FIG. 4A	FIG. 4B
FIG. 4C	FIG. 4D
FIG. 4E	FIG. 4F

FIG. 4

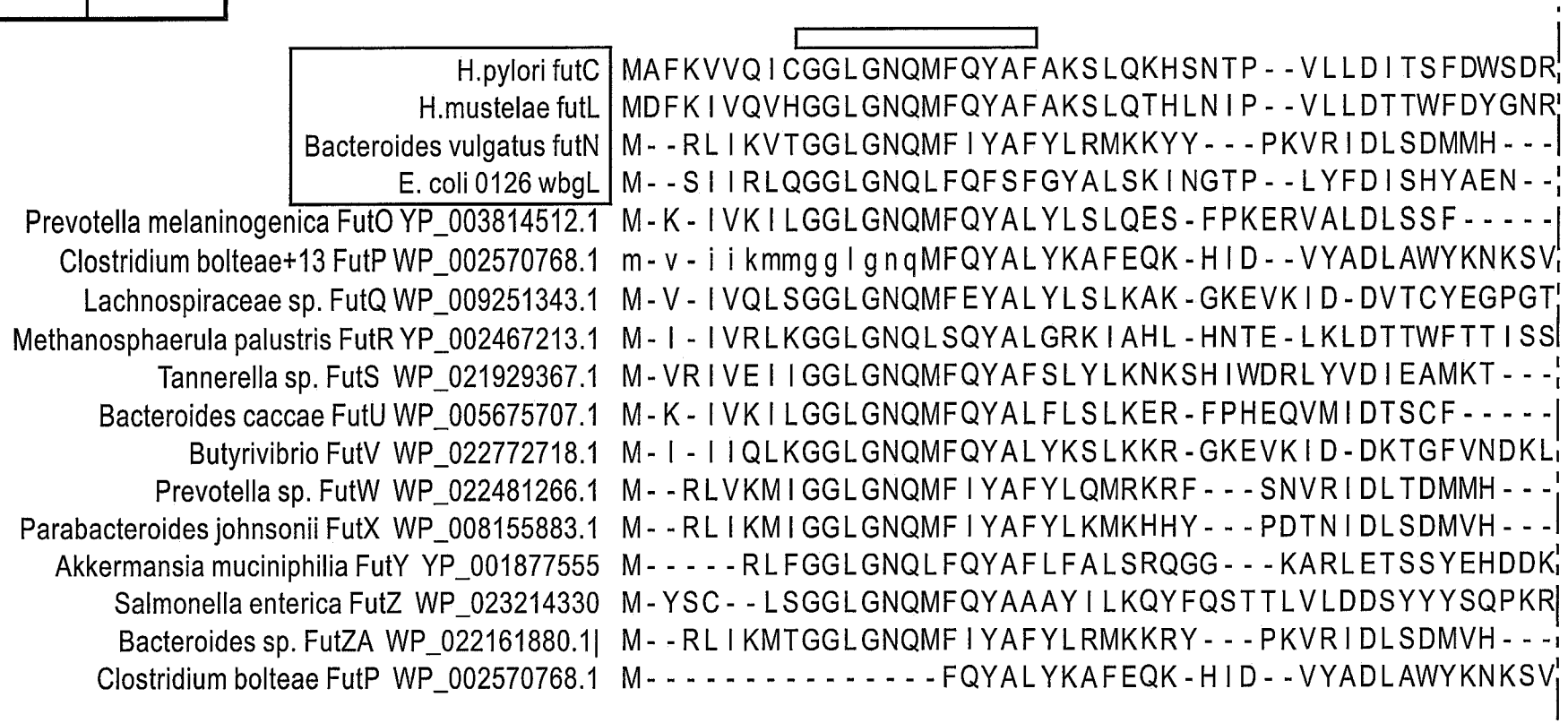


FIG. 4A

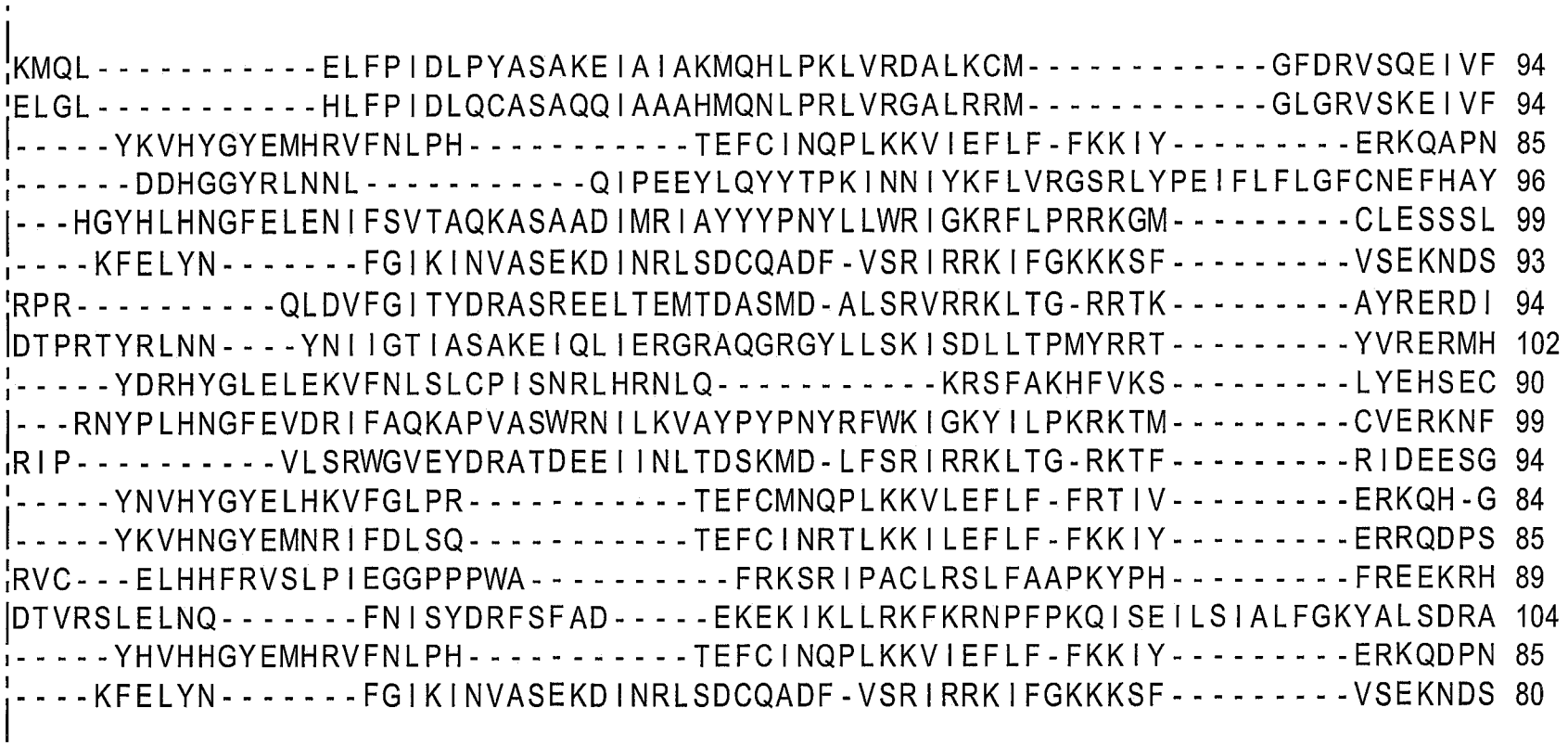

KMQL----------ELFPIDLPYASAKEIAIAKMQHLPKLVRDALKCM----------GFDRVSQEIVF 94
ELGL----------HLFPIDLQCASAQQIAAAHMQNLPRLVRGALRRM----------GLGRVSKEIVF 94
-----YKVHYGYEMHRVFNLPH----------TEFCINQPLKKVIEFLF-FKKIY---------ERKQAPN 85
------DDHGGYRLNNL----------QIPEEYLQYYTPKINNIYKFLVRGSRLYPEIFLFLGFCNEFHAY 96
---HGYHLHNGFELENIFSVTAQKASAADIMRIAYYYPNYLLWRIGKRFLPRRKGM---------CLESSSL 99
----KFELYN-------FGIKINVASEKDINRLSDCQADF-VSRIRRKIFGKKKSF---------VSEKNDS 93
RPR----------QLDVFGITYDRASREELTEMTDASMD-ALSRVRRKLTG-RRTK---------AYRERDI 94
DTPRTYRLNN----YNIIGTIASAKEIQLIERGRAQGRGYLLSKISDLLTPMYRRT---------YVRERMH 102
