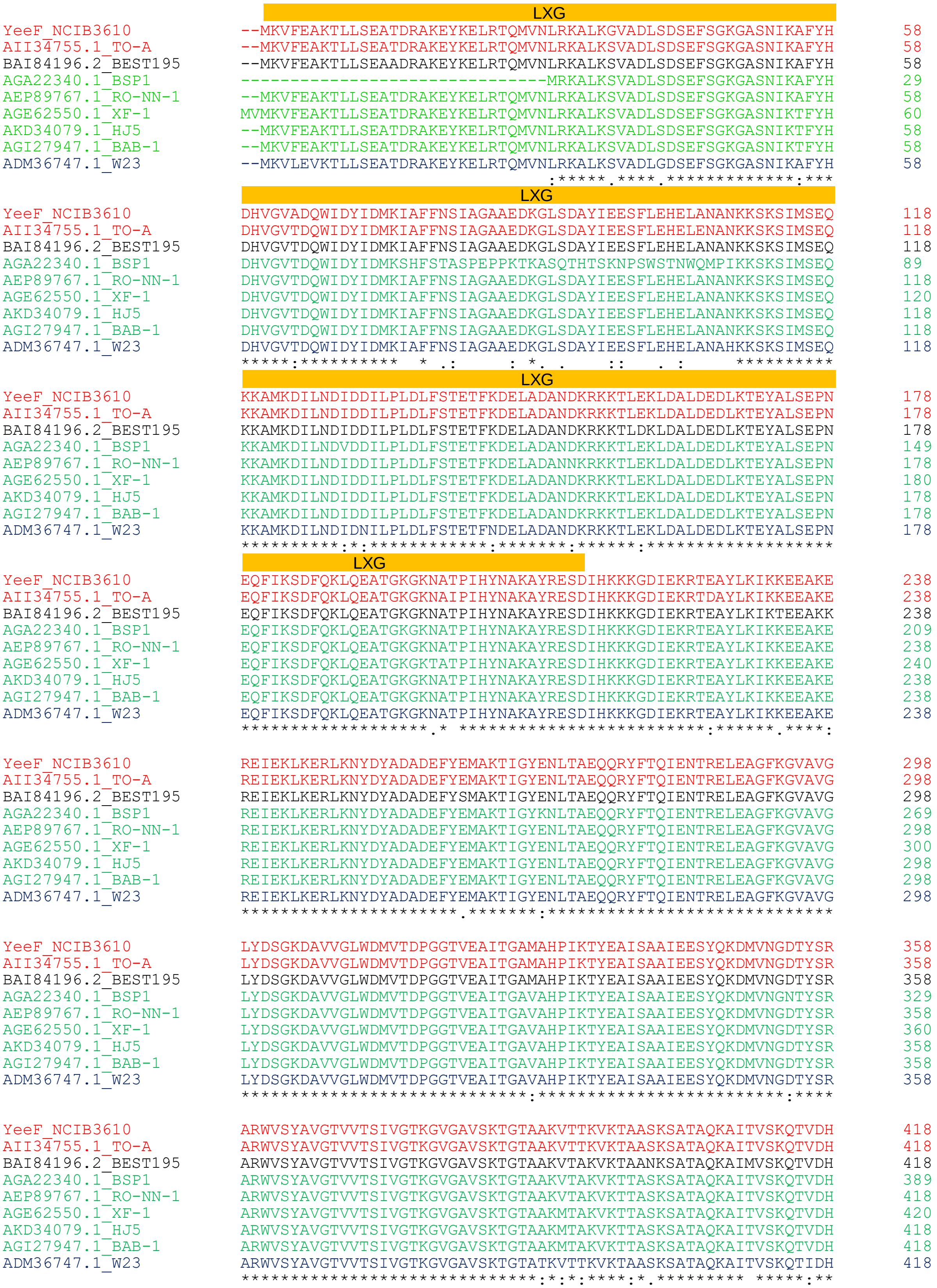
A



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                                                           LXG
YeeF_NCIB3610           --MKVFEAKTLLSEATDRAKEYKELRTQMVNLRKALKGVADLSDSEFSGKGASNIKAFYH       58
AII34755.1_TO-A         --MKVFEAKTLLSEATDRAKEYKELRTQMVNLRKALKSVADLSDSEFSGKGASNIKAFYH       58
BAI84196.2_BEST195      --MKVFEAKTLLSEAADRAKEYKELRTQMVNLRKALKSVADLSDSEFSGKGASNIKAFYH       58
AGA22340.1_BSP1         -------------------------------MRKALKSVADLSDSEFSGKGASNIKAFYH       29
AEP89767.1_RO-NN-1      --MKVFEAKTLLSEATDRAKEYKELRTQMVNLRKALKSVADLSDSEFSGKGASNIKAFYH       58
AGE62550.1_XF-1         MVMKVFEAKTLLSEATDRAKEYKELRTQMVNLRKALKSVADLSDSEFSGKGASNIKTFYH       60
AKD34079.1_HJ5          --MKVFEAKTLLSEATDRAKEYKELRTQMVNLRKALKSVADLSDSEFSGKGASNIKTFYH       58
AGI27947.1_BAB-1        --MKVFEAKTLLSEATDRAKEYKELRTQMVNLRKALKSVADLSDSEFSGKGASNIKTFYH       58
ADM36747.1_W23          --MKVLEVKTLLSEATDRAKEYKELRTQMVNLRKALKSVADLGDSEFSGKGASNIKAFYH       58
                                                       :*****.****.*************:***
                                                     LXG
YeeF_NCIB3610           DHVGVADQWIDYIDMKIAFFNSIAGAAEDKGLSDAYIEESFLEHELANANKKSKSIMSEQ       118
AII34755.1_TO-A         DHVGVTDQWIDYIDMKIAFFNSIAGAAEDKGLSDAYIEESFLEHELENANKKSKSIMSEQ       118
BAI84196.2_BEST195      DHVGVTDQWIDYIDMKIAFFNSIAGAAEDKGLSDAYIEESFLEHELANANKKSKSIMSEQ       118
AGA22340.1_BSP1         DHVGVTDQWIDYIDMKSHFSTASPEPPKTKASQTHTSKNPSWSTNWQMPIKKSKSIMSEQ       89
AEP89767.1_RO-NN-1      DHVGVTDQWIDYIDMKIAFFNSIAGAAEDKGLSDAYIEESFLEHELANANKKSKSIMSEQ       118
AGE62550.1_XF-1         DHVGVTDQWIDYIDMKIAFFNSIAGAAEDKGLSDAYIEESFLEHELANANKKSKSIMSEQ       120
AKD34079.1_HJ5          DHVGVTDQWIDYIDMKIAFFNSIAGAAEDKGLSDAYIEESFLEHELANANKKSKSIMSEQ       118
AGI27947.1_BAB-1        DHVGVTDQWIDYIDMKIAFFNSIAGAAEDKGLSDAYIEESFLEHELANANKKSKSIMSEQ       118
ADM36747.1_W23          DHVGVTDQWIDYIDMKIAFFNSIAGAAEDKGLSDAYIEESFLEHELANAHKKSKSIMSEQ       118
                        *****:**********  * .:     : *. .    ::   . :     **********
                                                     LXG
YeeF_NCIB3610           KKAMKDILNDIDDILPLDLFSTETFKDELADANDKRKKTLEKLDALDEDLKTEYALSEPN       178
AII34755.1_TO-A         KKAMKDILNDIDDILPLDLFSTETFKDELADANDKRKKTLEKLDALDEDLKTEYALSEPN       178
BAI84196.2_BEST195      KKAMKDILNDIDDILPLDLFSTETFKDELADANDKRKKTLDKLDALDEDLKTEYALSEPN       178
AGA22340.1_BSP1         KKAMKDILNDVDDILPLDLFSTETFKDELADANDKRKKTLEKLDALDEDLKTEYALSEPN       149
AEP89767.1_RO-NN-1      KKAMKDILNDIDDILPLDLFSTETFKDELADANNKRKKTLEKLDALDEDLKTEYALSEPN       178
AGE62550.1_XF-1         KKAMKDILNDIDDILPLDLFSTETFKDELADANDKRKKTLEKLDALDEDLKTEYALSEPN       180
AKD34079.1_HJ5          KKAMKDILNDIDDILPLDLFSTETFKDELADANDKRKKTLEKLDALDEDLKTEYALSEPN       178
AGI27947.1_BAB-1        KKAMKDILNDIDDILPLDLFSTETFKDELADANDKRKKTLEKLDALDEDLKTEYALSEPN       178
ADM36747.1_W23          KKAMKDILNDIDNILPLDLFSTETFNDELADANDKRKKTLEKLDALDEDLKTEYALSEPN       178
                        **********:*:************:*******:******:*******************
                                LXG
YeeF_NCIB3610           EQFIKSDFQKLQEATGKGKNATPIHYNAKAYRESDIHKKKGDIEKRTEAYLKIKKEEAKE       238
AII34755.1_TO-A         EQFIKSDFQKLQEATGKGKNAIPIHYNAKAYRESDIHKKKGDIEKRTDAYLKIKKEEAKE       238
BAI84196.2_BEST195      EQFIKSDFQKLQEATGKGKNATPIHYNAKAYRESDIHKKKGDIEKRTEAYLKIKTEEAKK       238
AGA22340.1_BSP1         EQFIKSDFQKLQEATGKGKNATPIHYNAKAYRESDIHKKKGDIEKRTEAYLKIKKEEAKE       209
AEP89767.1_RO-NN-1      EQFIKSDFQKLQEATGKGKNATPIHYNAKAYRESDIHKKKGDIEKRTEAYLKIKKEEAKE       238
AGE62550.1_XF-1         EQFIKSDFQKLQEATGKGKTATPIHYNAKAYRESDIHKKKGDIEKRTEAYLKIKKEEAKE       240
AKD34079.1_HJ5          EQFIKSDFQKLQEATGKGKNATPIHYNAKAYRESDIHKKKGDIEKRTEAYLKIKKEEAKE       238
AGI27947.1_BAB-1        EQFIKSDFQKLQEATGKGKNATPIHYNAKAYRESDIHKKKGDIEKRTEAYLKIKKEEAKE       238
ADM36747.1_W23          EQFIKSDFQKLQEATGKGKNATPIHYNAKAYRESDIHKKKGDIEKRTEAYLKIKKEEAKE       238
                        *******************.* *************************:******.****:

YeeF_NCIB3610           REIEKLKERLKNYDYADADEFYEMAKTIGYENLTAEQQRYFTQIENTRELEAGFKGVAVG       298
AII34755.1_TO-A         REIEKLKERLKNYDYADADEFYEMAKTIGYENLTAEQQRYFTQIENTRELEAGFKGVAVG       298
BAI84196.2_BEST195      REIEKLKERLKNYDYADADEFYSMAKTIGYENLTAEQQRYFTQIENTRELEAGFKGVAVG       298
AGA22340.1_BSP1         REIEKLKERLKNYDYADADEFYEMAKTIGYKNLTAEQQRYFTQIENTRELEAGFKGVAVG       269
AEP89767.1_RO-NN-1      REIEKLKERLKNYDYADADEFYEMAKTIGYENLTAEQQRYFTQIENTRELEAGFKGVAVG       298
AGE62550.1_XF-1         REIEKLKERLKNYDYADADEFYEMAKTIGYENLTAEQQRYFTQIENTRELEAGFKGVAVG       300
AKD34079.1_HJ5          REIEKLKERLKNYDYADADEFYEMAKTIGYENLTAEQQRYFTQIENTRELEAGFKGVAVG       298
AGI27947.1_BAB-1        REIEKLKERLKNYDYADADEFYEMAKTIGYENLTAEQQRYFTQIENTRELEAGFKGVAVG       298
ADM36747.1_W23          REIEKLKERLKNYDYADADEFYEMAKTIGYENLTAEQQRYFTQIENTRELEAGFKGVAVG       298
                        **********************.*******:*****************************

