```
S. agalactiae         -MMKIKPVKVESIENPKRFLNSRLLTKIEVEEAIEKALKQLYINIDYFGEEYPTPATFNN
C. perfringens        ---MIKEIRVEEIAKKDEFLKTKLLTRAEVKNAIDLVIKQIDANMEYFKEKFPSSATKNN
E. feacalis           ----MKKITQEKLLSSERFFGQGILTEDFIDQSIDKVLKKVEKNIQKLGDKFPTPATTDN
E. rhusiopathiae      MEKHIKQVTIEPIRDIDIFKNATLLTKEEVKQAIEDTIKKIDLNMEHIGERFPWSATKDL
M. fermentans         ---MVFRNLNNSLIYEKEFNDTKLLTKEEIKKALDLIIKQVDQNIDYFGKEFMIANTFNN
Bacillus              ----------------------------MWQQAIGDALGITARNLKKFGDRFPHVSDGSN
                                                    .:::   :     *:. : ..:      .

                               ↓                                             ↓
S. agalactiae         IYKVMDNTEWTNGFWTGCLWLAYEYNQDKKLKNIAHKNVLSFLNRINNRIALDHHDLGFL
C. perfringens        QYGIIENIEWTDGFWTGLLWLAYEYTGDEKYRELADKNVASFKNRVEKDIELDHHDLGFL
E. feacalis           TYIAMDNTEWTNGFWTGILWLCYEVSGEKHYREVAEQNVKSFIYRIENEIEVEHHDLGFL
E. rhusiopathiae      KYPIIDNIEWTDGFWTGLLWLAYEYTGDEKYRELADKNVDSFHHRVVNDIEIDHHDLGFL
M. fermentans         KYQKIYSSEWTDGFWTGILWLAYEYTNNNKYKELALEHVKWYKKRIKEKILVDHHDMGFL
Bacillus              KYVLNDNTDWTDGFWSGILWLCYEYTGDEQYREGAVRTVASFRERLDRFENLDHHDIGFL
                       *    . :**:***:* ***.** . ::: :: * . *  :  *: .   ::***:***

                                                                      ↓
S. agalactiae         YTPSCTAEYRINGDVKALEATIKAADKLMERYQEKGGFIQAWGELGYKEH-YRLIIDCLL
C. perfringens        YSLATVSGYKLTGSEDAREASIKAANKLISRYQEKGEFIQAWGELGSKDH-YRFIIDCLL
E. feacalis           YSLSCVSAYKLTGNEAAKNAAISAAEKLLQRYQSKGEFIQAWGELGNQDN-YRLIVDCLL
E. rhusiopathiae      YSLSCVASYKLTGSEKAKEAAVLAADKLITRWQEKGEFIQAWGEYNNPEH-YRFIIDCLL
M. fermentans         YSPSCVAAYKLTKNQEAKEAALLAADNLISRYQEKGKFIQAWGNIGANDN-YRLIIDCLL
Bacillus              YSLSAKAQWIVEKDESARKLALDAADVLMRRWRADAGIIQAWGPKGDPENGGRIIIDCLL
                      *: :  : : :  .  * : :: **: *: *:: .. :*****  .  ::  *:*:****

                                                                    ↓ ↓
S. agalactiae         NIQLLFFAYEQTGDEKYRQVAVNHFYASANNVVRDDSSAFHTFYFDPETGEPLKGVT R
C. perfringens        NIPLLYWASDETGDAKYRNIANKHFVTSCNNVIRDDASAFHTFYMDNETGKPLRGVT R
E. feacalis           NIPLLFWASTVTQDKRYREVAVKHYHTTIDNAIREDSSAYHTFFFDAETGDPLYGKT R
E. rhusiopathiae      NIPLLYWATEVTGDDKYANIAERHFYTSCQYVIRDDASAFHTFYMDPETGGPVRGAT R
M. fermentans         NIPLLYWASDYDR-KNYFDKALNHFNTSLHTVIREDGTTYHTYFFDAKTNKPLCGKT R
Bacillus              NLPLLLWAGEQTGDPEYRRVAEAHALKSRRFLVRGDDSSYHTFYFDPENGNAIRGGT H
                      *: ** :*       .*   *  *   :    :* * :::**:::* :.. .: * * :

