1) Phosphotransferase glucose transporter (PTSG)
Bacillus subtilis used as reference.

```
AIY92692.1|PTSG_BSU13890      MFKALFGVLQKIGRALMLPVAILPAAGILLAIGNAMQNKDMIQVLHFLSNDNVQLVAGVM    60
ADR25276.1|MBOVPG45_0417      ------------------------------------------------------------    0
ACF07467.1|MARTH_orf702       ------------------------------------------------------------    0
AJR12360.1|MDIS_03180         ------------------------------------------------------------    0
AAT27986.1|MMOB5000           ------------------------------------------------------------    0

AIY92692.1|PTSG_BSU13890      ESAGQIVFDNLPLLFAVGVAIGLANGDGVAGIAAIIGYLVMNVSMSAVLLANGTIPSDSV    120
ADR25276.1|MBOVPG45_0417      ------------------------------------------------------------    0
ACF07467.1|MARTH_orf702       ------------------------------------------------------------    0
AJR12360.1|MDIS_03180         ------------------------------------------------------------    0
AAT27986.1|MMOB5000           ------------------------------------------------------------    0

AIY92692.1|PTSG_BSU13890      ERAKFFTENHPAYVNMLGIPTLATGVFGGIIVGVLAALLFNRFYTIELPQYLGFFAGKRF    180
ADR25276.1|MBOVPG45_0417      ------------------------------------------------------------    0
ACF07467.1|MARTH_orf702       ------------------------------------------------------------    0
AJR12360.1|MDIS_03180         ------------------------------------------------------------    0
AAT27986.1|MMOB5000           ------------------------------------------------------------    0

AIY92692.1|PTSG_BSU13890      VPIVTSISALILGLIMLVIWPPIQHGLNAFSTGLVEANPTLAAFIFGVIERSLIPFGLHH    240
ADR25276.1|MBOVPG45_0417      ------------------------------------------------------------    0
ACF07467.1|MARTH_orf702       ------------------------------------------------------------    0
AJR12360.1|MDIS_03180         ------------------------------------------------------------    0
AAT27986.1|MMOB5000           ------------------------------------------------------------    0

AIY92692.1|PTSG_BSU13890      IFYSPFWYEFFSYKSAAGEIIRGDQRIFMAQIKDGVQLTAGTFMTGKYPFMMFGLPAAAL    300
ADR25276.1|MBOVPG45_0417      ------------------------------------------------------------    0
ACF07467.1|MARTH_orf702       ------------------------------------------------------------    0
AJR12360.1|MDIS_03180         ------------------------------------------------------------    0
AAT27986.1|MMOB5000           ------------------------------------------------------------    0

AIY92692.1|PTSG_BSU13890      AIYHEAKPQNKKLVAGIMGSAALTSFLTGITEPLEFSFLFVAPVLFAIHCLFAGLSFMVM    360
ADR25276.1|MBOVPG45_0417      ------------------------------------------------------------    0
ACF07467.1|MARTH_orf702       ------------------------------------------------------------    0
AJR12360.1|MDIS_03180         ------------------------------------------------------------    0
AAT27986.1|MMOB5000           ------------------------------------------------------------    0

AIY92692.1|PTSG_BSU13890      QLLNVKIGMTFSGGLIDYFLFGILPNRTAWWLVIPVGLGLAVIYYFGFRFAIRKFNLKTP    420
ADR25276.1|MBOVPG45_0417      --------MTT-------------GDKWKIATLTIFTLGFCWVYW---SVKNKKVK---K    33
ACF07467.1|MARTH_orf702       --------MSK-------------KNKLKYVLLIIFTLGLICIYW---RFKYRQVE---K    33
AJR12360.1|MDIS_03180         --------MKL-------------ISKIIYFLLQIFSFGFFAKHI---N---KKHN---K    30
AAT27986.1|MMOB5000           --------MSK-------------KDKFLYIFLIIITFGLILLYW---R-KYRQIK---P    32
                                      *.               .:     :  . :*:   :        :: :

AIY92692.1|PTSG_BSU13890      GREDAAEETAAPGKTGEAGDLPYEILQAMGDQENIKHLDACITRLRVTVNDQKKVDKDRL    480
ADR25276.1|MBOVPG45_0417      LKKGEINKLD-------SSMDTLELINLLGGKSNISSVSNTISRIKVIINDKSIVQKDKL    86
ACF07467.1|MARTH_orf702       -KDYLTVEHT-------LAFSFDELMNLIGSKDNIDNVSATQKIIKIYFKERSKVNLTGI    85
AJR12360.1|MDIS_03180         TKSDLTFEKK-------FDFKIEELINLLGGKKNIKSSDFSISRLKIQLKSTENLDFEKI    83
AAT27986.1|MMOB5000           -KKELSISTK-------ISFKLEDLIDSLGSKENIKSIKSSNQIVKIAINDNSLVKIDEV    84
                               :.    .               :::: :* :.**.  .     ::: .:. . :.   :

AIY92692.1|PTSG_BSU13890      KQL-GASGVLEVGNNIQAIFGPRSDGLKTQMQDIIAGRKPRPEPKTSAQEEVGQQVEEVI    539
ADR25276.1|MBOVPG45_0417      EQLKYVSGIMISSNNVSLVVGDYAKKLSEELNNEIAK-----------------------    123
ACF07467.1|MARTH_orf702       QKLPGISGISFQSKAISLVIGNSAKYLEELILKELDFNERS-------------------    126
AJR12360.1|MDIS_03180         KKLKGVSGIVVNSETISLIVGNKSKAISEAINNFE-------------------------    118
AAT27986.1|MMOB5000           KNLKGISGVVNNTTQISLVVGNSAPTIQKELENKLQKS----------------------    122
                              ::*   **:      :. :.*  :  :.  : .

