

Table S4. Anabaenolysin variants found in the *Anabaena* strain XPORK 15F.

Identification based on UV-spectra showing the triene specific absorption pattern, ion mass $[MH]^+$, product ion spectra and retention time (R_t). Product ions presented characterise the differences in the structures.

| Variant No | R_t (min) | MH^+ (m/z) | Relative area (%) | | | | | | | | | | |
|----------------|----------------|-----------------|-------------------|-----------------------------------|-----------------------------------|-------------------|------------------------|-----------------|---|--------------------------|--------------------|--|--|
| | | | | M-C ₁₁ H ₁₆ | M-C ₁₂ H ₁₈ | M-FA ^b | FA-(2H ₂ O) | FA-CO | FA-(2H ₂ O+NH ₃) | FA-(CO+H ₂ O) | FA-NH ₂ | FA-(CO+2H ₂ O+NH ₃) | |
| 1, Abl A | 23.5 | 559 | 78 | 411 | 397 | 272 | 270 | 260 | 253 | 242 | 230 | 225 | |
| 2, Abl B | 23.9 | 561 | 7 | 411 | 397 | 272 | 272 | 262 | 255 | 244 | 232 | 227 | |
| 3 | 21.7 | 531 | 2 | 411 | 397 | 272 | 242 | 232 | 225 | 214 | 202 | 197 | |
| 4 ^c | 21.7 | 553 | 2 | | | | | | | | | | |
| 5 | 22.4 | 555 | 1 | 411 | 397 | 272 | 266 | nd ^d | 251 | 240 | 228 | nd | |
| 6 | 22.5 | 545 | 1 | 411 | 397 | 272 | 256 | 246 | 239 | 228 | 216 | 211 | |
| 7 | 22.9 | 557 | 2 | 411 | 397 | 272 | 268 | 258 | 251 | 240 | 228 | 223 | |
| 8 | 23.3 | 573 | 2 | 425 | 411 | 286 | 270 | 260 | 253 | 242 | 230 | 225 | |
| 9 | 24.4 | 573 | 2 | 411 | 397 | 272 | 284 | 274 | 267 | 256 | 244 | 239 | |
| 10 | 24.7 | 563 | 3 | 411 | 397 | 272 | 274 | 264 | 257 | 246 | 234 | 229 | |

a: Calculated from the MH^+ signals, b: FA = unsaturated hydroxyamino-fatty acid

c: Ion assignment not done because of nontypical fragmentation, d: nd = not detected