                                ↓   ↓
S. agalactiae         QGYSDESSWARGQAWGIYGIPLSYRKMKDYQ-----QIILFKGMTNYFLNRLPED-KVSY
C. perfringens        QGYSDDSAWARGQAWGVYGIPLNYRYTRNES-----CFNLYEGMTNYFLNRLPKD-NVCY
E. feacalis           QGYSDSSSWARGQSWLIYGLALFRSYCPEEE-----NTEIFEAITNYFLNRLPKD-FVSY
E. rhusiopathiae      QGYNDESSWARGQAWGVYGIPLNYRYTHEDE-----VFPLHEGMTNYFLNRLPKD-FVCY
M. fermentans         QGYSDDSCWARGQAWGIYGIPLTLKYAKNNSKIDKNAYQIYQKVLNQFLNNLPQDDYVCY
Bacillus              QGNTDGSTWTRGQAWGIYGFALNSRYLGNAD-----LLETAKRMARHFLARVPED-GVVY
                      ** .* * *:***:* :**:.*      : .          : : . ** .:*:*  * *

S. agalactiae         WDLIFTDGSGQPRDTSATATAVCGIHEMLKYLPEVDPDKETYKYAMHTMLRSLIEQYSNN
C. perfringens        WDLIFNDGDDHSKDSSAAAIAVCGMHEMNKYLPEVDENKEVYKYAMHNILRSLMENYMNP
E. feacalis           WDLIFMDGSEQSRDTSATAIAVCGMSLMDAFLPETNSHKLVYKCAQHSMLRSLSENYTES
E. rhusiopathiae      WDLIFTDGDDQSRDSSAAAIAVCGMLEMIKYMKN-DELKTVYEGASHTILRSLIDNYTKT
M. fermentans         WDLIFNEKADQSRDSSASAIAVCGILEMLKITQK-DYKTDLYEKSAHLILRNLINKYHNK
Bacillus              WDFEVPQEPSSYRDSSASAITACGLLEIASQLDESDPERQRFIDAAKTTVTALRDGYAER
                      **: . :     :*:**:* :.**:  :     : :     :  : :  :  * : * :

                                   ↓
S. agalactiae         ELIAGRPLLLHGVY S WH S G K GVDEGNIWGDYYYLEALIRFYK-DWELYW-----
C. perfringens        EIEPGKPVLLHGVY S WH S G K GVDEGNIWGDYFFLEALIRFYK-DWNLYW-----
E. feacalis           KTDGITALLNEGVY S WH S G K GVNEGNIWGDYFYLEALVRFKK-NWKMYW-----
E. rhusiopathiae      THEPGNPVLYHGVY S WH S G K GVDEGNIWGDYYYLEALMRLYK-DWELYW-----
M. fermentans         KIEPGTPILLHGVY S WH S K K GVDEGNIWGDYYYFEALMRLYKKDWNPYW-----
Bacillus              DDGEAEGFIRRGSY H VR G G I SPDDYTIWGDYYYLEALLRLER-GVTGYWYERGR
                             .: .* *    : .     . :: .*****:::***:*: : .   **
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Supplemental Fig. S2. **Multiple sequence-alignment of bacterial UGLs.** Bacteria with UGL genes were as follows: *S. agalactiae*, *Streptococcus agalactiae* NEM 316; *C. perfringens*, *Clostridium perfringens* ATCC 13124; *E. faecalis*, *Enterococcus faecalis* V583; *E. rhusiopathiae*, *Erysipelothrix rhusiopathiae* ATCC 19414; *M. fermentans*, *Mycoplasma fermentans* PG18; and *Bacillus*, *Bacillus* sp. GL1. The motif "R-//-SXX(S)XK" responsible for recognition of the sulfate groups of Δ6S and Δ4S is boxed. Other residues binding to the substrate are indicated by arrows. Identical and similar amino acid residues among proteins are denoted by asterisks and dots, respectively.