-----YDRHYGLELEKVFNLSLCPISNRLHRNLQ----------KRSFAKHFVKS---------LYEHSEC 90
---RNYPLHNGFEVDRIFAQKAPVASWRNILKVAYPYPNYRFWKIGKYILPKRKTM---------CVERKNF 99
RIP----------VLSRWGVEYDRATDEEIINLTDSKMD-LFSRIRRKLTG-RKTF---------RIDEESG 94
-----YNVHYGYELHKVFGLPR----------TEFCMNQPLKKVLEFLF-FRTIV---------ERKQH-G 84
-----YKVHNGYEMNRIFDLSQ----------TEFCINRTLKKILEFLF-FKKIY---------ERRQDPS 85
RVC---ELHHFRVSLPIEGGPPPWA---------FRKSRIPACLRSLFAAPKYPH---------FREEKRH 89
DTVRSLELNQ-------FNISYDRFSFAD-----EKEKIKLLRKFKRNPFPKQISEILSIALFGKYALSDRA 104
-----YHVHHGYEMHRVFNLPH----------TEFCINQPLKKVIEFLF-FKKIY---------ERKQDPN 85
----KFELYN-------FGIKINVASEKDINRLSDCQADF-VSRIRRKIFGKKKSF---------VSEKNDS 80