AIY92692.1|PTSG_BSU13890      AEPLQNEIGEEVFVSPITGEIHPITDVPDQVFSGKMMGDGFAILPSEGIVVSPVRGKILN    599
ADR25276.1|MBOVPG45_0417      ------------------------------------------------------------    123
ACF07467.1|MARTH_orf702       ------------------------------------------------------------    126
AJR12360.1|MDIS_03180         ------------------------------------------------------------    118
AAT27986.1|MMOB5000           ------------------------------------------------------------    122

AIY92692.1|PTSG_BSU13890      VFPTKHAIGLQSDGGREILIHFGIDTVSLKGEGFTSFVSEGDRVEPGQKLLEVDLDAVKP    659
ADR25276.1|MBOVPG45_0417      ------------------------------------------------------------    123
ACF07467.1|MARTH_orf702       ------------------------------------------------------------    126
AJR12360.1|MDIS_03180         ------------------------------------------------------------    118
AAT27986.1|MMOB5000           ------------------------------------------------------------    122

AIY92692.1|PTSG_BSU13890      NVPSLMTPIVFTNLAEGETVSIKASGSVNREQEDIVKIEK       699
ADR25276.1|MBOVPG45_0417      ---------------------------------------       123
ACF07467.1|MARTH_orf702       ---------------------------------------       126
AJR12360.1|MDIS_03180         ---------------------------------------       118
AAT27986.1|MMOB5000           ---------------------------------------       122
```

BSU, *Bacillus subtilis*; MBOVPG45, *M. bovis* PG45; MARTH, *M. arthritidis*, MDIS, *M. dispar*.

2) Phosphotransferase glucose transporter (PTSI)
Staphylococcus simulans used as reference.

```
ERS92720.1|PTS_IIBC_SSIM_10465      -------------------------MYNFLQRLGRSLMLPVAVLPAAAIIIGIGNLLKAL
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                ------------------------------------------------------------
CAC13190.1|MYPU_0170                MTILKKLNFRKEKSEKSKINNNSGKLKKLLSKISGAFMLPIAIMSIAGIFLGVGAAIATG
AAP56484.2|MGA_0855                 MAS-TTNQVHSQKRSSERWKRFSGHFKEVVGKLSAGIMIPIALLPIAGLLLGIFAAVQNN

ERS92720.1|PTS_IIBC_SSIM_10465      E--V----TPTLAEFIFQSGIAVLEQLGLLFAIGVALGMAKKNDGSVALAAVVGYFVVTS
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                ------------------------------------------------------------
CAC13190.1|MYPU_0170                S--GANEGLKLFGLFIQNMGDPIFSSLPLLFAAAFVIAFTEE-AGAAVFAAIIAYLVFSA
AAP56484.2|MGA_0855                 VSQATHPGVFAMAAFFKNGAEAVFGNLPTLFAIAIAVAFTNQ-SGVAALSAFVGWLIFNA

ERS92720.1|PTS_IIBC_SSIM_10465      VLKTE------TLAKILS---------------VKEDSLNIGFTAMNNQNVFIGLIIGLI
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                ------------------------------------------------------------
CAC13190.1|MYPU_0170                LQAALIEPLRDSAQKIIGYKVLFESAGRDPESLIRLVGSSVGFTTL-QTSVFGGISVGLI
AAP56484.2|MGA_0855                 TQTALIFPNANSQTFTILYYNSVP---------ATALAMNVGLRSL-STSVFGGVIVGAI

ERS92720.1|PTS_IIBC_SSIM_10465      AAFCYNKFSGTELPTALSFFSGKRLVPIMTAFLSVILTIILLFVWPFVYSGIISFGKWIM
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                ------------------------------------------------------------
CAC13190.1|MYPU_0170                TSYLYNKFHKIQFHPAFSFFAGKRFVPLVAILAMVPLSLTFLLFWPWVGKGLSVFGTALG
AAP56484.2|MGA_0855                 TALLFNKFHTIQLPKVVGFFNGNRFVPIITLLTMLPVALVALMIWPAIGIGLNALGQSLG

ERS92720.1|PTS_IIBC_SSIM_10465      DF---GAFGAFLYGFFNRLLIPTGLHHALNSVFWFDLAGINDIAKFQT------------
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                ------------------------------------------------------------
CAC13190.1|MYPU_0170                KV--PYGIESFIFGFIERSLIPFGLHHVFYAPLWYSNAGGDAATALSQWQ----------