YeeF_NCIB3610           LYDSGKDAVVGLWDMVTDPGGTVEAITGAMAHPIKTYEAISAAIEESYQKDMVNGDTYSR       358
AII34755.1_TO-A         LYDSGKDAVVGLWDMVTDPGGTVEAITGAMAHPIKTYEAISAAIEESYQKDMVNGDTYSR       358
BAI84196.2_BEST195      LYDSGKDAVVGLWDMVTDPGGTVEAITGAMAHPIKTYEAISAAIEESYQKDMVNGDTYSR       358
AGA22340.1_BSP1         LYDSGKDAVVGLWDMVTDPGGTVEAITGAVAHPIKTYEAISAAIEESYQKDMVNGNTYSR       329
AEP89767.1_RO-NN-1      LYDSGKDAVVGLWDMVTDPGGTVEAITGAVAHPIKTYEAISAAIEESYQKDMVNGDTYSR       358
AGE62550.1_XF-1         LYDSGKDAVVGLWDMVTDPGGTVEAITGAVAHPIKTYEAISAAIEESYQKDMVNGDTYSR       360
AKD34079.1_HJ5          LYDSGKDAVVGLWDMVTDPGGTVEAITGAVAHPIKTYEAISAAIEESYQKDMVNGDTYSR       358
AGI27947.1_BAB-1        LYDSGKDAVVGLWDMVTDPGGTVEAITGAVAHPIKTYEAISAAIEESYQKDMVNGDTYSR       358
ADM36747.1_W23          LYDSGKDAVVGLWDMVTDPGGTVEAITGAVAHPIKTYEAISAAIEESYQKDMVNGDTYSR       358
                        *****************************:*************************:****

YeeF_NCIB3610           ARWVSYAVGTVVTSIVGTKGVGAVSKTGTAAKVTTKVKTAASKSATAQKAITVSKQTVDH       418
AII34755.1_TO-A         ARWVSYAVGTVVTSIVGTKGVGAVSKTGTAAKVTTKVKTAASKSATAQKAITVSKQTVDH       418
BAI84196.2_BEST195      ARWVSYAVGTVVTSIVGTKGVGAVSKTGTAAKVTAKVKTAANKSATAQKAIMVSKQTVDH       418
AGA22340.1_BSP1         ARWVSYAVGTVVTSIVGTKGVGAVSKTGTAAKVTAKVKTTASKSATAQKAITVSKQTVDH       389
AEP89767.1_RO-NN-1      ARWVSYAVGTVVTSIVGTKGVGAVSKTGTAAKVTAKVKTTASKSATAQKAITVSKQTVDH       418
AGE62550.1_XF-1         ARWVSYAVGTVVTSIVGTKGVGAVSKTGTAAKMTAKVKTTASKSATAQKAITVSKQTVDH       420
AKD34079.1_HJ5          ARWVSYAVGTVVTSIVGTKGVGAVSKTGTAAKMTAKVKTTASKSATAQKAITVSKQTVDH       418
AGI27947.1_BAB-1        ARWVSYAVGTVVTSIVGTKGVGAVSKTGTAAKMTAKVKTTASKSATAQKAITVSKQTVDH       418
ADM36747.1_W23          ARWVSYAVGTVVTSIVGTKGVGAVSKTGTATKVTTKVKTAASKSATAQKAITVSKQTIDH       418
                        ******************************:*:*:****:*.********* *****:**
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S4 Fig A. continued

A

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YeeF_NCIB3610           IKQKVNTGIEVSKKHVKTKLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQ       478
AII34755.1_TO-A         IKQKVNTGIEVSKKHVKTKLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQ       478
BAI84196.2_BEST195      IKQKVNTGIEVSKKHVKTRLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQ       478
AGA22340.1_BSP1         IKQKVNTGIEVSKKHVKTKLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQ       449
AEP89767.1_RO-NN-1      IKQKVNTGIEVSKKHVKTKLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQ       478
AGE62550.1_XF-1         IKQKVNTGIEGSKKHVKTKLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQ       480
AKD34079.1_HJ5          IKQKVNTGIEGSKKHVKTKLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQ       478
AGI27947.1_BAB-1        IKQKVNTGIEGSKKHVKTKLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQ       478
ADM36747.1_W23          IKQKVNKGIEVSKKHVKTKLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQ       478
                        ******.*** *******:*****************************************
                                                                toxin
YeeF_NCIB3610           KFAKVILPKPYGTSSSGRRTPAPHVPPVTVKYGEHFARWSRKKVLKPNIIYKTKEGYTYT       538
AII34755.1_TO-A         KFAKVILPKPYGTSSSGRRTPAPHVPPVTVKYGEHFARWSRKKVLKPNVIYKTKEGYTYT       538
BAI84196.2_BEST195      KFAKVILPKPYGTSSSGRRTPAPHVPPVTVKYGEHFARWSRKKVLKPNVIYKTKEGYTYT       538
AGA22340.1_BSP1         KFAKVILPKPYGTSSSGRRTPAPHVPPVTVKYGEHFARWSRKKVLKPNIIYKTKEGYTYT       509
AEP89767.1_RO-NN-1      KFAKVILPKPYGTSSSGRRTPAPHVPPVTVKYGEHFARWSRKKVLKPNIIYKTKEGYTYT       538
AGE62550.1_XF-1         KFAKVILPKPYGTSSSGRRTPAPHVPPVTVKYGEHFARWSRKKVLKPNIIYKTKEGYTYT       540
AKD34079.1_HJ5          KFAKVILPKPYGTSSSGRRTPAPHVPPVTVKYGEHFARWSRKKVLKPNIIYKTKEGYTYT       538
AGI27947.1_BAB-1        KFAKVILPKPYGTSSSGRRTPAPHVPPVTVKYGEHFARWSRKKVLKPNIIYKTKEGYTYT       538
ADM36747.1_W23          KFAKVILPKPYGTSSSGRRTPAPVVPPVTVKYGEHYARWSRKKVLKPNIIYKTKEGYTYT       538
                        *********************** ***********:************:***********
                                                     toxin
YeeF_NCIB3610           TDNYGRITSVKADLQLGEAKRNQYAQTNAGKPQDRKPDDDGGHLIATQFKGSGQFDNIVP       598
AII34755.1_TO-A         TDNYGRITSVKADLQLGEAKRNQYAQTNAGKPQDRKPDDDGGHLIATQFKGSGQFDNIVP       598
BAI84196.2_BEST195      TDNYGRITSVKADLQLGEAKRNQYAQTNAGKPQDRKPDDDGGHLIATQFKGSGQFDNIVP       598
AGA22340.1_BSP1         TDNYGRITSVKADLQLGEAKRNQYAQTNAGKPQDRKPDDDGGHLIATQFKGSGQFDNIVP       569
AEP89767.1_RO-NN-1      TDNYGRITSVKADLQLGEAKRNQYAQTNAGKPQDRKPDDDGGHLIATQFKGSGQFDNIVP       598
AGE62550.1_XF-1         TDNYGRITSVKADLQLGEAKRNQYAQTNAGKPQDRKPDDDGGHLIATQFKGSGQFDNIVP       600
AKD34079.1_HJ5          TDNYGRITSVKADLQLGEAKRNQYAQTNAGKPQDRKPDDDGGHLIATQFKGSGQFDNIVP       598
AGI27947.1_BAB-1        TDNYGRITSVKADLQLGEAKRNQYAQTNAGKPQDRKPDDDGGHLIATQFKGSGQFDNIVP       598
ADM36747.1_W23          TDNYGRITSVKADLQLGEAKRNQYAQSHAGKPQDRKPDDDGGHLIATQFKGSGQFDNIVP       598
                        **************************::********************************
                                              toxin
YeeF_NCIB3610           MNSQINRSGGKWYEMEQEWAKALSKKPPKKVAVQIEPVYSGDSLRPSYFDVTYKIGSRKE       658
AII34755.1_TO-A         MNSQINRSGGKWYEMEQEWAKALSKKPPKKVAVQIEPVYSGDSLRPSYFDVTYKIGSRKE       658
BAI84196.2_BEST195      MNSQINRSGGKWYNMEQVWSKALSQKPPKQVTVKINNIYEGDSLRPSKFIVVYKVGDKEP       658
AGA22340.1_BSP1         MNSQINRSGGRWYEMEQEWAKALKEEPPQKVNVNIKAIYKGDSLRPDKFIVKYRIGDADF       629
AEP89767.1_RO-NN-1      MNSQINRSGGRWYEMEQEWAKALKEEPPQKVNVNIKAIYKGDSLRPDKFIVKYRIGDADF       658
AGE62550.1_XF-1         MNSQINRSGGRWYEMEQEWAKALKEEPPQKVNVNIKAIYKGDSLRPDKFIVKYRIGDADF       660
AKD34079.1_HJ5          MNSQINRSGGRWYEMEQEWAKALKEEPPQKVNVNIKAIYKGDSLRPDKFIVKYRIGDADF       658
AGI27947.1_BAB-1        MNSQINRSGGRWYEMEQEWAKALKEEPPQKVNVNIKAIYKGDSLRPDKFIVKYRIGDADF       658
ADM36747.1_W23          MNSQINRSGGRWYEMEQEWAKALKEEPPQKVNVNIKAIYKGDSLRPDKFIVKFRIGDADF       658
                        **********:**:*** *:***.::**::* *:*: :*.******. * * :::*. .

YeeF_NCIB3610           ISVSIKNQPGG          669
AII34755.1_TO-A         ISVSIKNQPGG          669
BAI84196.2_BEST195      VRTIIKNKAGG          669
AGA22340.1_BSP1         EKVTLKNQSGG          640
AEP89767.1_RO-NN-1      EKVTLKNQSGG          669
AGE62550.1_XF-1         EKVTLKNQSGG          671
AKD34079.1_HJ5          EKVTLKNQSGG          669
AGI27947.1_BAB-1        EKVTLKNQSGG          669
ADM36747.1_W23          EKVTIKNQSGG          669
                          . :**: **
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S4 Fig A

B

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                                                   LXG
AMR62839.1_ATCC49760       MKVFEADSLLSEADKRTKEYKELRSQMVKLRKAFKAVADLDESEFSGKGANNIKAFYHDH      60
YobL_NCIB3610              MKVFEADSLLFEADKRTKEYKELRSQMVKLKKAFKEVANLDDSEFSGKGADNIKAFYHGH      60
AII35881.1_TO-A            MKVFEADSLLFEADKRTKEYKELRSQMVKLKKAFKEVANLDDSEFSGKGADNIKAFYHGH      60
AGA23389.1_BSP1            MKVFEADSLLFEADKRTKEYKELRSQMVKLRKAFQNVANLDDSEFSGKGADNIKAFYHDH      60
BAI85563.1_BEST195         MKVFEADSLLFEADKRTKEYKELRSQMVKLRKAFQNVANLDDSEFSGKGADNIKAFYHDH      60
AGI29216.1_BAB-1           MKVFEADSLLFEADKRTKEYKELRSQMVKLRKAFQNVATLDDSEFSGKGADNIKAFYHDH      60
AKD35310.1_HJ5             MKVFEADSLLFEADKRTKEYKELRSQMVKLRKAFQNVATLDDSEFSGKGADNIKAFYHDH      60
AGE63731.1_XF-1            --------------------------MVKLRKAFQNVATLDDSEFSGKGADNIKAFYHDH      34
YokI_NCIB3610              MKVFEADSLLSEADKRTKEYKELRSQMVKLKKAFKAVADLDDSKFSGKGADNIKAFYHDH      60
AEP89572.1_RO-NN-1         MKVFEAKSLLSEAENRAKDYKDLKNQMIKLRKAFKAVADLDDSEFSGKGANNIKAFYHDH      60
BAI84001.1_BEST195         MKVFEAKSLLSEAENRAKDYKELKNQMIKLRKAFKAVADLDDSEFSGKGANNIKAFYHDH      60
                                                     *:**:***: ** **:*:******:*******.*