FIG. 4B

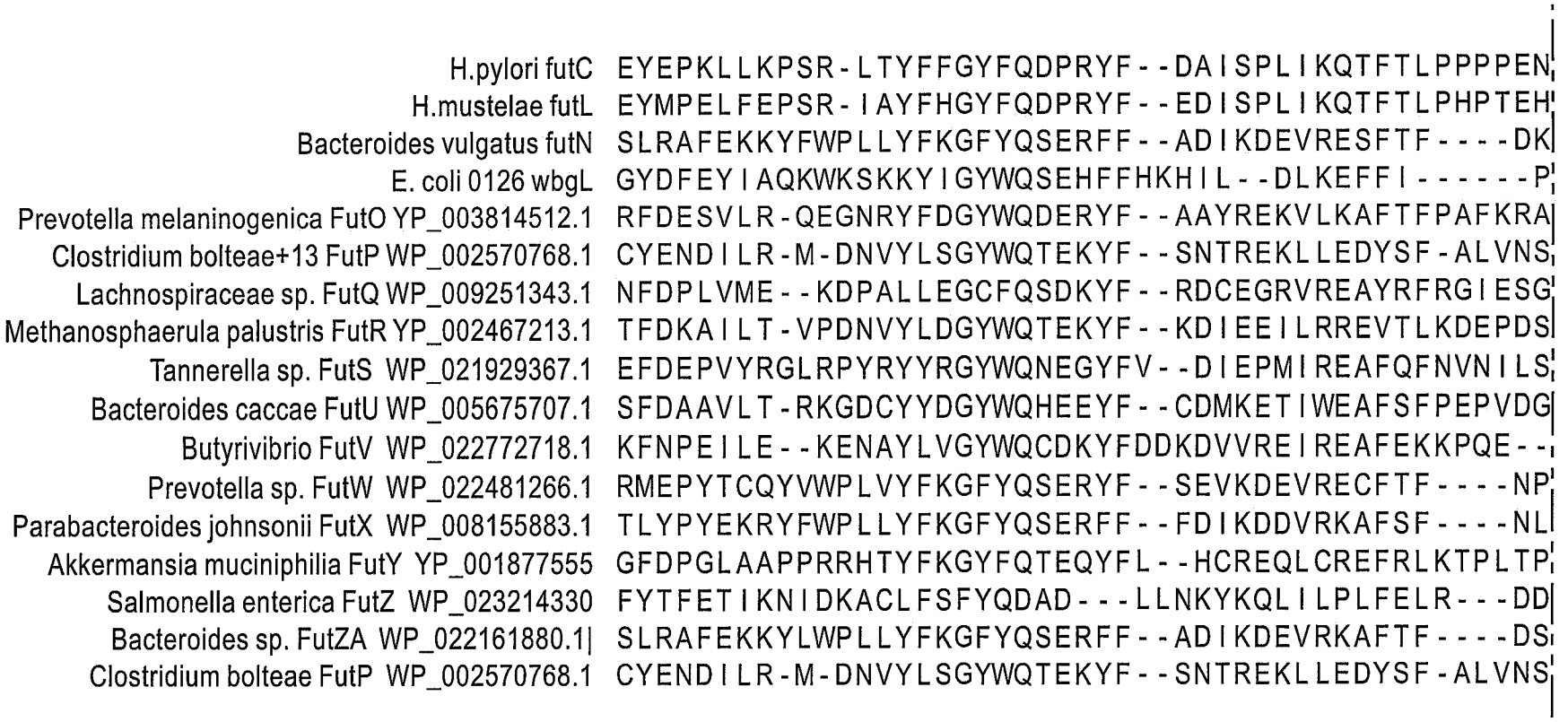

H.pylori futC EYEPKLLKPSR-LTYFFGYFQDPRYF--DAISPLIKQTFTLPPPPEN
H.mustelae futL EYMPELFEPSR-IAYFHGYFQDPRYF--EDISPLIKQTFTLPHPTEH
Bacteroides vulgatus futN SLRAFEKKYFWPLLYFKGFYQSERFF--ADIKDEVRESFTF----DK
E. coli 0126 wbgL GYDFEYIAQKWKSKKYIGYWQSEHFFHKHIL--DLKEFFI------P
Prevotella melaninogenica FutO YP_003814512.1 RFDESVLR-QEGNRYFDGYWQDERYF--AAYREKVLKAFTFPAFKRA
Clostridium bolteae+13 FutP WP_002570768.1 CYENDILR-M-DNVYLSGYWQTEKYF--SNTREKLLEDYSF-ALVNS
Lachnospiraceae sp. FutQ WP_009251343.1 NFDPLVME--KDPALLEGCFQSDKYF--RDCEGRVREAYRFRGIESG
Methanosphaerula palustris FutR YP_002467213.1 TFDKAILT-VPDNVYLDGYWQTEKYF--KDIEEILRREVTLKDEPDS
Tannerella sp. FutS WP_021929367.1 EFDEPVYRGLRPYRYYRGYWQNEGYFV--DIEPMIREAFQFNVNILS