AAP56484.2|MGA_0855                 VLSRNGNFNSFIFGYVERALVPFGLHHAFYAPLWFTSAGGSIANIIVNQAGSNAIAPLIV

ERS92720.1|PTS_IIBC_SSIM_10465      ---G--------------------------------------------------------
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                ------------------------------------------------------------
CAC13190.1|MYPU_0170                --QAGN-------------QFVESAGFTAANIQ-------ELIDSITKNADKWVGDSTGW
AAP56484.2|MGA_0855                 TDENGQRVIRSIVGVAANKDAVKPAGFTAQNWMYWGQVVTALNPNTQINTDSLSGDQRLW

ERS92720.1|PTS_IIBC_SSIM_10465      ------------------------------------------------------------
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                ------------------------------------------------------------
CAC13190.1|MYPU_0170                QAVNSLNFNVVSFRKQ---------------------------------------------
AAP56484.2|MGA_0855                 FTINSLFVNKSVYLSGSSDPYTFTFKSFADSTLNHPSLIQSITRNGTVISGAQLLTMIKE

ERS92720.1|PTS_IIBC_SSIM_10465      ----EG-------------AVKGITGRYMAGFFPVMMFGVPAAALAMYQTADSKQKKRVA
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                ------------------------------------------------------------
CAC13190.1|MYPU_0170                ---GSSEVQTLRVLDFFAQEFGIKLGRFLQGKYVFMSMGLPAAAFAMVMAAPKENRKVAF
AAP56484.2|MGA_0855                 SSTGSVVLQANDTLNF--AFPGVNPGQYEQGKHAFMIFGLPAAGAAMIMAAPKDQRKYAS

ERS92720.1|PTS_IIBC_SSIM_10465      GLMLAGSISAFFVGVTEPIEFAFMFAAPVLFV-IHALLTGLSLFIAALFHWTAGFSFSAG
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                ------------------------------------------------------------
CAC13190.1|MYPU_0170                ASLAPAAFTCFLTGITEPLEFTFLLLSPFLFWGFHAFMCALAFLLMNVLGAHIGMTFSGG
AAP56484.2|MGA_0855                 SIIISAAFTSFLTGITEPIEFTFLFLAPYLFWGFHAVFCAISFWLTSLLGGNIGQTFSGG

ERS92720.1|PTS_IIBC_SSIM_10465      LIDFLLSLINPVS----NHPWMLMVQGVVFFVIYYVVFRVAISVFNLNTPGRGDEKIADP
ADR25285.1|MBOVPG45_0573            ---------------------------------------------MA---------
ADN68838.1|MFE_02260                -----------MG----FVSWI------------------------KRVFGRKDNK----
CAC13190.1|MYPU_0170                FIDYVIYGLIPIQK--GTHAYWVYVVAPFYAPIYFFVFYFWIKFKNLDTPGRGQNIKLFT
AAP56484.2|MGA_0855                 IIDLTIYGFIPDALGAKTNSWLPLVIGLFYIPLYYFTFYFLITKRNIETPGRGAGTRLYT
                                                                                          .

ERS92720.1|PTS_IIBC_SSIM_10465      VDEEGVSSESGKG----------GKYSAMSTQIISGLGGKENITSLTNCATRLRLEVANI
ADR25285.1|MBOVPG45_0573            ----KANKILDTN----------TEEYKQPKQIIQALGGLENISKYRNCATKLRYDIVNK
ADN68838.1|MFE_02260                ----QKIKEVRKL----------VEISQLTRDIVNAMGGIENITGFNNCAVRLRYDVKDT
CAC13190.1|MYPU_0170                KKDF-RNKN-KNK----------NLVDPQVRAVVLGLGGWDNITKYENCASRLRYDVVDF
AAP56484.2|MGA_0855                 KADYQAKVASKNAASTNDGSANFKPIEITSYKLIKAFGGRDNISAVNACATKLRVSVKTK
                                              .                    :: .:** :**:    ** :** .:

ERS92720.1|PTS_IIBC_SSIM_10465      DQIDKAQIKQSGAAGVTTSGQHNVQVIIGTQVQQVADEVERQL---ESE-----------
ADR25285.1|MBOVPG45_0573            DLVNETELINSGASAVNFVGDNHVQVRFGLKTVKLAKNIREVRDSKSS---KNE------
ADN68838.1|MFE_02260                SLVNEEALKKVGASEVIFIGKRHVQAKFGEISEKLNLDIQEAAPFLEEEALKNKKIEVKS
CAC13190.1|MYPU_0170                SKIDENRIKSAGATAIRRVGSNHIQIIVGSIAEQLNQRVKASIGQSLEK---DSKQSDSN
AAP56484.2|MGA_0855                 EKVNFGEIGALGSLGTYAVSDTLVHAVYGGDADIIKSYMQKMINKDYDSSAIEKVIGDPA
                                    . ::   :   *:      ..  ::   *     :   :.       .

