Barnéoud-Arnoulet *et al*

Supplementary Fig. S1.

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                        10        20        30        40        50        60        70
                         |         |         |         |         |         |         |
Col5            -MDKVTDNSPDV-ESTESTEGSFPTVGVDTGDTITATLATGTENVGGGGGAFGGASESSAAIHAT-----
Col10           -MDKVTDNSPDV-ESTESTEGSFPTVGVDTGDTITATLATGTENVGGGGGAFGGASESSAAIHAT-----
ColK            MAKELSGYGPTAGESMGGTGANLNQQGGNNNSNSGVHWGGGSGHGNNGGQGNSNSSGSTSTVMKTGESYL
                  .:::. .* . **  .* ..:   * :....  .  . *: : ..** . ..:* *::::  *

                        80        90       100       110       120       130       140
                         |         |         |         |         |         |         |
Col5            AKWSTAQLKKHQAEQAARAAAAEAALAKAKSQRDALTQRLKDIVNDALRANAARS-------------PS
Col10           AKWSTAQLKKHQAEQAARAAAAEAALAKAKSQRDALTQRLKDIVNDALRANAARS-------------PS
ColK            TPWGDVVINNDGLPVMNGIVMTEENSTLVDNPFGGVSRVLNSLISDMPSLFAESSGNNNNNTASVNTAPT
                : *. . :::.        . :*   : ...  ..::: *:.::.*     *  *             *:

                       150       160       170       180       190       200       210
                         |         |         |         |         |         |         |
Col5            ---VTDLAHAN----NMAMQAEAERLRLAKAEQKAREEAEAAEKALR--------EAERQRDEIAR----
Col10           ---VTDLAHAN----NMAMQAEAERLRLAKAEQKAREEAEAAEKALR--------EAERQRDEIAR----
ColK            NAQVSDMDKSSKVVGNVINEKQKQKNKIATQISEKQKKIEEMKKVFKHHSYHGITDLERDVDELQKKSNQ
                   *:*: ::.    *:  : : :: ::*.  .: ::: *  :*.::        : **: **: :

                       220       230       240       250       260       270       280
                         |         |         |         |         |         |         |
Col5            --------------QQAETAHLLAMAEAAEAEKN-----RQDSLDEEHRAVEVAEKKLAEAKAELAKAES
Col10           --------------QQAETAHLLAMAEAAEAEKN-----RQDSLDEEHRAVEVAEKKLAEAKAELAKAES
ColK            LDADISKLNSYKNTLQSKIGDVNKQKEAEEKARENAEVAEHETLNEEKQAVAEAEKRLAEAKAELAKAES
                               *:: ..:    ** *  ::     .:::*:**::**  ***:*************

                       290       300       310       320       330       340       350
                         |         |         |         |         |         |         |
Col5            DVQSKQAIVSRVAGELENAQKSVDVKVTGFPGWRDVQKKLERQLQDKKNEYSSVTNALNSAVSIRDAKKT
Col10           DVQSKQAIVSRVAGELENAQKSVDVKVTGFPGWRDVQKKLERQLQDKKNEYSSVTNALNSAVSIRDAKKT
ColK            DVQSKQATVSRVAGELENAQKSVDVKVTGFPGWRDVQKKLQRQLEAKQAEYSAVENELKNAVSFRDGKAA
                ******* ********************************:***: *: ***:* * *:.***:**.* :

                       360       370       380       390       400       410       420
                         |         |         |         |         |         |         |
Col5            DVQNAEIKLKEAKDALEKSQVKDSVDTMVGFYQYITEQYGEKYSRIAQDLAEKAKGSKFSSVDEALAAFE
Col10           EVQNAEIKLKEAKDALEKSQVKDSVDTMVGFYQYITEQYGEKYSRIAQDLAEKAKGSKFNSVDEALAAFE
ColK            EVKEAEQKLKEAQDALEKSQIKDAVDTMVGFYQYITEQYGEKYAKIAQDLAEKSKGKKIQGVDEALAAFE
                :*::** *****:*******:**:*******************::********:**.*:..*********

                       430       440       450       460       470       480       490
                         |         |         |         |         |         |         |
Col5            KYKNVLDKKISKVDRDAIFNALESVNYDELSKNLTKISKSLKITSRVSFLYDVGSDFKNAIETGNWRPLF
Col10           KYKNVLDKKFSKVDRDDIFNALESITYDEWAKHLEKISRALKVTGYLSFGYDVWDGTLKGLKTGDWKPLF
ColK            KYKNVLDKKFSKVDRDAIFNALESVNYDELSKNLTKISKSLKITSRVSFLYDVGSDFKNAIETGNWRPLF
                *********:****** *******:.*** :*:* ***::**:*. :** ***  ..  :.::**:*:***

                       500       510       520       530       540
                         |         |         |         |         |
Col5            VTLEKSAVDVGVAKIVALMFSFIVGVPLGFWGIAIVTGIVSSYIGDDELNKLNELLGI
Col10           VTLEKSAVDFGVAKIVALMFSFIVGAPLGFWGIAIITGIVSSYIGDDELNKLNELLGI
ColK            VTLEKSAVDVGVAKIVALMFSFIVGVPLGFWGIAIVTGIVSSYIGDDELSKLNELLGI
                *********.***************.*********:*************.********
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Sequence aligment between colicins K, 5 and 10. These three pore-forming colicins using the Tsx protein as outer membrane receptor, their reception (central) and pore-formation (C-terminal) domains are similar whereas the translocation (N-terminal) domains are different. The sequence alignment highlights the sequence similarities and has been the base for the definition of the translocation domain. The sequence used in this study is indicated in brackets. The sequence alignment has been build by Clustal W on the pbil server (http://npsa-pbil.ibcp.fr/).