Bacteroides caccae FutU WP_005675707.1 SFDAAVLT-RKGDCYYDGYWQHEEYF--CDMKETIWEAFSFPEPVDG
Butyrivibrio FutV WP_022772718.1 KFNPEILE--KENAYLVGYWQCDKYFDDKDVVREIREAFEKKPQE--
Prevotella sp. FutW WP_022481266.1 RMEPYTCQYVWPLVYFKGFYQSERYF--SEVKDEVRECFTF----NP
Parabacteroides johnsonii FutX WP_008155883.1 TLYPYEKRYFWPLLYFKGFYQSERFF--FDIKDDVRKAFSF----NL
Akkermansia muciniphilia FutY YP_001877555 GFDPGLAAPPRRHTYFKGYFQTEQYFL--HCREQLCREFRLKTPLTP
Salmonella enterica FutZ WP_023214330 FYTFETIKNIDKACLFSFYQDAD---LLNKYKQLILPLFELR---DD
Bacteroides sp. FutZA WP_022161880.1 SLRAFEKKYLWPLLYFKGFYQSERFF--ADIKDEVRKAFTF----DS
Clostridium bolteae FutP WP_002570768.1 CYENDILR-M-DNVYLSGYWQTEKYF--SNTREKLLEDYSF-ALVNS