ERS92720.1|PTS_IIBC_SSIM_10465      ------------------------------------------------------------
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                DV---NLFEEKPVEVKKT-VDENIVYTPCKGTRKSIEDLSDQTFS--LLGCGYAIEIDKK
CAC13190.1|MYPU_0170                DK---NSTSKANLENPKTQNKNLSVYSVFEGNSHSIVELNDGVFSEKMLGDGVFVEPNEF
AAP56484.2|MGA_0855                 TKEIDPSMPKATPEVDHKLYDVVDVYSPVKGTVTDLADLPDPSFAGKIMGDGVSIEPEDG
```

```
ERS92720.1|PTS_IIBC_SSIM_10465      ------------------------------------------------------------
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                LNKLEVYAPINGKLIMSYPTKHAYGIANDNGLEVLVHIGIDTVKLNGLGFETNLKQ----
CAC13190.1|MYPU_0170                KGLQKVYAPVSGKLLTLFETKHAYGITTNEGIEILVHIGVDTVNLKGQGFKTNLVQ----
AAP56484.2|MGA_0855                 ----MFYSPVDGKLELAYNTGHAYFFD-VNGAKILIHIGIDTVSLNSNNSDSNNLVGFKM

ERS92720.1|PTS_IIBC_SSIM_10465      ------------------------------------------------------------
ADR25285.1|MBOVPG45_0573            ------------------------------------------------------------
ADN68838.1|MFE_02260                ----NDKVERGQ-LLATVDLKKLRNSKICSDVIVLITDNVNKNKQTKLL-CPLEIKEVNV
CAC13190.1|MYPU_0170                ----GQDVKIGD-VLAEVDYDFLSKQNLPSMSTIVVITNMEQSKITNLKQGPVAL---NQ
AAP56484.2|MGA_0855                 FAKSGDNVSFKKSPVVQANLEMIKKKELSTNSPILALKETLANYDLKVVVKPGDKVNVGD

ERS92720.1|PTS_IIBC_SSIM_10465      ----------
ADR25285.1|MBOVPG45_0573            ----------
ADN68838.1|MFE_02260                PWFKMVD---
CAC13190.1|MYPU_0170                KLFDLEQN--
AAP56484.2|MGA_0855                 LLFKLTKKNK
```

SSIM, *Staphylococcus simulans*; MFE, *M. fermentans*; MPYU, *M. pulmonis*; MGA, *M. gallisepticum*

3) Pfk family carbohydrate kinase (PFK)

Clostridium sordellii used as reference. Active site is not known but substrate binding sites are shown in red.

```
CEQ19350.1|PFKB_W2948_29021_CLOSR      MTDREKEILNILIEDPMVSQQELADKLNITRSSVAVHITNLMKKGHIKGKGYIINKGNFV    60
ADR25403.1|MBOVPG45_0026               ------------------------------------------------------MSV    3
CCO56448.1|VIBNI_A0244                 MTEREQQIFQLIKQDPMIPQQDIADKLGISRSAVAGHIMNMTNKGIILGKGYILSESQYA    60
WP_014584243.1|HF1_14770               ----------------------------------------MK--------------KSI    5

CEQ19350.1|PFKB_W2948_29021_CLOSR      TVIGGSNIDIQGSPNNTL-------------------TMFDSNPGKVDISLGGVGRNISE    101
ADR25403.1|MBOVPG45_0026               VVVGSINYDLYAKVNNKI-------------------SLRDSNPANIYSSLGGVAYNIAK    44
CCO56448.1|VIBNI_A0244                 VVIGGANMDILGQPQQAM-------------------HQGDSNPGVVSCSPGGVGRNIAE    101
WP_014584243.1|HF1_14770               LCLGNPVFDTFASVSDDILVSNNIEKGSAPILDPKKVIEIISKVNFISANCGGSASNIAK    65
                                         :*    *  .. .: :                       *:   :  . ** . **::

