### S10 Table. Results of the consensus analysis of LinA.

| Position | Residue | Frequency | ²Res_TOP | ²Freq_TOP | FoldX ΔΔG (kcal.mol⁻¹) | UniProt database | Mutant       |
|----------|---------|-----------|----------|-----------|------------------------|-----------------|--------------|
| 20       | K       | 0.62      | Y        | 0.15      | -1.437                 |                 | Halide-stabilizing |
| 23       | A       | 0.69      | G        | 0.23      | 1.778                  |                 |              |
| 32       | L       | 0.62      | F        | 0.38      | 4.379                  |                 |              |
| 50       | Y       | 0.54      | F        | 0.38      | -0.510                 |                 | LinA02       |
| 56       | A       | 0.54      | I        | 0.38      | 5.508                  |                 |              |
| 59       | L       | 0.62      | A        | 0.38      | 3.642                  |                 | LinA02       |
| 68       | F       | 0.62      | W        | 0.31      | 0.000                  |                 | LinA02       |
| 80       | L       | 0.54      | V        | 0.38      | 1.368                  |                 |              |
| 88       | V       | 0.62      | A        | 0.38      | 2.694                  |                 |              |
| 96       | L       | 0.77      | C        | 0.15      | 2.777                  |                 |              |
| 109      | I       | 0.62      | V        | 0.23      | 0.665                  |                 |              |
| 113      | F       | 0.69      | Y        | 0.23      | 0.138                  |                 | Activity decrease |
| 126      | F       | 0.54      | I        | 0.23      | 1.624                  |                 | LinA02       |
| 131      | A       | 0.62      | V        | 0.15      | -1.492                 |                 | LinA02       |
| 144      | F       | 0.54      | L        | 0.23      | 1.316                  |                 |              |

² The most conserved residue at a given position of the multiple sequence alignment; ³ Frequency of the most conserved residue at a given position of the multiple sequence alignment.