FIG. 4C

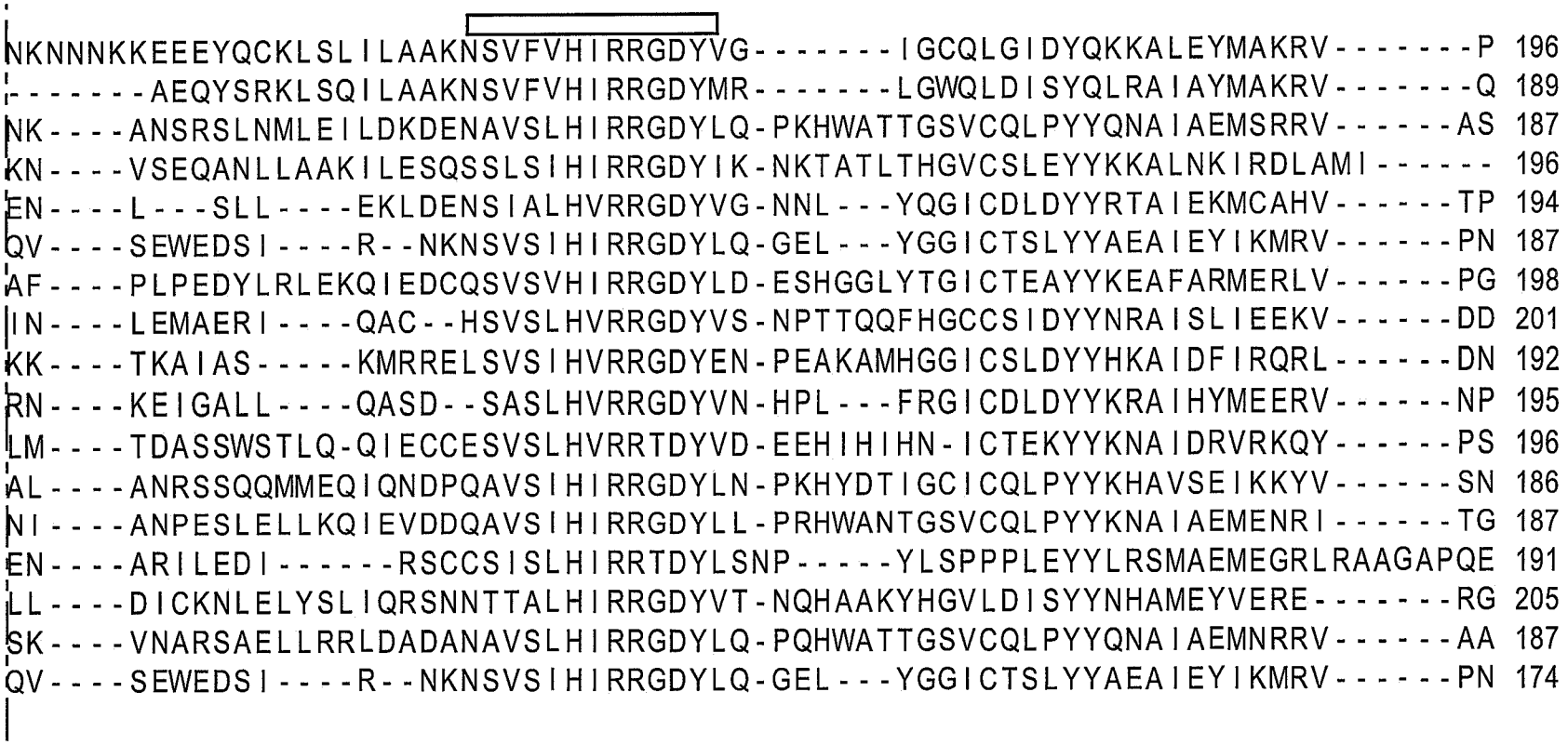

NKNNNKKEEEYQCKLSLILAAKNSVFVHIRRGDYVG-------IGCQLGIDYQKKALEYMAKRV-------P 196
-------AEQYSRKLSQILAAKNSVFVHIRRGDYMR-------LGWQLDISYQLRAIAYMAKRV-------Q 189
NK----ANSRSLNMLEILDKDENAVSLHIRRGDYLQ-PKHWATTGSVCQLPYYQNAIAEMSRRV------AS 187
KN----VSEQANLLAAKILESQSSLSIHIRRGDYIK-NKTATLTHGVCSLEYYKKALNKIRDLAMI------ 196
EN----L---SLL----EKLDENSIALHVRRGDYVG-NNL---YQGICDLDYYRTAIEKMCAHV------TP 194
QV----SEWEDSI----R--NKNSVSIHIRRGDYLQ-GEL---YGGICTSLYYAEAIEYIKMRV------PN 187
AF----PLPEDYLRLEKQIEDCQSVSVHIRRGDYLD-ESHGGLYTGICTEAYYKEAFARMERLV------PG 198
IN----LEMAERI----QAC--HSVSLHVRRGDYVS-NPTTQQFHGCCSIDYYNRAISLIEEKV------DD 201