                                                   LXG
AMR62839.1_ATCC49760       VGVTDQWIDLIDMKIAFLSSVSTKVEDAKMSDAYIEESFLEHELVNAYNKSKSIMSEQKK      120
YobL_NCIB3610              VGVTDQWIDLIDMKIAFLSSMSATLEDAKMSDAYIEESFLEHELANAYAKSKSIMSEQKK      120
AII35881.1_TO-A            VGVTDQWIDLIDMKIAFLSSMSATLEDAKMSDAYIEESFLEHELANAYAKSKSIMSEQKK      120
AGA23389.1_BSP1            VGVTDQWIDLIDMKIAFLSSISAKLEDAKMSDAYIEESFLEHELANAYTKSKSIMSEQKK      120
BAI85563.1_BEST195         VGVTDQWIDLIDMKIAFLSSMSAKLEDAKMSDAYIEESFLEHELANAYTKSKSIMSEQKK      120
AGI29216.1_BAB-1           VGVTDQWIDLIDMKIAFLSRMSAKLEDAKMSDAYIEESFLEHELANAYTKSKSIMSEQKK      120
AKD35310.1_HJ5             VGVTDQWIDLIDMKIAFLSRMSAKLEDAKMSDAYIEESFLEHELANAYTKSKSIMSEQKK      120
AGE63731.1_XF-1            VGVTDQWIDLIDMKIAFLSRMSAKLEDAKMSDAYIEESFLEHELANAYTKSKSIMSEQKK      94
YokI_NCIB3610              VGVTDQWIDLIDMKIVFLSSISAKLEDAKMSDAYIEESFLEHELVNAYTKSKSIMSEQKK      120
AEP89572.1_RO-NN-1         VGVTDQWIDLIEMKIAFLTSISGVLEEASLSDAYIEESFLEHELANAYKKSKSIMSEQKK      120
BAI84001.1_BEST195         VGVTDQWIDLIEMKIAFLTSISGVLEDASLSDAYIEESFLEHELTNAYKKSKSIMSEQKK      120
                           ***********:***.**: :*  :*:*.:**************.*** ***********

                                                   LXG
AMR62839.1_ATCC49760       AMKDILNDINDILPLEIFSTEDFKDKLSSAEDKREKTVDTLSNLDESLKTEYAETEPNEQ      180
YobL_NCIB3610              AMKDILNNINDILPLEIFSTEDFKDKLSSADDKREKTIDKLNKLDEDLKTEYAETEPNEQ      180
AII35881.1_TO-A            AMKDILNNINDILPLEIFSTEDFKDKLSSADDKREKTIDKLNKLDEDLKTEYAETEPNEQ      180
AGA23389.1_BSP1            AMKDILNDINDILPLEIFSTENFKDKLSSADDKREKTIDKLNKLDENLKSEYAETEPNEQ      180
BAI85563.1_BEST195         AMKDILNDINDILPLEIFSTEDFKDKLSSADDKREKTIDKLNKLDEDLKTEYAETEPNEQ      180
AGI29216.1_BAB-1           AMKDILNDINDILPLEIFSTEDFKDKLSSADDKREKTIDKLNKLDEDLKTEYVETEPNEQ      180
AKD35310.1_HJ5             AMKDILNDINDILPLEIFSTEDFKDKLSSADDKREKTIDKLNKLDEDLKTEYVETEPNEQ      180
AGE63731.1_XF-1            AMKDILNDINDILPLEIFSTEDFKDKLSSADDKREKTIDKLNKLDEDLKTEYVETEPNEQ      154
YokI_NCIB3610              AMKDILNDINDILPLEIFSTEDFKDKLSSADDKREKTIDKINKLDEDLKTEYAETEQNEQ      180
AEP89572.1_RO-NN-1         AMKDILNDIDDILPLDLFSTETFKDELSSAENKRKKTVDKICDVDENLKTEYAITEPNEQ      180
BAI84001.1_BEST195         AMKDILNDIDDILTLDLFSTETFKDELSSAENKRKKTVDKIGDVDENLKTEYAITEPNEQ      180
                           *******:*:*** *::**** ***:****::**:**:*.: .:**.**:**. ** ***

                                 LXG
AMR62839.1_ATCC49760       FIQQDFKKLQGSTGKGKNATPIHYNAKAYRESDIHKKKDDIEKHSEAYLSVKKEEAKERE      240
YobL_NCIB3610              FIQQDFKKLQESTGKGKNATPIHYNAKAYRESDIHKKKGDIEKHSEAYLSVKKEEAKERE      240
AII35881.1_TO-A            FIQQDFKKLQESTGKGKNATPIHYNAKAYRESDIHKKKGDIEKHSEAYLSVKKEEAKERE      240
AGA23389.1_BSP1            FIQQDFKKLQESTGKGKNATPIHYNAKAYRESDIHKKKGDIEKHSEAYLSVKQEEAKERE      240
BAI85563.1_BEST195         FIQQDFKKLQESTGKGKNATPIHYNAKAYRESDIHKKKGDIEKHSEAYLSVKKEEAKDRE      240
AGI29216.1_BAB-1           FIQQDFKKLQESTGKGKNATPIHYNAKAYRESDIHKKKGDIEKHSESYLSVKKEEAKERE      240
AKD35310.1_HJ5             FIQQDFKKLQESTGKGKNATPIHYNAKAYRESDIHKKKGDIEKHSESYLSVKKEEAKERE      240
AGE63731.1_XF-1            FIQQDFKKLQESTGKGKNATPIHYNAKAYRESDIHKKKGDIEKHSESYLSVKKEEAKERE      214
YokI_NCIB3610              FIQQDFKKLQESTGKGKNATPIHYSAKAYRESDIHKKKGDIEQHSEAYLTVKKEEAKERE      240
AEP89572.1_RO-NN-1         FIKADFQKLQESTGKGKNATPLHYNAKAYRESDIHKKKGDIEKQSEAYLKIKKEEAKKHE      240
BAI84001.1_BEST195         FIKADFQKLQESTGKGKNATPLHYNAKAYRESDIHKKKGDIEKQSEAYLKIKKEEANKCE      240
                           **: **:*** **********:**.*************.***::**:**.:*:***:. *

AMR62839.1_ATCC49760       IKELKKKLNDGVSDPDEYLEIAKKVGYENLEPAQVQLAVQIEQAKQLEGAGEITWDIVKG      300
YobL_NCIB3610              IKELKKKLNDGVSDPDEYLEIAKKVGYENLEPTQVQLAVQIEQAKQLEGAGEITWDIVKG      300
AII35881.1_TO-A            IKELKKKLNDGVSDPDEYLEIAKKVGYENLEPTQVQLAVQIEQAKQLEGAGEITWDIVKG      300
AGA23389.1_BSP1            IKELKKKLNDGVSDPDEYLEIAKKVGYENLEPAQVQLAVQIEQAKQLEGAGEITWDIVKG      300
BAI85563.1_BEST195         IKELKKKLNDGVSDPVEYLEIAKKVGYENLEPAQVQLAVQIEQAKQLEGAGEITWDIVKG      300
AGI29216.1_BAB-1           IKELKKKLNDGVSDPDEYLEIAKKVGYENLEPAQVQLAVQIEQAKQLEEAGEVTWDIVKG      300
AKD35310.1_HJ5             IKELKKKLNDGVSDPDEYLEIAKKVGYENLEPAQVQLAVQIEQAKQLEEAGEVTWDIVKG      300
AGE63731.1_XF-1            IKELKKKLNDGVSDPDEYLEIAKKVGYENLEPAQVQLAVQIEQAKQLEEAGEVTWDIVKG      274
YokI_NCIB3610              IKELKKKLNDGVSDPDEYLEIAKKVGYENLEPAQVQLAVQIEQAKQLEGAGEITWDIVKG      300
AEP89572.1_RO-NN-1         IKDLKRQLV-KVTDPDEYLKIAKKIGYENLEPEQQVYFRQLEELQQK-------AEIGKG      292
BAI84001.1_BEST195         IKDLKKQLV-KVTDPDEYLKIAKKIGYENLEPEQQVYFRQLEELQQK-------AEIGKG      292
                           **:**::*   *:** ***:****:******* *     *:*: :*         :* **
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S4 Fig B continued

B

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AMR62839.1_ATCC49760      VGVGLYDVGKDTVTGIWDFITDPGETLSALGNAVIHPVKTYDAISAAIEESYQKDMVNGD     360
YobL_NCIB3610             VGVGLYDVGKDTVTGIWDFITDPGETLSALGNAAMHPVKTYDAISAAIEESYQKDMVNGD     360
AII35881.1_TO-A           VGVGLYDVGKDTVTGIWDFITDPGETLSALGNAAMHPVKTYDAISAAIEESYQKDMVNGD     360
AGA23389.1_BSP1           VGVGLYDVGKDTVTGLWDFITDPGETLSALGNAVIHPVKTYDAISAAIEESYQKDMVNGD     360
BAI85563.1_BEST195        VGVGLYDVGKDTVTGIWDFITDPGETLSALGNAVIHPVKTYDAISAAIEESYQKDMVNGD     360
AGI29216.1_BAB-1          VGVGLYDVGKDTVTGIWDFITDPGETLSALGNAVIHPVKTYDAISAAIEESYQKDMVNGD     360
AKD35310.1_HJ5            VGVGLYDVGKDTVTGIWDFITDPGETLSALGNAVIHPVKTYDAISAAIEESYQKDMVNGD     360
AGE63731.1_XF-1           VGVGLYDVGKDTVTGIWDFITDPGETLSALGNAVIHPVKTYDAISAAIEESYQKDMVNGD     334
YokI_NCIB3610             VGVGLYDVGKDTVTGLWDFITDPGETLSALGNAVIHPVKTYDAISAAIEESYQKDMVNGD     360
AEP89572.1_RO-NN-1        IAMGMYEAGKDTVMGLYQLARHPIETLSGTVNAALHPIDTYKIIAKDIEDTFQRDMINGD     352
BAI84001.1_BEST195        IAMGMYEAGKDTVMGLYQLARHPIESLSGTVNAALHPIDTYKIIAKDIEDTFQREMINGD     352
                          :.:*:*:.***** *::::  .* *:**.  **.:**:.**. *:  **:::*::*:***

AMR62839.1_ATCC49760      AYSRSRWVTYAVGSVAAAIVGTKGAGAINKADAAGKVINKA-----SQ--AGKKLKDVKL     413
YobL_NCIB3610             AYSRSRWVTYAIGSVAVAVVGTKGAGAINKADAAGKVINKA-----SQ--AGKKIKDVKI     413
AII35881.1_TO-A           AYSRSRWVTYAIGSVAVAVVGTKGAGAINKADAAGKVINKA-----SQ--AGKKIKDVKI     413
AGA23389.1_BSP1           AYSRSRWVTYAIGSVAAAVVGTKGAGAINKADAAGKVINKA-----SQ--AGKKIKDVKI     413
BAI85563.1_BEST195        AYSRSRWVTYAVGSVAVAVFGTKGAGAINKADAAGKVINKA-----SQ--AGKKIKDVKI     413
AGI29216.1_BAB-1          AYSRSRWVTYAVGSVAVAVFGNKGAGAINKADAAGKVINKA-----SQ--AGKKIKDVKI     413
AKD35310.1_HJ5            AYSRSRWVTYAVGSVAVAVFGTKGAGAINKADAAGKVINKA-----SQ--AGKKIKDVKI     413
AGE63731.1_XF-1           AYSRSRWVTYAVGSVAVAVFGTKGAGAINKADAAGKVINKA-----SQ--AGKKIKDVKI     387
YokI_NCIB3610             AYSRSRWVTYAIGSVAAAVIGTKGAGAINKADAAGKVINKA-----SQ--AGKKIKDVKI     413
AEP89572.1_RO-NN-1        SYSRAKWVSYVGSTVVLAIVGPKGIDKVSKVAKAGSKVAAIKALEASKAGIKKGIEYVKI     412
BAI84001.1_BEST195        SHSRAKWVSYVGSTVVLAIVGPKGIDKVSKVAKAGSKVAALKTLEVSKTGIKKGIEYVKI     412
                          ::**::**:*. .:*. *:.* ** . :.*.  **. :        *:    * :: **:

AMR62839.1_ATCC49760      PDLLPYNPKNKL-ALADNVPYNVVDSQNLKNELLTNAKKLPDG----TRKPFTGQKIIP-     467
YobL_NCIB3610             PDLLPYNPKYKL-ALADNVPYNVVDSQNLKNELLTNAKKIPDG----TRKPFTGQKKSP-     467
AII35881.1_TO-A           PDLLPYNPKYKL-ALADNVPYNVVDSQNLKNELLTNAKKIPDG----TRKPFTGQKKSP-     467
AGA23389.1_BSP1           PDLLPYNPKYDF-ALADNVPYNVVDSQSLKNELLTNAKKIPDG----TRKPFTGQKISP-     467
BAI85563.1_BEST195        PDLLPYNPKYDF-PLADNVPYNVVDSQSLKNELLTNAKKIPDG----TRKPFTGQKISP-     467
AGI29216.1_BAB-1          PDLLPYNPKYDF-ALADNVPYNVVDSQSLKNELLTNAKKIPDG----TRKPFTGQKISP-     467
AKD35310.1_HJ5            PDLLPYNPKYDF-ALADNVPYNVVDSQSLKNELLTNAKKIPDG----TRKPFTGQKISP-     467
AGE63731.1_XF-1           PDLLPYNPKYDF-ALADNVPYNVVDSQSLKNELLTNAKKIPDG----TRKPFTGQKISP-     441
YokI_NCIB3610             PDLLPYNPKYDL-AMAGDVPYNVVDGENLKNQLMSFAKGSD-K----EVKPFDVVDYRPS     467
AEP89572.1_RO-NN-1        PNVFEQ--HYAMAGGSGTFPFNVIDGENYKSSALEIFKTSSTVQGLKKAKPHEVVNELK-     469
BAI84001.1_BEST195        PSVFEQ--QFAMAGGSGTFPFNVLDGENYKNSALEIFKNSSTVQGLKKAKPHEVVNELK-     469
                          *.::    :  :   :. .*:**:*.:. *.. :   *           **.   .

