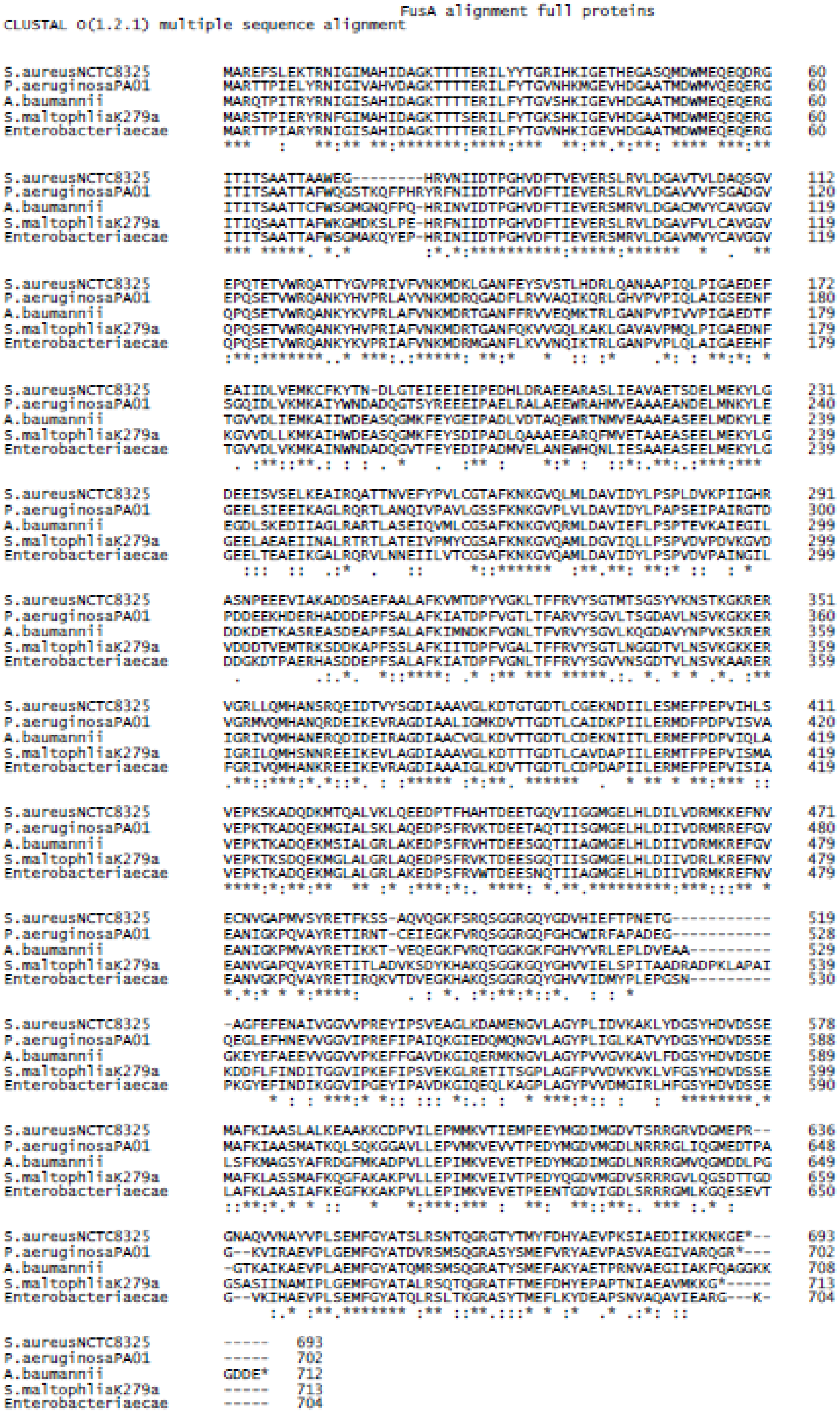
Supplementary Figure 1: Homology between amino acid sequences of FusA like proteins in *S. aureus, Enterobacteriacae, A. baumannii, Pseudomonas aeruginosa* and *Stenotrophomonas maltophilia.*



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                                                FusA alignment full proteins
CLUSTAL O(1.2.1) multiple sequence alignment