KK----TKAIAS-----KMRRELSVSIHVRRGDYEN-PEAKAMHGGICSLDYYHKAIDFIRQRL------DN 192
RN----KEIGALL----QASD--SASLHVRRGDYVN-HPL---FRGICDLDYYKRAIHYMEERV------NP 195
LM----TDASSWSTLQ-QIECCESVSLHVRRTDYVD-EEHIHIHN-ICTEKYYKNAIDRVRKQY------PS 196
AL----ANRSSQQMMEQIQNDPQAVSIHIRRGDYLN-PKHYDTIGCICQLPYYKHAVSEIKKYV------SN 186
NI----ANPESLELLKQIEVDDQAVSIHIRRGDYLL-PRHWANTGSVCQLPYYKNAIAEMENRI------TG 187
EN----ARILEDI------RSCCSISLHIRRTDYLSNP-----YLSPPPLEYYLRSMAEMEGRLRAAGAPQE 191
LL----DICKNLELYSLIQRSNNTTALHIRRGDYVT-NQHAAKYHGVLDISYYNHAMEYVERE-------RG 205
SK----VNARSAELLRRLDADANAVSLHIRRGDYLQ-PQHWATTGSVCQLPYYQNAIAEMNRRV------AA 187
QV----SEWEDSI----R--NKNSVSIHIRRGDYLQ-GEL---YGGICTSLYYAEAIEYIKMRV------PN 174