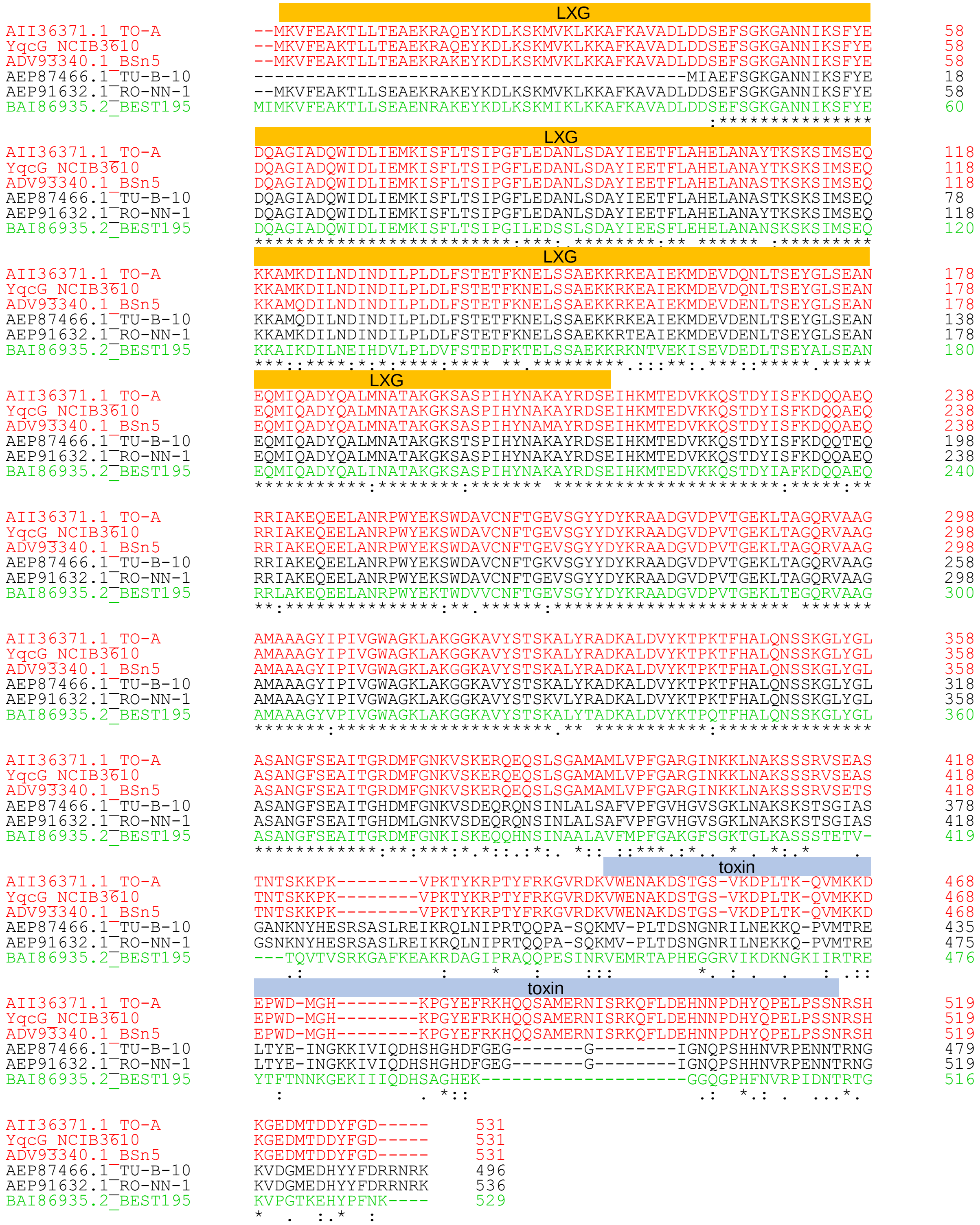
AMR62839.1_ATCC49760      ------------PWLNKEKYEAYEIEGKVKAK----GKVKDVSRRVYTMKDIDINQKTEF     511
YobL_NCIB3610             ------------PWLNKEKYDAYEIEGKVKAK----GKVKDVSRRVYTMKDIDINQKTEF     511
AII35881.1_TO-A           ------------PWLNKEKYDAYEIEGKVKAK----GKVKDVSRRVYTMKDIDINQKTEF     511
AGA23389.1_BSP1           ------------PWLNKEKYDAYEIEGKVKAK----GKVKDVSRRVYTMKDIDINQKTEF     511
BAI85563.1_BEST195        ------------PWLNKEKYDAYEIEGKVKAK----GKVKDVSRRVYTMKDIDINQKTEF     511
AGI29216.1_BAB-1          ------------PWLNKEKYEAYEIEGKVKAK----GKVKDVSRRVYTMKDIDINQKTEF     511
AKD35310.1_HJ5            ------------PWLNKEKYEAYEIEGKVKAK----GKVKDVSRRVYTMKDIDINQKTEF     511
AGE63731.1_XF-1           ------------PWLNKEKYEAYEIEGKVKAK----GKVKDVSRRVYTMKDIDINQKTEF     485
YokI_NCIB3610             NSPLENHHGVMDVWAKHN-VPNYVSRGSNTPTVALTKEQHNATKKVYREWL---------     517
AEP89572.1_RO-NN-1        ------------TF----QSRKYTFGGQS-FLIDKRGMKHILERHHPNLWDGSIKSQQSF     512
BAI84001.1_BEST195        ------------TF----QSRKYTFGGQS-FLIDKRGMKHILERHHPNLWDGSIKSQQSF     512
                                                        toxin

AMR62839.1_ATCC49760      GVTNL----------QLMKNGNAPYAKDGTQINLHHL----IQEEPGPMLE---IPNSLH     554
YobL_NCIB3610             GVTNL----------QLMKNGNAPYAKDGTQINLHHL----IQEEPGPMLE---IPNSLH     554
AII35881.1_TO-A           GVTNL----------QLMKNGNAPYAKDGTQINLHHL----IQEEPGPMLE---IPNSLH     554
AGA23389.1_BSP1           GVTNL----------QLMKNGNAPYAKDGTQINLHHL----IQEEPGPMLE---IPNSLH     554
BAI85563.1_BEST195        GVTNL----------QLMKNGNAPYAEDGTQINLHHL----IQEEPGPMLE---IPNSLH     554
AGI29216.1_BAB-1          GVTNL----------QLMKNGNAPYAKDGTQINLHHL----IQEEPGPMLE---IPNSLH     554
AKD35310.1_HJ5            GVTNL----------QLMKNGNAPYAKDGTQINLHHL----IQEEPGPMLE---IPNSLH     554
AGE63731.1_XF-1           GVTNL----------QLMKNGNAPYAKDGTQINLHHL----IQEEPGPMLE---IPNSLH     528
YokI_NCIB3610             ----------------FEKTGK----KVGGKVNWKEVSPREIQELTEKMFDAANVPKEAR     557
AEP89572.1_RO-NN-1        LNKEMTVNDVADAIESIMKQNREELTKKGTKFSYQIRGTYEGQ-----------------     555
BAI84001.1_BEST195        LNKEMTVNDVADAIESIMKQNREELTKKGTKFSYQIRGSYEGQ-----------------     555
                                              toxin                 *

