

Supplemental Figure S1

CLUSTAL 2.1 Multiple Sequence Alignments

```
Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: CMH-4          381 aa
Sequence 2: CNE-1          382 aa
Sequence 3: CNE-2          382 aa
Sequence 4: CDA-1          382 aa
Sequence 5: C_lapagei      380 aa
Start of Pairwise alignments
Aligning...
```

```
Sequences (1:2) Aligned. Score: 74.0157
Sequences (1:3) Aligned. Score: 73.4908
Sequences (1:4) Aligned. Score: 74.2782
Sequences (1:5) Aligned. Score: 78.9474
Sequences (2:3) Aligned. Score: 93.4555
Sequences (2:4) Aligned. Score: 86.1257
Sequences (2:5) Aligned. Score: 74.2105
Sequences (3:4) Aligned. Score: 86.3874
Sequences (3:5) Aligned. Score: 74.4737
Sequences (4:5) Aligned. Score: 77.8947
Guide tree file created: \[clustalw.dnd\]
```

```
There are 4 groups
Start of Multiple Alignment
```

```
Aligning...
Group 1: Sequences: 2      Score:6105
Group 2: Sequences: 3      Score:5904
Group 3: Sequences: 2      Score:6278
Group 4: Sequences: 5      Score:5955
Alignment Score 19417
```

```
CLUSTAL-Alignment file created \[clustalw.aln\]
```

[clustalw.aln](#)

CLUSTAL 2.1 multiple sequence alignment

```
CNE-1      -MKKSLCLTLLLAASCSSFAAQKELTAQQIEKLVNRTVAPLMKEQAIPGMMAVAVIYKGY
CNE-2      -MKKSLCLTLLLAASCSSLAAQKELTAQQIEKVVNRTVAPLMKEQAIPGMMAVAVIYKGY
CDA-1      -MKKSLCLTLLLAASCSTFAAPKQLTAQQIEKIVNRTISPLLKEQAIPGMMAVAVIYKGY
CMH-4      MMKKSLSALLSVACSAFAAP--MSEKQLADVVERTVTPLMKAQAIPGMMAVAVIYQGQP
C_lapagei  -MKKSLCCALLLSASFSTLAAP--VTDKQLADIVNRTIAPLMQEQAIPGMMAVAVIYQGKP
          ***** :***:: *::**  :: **: :*: :*:***::**:: *****:* *

CNE-1      LYFTWGKADVQRNQPVTRQTLFELGSVSKTFTGVLGGDALARGEISLSDPAQKYWP
CNE-2      LYFTLGKADVQRNVPVTRQTLFELGSVSKTFTGVLGGDALARGEVSLSDPAQKYWP
CDA-1      LYFTWGKADVQHNPVTRQTLFELGSVSKTFTGVLGGDTLARGEISLSDPAQKYWP
CMH-4      HYFTFGKADVAANKPVPQTLFELGSVSKTFTGVLGGDAIARKEISLADPVTKYWP
C_lapagei  HIFTWGKADIEANRPVTRQTLFELGSVSKTFTGVLGGDAIARGEIRLSDPVTKYWP
          ** ***:  * *** :*****::** *: *:* . *****.*

CNE-1      DRWREITLLQLATYTAGGLPLQVPDEVNTNDALLKFYQWQPQWAPGTQRLYANASIGLF
```

```

CNE-2      NQWKGITLLQLATYTTGGLPLQVPDEVTSNDELKIFYQDWQPQWAPGTQRLYANASIGLF
CDA-1      SQWKGITLLQLATYTAGGLPLQVPDEVTDASLLNFYQSWQPQWAPGSKRLYANASIGLF
CMH-4      KQWQGIRLLDLATYTAGGLPLQVPDDVTDNASLLRFYQSWQPKWAPGTTRLYANTSIGLF
C_lapagei  KQWQHINLLHLATYTAGGLPLQVPDDVTDRAALLTFYQNWQPQWAPGEKRLYANASIGLF
           .: *: * *.*****:*****: *:  ** *** ***:***** *****:*****

CNE-1      GALMVKPSGMSFDMKAMSKRVFEPLNLHTWINVPATEESRYAWGYRDGKAVRVSPGMLDA
CNE-2      GALMVKPSGMSFEQAMSKRVFEPLNLHTWIKVPATEESHYAWGYRDGKAVRVSPGMLDA
CDA-1      GALMVKPSGMGFEQAMTTRVLEPLKLAHTWITVPPAEESHYAWGYRNDKAVRVSPGMLDA
CMH-4      GSLAVKPSGMRFEQAMAERVFVKPLKLNHTWINVPHAEEPHYAWGYREGKAVHVSFGMLDA
C_lapagei  GSLAVKPSGMSFEQAMTTRVLQPLKLNHTWLTVPPESEQQHYAWGYRDGKAVHVSFGQLDA
           *: * ***** *: : *: *: : *: : *: : *: : *****: ***** **

CNE-1      EAYGVKSSIEDMAHWVQANMAPDRLEDKTLQQGIRLAQSRYWRVGS MYQGLGWEMLNWPV
CNE-2      EAYGVKSSIEDMAHWVQANMAPHRVEDKTLAQGIQLAQSR YWRVGS MYQGLGWEMLNWPV
CDA-1      EAYGVKSSIEDMAHWVQANMVPERVEDQNLQQGIKLAQSR YWRIGS MYQGLGWEMLNWPL
CMH-4      EAYGVKSNVKDMASWVMANMAPETLPQSTLQQGIALAQSR YWRVGAM YQGLGWEMLNWPV
C_lapagei  EAYGVKTTIEDMASWVQANMNPATVSDQKLQQGITLAQSR YWQIGEM YQGLGWEMLNWPV
           *****: : : : * * * * * : : * * * *****: : * *****: : :

CNE-1      KGKTIIDGSDNKVALAPHPATLIDPPVPAVKASWVHKTGSTGGFGSYVAFIPEKQLGIVM
CNE-2      KGKTIIDGSDNKVALAPHPATLIDPPVTAVKASWVHKTGSTGGFGSYVAFIPEKQLGIVM
CDA-1      KGKVIIDGSDNKVALAPQTAVAIIDPPAPLVKASWVHKTGSTGGFGSYVAFIPEKQLGIVM
CMH-4      DAKTVVDGSDNKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIVM
C_lapagei  KAKTVVTGSDNKVALAPATAVEINPPAPAVKASWVHKTGSTGGFGSYVAFIPQKDLGIVM
           ..*.: : ***** .. : : * .. *****: : : *****

CNE-1      LANKSYPNTERVKAAYAILEALQ
CNE-2      LANKSYPNTERVKAAYAILEALQ
CDA-1      LANKSYPNPERVKAAYAILEALQ
CMH-4      LANKSYPNPVRVETAYRILDALQ
C_lapagei  LANKSYPNPARVDAAFRILDALQ
           *****. **.: *: **:***