FIG. 4D


H.pylori futC NMELFVFCEDLEFT-QNLDLGYP---FMDMTTRDKEEEAYWDMLLMQ
H.mustelae futL NLELFLFCEDLEFV-QNLDLGYP---FVDMTTRDGA--AHWDMMLMQ
Bacteroides vulgatus futN PS-YYIFSDDIAWVKENL----PLQNAVYIDWNTDE-DSWQDMMLMS
E. coli 0126 wbgL -RDVFIFSDDIFWCKENIETLLSKKYNIYYSEDLSQEE---DLWLMS
Prevotella melaninogenica FutO YP_003814512.1 SL-FCIFSNDITWCQQHLQPYLKAP-VVYVTWNTGV-ESYRDMQLMS
Clostridium bolteae+13 FutP WP_002570768.1 AK-FFVFSDDVEWVKQQED----FKGFVIVDRNEYS-SALSDMYLMS
Lachnospiraceae sp. FutQ WP_009251343.1 AR-FFLFSNDPEWTREHFE----SKNCVLVEGSTED-TGYMDLYLMS
Methanosphaerula palustris FutR YP_002467213.1 PS-FFIFSDDLPWAKENLD--IPGEKT-FVAHNGPE-KEYCDLWLMS
Tannerella sp. FutS WP_021929367.1 NICFYLFSDDINWVEENLQL----ENRCIIDWNQGE-DSWQDMYLMS
Bacteroides caccae FutU WP_005675707.1 QL-YCVFSNDMAWCESHLRALLPGKEVVYVDWNKGA-ESYVDMRLMS
Butyrivibrio FutV WP_022772718.1 AV-FFIFTDDKEWCRDHFK----GPNFIVVELEEGDGTDIAEMTLMS
Prevotella sp. FutW WP_022481266.1 PH-FYVFSEDLDWVKANL----PLENAQYIDWNKGA-DSWQDMMLMS
Parabacteroides johnsonii FutX WP_008155883.1 PS-YYVFSDDISWVKENI----PLKKAVYVTWNKGE-DSWQDMMLMS
Akkermansia muciniphilia FutY YP_001877555 SLRYFIFSDDIEWARQNLRPALP---HVHVDINDG-GTGYFDLELMR
Salmonella enterica FutZ WP_023214330 KQNFIIFSDDVRWAQKAFLE----NDNCYVINNSDYDFSAIDMYLMS
Bacteroides sp. FutZA WP_022161880.1 PS-YYVFSDDIAWVKENI----PLQNAVYIDWNKGE-ESWQDMMLMS
Clostridium bolteae FutP WP_002570768.1 AK-FFVFSDDVEWVKQQED----FKGFVIVDRNEYS-SALSDMYLMS