S.aureusNCTC8325        MAREFSLEKTRNIGIMAHIDAGKTTTTERILYYTGRIHKIGETHEGASQMDWMEQEQDRG      60
P.aeruginosaPA01        MARTTPIELYRNIGIVAHVDAGKTTTTERILFYTGVNHKMGEVHDGAATMDWMVQEQERG      60
A.baumannii             MARQTPITRYRNIGISAHIDAGKTTTTERILFYTGVSHKIGEVHDGAATMDWMEQEQERG      60
S.maltophliaK279a       MARSTPIERYRNFGIMAHIDAGKTTTSERILFYTGKSHKIGEVHDGAATMDWMEQEQERG      60
Enterobacteriaecae      MARTTPIARYRNIGISAHIDAGKTTTTERILFYTGVNHKIGEVHDGAATMDWMEQEQERG      60
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S.aureusNCTC8325        ITITSAATTAAWEG--------HRVNIIDTPGHVDFTVEVERSLRVLDGAVTVLDAQSGV      112
P.aeruginosaPA01        ITITSAATTAFWQGSTKQFPHRYRFNIIDTPGHVDFTIEVERSLRVLDGAVVVFSGADGV      120
A.baumannii             ITITSAATTCFWSGMGNQFPQ-HRINVIDTPGHVDFTIEVERSMRVLDGACMVYCAVGGV      119
S.maltophliaK279a       ITIQSAATTAFWKGMDKSLPE-HRFNIIDTPGHVDFTIEVERSLRVLDGAVFVLCAVGGV      119
Enterobacteriaecae      ITITSAATTAFWSGMAKQYEP-HRINIIDTPGHVDFTIEVERSMRVLDGAVMVYCAVGGV      119
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S.aureusNCTC8325        EPQTETVWRQATTYGVPRIVFVNKMDKLGANFEYSVSTLHDRLQANAAPIQLPIGAEDEF      172
P.aeruginosaPA01        EPQSETVWRQANKYHVPRLAYVNKMDRQGADFLRVVAQIKQRLGHVPVPIQLAIGSEENF      180
A.baumannii             QPQSETVWRQANKYKVPRLAFVNKMDRTGANFFRVVEQMKTRLGANPVPIVVPIGAEDTF      179
S.maltophliaK279a       QPQSETVWRQANKYHVPRIAFVNKMDRTGANFQKVVGQLKAKLGAVAVPMQLPIGAEDNF      179
Enterobacteriaecae      QPQSETVWRQANKYKVPRIAFVNKMDRMGANFLKVVNQIKTRLGANPVPLQLAIGAEEHF      179
                        :**:*******..* ***:.:*****: **:*   *  :: :*    .*: : **:*: *

S.aureusNCTC8325        EAIIDLVEMKCFKYTN-DLGTEIEEIEIPEDHLDRAEEARASLIEAVAETSDELMEKYLG      231
P.aeruginosaPA01        SGQIDLVKMKAIYWNDADQGTSYREEEIPAELRALAEEWRAHMVEAAAEANDELMNKYLE      240
A.baumannii             TGVVDLIEMKAIIWDEASQGMKFEYGEIPADLVDTAQEWRTNMVEAAAEASEELMDKYLE      239
S.maltophliaK279a       KGVVDLLKMKAIHWDEASQGMKFEYSDIPADLQAAAEEARQFMVETAAEASEELMEKYLG      239
Enterobacteriaecae      TGVVDLVKMKAINWNDADQGVTFEYEDIPADMVELANEWHQNLIESAAEASEELMEKYLG      239
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S.aureusNCTC8325        DEEISVSELKEAIRQATTNVEFYPVLCGTAFKNKGVQLMLDAVIDYLPSPLDVKPIIGHR      291
P.aeruginosaPA01        GEELSIEEIKAGLRQRTLANQIVPAVLGSSFKNKGVPLVLDAVIDYLPAPSEIPAIRGTD      300
A.baumannii             EGDLSKEDIIAGLRARTLASEIQVMLCGSAFKNKGVQRMLDAVIEFLPSPTEVKAIEGIL      299
S.maltophliaK279a       GEELAEAEIINALRTRTLATEIVPMYCGSAFKNKGVQAMLDGVIQLLPSPVDVPDVKGVD      299
Enterobacteriaecae      GEELTEAEIKGALRQRVLNNEIILVTCGSAFKNKGVQAMLDAVIDYLPSPVDVPAINGIL      299
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S.aureusNCTC8325        ASNPEEEVIAKADDSAEFAALAFKVMTDPYVGKLTFFRVYSGTMTSGSYVKNSTKGKRER      351
P.aeruginosaPA01        PDDEEKHDERHADDDEPFSALAFKIATDPFVGTLTFARVYSGVLTSGDAVLNSVKGKKER      360
A.baumannii             DDKDETKASREASDEAPFSALAFKIMNDKFVGNLTFVRVYSGVLKQGDAVYNPVKSKRER      359
S.maltophliaK279a       VDDDTVEMTRKSDDKAPFSSLAFKIITDPFVGALTFFRVYSGTLNGGDTVLNSVKGKKER      359
Enterobacteriaecae      DDGKDTPAERHASDDEPFSALAFKIATDPFVGNLTFFRVYSGVVNSGDTVLNSVKAARER      359
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S.aureusNCTC8325        VGRLLQMHANSRQEIDTVYSGDIAAAVGLKDTGTGDTLCGEKNDIILESMEFPEPVIHLS      411
P.aeruginosaPA01        VGRMVQMHANQRDEIKEVRAGDIAALIGMKDVTTGDTLCAIDKPIILERMDFPDPVISVA      420
A.baumannii             IGRIVQMHANERQDIDEIRAGDIAACVGLKDVTTGDTLCDEKNIITLERMEFPDPVIQLA      419
S.maltophliaK279a       IGRILQMHSNNREEIKEVLAGDIAAAVGLKDTTTGDTLCAVDAPIILERMTFPEPVISMA      419
Enterobacteriaecae      FGRIVQMHANKREEIKEVRAGDIAAAIGLKDVTTGDTLCDPDAPIILERMEFPEPVISIA      419
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S.aureusNCTC8325        VEPKSKADQDKMTQALVKLQEEDPTFHAHTDEETGQVIIGGMGELHLDILVDRMKKEFNV      471
P.aeruginosaPA01        VEPKTKADQEKMGIALSKLAQEDPSFRVKTDEETAQTIISGMGELHLDIIVDRMRREFGV      480
A.baumannii             VEPKTKADQEKMSIALGRLAKEDPSFRVHTDEESGQTIIAGMGELHLDIIVDRMKREFGV      479
S.maltophliaK279a       VEPKTKSDQEKMGLALGRLAQEDPSFRVKTDEESGQTIISGMGELHLDIIVDRLKREFNV      479
Enterobacteriaecae      VEPKTKADQEKMGLALGRLAKEDPSFRVWTDEESNQTIIAGMGELHLDIIVDRMKREFNV      479
                        ****:*:**:**  ** :* :***:*:. ****: *.**.*********:***:::** *

