4 | 2 |
| N8 | N8ABP | NA | Normal | NA | NA | TM1, stabilises TM2-AH loop | 4 | 2 |
| K59 | K59ABP | NA | Normal | NA | NA | AH helix; facing the cytoplasm | 4 | 2 |
| K66 | K66ABP | NA | Normal | NA | NA | AH helix; facing the cytoplasm | 4 | 2 |
| E67 | E67ABPE67ABS | NA~80%KNabc | Normal28%KNabc | NA68%KNabc | NANA | AH helix; facing the cytoplasm, interacts with ferredoxin-like fold | 42\* | 26 |
| E67 | E67DBSE67DBS | ~100%KNabc~90%BS | 89%KNabc100%BS | >100%KNabc>100%BS | NANA | 44 | 66 |
| E67 | E67QBSE67QBS | ~100%KNabc~100%BS | 58%KNabc>100%BS | 97%KNabc>100%BS | NANA | 24 | 66 |
| T113 | T113ABPT113ABP | >0.070.02 | 1%- | -NA | DXX | MX✓ | A-D✓X | Loop before HH2 helix in ferredoxin-like fold, stabilises the helix | 11 | 32 |
| T113 | T113YBP | >1 | 2% | - | D✓ | M✓ | A-D✓ | 2/3 | 3 |
| P114 | P114ABP | >0.91 | 79%Km 0.11 mM | + | D✓ | M✓ | A-D✓ | Loop before HH2 helix in ferredoxin-like fold, interacts with AH helix | 4 | 3 |
| P114 | P114GBPP114GBP | >0.950.73 | 12%Km 1.6 mM-Km 1.3 | +NA | D✓✓ | M✓✓ | A-D✓✓ | 2\*2 | 32 |
| P114 | P61L | NA | NA | + | NA | 4 | 5 |
| H131 | H131ABP | NA | Normal | NA | NA | On β-strand, part of Na+ pathway | 4 | 2 |

**MrpF**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Residue in *A. flavi-thermus* | Homologous residue, species, mutationa | Expressionb | Effect | Amino acid locationg | Cate-gory | Refe-rence |
| Antiport activityc | Growth in NaCld | Assemblyof the mutante |
| R20 | R35HCG | NA | NA | + | NA | Top of TM1 | 4 | 5 |
| P25 | P28GBP | >0.97 | 94% | + | D✓ | M✓ | A-D✓ | Loop between TM1 & TM2; cytoplasmic surface | 4 | 3 |
| D29 | D32ABP | >0.27 | 0% | - | DX | MX | A-D✓ | Cytoplasmic surface of TM2, salt bridge to R40*g* | 1 | 3 |
| R30 | R33ABP | >0.81 | 46%Km 0.082 mM | + | D✓ | M✓ | A-D✓ | Cytoplasmic surface of TM2 | 2 | 3 |
| D35 | D38ABS | ~5%KNabc | 1%KNabc | 0%KNabc | NA | Middle of TM2, part of Na+ pathway | 2/3 | 6 |
| D35 | D38EBSD38EBS | ~40%KNabc~100%BS | 3%KNabc80%BS | 0%KNabc>100%BS | NANA | 2/34 | 66 |
| D35 | D38NBSD38NBS | ~40%KNabc~100%BS | 4%KNabc>100%BS | 0%KNabc75%BS | NANA | 2/34 | 66 |

**MrpG**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Residue in *A. flavi-thermus* | Homologous residue, species, mutationa | Expressionb | Effect | Amino acid locationg | Cate-gory | Refe-rence |
| Antiport activityc | Growth in NaCld | Assemblyof the mutante |
| R33 | R28H | NA | NA | + | NA | End of TM1 | 4 | 5 |
| P86 | P81GBP | >1 | 8% | + | D✓ | M✓ | A-D✓ | on a kink in TM3, interacting with MrpE | 2\* | 3 |
| P86 | P81ABP | >0.96 | 8% | + | D✓ | M✓ | A-D✓ | 2\* | 3 |

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