

The diagram illustrates the chemical structure of a complex glycoside, showing a steroid core linked to multiple sugar units. The structure is labeled with various glycosylation sites:

- C13 1-3'-glycosylation**: Linkage between the C13 of the steroid and the 1' of the top sugar.
- C13 O-glycosylation**: Linkage between the C13 of the steroid and the oxygen of the top sugar.
- C13 1-2'-glycosylation**: Linkage between the C13 of the steroid and the 2' of the top sugar.
- C19 1-3'-glycosylation**: Linkage between the C19 of the steroid and the 1' of the bottom sugar.
- C19 O-glycosylation**: Linkage between the C19 of the steroid and the oxygen of the bottom sugar.
- C19 1-2'-glycosylation**: Linkage between the C19 of the steroid and the 2' of the bottom sugar.

An inset shows the steroid core with numbered carbons (1-17) and functional groups (CH₂, H, H₃C, O).

FIG. 3A

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76G1_1 (1-306)      MAENKTETTVRRRRRIILFPVPFQGHINPILQLANVLYSKGFSITIFHTNFKPKTSNYP
MbUGT13_2 (156-455) GSGGSG-----RRRRRIILFPVPFQGHINPMLQLANVLYSKGFSITIFHTNFKPKTSNYP
                   : .. *****:*****

76G1_1 (1-306)      HFTFRFILDNDPQDERISNLPTHGPLAGMRIPIINEHGADELRRLELELLMLASEEDEEVS
MbUGT13_2 (156-455) HFTFRFILDNDPQDERISNLPTHGPLAGMRIPIINEHGADELRRLELELQMLASEEDEEVS
                   *****

76G1_1 (1-306)      CLITDALWYFAQSVADSLNLRRLVLMTSSLFNFHAHVSLPQFDELGYLDPDDKTRLEEQA
MbUGT13_2 (156-455) CLITDALWYFAQSVADSLNLRRLVLMTSSLFNFHAHVSLPQFDELGYLDPDDKTRLEEQA
                   *****

76G1_1 (1-306)      SGFPMLKVVDIKSAYS SNWQIAKEILGKMIKQTKASSGVIWNSFKELEESELETVIREIPA
MbUGT13_2 (156-455) SGFPMLKVVDIKSAYS SNWQIAKEILGKMIKQTKASSGVIWNSFKELEESELETVIREIPA
                   *****

76G1_1 (1-306)      PSFLIPLPKHLTASSSSLLDHDRTVFQWLDQQPPSSVLYVSFGSTSEVDEKDFLEIARGL
MbUGT13_2 (156-455) PSFLIPLPKHLTASSSSLLDHDRTVFQWLDQQPPSSVLYVSFGSTSEVDEKDFLEIARGL
                   *****:*****

76G1_1 (1-306)      VDSKQS
MbUGT13_2 (156-455) VDSQS-
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FIG. 3B

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76G1_1 (307-459)      --FLWVVRPGFVKGSTWVEPLPDGFLGERGRIVKWVPQQEVLAHGAIGAFWTHSGWNSTL
MbUGT13_2 (1-155)      MAFLWVVRPGFVKGSTWVEPLPDGFLGERGRIVKWVPQQEVLAHGAIGAFWTHGGWNSTL
                   *****:*****

76G1_1 (307-459)      ESVCEGVPMIFSDFGLDQPLNARYMSDVLKGVYLENGWERGEIANAIRRMVDEEGEYI
MbUGT13_2 (1-155)      ESVCEGVPMIFSDFGLDQPLNARYMSDVLKGVYLENGWERGEIANAIRRLMVDEEGEYI
                   *****:*****

76G1_1 (307-459)      RQNARVLKQKADVSLMKGGSSYESLESLSVSYISSL
MbUGT13_2 (1-155)      RQNARVLKQKADVSLMKGGSSYESLESLSVSYISSL
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FIG. 4

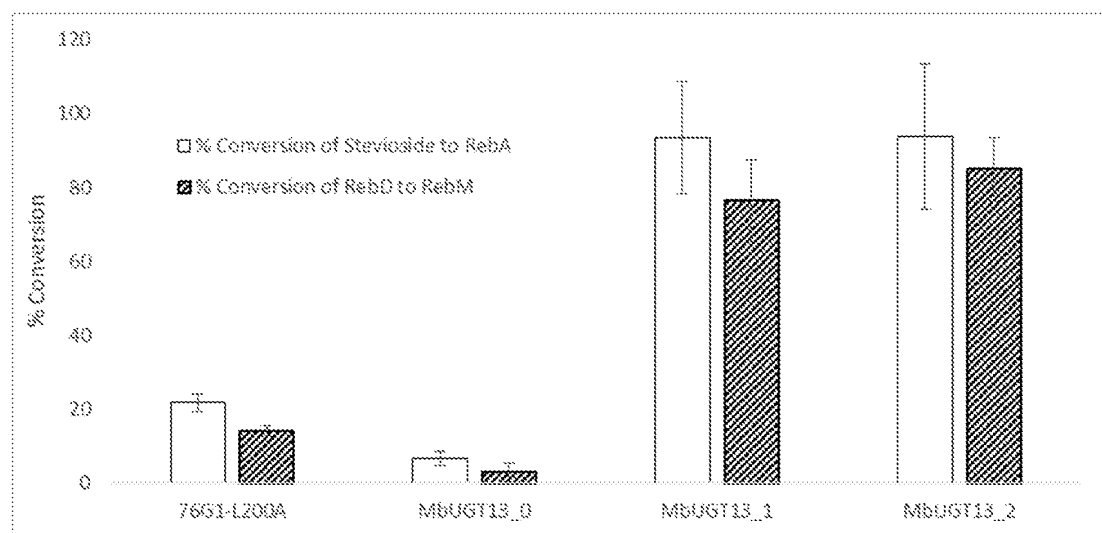


FIG. 5