AMR62839.1_ATCC49760      TKYSDIIHKLKSDGESFRNDKVLKAQYESFRS--------------    586
YobL_NCIB3610             TKYSDVIHQLKSDGESFRNDKVLKAQYESFRKRYWKWRAKQFENEN    600
AII35881.1_TO-A           TKYSDVIHQLKSDGESFRNDKVLKAQYESFRKRYWKWRAKQFENEN    600
AGA23389.1_BSP1           TKYSDVIHQLKSDGESFRNDKVLKAQYESFRKRYWKWRAKQFENEN    600
BAI85563.1_BEST195        TKYSDVIHQLKSDGESFRNDKVLKAQYESFRKRYWKWRAKQFENEN    600
AGI29216.1_BAB-1          TKYSDVIHQLKSDGESFRNDKVLKAQYESFRKRYWKWRAKQFENEN    600
AKD35310.1_HJ5            TKYSDVIHQLKSDGESFRNDKVLKAQYESFRKRYWKWRAKQFENEN    600
AGE63731.1_XF-1           TKYSDVIHQLKSDGESFRNDKVLKAQYESFRKRYWKWRAKQFENEN    574
YokI_NCIB3610             QQYYN-----------------------AFNQY--NFRK-------    571
AEP89572.1_RO-NN-1        -KY---------------------------VVGFQKGRVGQFYPEK    573
BAI84001.1_BEST195        -QY---------------------------VVGFQKGRVGQFYPEK    573
                           :*
```

S4 Fig B

C



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                                                       LXG
AII36371.1_TO-A          --MKVFEAKTLLTEAEKRAQEYKDLKSKMVKLKKAFKAVADLDDSEFSGKGANNIKSFYE       58
YqcG_NCIB3610            --MKVFEAKTLLTEAEKRAQEYKDLKSKMVKLKKAFKAVADLDDSEFSGKGANNIKSFYE       58
ADV93340.1_BSn5          --MKVFEAKTLLTEAEKRAKEYKDLKSKMVKLKKAFKAVADLDDSEFSGKGANNIKSFYE       58
AEP87466.1_TU-B-10       --------------------------------------------MIAEFSGKGANNIKSFYE     18
AEP91632.1_RO-NN-1       --MKVFEAKTLLSEAEKRAKEYKDLKSKMVKLKKAFKAVADLDDSEFSGKGANNIKSFYE       58
BAI86935.2_BEST195       MIMKVFEAKTLLSEAENRAKEYKDLKSKMIKLKKAFKAVADLDDSEFSGKGANNIKSFYE       60
                                                                     :***************
                                                      LXG
AII36371.1_TO-A          DQAGIADQWIDLIEMKISFLTSIPGFLEDANLSDAYIEETFLAHELANAYTKSKSIMSEQ       118
YqcG_NCIB3610            DQAGIADQWIDLIEMKISFLTSIPGFLEDANLSDAYIEETFLAHELANAYTKSKSIMSEQ       118
ADV93340.1_BSn5          DQAGIADQWIDLIEMKISFLTSIPGFLEDANLSDAYIEETFLAHELANASTKSKSIMSEQ       118
AEP87466.1_TU-B-10       DQAGIADQWIDLIEMKISFLTSIPGFLEDANLSDAYIEETFLAHELANASTKSKSIMSEQ       78
AEP91632.1_RO-NN-1       DQAGIADQWIDLIEMKISFLTSIPGFLEDANLSDAYIEETFLAHELANAYTKSKSIMSEQ       118
BAI86935.2_BEST195       DQAGIADQWIDLIEMKISFLTSIPGILEDSSLSDAYIEESFLEHELANANSKSKSIMSEQ       120
                         *************************:***:.********:** ****** :*********
                                                      LXG
AII36371.1_TO-A          KKAMKDILNDINDILPLDLFSTETFKNELSSAEKKRKEAIEKMDEVDQNLTSEYGLSEAN       178
YqcG_NCIB3610            KKAMKDILNDINDILPLDLFSTETFKNELSSAEKKRKEAIEKMDEVDQNLTSEYGLSEAN       178
ADV93340.1_BSn5          KKAMQDILNDINDILPLDLFSTETFKNELSSAEKKRKEAIEKMDEVDENLTSEYGLSEAN       178
AEP87466.1_TU-B-10       KKAMQDILNDINDILPLDLFSTETFKNELSSAEKKRKEAIEKMDEVDENLTSEYGLSEAN       138
AEP91632.1_RO-NN-1       KKAMKDILNDINDILPLDLFSTETFKNELSSAEKKRTEAIEKMDEVDENLTSEYGLSEAN       178
BAI86935.2_BEST195       KKAIKDILNEIHDVLPLDVFSTEDFKTELSSAEKKRKNTVEKISEVDEDLTSEYALSEAN       180
                         ***::****:*:*:****:**** **.*********.:::**:.***::*****.*****
                                      LXG
AII36371.1_TO-A          EQMIQADYQALMNATAKGKSASPIHYNAKAYRDSEIHKMTEDVKKQSTDYISFKDQQAEQ       238
YqcG_NCIB3610            EQMIQADYQALMNATAKGKSASPIHYNAKAYRDSEIHKMTEDVKKQSTDYISFKDQQAEQ       238
ADV93340.1_BSn5          EQMIQADYQALMNATAKGKSASPIHYNAMAYRDSEIHKMTEDVKKQSTDYISFKDQQAEQ       238
AEP87466.1_TU-B-10       EQMIQADYQALMNATAKGKSTSPIHYNAKAYRDSEIHKMTEDVKKQSTDYISFKDQQTEQ       198
AEP91632.1_RO-NN-1       EQMIQADYQALMNATAKGKSASPIHYNAKAYRDSEIHKMTEDVKKQSTDYISFKDQQAEQ       238
BAI86935.2_BEST195       EQMIQADYQALINATAKGKSASPIHYNAKAYRDSEIHKMTEDVKKQSTDYIAFKDQQAEQ       240
                         ***********:********:******* **********************:*****:**

AII36371.1_TO-A          RRIAKEQEELANRPWYEKSWDAVCNFTGEVSGYYDYKRAADGVDPVTGEKLTAGQRVAAG       298
YqcG_NCIB3610            RRIAKEQEELANRPWYEKSWDAVCNFTGEVSGYYDYKRAADGVDPVTGEKLTAGQRVAAG       298
ADV93340.1_BSn5          RRIAKEQEELANRPWYEKSWDAVCNFTGEVSGYYDYKRAADGVDPVTGEKLTAGQRVAAG       298
AEP87466.1_TU-B-10       RRIAKEQEELANRPWYEKSWDAVCNFTGKVSGYYDYKRAADGVDPVTGEKLTAGQRVAAG       258
AEP91632.1_RO-NN-1       RRIAKEQEELANRPWYEKSWDAVCNFTGEVSGYYDYKRAADGVDPVTGEKLTAGQRVAAG       298
BAI86935.2_BEST195       RRLAKEQEELANRPWYEKTWDVVCNFTGEVSGYYDYKRAADGVDPVTGEKLTEGQRVAAG       300
                         **:***************:**.******:*********************** *******

AII36371.1_TO-A          AMAAAGYIPIVGWAGKLAKGGKAVYSTSKALYRADKALDVYKTPKTFHALQNSSKGLYGL       358
YqcG_NCIB3610            AMAAAGYIPIVGWAGKLAKGGKAVYSTSKALYRADKALDVYKTPKTFHALQNSSKGLYGL       358
ADV93340.1_BSn5          AMAAAGYIPIVGWAGKLAKGGKAVYSTSKALYRADKALDVYKTPKTFHALQNSSKGLYGL       358
AEP87466.1_TU-B-10       AMAAAGYIPIVGWAGKLAKGGKAVYSTSKALYKADKALDVYKTPKTFHALQNSSKGLYGL       318
AEP91632.1_RO-NN-1       AMAAAGYIPIVGWAGKLAKGGKAVYSTSKVLYRADKALDVYKTPKTFHALQNSSKGLYGL       358
BAI86935.2_BEST195       AMAAAGYVPIVGWAGKLAKGGKAVYSTSKALYTADKALDVYKTPQTFHALQNSSKGLYGL       360
                         *******:*********************.** ***********:***************

AII36371.1_TO-A          ASANGFSEAITGRDMFGNKVSKERQEQSLSGAMAMLVPFGARGINKKLNAKSSSRVSEAS       418
YqcG_NCIB3610            ASANGFSEAITGRDMFGNKVSKERQEQSLSGAMAMLVPFGARGINKKLNAKSSSRVSEAS       418
ADV93340.1_BSn5          ASANGFSEAITGRDMFGNKVSKERQEQSLSGAMAMLVPFGARGINKKLNAKSSSRVSETS       418
AEP87466.1_TU-B-10       ASANGFSEAITGHDMFGNKVSDEQRQNSINLALSAFVPFGVHGVSGKLNAKSKSTSGIAS       378
AEP91632.1_RO-NN-1       ASANGFSEAITGHDMLGNKVSDEQRQNSINLALSAFVPFGVHGVSGKLNAKSKSTSGIAS       418
BAI86935.2_BEST195       ASANGFSEAITGRDMFGNKISKEQQHNSINAALAVFMPFGAKGFSGKTGLKASSSTETV-       419
                         ************:**:***:*.*::.:*:. *:: ::***.:*.. * . *:.*    .
                                                                 toxin
AII36371.1_TO-A          TNTSKKPK--------VPKTYKRPTYFRKGVRDKVWENAKDSTGS-VKDPLTK-QVMKKD       468
YqcG_NCIB3610            TNTSKKPK--------VPKTYKRPTYFRKGVRDKVWENAKDSTGS-VKDPLTK-QVMKKD       468
ADV93340.1_BSn5          TNTSKKPK--------VPKTYKRPTYFRKGVRDKVWENAKDSTGS-VKDPLTK-QVMKKD       468
AEP87466.1_TU-B-10       GANKNYHESRSASLREIKRQLNIPRTQQPA-SQKMV-PLTDSNGNRILNEKKQ-PVMTRE       435
AEP91632.1_RO-NN-1       GSNKNYHESRSASLREIKRQLNIPRTQQPA-SQKMV-PLTDSNGNRILNEKKQ-PVMTRE       475
BAI86935.2_BEST195       ---TQVTVSRKGAFKEAKRDAGIPRAQQPESINRVEMRTAPHEGGRVIKDKNGKIIRTRE       476
                            .:             :    *   :    :::        *. : .  .   : .::
                                                toxin
AII36371.1_TO-A          EPWD-MGH--------KPGYEFRKHQQSAMERNISRKQFLDEHNNPDHYQPELPSSNRSH       519
YqcG_NCIB3610            EPWD-MGH--------KPGYEFRKHQQSAMERNISRKQFLDEHNNPDHYQPELPSSNRSH       519
ADV93340.1_BSn5          EPWD-MGH--------KPGYEFRKHQQSAMERNISRKQFLDEHNNPDHYQPELPSSNRSH       519
AEP87466.1_TU-B-10       LTYE-INGKKIVIQDHSHGHDFGEG-------G--------IGNQPSHHNVRPENNTRNG       479
AEP91632.1_RO-NN-1       LTYE-INGKKIVIQDHSHGHDFGEG-------G--------IGNQPSHHNVRPENNTRNG       519
BAI86935.2_BEST195       YTFTNNKGEKIIIQDHSAGHEK-------------------GGQGPHFNVRPIDNTRTG       516
                           :             . *::                      .:  *.: .  ...*.

AII36371.1_TO-A          KGEDMTDDYFGD-----     531
YqcG_NCIB3610            KGEDMTDDYFGD-----     531
ADV93340.1_BSn5          KGEDMTDDYFGD-----     531
AEP87466.1_TU-B-10       KVDGMEDHYYFDRRNRK     496
AEP91632.1_RO-NN-1       KVDGMEDHYYFDRRNRK     536
BAI86935.2_BEST195       KVPGTKEHYPFNK----     529
                         *  .  :.*  :
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S4 Fig C

D

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                                                       LXG
YwqJ_NCIB3610             MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQGVADLGDNFKGNGADNIKDFFQGQ       60
AKD36832.1_HJ5            MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQGVADLGDNFKGKGADNIKDFFQGQ       60
BAO93629.1_BEST195        MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQGVADLGDNFKGKGADNIKDFFQGQ       60
AGE65222.1_XF-1           MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQGVADLGDNFKGKGADNIKDFFQGQ       60
ADV94423.1_BSn5           MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQGVADLGDNFKGNGADNIKDFFQGQ       60
AGA21789.1_BSP1           MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQGVADLGDNFKGKGADNIKDFFQGQ       60
AII38166.1_TO-A           MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQGVADLGDNFKGKGADNIKDFFQGQ       60
AEP92663.1_RO-NN-1        MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQGVADLGDNFKGKGADNIKDFFQGQ       60
AIC99919.1_OH131.1        MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQGVADLGDNFKGKGADNIKDFFQGQ       60
AEP88550.1_TU-B-10        MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQEVADLGDNFKGKGADNIKDFFQGQ       60