CEQ19350.1|PFKB_W2948_29021_CLOSR      NIAKLGLNTKLLSAVGNDIYGNKILSECKQLNIDVSDCYVSDAFPTSMY-----------    150
ADR25403.1|MBOVPG45_0026               NLALSGIDTTLISAVGNDLEANWIKKQLENDSLN-SILIAKNDYKTAKY-----------    92
CCO56448.1|VIBNI_A0244                 NIARLGTEVRLISVVGNDTYGQLIIDKTRQAGVDVSPVMKLSDGTTSTY-----------    150
WP_014584243.1|HF1_14770               GIALVGGKAGLFGQYADDKEGDIIKDSLKEHGVI-DHCSVEKGGITTQINCLVTPDAQRT    124
                                        :*  * .. *:.  .:*  .: * .. .:  :  .     .   *:

CEQ19350.1|PFKB_W2948_29021_CLOSR      -LSILNSDYDMQLAISHMDIIEKIDIDYIVSKHNSIKDSLAIVLDTNLSYEVIDYISRTY    209
ADR25403.1|MBOVPG45_0026               -VALIDNNSDMNVAASDTKITESIDYNDLFAYKKLLDKSTYLCLDANLSSYLIVKLCKNF    151
CCO56448.1|VIBNI_A0244                 -LSLLNEDGDMQVAVSDMSILDKLTIESLEPHIEVLKRAEVIVVDTNLSESVLEYIFSQF    209
WP_014584243.1|HF1_14770               MIPLFGASHFMNPEAVDYSVVDNYDYFLLEGYQFCNQ-----CL-VDISYAFLDRVKEKN    178
                                        : ::  .  *:    . .: :.     :       .      : .::*  .:  :

CEQ19350.1|PFKB_W2948_29021_CLOSR      TNIPIFIDTVSTQKSLKI-------KDIIGRFNTIKPNKLEAEILSDIKINTQDDLKQCA    262
ADR25403.1|MBOVPG45_0026               SDKFIVAEAVSSQKILKF-------KPVLKHISLLKGNKLEFQALLNT---SETDLFILA    201
CCO56448.1|VIBNI_A0244                 ADKPIFVDTVSSTKAVKI-------KPYLSHIHTLKPNIKEAQSLSDLPHHDADDLETIA    262
WP_014584243.1|HF1_14770               IS-----LILSISNIFCVESYYQHMKHFAEAARMIVGNEEEFLKLFNF-----DDVNKLL    228
                                        .       :*  : . .       *        :  *  *   * :       *:

CEQ19350.1|PFKB_W2948_29021_CLOSR      QYF----LEK-GVKNVFITLGQDGVFCANENESLLL-RGVKVNAVNATGAGDAFISALVY    316
ADR25403.1|MBOVPG45_0026               SKV----LEL-GIKSVVITDGENGCIYANNEGVVEFYRPTIVKALSTSGAGDAFCAGLIY    256
CCO56448.1|VIBNI_A0244                 DWF----LNQ-GTQRIFLSLGEEGVFYKDAQGSQHF-PTVSTDIKNANGAGDAFLAGLVH    316
WP_014584243.1|HF1_14770               DHLQSQCVKGGKYEMIMVTAGPKGANILWEGKRFFVEAPDVKTPVDTTGAGDYFVAGLLY    288
                                       . .    ::    : :.:: * .*           .         .:.**** * :.*::

CEQ19350.1|PFKB_W2948_29021_CLOSR      SYLNHFNLKDTAEFSTAASILTLLHKD-TINPSMSVDSVEKILKEMI-       362
ADR25403.1|MBOVPG45_0026               GLINKMQILKVGASF---AKFSLLSLM-TINDKLNKSSLSKELMEVN-       299
CCO56448.1|VIBNI_A0244                 SYINKWSVERSSEFAMAAASVALSDVA-TINPNFSENAVKRVLNEAEC       363
WP_014584243.1|HF1_14770               GYFQGYDMSISNKIAQIMAKDIISKFGSTLSPS-VVDEVKKVLP----       331
                                       . ::  .:          :   :     *:. .   . :.: *
```

W2948_29021, *Clostridium sordellii*; VIBNI, *Vibrio nigripulchritudo;* HF1_14770, *M. haemofelis*

4) Acetaldehyde dehydrogenase (ADH)

