

SEQUENCE LISTING

<110> Glycom A/S

<120> NEW MAJOR FACILITATOR SUPERFAMILY (MFS) PROTEIN (FRED) IN HMO PRODUCTION

<130> P2876W000

<150> DK202000087

<151> 2020-01-23

<160> 33

<170> BiSSAP 1.3.6

<210> 1

<211> 393

<212> PRT

<213> *Yersinia frederiksenii*

<220>

<223> fred_WP_087817556.1\optimized translation:

<400> 1

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Ala Pro Thr Leu Ser Leu Phe Leu Ser Thr Glu Val Lys Val Arg Pro
          35          40          45
Leu Trp Val Gly Leu Phe Tyr Thr Val Asn Ala Ile Ala Gly Ile Thr
          50          55          60
Val Ser Phe Val Leu Ala Lys Arg Ser Asp Leu Arg Gly Asp Arg Arg
65          70          75          80
Lys Leu Ile Leu Val Cys Tyr Leu Met Ala Val Gly Asn Cys Leu Leu
          85          90          95
Phe Ala Phe Asn Arg Asp Tyr Leu Thr Leu Ile Thr Ala Gly Val Leu
          100         105         110
Leu Ala Ala Val Ala Asn Thr Ala Met Pro Gln Ile Phe Ala Leu Ala
          115         120         125
Arg Glu Tyr Ala Asp Asn Ser Ala Arg Glu Val Val Met Phe Ser Ser
          130         135         140
Ile Met Arg Ala Gln Leu Ser Leu Ala Trp Val Ile Gly Pro Pro Leu
145         150         155         160
Ser Phe Met Leu Ala Leu Asn Tyr Gly Phe Thr Leu Met Phe Cys Ile
          165         170         175
Ala Ala Gly Ile Phe Val Leu Ser Ala Leu Val Val Trp Phe Ile Leu
          180         185         190
Pro Ser Val Gln Arg Ala Glu Pro Val Met Asp Ala Pro Thr Val Ala
          195         200         205
Gln Gly Ser Leu Phe Ala Asp Lys Asp Val Leu Leu Leu Phe Ile Ala
          210         215         220
Ser Met Leu Met Trp Thr Cys Asn Thr Met Tyr Ile Ile Asp Met Pro

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225					230					235				240	
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Leu	Met	Gly	Thr	Ala	Ala	Gly	Leu	Glu	Ile	Pro	Ile	Met	Leu	Leu	Ala
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Gly	Tyr	Ser	Val	Arg	Arg	Phe	Gly	Lys	Arg	Lys	Ile	Met	Leu	Phe	Ala
		275					280					285			
Val	Leu	Ala	Gly	Val	Leu	Phe	Tyr	Thr	Gly	Leu	Val	Leu	Phe	Lys	Phe
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Lys	Ser	Ala	Leu	Met	Leu	Leu	Gln	Ile	Phe	Asn	Ala	Ile	Phe	Ile	Gly
305					310					315					320
Ile	Val	Ala	Gly	Ile	Gly	Met	Leu	Tyr	Phe	Gln	Asp	Leu	Met	Pro	Gly
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Arg	Ala	Gly	Ala	Ala	Thr	Thr	Leu	Phe	Thr	Asn	Ser	Ile	Ser	Thr	Gly
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Val	Ile	Leu	Ala	Gly	Val	Leu	Gln	Gly	Val	Leu	Thr	Glu	Thr	Trp	Gly
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His	Asn	Ser	Val	Tyr	Val	Met	Ala	Met	Ile	Leu	Ala	Ile	Leu	Ser	Leu
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cgtgactatc tgaccctgat taccgcgggc gtgctgctgg cggcggttgc gaacaccgcg	360
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ttcgtgctga gcgcgctggt tgtgtggttt attctgccga gcgtgcagcg tgcggaaccg	600
gttatggatg cgccgaccgt ggcgcaaggc agcctgttcg cggacaagga tgttctgctg	660

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atcgtggcgg gtatcggcat gctgtacttc caagacctga tgccgggtcg tgcgggtgcg	1020
gcgaccaccc tgtttaccaa cagcattagc accggcgтта tcctggcggg cgtgctgcaa	1080
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gaggccgttt ttttgccttt cactcctcga ataattttca tattgtcgtt tttgtgatcg	180
ttatctcgat atttaaaaac aaataatttc attatatattt gtgcctacaa gcacgtgga	240
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 <223> PglpF regulatory sequence

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 <311> 19.12.2018
 <312> 27.06.2019
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tttaagtctg atatttctcg tttttgctcg ttaacgataa gtttacagca tgcctacaag 240
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tgtacaatca gatggaataa atggcgcgat aacgctcatt ttatgacgag gcacacacat 180
tttaagtctg atatttctcg tttttgctcg ttaacgataa gtttacagca tgcctacaag 240
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tgtacaatca gatggaataa atggcgcgat aacgctcatt ttatgacgag gcacacacat 180
tttaagttcg atatttctcg tttttgctcg ttaacgataa gtttacagca tgcctacaag 240
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cattaaccaa ggaggaaaca gct 203

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cattaaccaa ctaggaaaca gct 203

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cggctcgtat gttgtgtgga attgtgagcg gataacaatt tcacacagga aacagctatg 120

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aaggaggaaa cagct 195

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<223> Primer 068, Plac.for

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<400> 20

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<223> Primer 0133, Plac.rev

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<400> 21

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