ADM39597.1_W23            MSKVFESKSLIEEAKSRKKQYETLEEQLNTLKKAFQEVADLGDNFKGKGADNIKDFFQGQ       60
AMR61191.1_ATCC49760      MSKVFESQSLIDEAEKRKKQYETFEEQLNTLKKAFQGVADLGDDFKGKGADNIKDFFQGQ       60
                          *******:***:**:.*******:************ ******:***:************
                                                       LXG
YwqJ_NCIB3610             AEIVDSWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELPNGDLKASEIVSAHKE      120
AKD36832.1_HJ5            AEIVDSWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELPNGDLKASEIVSAHKE      120
BAO93629.1_BEST195        AEIVDSWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELPNGDLKASEIVSAHKE      120
AGE65222.1_XF-1           AEIVDSWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELPNGDLKASEIVSAHKE      120
ADV94423.1_BSn5           AEIVDSWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELPNGDLKASEIVSAHKE      120
AGA21789.1_BSP1           AEIVDSWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELPNGDLKASEIVSAHKE      120
AII38166.1_TO-A           AEIVDSWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELPNGDLKASEIVSAHKE      120
AEP92663.1_RO-NN-1        AEIVDSWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELPNGDLKASEIVSAHKE      120
AIC99919.1_OH131.1        AEIVDSWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELPNGDLKASEMVSAHKE      120
AEP88550.1_TU-B-10        AEIVESWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELSNGDLKASEIVSAHKE      120
ADM39597.1_W23            AEIVESWLTLVSAQIAFLNGISGDIKDQELNDSYVETSFLDHELPNGDLKASEIVSAHKE      120
AMR61191.1_ATCC49760      AEIVDSWLTLVSSQIAFLKGISGDIKDQELSDSYVETSFLDHELPNGDLKASEIVSAHKA      120
                          ****:*******:*****:***********.************* ********:***** 
                                                       LXG
YwqJ_NCIB3610             EIDSILSGISDIIDLDMYTLDDYADKMGDAQKIRRDTITAVDKLDESLTTEYQNLESLDN      180
AKD36832.1_HJ5            EIDSILSGISDIIDLDMYTLDDYADKMGDAQKTRRDTITAVDKLDESLTTEYQNLESLDN      180
BAO93629.1_BEST195        EIDSILSGISDIIDLDMYTLDDYADKMGDAQKIRRDTITAVDKLDESLTTEYQNLESLDN      180
AGE65222.1_XF-1           EIDSILSGISDIIDLDMYTLDDYADKMGDAQKTRRDTITAVDKLDESLTTEYQNLESLDN      180
ADV94423.1_BSn5           EIDSILSGISDIIDLDMYTLDDYADKMGDAQKIRRDTITAVDKLDESLTTEYQNLESLDN      180
AGA21789.1_BSP1           EIDSILSGISDIIDLDMYTLDEYADKMGDAQKIRRDTITAVDKLDESLTTEYQNLESLDN      180
AII38166.1_TO-A           EIDSILSGISDIIDLDMYTLDEYADKMGDAQKVRRDTITAVDKLDESLTTEYQNLESLDN      180
AEP92663.1_RO-NN-1        EIDSILSGISDIIDLDMYTLDDYADKMGDAQKIRRDTITAVDKLDESLTTEYQNLESLDN      180
AIC99919.1_OH131.1        EIDSILSGISDIIDLDMYTLDDYADKMGDAQKIRRDTITAVDKLDESLTTEYQNLESLDN      180
AEP88550.1_TU-B-10        EIDSILSGISDIIDLDMYTLDDYADKMGDAQKIRRETITAVDKLDESLTTEYQNLESLDN      180
ADM39597.1_W23            EIDSILSGISDIIDLDMYTLDDYADKMGDAQKIRRDTITAVDKLDESLTTEYQNLESLDN      180
AMR61191.1_ATCC49760      EIDSILSGISDIIDLDMYSLDNYADKMDNAQKVRRDTITAVDQLDESLTTEYQNLESLDN      180
                          ******************:**:*****.:*** **:******:*****************
                                    LXG
YwqJ_NCIB3610             AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVENQGTTYIDAKTQQAEARR      240
AKD36832.1_HJ5            AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVENQGTTYIDAKTQQAEARR      240
BAO93629.1_BEST195        AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVENQGTTYIDAKTQQAEARR      240
AGE65222.1_XF-1           AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVENQGTTYIDAKTQQAEARR      240
ADV94423.1_BSn5           AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVENQGTTYIDAKTQQAEARR      240
AGA21789.1_BSP1           AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVENQGTTYIDAKAQQAEARR      240
AII38166.1_TO-A           AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVENQGTTYIDAKAQQAEARR      240
AEP92663.1_RO-NN-1        AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVENQGTTYIDAKTQQAEARR      240
AIC99919.1_OH131.1        AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVENQGTTYIDAKTQQAEARR      240
AEP88550.1_TU-B-10        AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVEKQGTTYIDAKAQQAEARR      240
ADM39597.1_W23            AVLTKYSVLMQATSNGKSASPMYYDKKAFHSNEVYKSVIEVEKQGTTYIDAKAQQAEARR      240
AMR61191.1_ATCC49760      AVLSKYSVLMQATSNGKSATPMYYDKKAFHSNEVYKSVIEVEKQGTSYIEAKEQQAEARR      240
                          ***:***************:**********************:***:**:** *******

YwqJ_NCIB3610             LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGVDPVTGEKLSTAERVTAGAM      300
AKD36832.1_HJ5            LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGVDPVTGEKLSTAERVTAGAM      300
BAO93629.1_BEST195        LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGVDPVTGEKLSTAERVTAGAM      300
AGE65222.1_XF-1           LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGVDPVTGEKLSTAERVTAGAM      300
ADV94423.1_BSn5           LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGVDPVTGEKLSTAERVTAGAM      300
AGA21789.1_BSP1           LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGIDPVTGEKLSTAERVTAGAM      300
AII38166.1_TO-A           LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGIDPVTGEKLSTAERVTAGAM      300
AEP92663.1_RO-NN-1        LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGVDPVTGEKLSTAERVTAGAM      300
AIC99919.1_OH131.1        LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGVDPVTGEKLSTAERVTAGAM      300
AEP88550.1_TU-B-10        LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGVDPVTGEKLSTAERVTAGAM      300
ADM39597.1_W23            LQEKAEEEANKPWYEKTWDGVCNFTGEVTGYYDYKRATEGVDPVTGEKLSTAERVTAGAM      300
AMR61191.1_ATCC49760      LQEKAEEEANKPWYEKTWDGICTFTGEVSGYYDYKRATEGVDPVTGEKLSAAERVTAGAM      300
                          ********************:*.*****:***********:*********:*********
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S4 Fig D continued

D

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YwqJ_NCIB3610             AAAGFIPVVGWAGRAFKGGKAIYKTGKAAIAAEHALDAYKTGKSLDILKMTEMGAYGLVA     360
AKD36832.1_HJ5            AAAGFIPVVGWAGRAFKGGKAIYKTGKAAIAAEHALDAYKTGKSLDILKMTEMGAYGLVA     360
BAO93629.1_BEST195        AAAGFIPVVGWAGRAFKGGKAIYKTGKAAIAAEHALDAYKTGKSLDILKMTEMGAYGLVA     360
AGE65222.1_XF-1           AAAGFIPVVGWAGRAFQGGKAIYKTGKAAIAAEHALDAYKTGKSLDILKMTEMGAYGLVA     360
ADV94423.1_BSn5           AAAGFIPVVGWAGRAFKGGKAIYKTGKAAIAAEHALDAYKTGKSLDILKMTEMGAYGLVA     360
AGA21789.1_BSP1           AAAGFIPVVGWAGRAFKGGKAIYKTGKAAIAAEHALDAYKTGKSLDILKMTEMGAYGLVA     360
AII38166.1_TO-A           AAAGFIPVVGWAGRAFKGGKAIYKTGKAAIAAEHALDAYKTGKSLDILKMTEMGAYGLVA     360
AEP92663.1_RO-NN-1        AAAGFIPVVGWAGRAFKGGKAIYKTGKAAIAAEHALDAYKTGKSLDILKMTEMGAYGLVA     360
AIC99919.1_OH131.1        AAAGFIPVVGWAGRAFKGGKAIYKTGKAAIAAEHALDAYKTGKSLDILKMTEMGAYGLVA     360
AEP88550.1_TU-B-10        AAAGFIPVVGWAGRAFKGGKAIYKTGKAAIAADHALDAYKTGKSLDILKMSEMGAYGLVA     360
ADM39597.1_W23            AAAGFIPVVGWAGRAFKGGKAIYKTGKAAIAADHALDAYKTGKSLDILKMSEMGAYGLVA     360
AMR61191.1_ATCC49760      AAAGFIPVVGWAGRAFKGGKAIYKTGKAAITAEHALDAYKTGKSLDILKMSEMGAYGLIA     360
                          ****************:*************:*:*****************:*******:*

YwqJ_NCIB3610             SNGFSEAVTGRDMFGNKVSEEKRKQGALEAITIIGGAGL-AHYFDRLYQKNAPYVNKVSN     419
AKD36832.1_HJ5            SNGFSEAVTGRDMFGNKVSEEKRKTGALEAALSLVGAGALAKSVDNTL----SMGRNLDK     416
BAO93629.1_BEST195        SNGFSEAVTGRDMFGNKVSEEKRKTGALEAALSLVGAGALAKSVDNTL----SMGRNLDK     416
AGE65222.1_XF-1           SNGFSEAVTGRDMFGNKVSEEKRKQGALEAVLSLVGAGALAKHIDKGI----PLATHSKV     416
ADV94423.1_BSn5           SNGFSEAVTGRDMFGNKVSEEKRKQGALEAALSLVGAGALAKHIDKGI----PLATHSKV     416
AGA21789.1_BSP1           SNGFSEAVTGRDMFGNKVSEEKRKQGALEAALSLVGAGALAKHIDKGI----PLATHSKV     416
AII38166.1_TO-A           SNGFSEAVTGRDMFGNKVSEEKRKQGALEAALSLVGVGALAKHIDKGI----PLATHSKV     416
AEP92663.1_RO-NN-1        SNGFSEAVTGRDMFGNKVSEEKRKQGALEAALSLVGAGALAKHIDKGI----PLATHSKV     416
AIC99919.1_OH131.1        SNGFSEAVTGRDMFGNKVSEEKRKQGALEAALSLVGAGALAKHIDKGI----PLATHSKV     416
AEP88550.1_TU-B-10        SNGFSEAVTGRDMFGNKVSEEKRKQGALEAALSLVGAGALAKHINKGI----PLATHSKV     416
ADM39597.1_W23            SNGFSEAVTGRDMFGNKVSEEKRKQGALEAALSLVGAGALAKHINKGI----PLATHSKV     416
AMR61191.1_ATCC49760      SNGFSEAVTGRDMFGNKVSDEKRKTGALEAALSLVGAGALAKHIDKGI----PLATHTKV     416
                          *******************:**** *****   : *.*  *: .:.          : .
                                                                       toxin
YwqJ_NCIB3610             ESLISNIAKTTEEKQTRLQYLRNKH----GVLSKEDLH-----HRINLRAEVLNELSRIK     470
AKD36832.1_HJ5            SY-----S---FSK-----IKQSGHINKEQIVTSTGHTFDLKPEKKQLYTKK------VN     457
BAO93629.1_BEST195        SY-----S---FSK-----IKQSGHINKEQIVTSTGHTFDLKPEKKQLYTKK------VN     457
AGE65222.1_XF-1           QT-----ANKTLEKVKQFKVPTNVRVYAERPVTPDGFTFGIPTVRVDVEKTA------VK     465