```

Supplemental Figure S1. ClustalW (www.genome.jp/tools-bin/clustalw) (Accessed 4 Jan. 2023) multiple sequence alignment of *Cedecea* AmpCs and CMH-4 from *E. cloacae*. CDA-1, CNE-1, CNE-2, CMH-4 from *E. cloacae* ATCC 13047, and *C. lapagei* AmpC.

Supplemental Figure S2

CLUSTAL 2.1 Multiple Sequence Alignments

```

Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: GC1          384 aa
Sequence 2: CMH-4       381 aa
Sequence 3: CHE         375 aa
Start of Pairwise alignments
Aligning...

```

```

Sequences (1:2) Aligned. Score: 83.4646
Sequences (1:3) Aligned. Score: 97.8667
Sequences (2:3) Aligned. Score: 83.4667
Guide tree file created:  \[clustalw.dnd\]

```

There are 2 groups
Start of Multiple Alignment

Aligning...

Group 1: Sequences: 2 Score:6093
Group 2: Sequences: 3 Score:5760
Alignment Score 6454

CLUSTAL-Alignment file created [\[clustalw.aln\]](#)

[clustalw.aln](#)

CLUSTAL 2.1 multiple sequence alignment

```
GC1      MMKKSLLCCALLLGISCSALATPVSEKQLAEVVANTVTPLMKAQSVPGMAVAVIYQGKPHY
CHE      MMKKSLLCCALLLGISCSALATPVSEKQLAEVVANTVTPLMKAQSVPGMAVAVIYQGKPHY
CMH-4    MMKKSLLSCALLLSVACSAFAAPMSEKQLADVVERTVTPLMKAQAIPGMAVAVIYQGQPHY
          *****.:***.:*:*:*****:* .*****.:*****:***

GC1      YTFGKADIAANKPVTPQTLFELGSISKFTFTGVLGGDAIARGEISLDDPVTRYWPQLTGKQ
CHE      YTFGKADIAANKPVTPQTLFELGSISKFTFTGVLGGDAIARGEISLDDPVTRYWPQLTGKQ
CMH-4    FTFGKADVAANKPVTPQTLFELGSVSKFTFTGVLGGDAIARKEISLADPVTKYWPELTGKQ
          :*****:*****:*****:***** *****:***:*****

GC1      WQGIRMLDLATYTAGGLPLQVPDEVTDNASLLAFYQNWQPQWKPGTTRLYANASIGLFGA
CHE      WQGIRMLDLATYTAGGLPLQVPDEVTDNASLLRFYQNWQPQWKPGTTRLYANASIGLFGA
CMH-4    WQGIRLLDLATYTAGGLPLQVPDDVTDNASLLRFYQSWQPKWAPGTTRLYANTSIGLFGS
          *****:*****:***** * .*:.* *****:*****:

GC1      LAVKPSGMPYEQAMTTRVLKPLKLDHTWINVPKAEAAHYAWGYRDGKAVRAVRVSPGMLD
CHE      LAVKPSGMPYEQAMTTRVLKPLKLDHTWINVPKAEAAHYAWGYRDG---KAVRVSPGMLD
CMH-4    LAVKPSGMRFEQAMAERVFVKPLKLNHTWINVPKAEAPHYAWGYREG---KAVHVSFGMLD
          ***** :***: *:*:*****:*****:***.*****:* :*:*****

GC1      AQAYGVKTNVQDMANWVMANMAPENVADASLKQGIALAQSRYWIRIGSMYQGLGWEMLNWP
CHE      AQAYGVKTNVQDMANWVMANMAPENVADASLKQGIALAQSRYWIRIGSMYQGLGWEMLNWP
CMH-4    AEAYGVKSNVKDMASWVMANMAPETLPQSTLQOGIALAQSRYWIRVGAMYQGLGWEMLNWP
          *:*****:*:*:***.*****.:*:*:*:*****:*****:*****

GC1      VEANTVVEGSDSKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIV
CHE      VEANTVVEGSD-----PLPVVEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIV
CMH-4    VDAKTVDGSDNKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIV
          *:*.***:*** *****.*****:*****:*****

GC1      MLANTSYPNPARVEAAYHILEALQ
CHE      MLANTSYPNPARVEAAYHILEALQ
CMH-4    MLANKSYPNPVRVETAYRILDALQ
          ****.*****.***:*.***:***
```

Supplemental Figure S2. ClustalW(www.genome.jp/tools-bin/clustalw) (Accessed 2 Dec. 2022) multiple sequence alignment of *E. cloacae* species AmpCs. CMH-4 from *E. cloacae* ATCC 13047, GC1 and CHE.