FIG. 4E

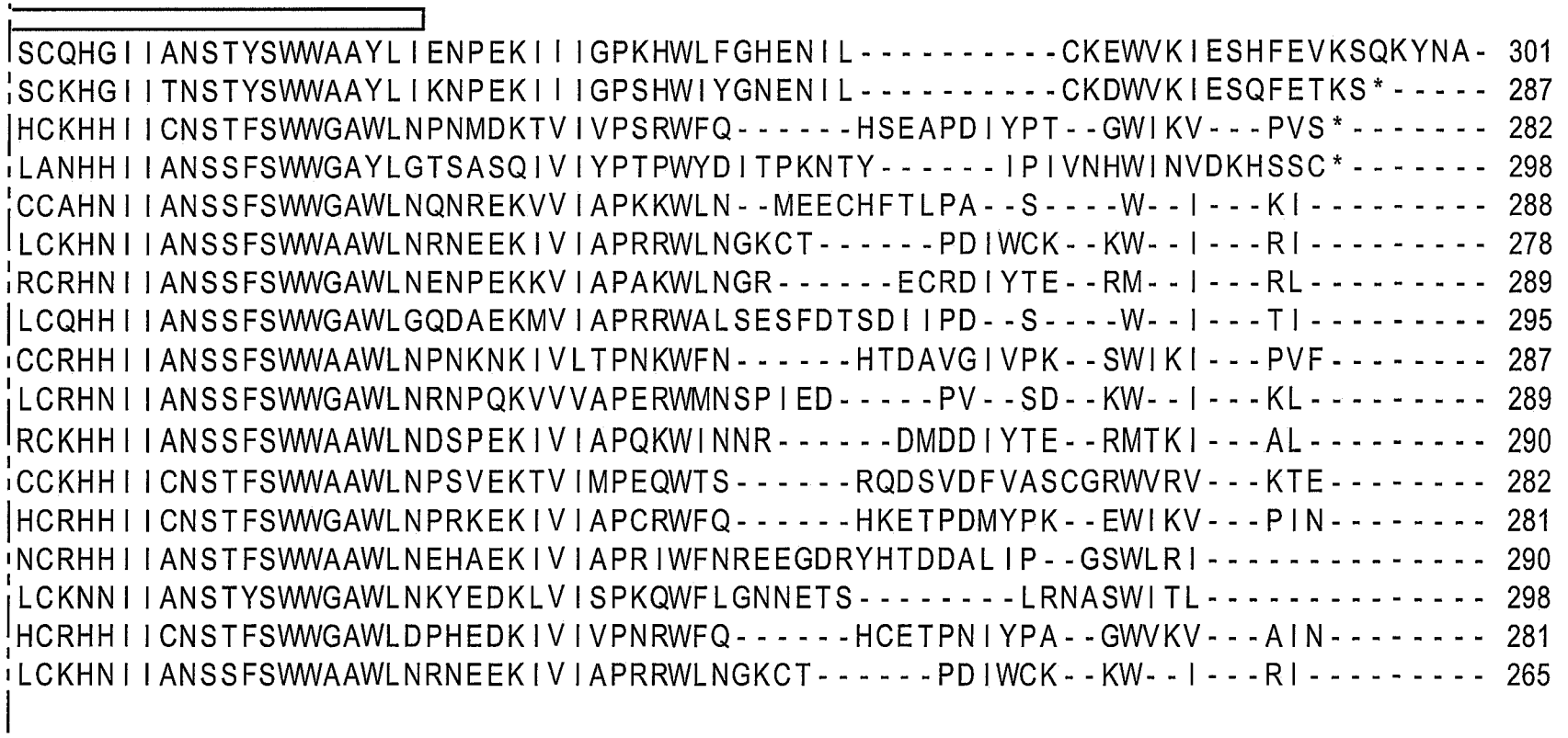

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SCKHGIITNSTYSWWAAYLIKNPEKIIIGPSHWIYGNENIL----------CKDWVKIESQFETKS*----- 287
HCKHHIICNSTFSWWGAWLNPNMDKTVIVPSRWFQ------HSEAPDIYPT--GWIKV---PVS*------- 282
LANHHIIANSSFSWWGAYLGTSASQIVIYPTPWYDITPKNTY------IPIVNHWINVDKHSSC*------- 298
CCAHNIIANSSFSWWGAWLNQNREKVVIAPKKWLN--MEECHFTLPA--S----W--I---KI--------- 288
LCKHNIIANSSFSWWAAWLNRNEEKIVIAPRRWLNGKCT------PDIWCK--KW--I---RI--------- 278
RCRHNIIANSSFSWWGAWLNENPEKKVIAPAKWLNGR------ECRDIYTE--RM--I---RL--------- 289
LCQHHIIANSSFSWWGAWLGQDAEKMVIAPRRWALSESFDTSDIIPD--S----W--I---TI--------- 295
CCRHHIIANSSFSWWAAWLNPNKNKIVLTPNKWFN------HTDAVGIVPK--SWIKI---PVF-------- 287
LCRHNIIANSSFSWWGAWLNRNPQKVVVAPERWMNSPIED-----PV--SD--KW--I---KL--------- 289
RCKHHIIANSSFSWWAAWLNDSPEKIVIAPQKWINNR------DMDDIYTE--RMTKI---AL--------- 290
CCKHHIICNSTFSWWAAWLNPSVEKTVIMPEQWTS------RQDSVDFVASCGRWVRV---KTE-------- 282
HCRHHIICNSTFSWWGAWLNPRKEKIVIAPCRWFQ------HKETPDMYPK--EWIKV---PIN-------- 281
NCRHHIIANSTFSWWAAWLNEHAEKIVIAPRIWFNREEGDRYHTDDALIP--GSWLRI------------- 290
LCKNNIIANSTYSWWGAWLNKYEDKLVISPKQWFLGNNETS--------LRNASWITL------------- 298
HCRHHIICNSTFSWWGAWLDPHEDKIVIVPNRWFQ------HCETPNIYPA--GWVKV---AIN-------- 281
LCKHNIIANSSFSWWAAWLNRNEEKIVIAPRRWLNGKCT------PDIWCK--KW--I---RI--------- 265

FIG. 4F