ADV94423.1_BSn5           QK-----ANKTLEKVKQFKVPTNVRVYAERPVTPDGFTFGIPTVRVDVEKTA------VK     465
AGA21789.1_BSP1           QK-----ANKTLEKVKQFKVPTNVRVYAERPVTPEGFTFGIPTVRVDVEKTA------VK     465
AII38166.1_TO-A           QK-----ANKTLEKVKQFKVPTNVRVYAERPVTPDGFTFGIPTVRVDVEKTA------VK     465
AEP92663.1_RO-NN-1        QK-----ANKTLEKVKQFKVPTNVRVYAERPVTPEGFTFGIPTVRVDVEKTA------VK     465
AIC99919.1_OH131.1        QK-----ANKTLEKVKQFKVPTNVRVYAERPVTPEGFTFGIPTVRVDVEKTA------VK     465
AEP88550.1_TU-B-10        QK-----ANKTLEKVKQFKVPTNVRVYAERPVTPDGLTFGFPTVRVDVETKS------VK     465
ADM39597.1_W23            QK-----ANKTLEKVKQFKVPTNVRVYAERPVTPDGLTFGFPTVRVDVGTKS------VK     465
AMR61191.1_ATCC49760      QK-----ANTILEKAKQFKVPTNVRVYAERPVTTNGFTFGFPTVRVDVGTKS------VK     465
                          .      :    .*        . :      ::  .        : ::          ::
                                                     toxin
YwqJ_NCIB3610             SSGLTKKQ--RGPAVA----------GVLDKKTGNYYFGINNIDGKPPKVLHPLIHDRIV     518
AKD36832.1_HJ5            NDKLQSSKKAVDPVEQSVSYYRVQGGGAGNK-TSQYRIKVNS-DGS---IAIPI-KNADL     511
BAO93629.1_BEST195        NDKLQSSKKSVDPVEQSVSYYRVQGGGAGNK-TSQYRIKVNS-NGS---IVIPI-KNADL     511
AGE65222.1_XF-1           DLGI----------------VKMVSDGGRK-GSSHS---------P---NISEN-HDKVA     495
ADV94423.1_BSn5           DLGI----------------VKMVSDGGRK-GSSHS---------P---NISKN-HDKVA     495
AGA21789.1_BSP1           DLGI----------------VKMVSDGGRK-GSSHS---------P---NISKN-HDKVA     495
AII38166.1_TO-A           DLGI----------------VKMVSDGGRK-GSSHS---------P---NISKN-HDKVA     495
AEP92663.1_RO-NN-1        DLGI----------------VKMVSSGKGIKGTGKS---------S---NKNPL-P-SWL     495
AIC99919.1_OH131.1        DLGI----------------VKMVSSGKGIKGTGKS---------S---NKNPL-P-SWL     495
AEP88550.1_TU-B-10        DLGI----------------VKMMGKWSNGGEYDRIR---GY-TGR---DLSKY-DNKYL     501
ADM39597.1_W23            DLGI----------------VKMMGKWSNGGEYDRIR---GY-TGR---DLSKY-DNKYL     501
AMR61191.1_ATCC49760      DLGI----------------VKMASGPSKKPQ--------------------------WV     483
                          .  :
                                                     toxin
YwqJ_NCIB3610             N--MPTELK-EGYIKTSGAGSHAE-------VNALNEALLQRPDADLKDLMV--------     560
AKD36832.1_HJ5            NISAYNLEHAKYYRDVARPGGEIVEFKVPK---EVDDLIKE-------------------     549
BAO93629.1_BEST195        NISAYNLEHAKYYRDVARPGGEIVEFKVPK---EVDDLIKE-------------------     549
AGE65222.1_XF-1           H----------------------DGYYG---RKEFRTMLNNASFTPHGHKHVKAKTPEEA     530
ADV94423.1_BSn5           H----------------------DGYYG---RKEFRTMLNNASFTPHGHKHVKAKTPEEA     530
AGA21789.1_BSP1           H----------------------DGYYG---RKEFRTMLNNASFTPHGHKHVKAKTPEEA     530
AII38166.1_TO-A           H----------------------DGYYG---RKEFRTMLNNASFTPHGHKHVKAKTPEEA     530
AEP92663.1_RO-NN-1        K----------------------ERWEA---GNNFNKE--NRPRYPYNEVELEAKEAG-G     527
AIC99919.1_OH131.1        K----------------------ERWEA---GNNFNKE--NRPRYPYNEVELEAKEAG-G     527
AEP88550.1_TU-B-10        ID--PRLVVEMNFKGKGKPGTNAAGWERN-AKKFFNTLLKSNPEFWSAENTAKIK-----     553
ADM39597.1_W23            ID--PRLVVEMNFKGKGKPGTNAAGWERN-AKKFFNTLLKSNPEFWSAENTAKIK-----     553
AMR61191.1_ATCC49760      QK--PEDMTQNDYVAHNG-----NNYSKKKRTEEYNAAIADR------------------     518
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S4 Fig D continued

D

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                                                    toxin
YwqJ_NCIB3610          --YVVSARK--------------------INKKMPE----------------------GV     576
AKD36832.1_HJ5         ---TVIDQ--YGYTKNPRNQG--R--------TAPK---LVDPT----------TPGVSY     581
BAO93629.1_BEST195     ---TVIDQ--YGYTKNPRNQG--R--------TAPK---LVDPT----------TPGVSY     581
AGE65222.1_XF-1        KRFSMTGKKAAQYLPDVNNKALEK--------KALLKGHIIDNGNNNYYFIYDAGKTVGY     582
ADV94423.1_BSn5        KRFSMTGKKAAQYLPDVNNKALEK--------EALLKGHIIDNGNNNYYFIYDAGKTVGY     582
AGA21789.1_BSP1        KRFSMTGKKAAQYLPDVNNKALEK--------EALLKGHIIDNGNNNYYFIYDAGKTVGY     582
AII38166.1_TO-A        KRFSMTGKKAAQYLPDVNNKALEK--------EALLKGHIIDNGNNNYYFIYDAGKTVGY     582
AEP92663.1_RO-NN-1     KKYVV-----DSYSPNKE--IVSR--------KYTQLSDVQEKT----ALSYLNEITKKY     568
AIC99919.1_OH131.1     KKYVV-----DSYSPNKE--IVSR--------KYTQLSDVQEKT----ALSYLNEITKKY     568
AEP88550.1_TU-B-10     ----------RGRVPVVDEQFI-K--------HFP------------QYADYLKDPMRHH     582
ADM39597.1_W23         ----------RGRVPVVDEQFI-K--------HFP------------QYADYLKDPMRHH     582
AMR61191.1_ATCC49760   --EKIIGDNSNGYRLKEPTKWMENRGMVQIKERLKRKS-WTDNEGFNW----------QW     565

                        toxin
YwqJ_NCIB3610          PMPRCPHCEY----ITQNTNYIPEALKYGK------------------------------     602
AKD36832.1_HJ5         ELPAEPWIEWLEEYGHSAKKIE--------------------------------------     603
BAO93629.1_BEST195     ELPAEPWIEWLEEYGHSAKKIE--------------------------------------     603
AGE65222.1_XF-1        DLGT--PTSWIRAEF-SGGEYHGHPIAGSRLDKYL-----------KQLGIDK-------     621
ADV94423.1_BSn5        DLGT--PTSWIRAEF-SGGEYHGHPIAGSRLDKYL-----------KQLGIDK-------     621
AGA21789.1_BSP1        DLGT--PTSWIRAEF-SGGEYHGHPIAGSRLDKYL-----------KQLGIDK-------     621
AII38166.1_TO-A        DLGT--PTSWIRAEF-SGGEYHGHPIAGSRLDKYL-----------KQLGIDK-------     621
AEP92663.1_RO-NN-1     SSG---------SKI-SNGPFNPKALKGGRLKGELILEVPVQNKAIPQKILDEATKNRI-     617
AIC99919.1_OH131.1     SSG---------SKI-SNGPFNPKALKGGRLKGELILEVPVQNKAIPQKILDEATKNRI-     617
AEP88550.1_TU-B-10     HIGEGGQAAALPK--------SLHPGYGGIHNVE---------KEWGITGVDDQIANRLE     625
ADM39597.1_W23         HIGEGGQAAALPK--------SLHPGYGGIHNVE---------KEWGITGVDDQIANRLE     625
AMR61191.1_ATCC49760   DSQHGKLEKWNRRRTEHLGEFDPVTGKQ--TKK------GEPSRRWDG------------     605

YwqJ_NCIB3610          -----------        602
AKD36832.1_HJ5         -----------        603
BAO93629.1_BEST195     -----------        603
AGE65222.1_XF-1        -----------        621
ADV94423.1_BSn5        -----------        621
AGA21789.1_BSP1        -----------        621
AII38166.1_TO-A        -----------        621
AEP92663.1_RO-NN-1     IIRDINGKVYN        628
AIC99919.1_OH131.1     IIRDINGKVYN        628
AEP88550.1_TU-B-10     TFRKESGR---        633
ADM39597.1_W23         TFRKESGR---        633
AMR61191.1_ATCC49760   -----------        605
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S4 Fig D

E

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                                                     LXG
AID00230.1_OH131.1      MKTLDVHALHEGIQHTIEKLDKQKQQLEKLEKSVEHLAGMKDALKGKGGDAIRTFYEECH      60
AII38200.1_TO-A         MKTLDVHALHEGIQHTIEKLDKQKQQLEKLEKSVEHLAGMKDALKGKGGDAIRTFYEECH      60
YxiD_NCIB3610           MKTLDVHALHEGIQHTIEKLDKQKQQLEKLEKSVEHLAGMKDALKGKGGDAIRTFYEECH      60
ADM39953.1_W23          MKTLDVHALHEGIQHTIEKLDKQKQQLEKLEKSVEHLAGMKDALKGKGGDAIRTFYEECH      60
BAI87628.2_BEST195      MKTLDVHALHEGIQHTIEKLDKQKQQLEKLEKSVEHLAGMKDALKGKGGDAIRTFYEECH      60
AEP88894.1_TU-B-10      MKTLDVHALHEGIQHTIEKLDKQKQQLEKLEKSVEHLAGMKDALKGKGGDAIRTFYEECH      60
AEP92997.1_RO-NN-1      MKTLDVHALHEGIQHTIEKLDKQKQQLEKLEKSVEHLAGMKDALKGKGGDAIRTFYEECH      60
AGE65543.1_XF-1         MKTLDVHALHEGIQHTIEKLDKQKQQLEKLEKSVEHLAGMKDALKGKGGDAIRTFYEECH      60
AGI31091.1_BAB-1        MKTLDVHALHEGIQHTIEKLDKQKQQLEKLEKSVEHLAGMKDALKGKGGDAIRTFYEECH      60
AKD37149.1_HJ5          MKTLDVHALHEGIQHTIEKLDKQKQQLEKLEKSVEHLAGMKDALKGKGGDAIRTFYEECH      60
                        ************************************************************
                                                     LXG
AID00230.1_OH131.1      KPFLLFFGMFIDEYKKVLKQTQHAISSVESDSHGMIAEAFLSHDARHGVKHAREVTEQLT      120
AII38200.1_TO-A         KPFLLFFGMFIDEYKKVLKQTQHAISSVESDSHGMIAEAFLSHDARHGVKHAREVTEQLT      120
YxiD_NCIB3610           KPFLLFFGIFIDEYKKVLKQTQHAISSVESNSHGMIAEAFLSHDARHGVKHAREVTEQLT      120
ADM39953.1_W23          KPFLLFFGMFIDEYKKVLKQTQHAISSVESDSHGMIAEAFLSHDARHGVKHAREVTEQLT      120
BAI87628.2_BEST195      KPFLLFFGMFIDEYKKVLKQTQHAISSVESDSHGMIAEAFLSHDARHGVKHAREVTEQLT      120
AEP88894.1_TU-B-10      KPFLLFFGIFIDEYKKVLKQTQHAISSVESDSHGMIAEAFLSHDARHGVKHAREVTEQLT      120
AEP92997.1_RO-NN-1      KPFLLFFGMFIDEYKKVLKQTQHAISSVESDSHGMIAEAFLSHDARHGVKHAREVTEQLT      120
AGE65543.1_XF-1         KPFLLFFGMFIDEYKKVLKQTQHAISSVESDSHGMIAEAFLSHDARHGVKHAREVTEQLT      120
AGI31091.1_BAB-1        KPFLLFFGMFIDEYKKVLKQTQHAISSVESDSHGMIAEAFLSHDARHGVKHAREVTEQLT      120
AKD37149.1_HJ5          KPFLLFFGMFIDEYKKVLKQTQHAISSVESDSHGMIAEAFLSHDARHGVKHAREVTEQLT      120
                        ********:*********************:*****************************
                                                     LXG
AID00230.1_OH131.1      DAVNRQTSAIDHIVSLPTVNDSFFRMETEQAERLISDTLNKLFQFDGQQTQALETAKSDF      180
AII38200.1_TO-A         DAVNRQTSAIDHIVSLPTVNDSFFRMETEQAERLISDTLNKLFQFDGQQTQALEAAKSDF      180
YxiD_NCIB3610           DAVNRQTSAIDHIVSLPTVNDSFFRMETEQAERLISDTLNKLFQFDGQQTQALEAAKSDF      180