S.aureusNCTC8325        ECNVGAPMVSYRETFKSS-AQVQGKFSRQSGGRGQYGDVHIEFTPNETG-----------      519
P.aeruginosaPA01        EANIGKPQVAYRETIRNT-CEIEGKFVRQSGGRGQFGHCWIRFAPADEG-----------      528
A.baumannii             EANIGKPMVAYRETIKKT-VEQEGKFVRQTGGKGKFGHVYVRLEPLDVEAA---------      529
S.maltophliaK279a       EANVGAPQVAYRETITLADVKSDYKHAKQSGGKGQYGHVVIELSPITAADRADPKLAPAI      539
Enterobacteriaecae      EANVGKPQVAYRETIRQKVTDVEGKHAKQSGGRGQYGHVVIDMYPLEPGSN---------      530
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S.aureusNCTC8325        -AGFEFENAIVGGVVPREYIPSVEAGLKDAMENGVLAGYPLIDVKAKLYDGSYHDVDSSE      578
P.aeruginosaPA01        QEGLEFHNEVVGGVIPREFIPAIQKGIEDQMQNGVLAGYPLIGLKATVYDGSYHDVDSSE      588
A.baumannii             GKEYEFAEEVVGGVVPKEFFGAVDKGIQERMKNGVLAGYPVVGVKAVLFDGSYHDVDSDE      589
S.maltophliaK279a       KDDFLFINDITGGVIPKEFIPSVEKGLRETITSGPLAGFPVVDVKVKLVFGSYHDVDSSE      599
Enterobacteriaecae      PKGYEFINDIKGGVIPGEYIPAVDKGIQEQLKAGPLAGYPVVDMGIRLHFGSYHDVDSSE      590
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S.aureusNCTC8325        MAFKIAASLALKEAAKKCDPVILEPMMKVTIEMPEEYMGDIMGDVTSRRGRVDGMEPR--      636
P.aeruginosaPA01        MAFKIAASMATKQLSQKGGAVLLEPVMKVEVVTPEDYMGDVMGDLNRRRGLIQGMEDTPA      648
A.baumannii             LSFKMAGSYAFRDGFMKADPVLLEPIMKVEVETPEDYMGDIMGDLNRRRGMVQGMDDLPG      649
S.maltophliaK279a       MAFKLASSMAFKQGFAKAKPVLLEPIMKVEIVTPEDYQGDVMGDVSRRRGVLQGSDTTGD      659
Enterobacteriaecae      LAFKLAASIAFKEGFKKAKPVLLEPIMKVEVETPEENTGDVIGDLSRRRGMLKGQESEVT      650
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S.aureusNCTC8325        GNAQVVNAYVPLSEMFGYATSLRSNTQGRGTYTMYFDHYAEVPKSIAEDIIKKNKGE*--      693
P.aeruginosaPA01        G--KVIRAEVPLGEMFGYATDVRSMSQGRASYSMEFVRYAEVPASVAEGIVARQGR*---      702
A.baumannii             -GTKAIKAEVPLAEMFGYATQMRSMSQGRATYSMEFAKYAETPRNVAEGIIAKFQAGGKK      708
S.maltophliaK279a       GSASIINAMIPLGEMFGYATALRSQTQGRATFTMEFDHYEPAPTNIAEAVMKKG*-----      713
Enterobacteriaecae      G--VKIHAEVPLSEMFGYATQLRSLTKGRASYTMEFLKYDEAPSNVAQAVIEARG---K-      704
                             :.* :**.******* :** ::**.:::* * :*  .* .:*: ::

S.aureusNCTC8325        -----   693
P.aeruginosaPA01        -----   702
A.baumannii             GDDE*   712
S.maltophliaK279a       -----   713
Enterobacteriaecae      -----   704
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