M. pneumoniae used as reference. No known active site.

```
NP_110253.1|ADH_MPN564          MKAYAMLKIGAT----GWIEKPRPVCGPNDAIIRPLAVAPCTSDVHTVWEGGIGERHNMV        56
ADR25320.1|MBOVPG45_0543        MKMKALVYHGDHKIALETVDK-PVILKPTDAIVKVTKTTICGTDLGIYKGKNPEVADGRI        59
                                **  *::  *         ::*   :  *.***::   .: * :*:            .  :

NP_110253.1|ADH_MPN564          LGHEGCGVVDEVGSEVKSFKVGDRVLVAAITPEWNSVNAQAGYPMHSGGMLGGWKFSNVK        116
ADR25320.1|MBOVPG45_0543        LGHEGIGIVEEVGSSVSNVKVGDKVLIGCVTPCGKCDNCRQQLYSHCREAEGGWKFGYMI        119
                                ***** *:*:****.*...****:**:..:**  :. *.:     *.    *****. :

NP_110253.1|ADH_MPN564          DGMFAEYFHVNDAEGNLALMPEGMDLADACMLSDMIPTGFHAN-ELADIQYGVALSFFCA        175
ADR25320.1|MBOVPG45_0543        NGTQAEYVRVPFADNSLYKYPESISDEVAVMLSDALPTGHEIGVQYGNVAPGKSVAIVGA        179
                                :*  ***.:*  *: .*   **.:.   * **** :***..   : .::  * ::::. *
```

```
NP_110253.1|ADH_MPN564        GPVGLMAIAGAALKGAGRIIVVDSRPDIVEIAKAYGATDYIDFKKVSVVDEILKWTNNEG        235
ADR25320.1|MBOVPG45_0543      GPVGMGALLTAQLYSPAHLIVIDFDKNRLEMAKKLGATHTLVPDET-LLTKLQEIVGTDG        238
                              ****: *:  * * . .::**:*   : :*:**  ***. :  .:. :: :: : . .:*

NP_110253.1|ADH_MPN564        VEKVLISGGGSTILETAIKVLRPGGKIGNVNYFGAGEFLTIPRVEWGVGMAHKAIHGGLM        295
ADR25320.1|MBOVPG45_0543      VDVAIEAVGVPQSWDTCQKIVKAGGNISVVGVHGKKVDFNVQE-LWIKNL---TVTTGLV        294
                              *: .: : *     :*. *::: **:*. *  .*    :.: .  *   :   ::  **:

NP_110253.1|ADH_MPN564        LGGRLRLEKLARLIMTKKLDPSKMITHRFKGFEHIEEALFLMKDKPKDLIKSVVIF----        351
ADR25320.1|MBOVPG45_0543      NTN--TLPMLINAVSTGKLPVQGLITHRFNLSDMMKAYDTFLNASDN---KAMKIFIDAT        349
                                    *  * . : * **  . :*****:  : ::    ::: . :   *:: **

NP_110253.1|ADH_MPN564        -       351
ADR25320.1|MBOVPG45_0543      K       350
```

MPN, *M. pneumoniae.*

6) 5'-nucleotidase (NT5; USHA)

E. coli used as reference.

```
NP_415013.1|USHA_b0480_ECOLI      ------------------------------------------------------------    0
ADR25153.1|MBOVPG45_0690          MKRKFILGLGA-ISAFAAIPMVAATCGVSSPK-----------------QVAKARAAYDE    42
ENY68833.1|MAU_3200               MKKKMLLSLGGILTAFSALPMIAISCGQPNEE-----------------KVAKAKAAYEN    43
ENY69482.1|MBVG_3940              MKKRLFLNLMP-VAALSMLPTIAISCINTKQKDKD---------TQSNTQFEVQLAEYEK    50
ADE19785.1|MCRO_0158              MKIKKLMLVGAIAPLVILPATISAACDDKNKPVKPVTPSTNEMTAEEKKALDAARVEFKD    60

NP_415013.1|USHA_b0480_ECOLI      --------------------------------------------------MKLLQRGVAL    10
ADR25153.1|MBOVPG45_0690          AFKKFNDAVESDIKELVQKKEAINAKDIDKEKKKKLTEEKDAWVKTRTPILQGLRKKAND    102
ENY68833.1|MAU_3200               AFKNFDEAINADMQSLKDKKAEIE-KEKDETKKKELIAKKEEFVKQRSPILLALRKKVND    102
ENY69482.1|MBVG_3940              HYKLFNDTISKYKKELEEKYKNIQKRGNTKEQTKQLTAKKDAWVKEKTIELQALRKNVDD    110
ADE19785.1|MCRO_0158              AMGNYNAQLLTFSKELAAKKKAID-KEKDKTKKEALQKERKQFVAEKSKIVAPLREEINK    119
                                                                                :  *:.

