



Supplementary Figure

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2

3

Cluster A 70 GLASKEDGRRVTPETLFEIGSVSKTFTATLAGYALTQDKMRLDDRA 115

Cluster B 70 GLASKEDGRRVTPETLFEIGSVSKTFTATLAGYALAQDKMRLDDRA 115

Cluster C 70 GLASKEDGRRVTPETLFEIGSVSKTFTVTLAGYALAQDKMRLDARA 115

Cluster D 70 GLASKEDGRRVTPETLFEIGSVSKTFTATLAGYALAQDKMRLDDRA 115

Cluster E 70 GLASKEDGRQVTPETLFEIGSVSKTFTATLAGYALAQDKMRLDDRA 115

Cluster F 70 GLASKEDGRRVTPETLFEIGSVSKTFTATLAGYALAQDKMRLDDRA 115

Cluster G 70 GLASKEDGRRVTPETLFEIGSVSKTFTATLAGYALAQDKMRLDDRA 115

Cluster H 70 GVASKEDARKVTPETLFEIGSVSKTFTATLAGYALAQDKMRLDDRA 115

Cluster A 160 DYYRQWQPTYAPGSQRLYSNPSIGLFGYLAARSLGQPFERLMEQQV 205

Cluster B 160 DYYRQWQPTYAPGSQRLYSNPSIGLFGYLAARSLGQPFERLMEQQV 205

Cluster C 160 DYYRQWQPTYAPGSQRLYSNPSIGLFGYLAARSLGQPFERLMEQQ 205

Cluster D 160 DYYRQWQPTYAPGSQRLYSNPSIGLFGYLAARSLGQPFERLMEQQ 205

Cluster E 160 DYYRQWQPTYAPGSQRLYSNPSIGLFGYLAARSLGQPFERLMEQQ 205

Cluster F 160 DYYRQWQPTYTPGSQRLYSNPSIGLFGYLAARSLGQPFERIMEQQ 205

Cluster G 160 DYYRQWQPTYAPGSQRLYSNPSIGLFGYLAARSLGQPFERIMEQRL 205

Cluster H 160 DYYRQWQPTYAPGSHRQYSNPSIGLFGYLAARSLGQPFERSMERQL 205

| | | | |
|-----------|-----|--|-----|
| Cluster A | 322 | PHRIARLPAPQALEGQRLLNKTGSTNGFGAYVAFVPGRDLGLVILA | 367 |
| Cluster B | 322 | PHRIARLPAPQALEGQRLLNKTGSTNGFGAYVAFVPGRDLGLVILA | 367 |
| Cluster C | 322 | PHRIARLPAPQALEGQRLLNKTGSTNGFGAYVAFVPGRDLGLVILA | 367 |
| Cluster D | 322 | PHRIARLPAPQALEGQRLLNKTGSTNGFGAYVAFVPGRDLGLVILA | 367 |
| Cluster E | 322 | PHRIARLSAPQALEGQRLLNKTGSTNGFGAYVAFIPGRDLGLVILA | 367 |
| Cluster F | 322 | PHRIARLPAPQAPEGQRLLNKTGSTNGFGAYVAFIPGRDLGLVILA | 367 |
| Cluster G | 322 | PHRVARLPAPQALEGQRLLNKTGSTNGFGAYVAFIPGRDLGLVILA | 367 |
| Cluster H | 322 | AHKVARLPAPQALDGQRLLNKTGSTNGFGAYLAFIPGRDVGLVILA | 367 |

Supplementary Figure S1. Multiple sequence alignment of representative *Pseudomonas*-derived cephalosporinase (PDC) amino acid sequences from clusters A to H. Each active site motif of PDC is highlighted in light yellow, light blue, and light green, respectively.