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logo
hasA      MRTLKNLITVVAFSIFWVLLIYVNVYLFGAKGSLSIYGFLLIAYLLVKMSLSFFYKPF...........KGRAGQYKVAAIIPSYNEDAESLLETLKSVQQQTYPLAEIY   99
sleD      ..............................................MEG...........PGHSGIRTL.IVIPCLNE.AKTIEGLLVKFTGAMQGRLFRI   42
exoA      ..............................................MSS...........DELTSTSSL.IVIPCLNE.ASHIEALIEKLRPSLTPLNARV   42
icaA      ........................MHVFNFLLFYPIFMSIYWIVGSIYYFFIKEK..PFNRSLLVKSEHQQVEGISFLLACYNE.SETVQDTLSSVLSLEYPEKEII   80
pgaC      MINRIVSFFILCLVLCIPLCVAYFHSGELMMRFVFFWPFFMSIMWIVGGVYFWVYRERHWPWGENAPA.PQLKDNPSISIIIPCFNE.EKNVEETIHAALAQRYENIEVI  108
consensus *                 *            ** ************  * *** *   *        *   *  * ** *** !! * * ****  ** * *** * *

logo
hasA      VVDD.GSADETGIKRIEDYVRDTGDLSSNVIVHRSEKNQGKRHAQAWAFERSDADVFLTVDSDTYIYPDA.....LEELLKTFNDPTVFAA..TGHLNVRNRQTNLLTRL  201
sleD      VVADGGSTDGTR.DIVAAFAAKDERV...TLLANPKRIQSAGINLAVATFGEDFDYLIRIDAHG.DYPDDYCQRLIEDAERTGADSVVVAMDTVGHGLFQKA.TAIAQNS  146
exoA      VIADGGSTDGTR.EIARRLATEDFRV...LFLDNPKRIQSAAVNRAVAELGAGSDYLIRIDAHG.TYPDDYCERLVEDALATGADSVVVAMQTVGFSTFQKA.TAFAQNS  146
icaA      IIND.GSSDNTA.EIIYDFKKN.HDF...KFVD.LEVNRGKANALNEGIKQASYEYVMCLDADT.VIDDDAPFYMIEDFKK...NPKLGAV..TGNPRIRNK.SSILGKI  176
pgaC      AVND.GSTDKTR.AILDRMAAQIPHL...RVIH.LAQNQGKAIALKTGAAAAKSEYLVCIDGDA.LLDRDAAAYIVEPMLY...NPRVGAV..TGNPRIRTR.STLVGKI  205
consensus ** !*!!*!*!* ***  *** **      *  *  ***********  ******* *!**   **** *  * !*********** !  **! ** *   **

logo
hasA      TDIRYDNAFGVERAAQSVTGNILVCSGPLSVYRREVVVPNIDRYINQTFLGIPVSIGDDRCLTN...YATDLGKTVYQSTAKCITDVPDKMSTYLKQQNRWNKSFFRESI  308
sleD      KLGN.....GGSKHREGAKGH.WIDHGHHALMRIA.AFDAVGGYDESFSHNEDAELDFRLRKSGFRIWMTDKTRMTYYPRAS...VMP.....LFKQYLAYGRG......  235
exoA      KLGN.....GGSKHRTGAVGH.WAEHGHHALMRIE.AFKAVGGYDESFSHNEDAELDYRLGKAGYRIWMTDKTSMVYYPRAK...LVP.....LFWQYFGYGRG......  235
icaA      QTIEYASIIGCIKRSQSLAGAINTISGVFTLFKKS.ALKDVGYWDTDM.ITEDIAVSWKLHLFD...Y.....EIKYEPRALCWMLVPETIGGLWKQRVRWAQG......  270
pgaC      QVGEYSSIIGLIKRTQRIYGNVFTVSGVIAAFRRS.ALAEVGYWSDDM.ITEDIDISWKLQLNQ...W.....TIFYEPRALCWILMPETLKGLWKQRLRWAQG......  299
consensus  ** * ***!* * ** * ! *** *! *** *   * **** ***  *  ** *  * * * * ********  *! **! ** **!**  ** *! ***  *

logo
hasA      ISVKKIM.NNPFVALWTILEVSMFMMLVYSVVDFFVGNVREFDWLRVLAFLVIIFIVAL.......................CRNIHYMLKHPLSFLLSPFYGVLHLFVLQ  395
sleD      .RAKNLLKHRSIPKIRQMIPLAVLPVFIFALLSL.......VHWAAL..IPLGLWIAAC.........................VGYGLWMAIGQKNPYGPLAAFS  306
exoA      .RAKNFLKHRAMPGLRQMLPLAVAPIAFGALLAI.......VNWMAV..VPVGVWAAAC.........................LGYGVWMALGQRNPYGPLAAVA  306
icaA      .GHEVLL..RDFWPTIKTKKLSLYILMFEQIASI.......T.WVYIVLCYLSFLVITANI..LDYTYLKYSFSIFFFSSFTMTFINIIQFTVALFIDSRYEKKNIVGLI  367
pgaC      .GAEVFL..KNMTRLWRKENFRMWPLFFEYCLTT.......I.WAFT..CLVGFIIYAVQLAGVPLNIELTHIAATHTAGILLCTLCLLQFIVSLMIENRYEHNLTSSLF  396
consensus   **  ****  * * *****   *********        * !***  * ********                                *  **  ****** *******

logo
hasA      PLKLYSLFTIRNADWGT....RKKLL...................  417
sleD      AMVMH..LAWSTGFWLELLKFRGRKAVS.................  332
exoA      AMVMH..LAWSAGFWRELLDFRRRVA...................  330
icaA      FLSWYPTLYWVINAAVVIMAFPKALKRKKGGYATWSSPDRGNIQR  412
pgaC      WIIWFPVIFWMLSLATTLVSFTRVMLMPKKQRARWVSPDRGILRG  441
consensus * *  * **** ***  ** ** **   *   * * *****
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X non-conserved

X ≥50% conserved