NP_415013.1|USHA_b0480_ECOLI      ALLTTFTLASETALAYEQDKTYKITVLHTNDHHGHFWRN--EYGEYGLAAQKTLVDGIRK    68
ADR25153.1|MBOVPG45_0690          AFINL-------RKVQKNFKTQVVKVVHTNDEHGRLVFDDGKYNNYS------GMQGLAE    149
ENY68833.1|MAU_3200               AYKNL-------RVAQKGAGTQLIKIVHTNDEHGRLVFDDGKYNNYS------GMQGLAE    149
ENY69482.1|MBVG_3940              NYLKL-------RNLK-DHKTRLVKLIHTNDEHGRLVFDNGKYNKYS------GMQGHAE    156
ADE19785.1|MCRO_0158              ALVKV-------NKLEAKSDTQTIKIFNTNDEHGRLVFDDGKYNNFS------GMDTLAK    166
                                     .                *  :.:..***.**::  :  :* ::.       ::   :

NP_415013.1|USHA_b0480_ECOLI      EVAAEGGSVLLLSGGDINTGVPESDLQDAEPDFRGMNLVGYDAMAIGNHEFDNPLTVLRQ    128
ADR25153.1|MBOVPG45_0690          VLNKDFDRDLLLSAGDLIQGLPLSDSDKGLTISKVAKEMKYQAVAIGNHEFDYGLEHMFN    209
ENY68833.1|MAU_3200               ILSRDFDRDLLLSAGDLIQGLPLSDSDKGLTISKIAKEMKYNAVAIGNHEFDYGLDHMFK    209
ENY69482.1|MBVG_3940              ILGLNFTRDLLLSAGDLIQGQPLSDSDKGVTISEIAALMNYNAVAVGNHEFDYGLMHLFE    216
ADE19785.1|MCRO_0158              FM-QNVEHSLLLSAGDLIQGLPMNDSDKGVTISLVAKEMNYDAIAIGNHEFDFGLEHMIN    225
                                   :  :    ****.**:  * * .* :..         : *:*:*:******  *  : :

NP_415013.1|USHA_b0480_ECOLI      QEK--WAKFPLLSANIYQK----------------STGERLFKPWALFK-RQDLKIAVIG    169
ADR25153.1|MBOVPG45_0690          IEKQT-AGMPFLSANIVWNDKAVAEKVKTKDGKLAVKNEQVFTPYIIKTLESGIKVGIMG    268
ENY68833.1|MAU_3200               IEKET-EGMPFLSANIVWNKKAVTDQVKDKNGKLAIEGQKVFSPYIIKELPSGLKVAIMG    268
ENY69482.1|MBVG_3940              IQKKT-PNMPFLSANIVWNQKAVTDKVKDIDGKDAVADELVFKPYIIKELASGIKVGIMG    275
ADE19785.1|MCRO_0158              IDKQTKDKMPFLSANVVYKDTMP----------EGVKGTRPFTPYKVVTLANGFKVALIG    275
                                   :*     :*:****:  :                      *.*: :    . :*:.::*

NP_415013.1|USHA_b0480_ECOLI      LTTDDTAKIGNPEYFTDIEFRKPADEAKLVIQELQQTEKPDIIIAATHMGHYDNGEHGSN    229
ADR25153.1|MBOVPG45_0690          ITTPDTQWTSNPKNSVHVTFLDPIESGKKTVEELKSK-GVNFIIALTHLGVNRPDTRWDS    327
ENY68833.1|MAU_3200               ITTPDTQWTSAPRNSVHVTFLDPIDTAKEVVKELKAK-GINFIVALTHLGVNRPDTRWDS    327
ENY69482.1|MBVG_3940              ITTPDTAWTSSPKNSVHVTFKDPVQEGTKYAKELRDK-GVNIVIALTHLGVDRQNKEWDS    334
ADE19785.1|MCRO_0158              ITTPDTTITSHPRNSKDVIFKDPVTAAKEIVTEIENKEKINFIIALTHLGVGRNQVEWDS    335
                                  :** **   . *.   .: * .*   ..    *:. .   ::::* **:*      . ..

NP_415013.1|USHA_b0480_ECOLI      APGDVEMARALPAGSLAMIVGGHSQDPVCMAAENKKQVDYVPGTPCKPDQQNGIWIVQAH    289
ADR25153.1|MBOVPG45_0690          R----EF--TKNVAGVDLVLDGHSHTRVDIE----------------RKDEEKGFLTQAE    365
ENY68833.1|MAU_3200               R----EF--TKNVEGIDLVLDGHSHTLVPIE----------------EGKDENGFLTQAE    365
ENY69482.1|MBVG_3940              R----TF--ANNVEGVDLVLDGHSHTLVKAE----------------K--INNTILTQAD    370
ADE19785.1|MCRO_0158              R----YF--ADNATGVDLTIDGHSHTKVDLE----------------K--NKESWLTQTE    371
                                        :  :  . .: : : ***:  *                      :   :.*:.