ADM39953.1_W23          DAVNRQTSAIGHIVSLPAVNDTFFRMETEQAERLISDTLNKLFQFDGQQTQALETAKSDF      180
BAI87628.2_BEST195      DAVNRQTSAIGHIVSLPAVNDTFFRMETEQAERLISDTLNKLFQFDGQQTQALEAAKSDF      180
AEP88894.1_TU-B-10      DAVNRQTSAIDHIVSLPTVNDTFFRMETEQAERLISDTLNKLFQFDGQQTQALETAKSDF      180
AEP92997.1_RO-NN-1      DAVNRQTSAIGHIVSLPAVNDTFFRMETEQAERLISDTLNKLFQFDGQQTQALEAAKSDF      180
AGE65543.1_XF-1         DAVNRQTSAIDHIVSLPTVNDSFFRMETEQAERLISDTLNKLFQFDGQQTQALETAKSDF      180
AGI31091.1_BAB-1        DAVNRQTSAIDHIVSLPTVNDSFFRMETEQAERLISDTLNKLFQFDGQQTQALETAKSDF      180
AKD37149.1_HJ5          DAVNRQTSAIDHIVSLPTVNDSFFRMETEQAERLISDTLNKLFQFDGQQTQALETAKSDF      180
                        **********.******:***:********************************:*****
                                  LXG
AID00230.1_OH131.1      QTMKKYIDQLETMYTGPKIEITGYKSGSILKSQEEENINQTFGAINPQMKQAVDSPMEMM      240
AII38200.1_TO-A         QTMKKYIDQLETMYTGPKIEITGYKSGSILKSQEEENINQIFGAINPQMKQADDSPMEMM      240
YxiD_NCIB3610           QTMKKYIDQLETMYTGPKIEITGYKSGSILKSQEEENINQIFGAINPQMKQADDSPMEMM      240
ADM39953.1_W23          QTMKKYIDQLETMYTGPKIEITGYKSGSILKSQEEENINQTFGTINPQMKEADDSPMEMM      240
BAI87628.2_BEST195      QTMKKYIDQLETMYTGPKIEITGYKSGSILKSQEQENINQTFGAINPQMKQPDDSPMEMM      240
AEP88894.1_TU-B-10      QTMKKYIDQLETMYTGPKIEITGYKSGSILKSQEEEKINQTFGGINSQMKQADDSPMELM      240
AEP92997.1_RO-NN-1      QTMKKYIDQLETMYTGPKIEITGYKSGSILKSQEEENINQTFGAINPQMKQSDDSPMEMM      240
AGE65543.1_XF-1         QTMKKYMDQLETMYTGPKIEITGYKTGSILKSQEEENINQTFGGINSQMKQPDDSPMEMM      240
AGI31091.1_BAB-1        QTMKKYMDQLETMYTGPKIEITGYKTGSILKSQEEENINQTFGGINSQMKQPDDSPMEMM      240
AKD37149.1_HJ5          QTMKKYMDQLETMYTGPKIEITGYKTGSILKSQEEENINQTFGGINSQMKQPDDSPMEMM      240
                        ******:******************:********:*:*** ** ** ***:  *****:*

AID00230.1_OH131.1      LKKLAENEKSKVDSVVKTGDSKKVSKN------------------------IIVINGKVY      276
AII38200.1_TO-A         LKKLAENEKSKVDSVVKTGDSKKVSKN------------------------IIVINGKVY      276
YxiD_NCIB3610           LKKLAENEKSKVDSVVKTGDSKKVSKN------------------------IIVINGKVY      276
ADM39953.1_W23          LKKLAENEKSKVDSVVKTGHSKKVSKN------------------------IIVINGKVY      276
BAI87628.2_BEST195      LKKIEKHKQSNVDIVMKDGKQQKIEREIHADDSNVTVLQKEAAAHPKVYGDIRVINDKLY      300
AEP88894.1_TU-B-10      LKKLEKHKQSNVDTVMKDGKQQKIEREIHADDSNLTVLQKEAAAHPKVYGDIRVINDKLY      300
AEP92997.1_RO-NN-1      LKKLEKHKQSNVDSVMMDDKQQKIEREIHADDSNVTVLQKEAAAHPKVYGDIRVINDKLY      300
AGE65543.1_XF-1         LKKLEKHKQSNVDSVMMDDKQQKIEREIHADDSNLTVLQKEAAAHPKVYGDIRVINDKIY      300
AGI31091.1_BAB-1        LKKLEKHKQSNVDSVMMDDKQQKIEREIHADDSNLTVLQKEAAAHPKVYGDIRVINDKIY      300
AKD37149.1_HJ5          LKKLEKHKQSNVDSVMMDDKQQKIEREIHADDSNLTVLQKEAAAHPKVYGDIRVINDKIY      300
                        ***: ::::*:** *:  ...:*:.::                        * ***.*:*

AID00230.1_OH131.1      NTSEHREHIKTDFS---NAEVKQVVYNDTLYNVYIS---------GNDMKLEPVVSLSDI      324
AII38200.1_TO-A         NTSEHREHIKTDFS---NAEVKQVVYNDTLYNVYIS---------GNDMKLEPVVSLSDI      324
YxiD_NCIB3610           NTSEHREHIKTDFS---NAEVKQVVYNDTLYNVYIS---------GNDMKLEPVVSLSDI      324
ADM39953.1_W23          NTSEHREHIKTDFS---NAEVKQVVYNDTLYNVYIS---------GNDMKLEPVVSLSDI      324
BAI87628.2_BEST195      NNKRLKKIDTIEVIDELTRNTASIDYVGGKYYVYENGQIVREFYAGGKKRLEEVSYIPED      360
AEP88894.1_TU-B-10      NHKGLKKIDTIEVIDELTRDTASIDYVGGKYFVYENGQIVREFYAGGKKRLEEVSYIPED      360
AEP92997.1_RO-NN-1      NNKRLKKIDTIEVIDELTRNTASIDYVGGKYYVYENGQIVREFYAGGKKRLEEVSYIPED      360
AGE65543.1_XF-1         NHKGLKKIDTIEVIDELTRDTASIDYVGGKYYIYENGQIVRELYAGGKKRLEEVSYIPED      360
AGI31091.1_BAB-1        NHKGLKKIDTIEVIDELTRDTASIDYVGGKYYIYENGQIVRELYAGGKKRLEEVSYIPED      360
AKD37149.1_HJ5          NHKGLKKIDTIEVIDELTRDTASIDYVGGKYYIYENGQIVRELYAGGKKRLEEVSYIPED      360
                        * .  ::  . :.    . :. .: * .  * :* .         *.. :** *  : :

AID00230.1_OH131.1      KVDENGYVKILETAVELTGVYDLFKAATGRDPVSGEKVTGKDRVVASINSVPLAKIAKLE      384
AII38200.1_TO-A         KVDENGYVKILETAVELTGVYDLFKAATGRDPVSGEKVTGKDRVVASINSVPFAKIAKLE      384
YxiD_NCIB3610           KVDENGYVKILETAVELTGVYDLFKAATGRDPVSGEKVTGKDRVVASINSVPFAKIAKLE      384
ADM39953.1_W23          KVDENGNVKILETAVELTGVYDLFKAATGRDPVSGEKVTGKDRVVASINSVPFAKIAKLE      384
BAI87628.2_BEST195      K---VGGAKSLDSFLA-GTQYEFIEWVSPQGAVKKLAVRGGKRVVTDVAKHVVEKD----      412
AEP88894.1_TU-B-10      K---VGGAKSLDSFLA-GTQYEFIEWVSPQGAVKKLAVRGGKRVVTDVAKHVAEKD----      412
AEP92997.1_RO-NN-1      K---VGGAKSLDSFLA-GTQYEFIEWVSPQGAVKKLAVRGGKRVVTDVAKQVTEKE----      412
AGE65543.1_XF-1         K---VGGAKPIDSFLA-GTQYEFIEWVSPQGAVKKLAVRGGKRVVTDVAKHVAGKE----      412
AGI31091.1_BAB-1        K---VGGAKPIDSFLA-GTQYEFIEWVSPQGAVKKLAVRGGKRVVTDVAKHVAGKE----      412
AKD37149.1_HJ5          K---VGGAKPIDSFLA-GTQYEFIEWVSPQGAVKKLAVRGGKRVVTDVAKHVAGKE----      412
                        *    * .* ::: :     *:::: .: :. *.   * * .***:.: .    *
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S4 Fig E continued

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                                                              toxin
AID00230.1_OH131.1      KLIDINKLINDGKKAKKASEVKNVAKDKGKIANDVSGSANKINSDLIKKYARDIEQRTGR       444
AII38200.1_TO-A         KLIDINKLINNGKKAKKASEVKNVAKDKGKIANDVSGSANKINSDLIKKYARDIEQRTGR       444
YxiD_NCIB3610           KLIDINKLINNGKKAKKASEVKNVAKDKGKIANDVSGSANKINSDLIKKYARDIEQRTGR       444
ADM39953.1_W23          KLIDINKLINDGKKAKKASEVKNVAKDTGNGVPSYGKKS------LPKGPYREVHGFPVK       438
BAI87628.2_BEST195      IKGDVKKKPSKGS-----VNS-------KWWHPGYVDNLSSSQTVIGIKNSPKGLSTLGS       460
AEP88894.1_TU-B-10      IKGDVKKKTPKGS-----VNS-------KWWHPGYVDNLSSSQTVIGIKNSPKGLSTLGS       460
AEP92997.1_RO-NN-1      IKGEVNKVASKGT-----SEI-------GWNMSKGGGQIN------GRKYSQHALERMAP       454
AGE65543.1_XF-1         SKGEVNKVASKGA-----SEG-------KKLV--------SSKTVISSDMEAKILEGQ-R       451
AGI31091.1_BAB-1        SKGEVNKVASKGA-----SEG-------KKLV--------SSKTVISSDMEAKILEGQ-R       451
AKD37149.1_HJ5          SKGEVNKVASKGA-----SEG-------KKLV--------SSKTVISSDMEAKILEGQ-R       451
                           :::*   .*       :                                .
                                                    toxin
AID00230.1_OH131.1      ELPKNQIDKLKEA-------LRNK--EYK--KMSPIETAKHR----TKFD----K---VK       482
AII38200.1_TO-A         ELPKNQIDKLKEA-------LRNK--EYK--KMSPIETAKHR----TKFD----K---VK       482
YxiD_NCIB3610           ELPKNQIDKLKEA-------LRNK--EYK--KMSPIETAKHR----TKFD----K---VK       482
ADM39953.1_W23          VKPGAQEKHIP----------NTP--NYK--QE--IANGKNK----SIFY----GDNKTA       474
BAI87628.2_BEST195      STRQNALDAGKGWVGQGAEKMYDKAGNFL---------GYKSVDKMRAFRLQYKPKEKMW       511
AEP88894.1_TU-B-10      STRQNALDAGKGWVGEGAEKMYDKAGNFL---------GYKSVDKMRAFRLQYKPKEKMW       511
AEP92997.1_RO-NN-1      DIPEV-----KAT---------------L---------TNR--AIKKAEELGYKPQTKEF       483
AGE65543.1_XF-1         KVPKNILIGGHSS------SINNANDNFAVEVLSTNADGTKSVMFTKQFVDGNISKIKKS       505
AGI31091.1_BAB-1        KVPKNILIGGHSS------SINNANDNFAVEVLSTNADGTKSVMFTKQFVDGNISKIKKS       505
AKD37149.1_HJ5          KVPKNILIGGHSS------SINNANDNFAVEVLSTNADGTKSVMFTKQFVDGNISKIKKS       505

                                                    toxin
AID00230.1_OH131.1      NKVIKEWEENTGQKWPVYKENVVSEKTGKIIRKKGDKYDAHHIIENTFGGEHEWWNMHPA       542
AII38200.1_TO-A         NKVIKEWEENTGQKWPVYKENVVSEKTGKIIRKKGDKYDAHHIIENTFGGEHEWWNMHPA       542
YxiD_NCIB3610           NKVIKEWEENTGQKWPVYKENVVSEKTGKIIRKKGDKYDAHHIIENTFGGEHEWWNMHPA       542
ADM39953.1_W23          QELLDKYAG-----------------KGDFLKNGRERVDFGKPIG-------KYYDRNTG       510
BAI87628.2_BEST195      RANFT-------------ENEI-------------TVVGSKT----------------EL       529
AEP88894.1_TU-B-10      RANFT-------------ENEI-------------TVVGSKT----------------EL       529
AEP92997.1_RO-NN-1      SDFIKKYVDPRNISPSVIEDAI--------M-NTKKIPGNRS---------GTF--VHET       523
AGE65543.1_XF-1         TLFPESWN----------DDQI--------L-KSIIEVGNTPPISTRLRDRSTWH-RASK       545
AGI31091.1_BAB-1        TLFPESWN----------DDQI--------L-KSIIEVGNTPPISTRLRDRSTWH-RASK       545
AKD37149.1_HJ5          TLFPESWN----------DDQI--------L-KSIIEVGNTPPISTRLRDRSTWH-RASK       545
                                                              .
                              toxin
AID00230.1_OH131.1      KFPNEHQAGIHGTGSPANELFKGGKKK-------   569
AII38200.1_TO-A         KFPNEHQAGIHGTGSPANELFKGGKKK-------   569
YxiD_NCIB3610           KFPNEHQAGIHGTGSPANELFKGGKKK-------   569
ADM39953.1_W23          EYVETT-KGLIHYGKDGAHIVPSRP---------   534
BAI87628.2_BEST195      RN---VHVDILD----------------------   538
AEP88894.1_TU-B-10      RN---VHVDILD----------------------   538
AEP92997.1_RO-NN-1      QD---VKVIINEAGDVIT-VIPK-----------   542
AGE65543.1_XF-1         NG---VEIDVIKNGDEVTSGYPTGKVNAPRPSGF   576
AGI31091.1_BAB-1        NG---VEIDVIKNGDEVTSGYPTGKVNAPRPSGF   576
AKD37149.1_HJ5          NG---VEIDVIKNGDEVTSGYPTGKVNAPRPSGF   576
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S4 Fig E