NP_415013.1|USHA_b0480_ECOLI      EWGKYVGRADFEFRNGEMKMVNYQLIPVNLKKKVTWEDGKSERVL--------YTPEIAE    341
ADR25153.1|MBOVPG45_0690          CYTKYLSELDLVVDKETGKVTEVKQY-LRTIEYTELLGGKENSIASIKDMIGKLKEKFDA    424
ENY68833.1|MAU_3200               CYTKYLSELDLIVNTKTGKISSVKQR-LWTIEYTELMDGKKNTITPIKNMIDALKTKFDA    424
ENY69482.1|MBVG_3940              SYTKYLSELDIYIDTETNKITKVNQQ-LRTMEETELLGGAVNNNKIIDEKITKLKAEFEK    429
ADE19785.1|MCRO_0158              CYTKYLSEIDLLVDKKTGKIVENLGQVQRDINEVEIA-SHGKENKKVDELIAALTKKFGE    430
                                   : **:.. *: . .   *: .         : .    .  :            . ::

NP_415013.1|USHA_b0480_ECOLI      NQQMISLLSPFQNKGKAQLEVKIGETNGRLEGDRDKVRFVQTNMGRLILAAQMD------    395
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ADR25153.1|MBOVPG45_0690          VNDKVVFNLPIEFKH--TEEVKIKPGNGEKEVSIWRGRAQQTNLGTFAADAAAYDFIENN   482
ENY68833.1|MAU_3200               VNNEVVFSLPFDFKH--TEEVKIKPGNGSKEVPIWKGRSQQTNLGSFTTDATAWDFIENS   482
ENY69482.1|MBVG_3940              INGVKVFDNPIDFIH--TTSHKVEEANKS----SALGRQKQTNLGMFVADALGWSFISDK   483
ADE19785.1|MCRO_0158              VNNVLAFKNTVHFKH--IENIKVD------GIEFWRGRVEQTNLGVLAANAIADELAKAK   482
                                   :    :   ..       . *:              *  ***:* :   *

NP_415013.1|USHA_b0480_ECOLI      ----------RTGADFAVMSGGGIRDSIEAGDISYKNVLKVQPFGNVVVYADMTGKEVID   445
ADR25153.1|MBOVPG45_0690          PKVNGQVVQFNADNVIGLVNGGGLRQDTQSGDIKRADLLGISPFGNRIAAVQVKGSVLLE   542
ENY68833.1|MAU_3200               PKVNNEAVVFNADNVIGLEVGGALRQDTQKGAIKRADLLGIAPFGNRIAAVQVKGEVLLE   542
ENY69482.1|MBVG_3940              STADGQ--KYNLDNTIAFVGGGSIRENLVKGPITRGNMFAVSPYGNRIAAVELKGDKLIE   541
ADE19785.1|MCRO_0158              KDTKDFDKYYSEDKMIGLMNGGGLRADLPVGDVKRGDVLGVLPFGNRIAAVRVDGQTLID   542
                                                 :..  **.:* .   * :.  ::: : *:** :. . : *. :::

NP_415013.1|USHA_b0480_ECOLI      YLTAVAQMKPDSGAYPQFANV-SFVA------KDG--------KLNDLKIKGEPVDPAKT   490
ADR25153.1|MBOVPG45_0690          AMKHG-ASKVFSGAYAQYSHNVSAKISYKET-KDG--KFIYELDEDSVMINNKKVEKDKD   598
ENY68833.1|MAU_3200               AMKHG-AKKIFSGGYAQYSHNVSAKINFKEE-KDN--KFVYELDESSVKINGKSVNKDQN   598
ENY69482.1|MBVG_3940              VVAHG-AKKIFSGGFAQWSKNVKLDINFDPT-D-----KIYKPVEESIKINDKAIDRNAT   594
ADE19785.1|MCRO_0158              AIKHG-ASKVKSGAYPQFSQNVSFTIKKTETIKDGKKVYTYEADESTIKIHDKEINKTET   601
                                   :      *  **.: *::.  .         .            . : *. : ::

NP_415013.1|USHA_b0480_ECOLI      YRMATLNFNATGGDGYPRLDN---KPGYVNTGFIDAEVLKAYIQKSSPLDVSVYEPKGEV   547
ADR25153.1|MBOVPG45_0690          YYIVTNDFILIGGDGYEMLDYVKHPE-KAKSVFEGGDILESYIKFGQLITNKEQ-K--ES   654
ENY68833.1|MAU_3200               YYIVTNGFVLEGGDGYDMLNYTKNPT-KAKSVFEGGDILETYIKYGKLITSSNN-T--NS   654
ENY69482.1|MBVG_3940              YYLVTDDYILVGGDEYNMLNYAKITDGSVKLIFEGSDMLQELIKYGQHITKTDF-KA-TE   652
ADE19785.1|MCRO_0158              YTIVTNDFILAGGDGYKMLNFMENK--KATTDYEGGDLLEVMINHFKYSTDSTNFAEGKT   659
                                  * :.*  :   *** *  *:        ..  :  .::*:  *:  .    .

NP_415013.1|USHA_b0480_ECOLI      SWQ---------------------------   550
ADR25153.1|MBOVPG45_0690          TNAFGKRKVDDYKNI-SPNNIEVKHSK---   680
ENY68833.1|MAU_3200               SNPFAKYKTDDYKDP-NPTYIQVNHNKK--   681
ENY69482.1|MBVG_3940              NNPFGDAQIDFYNQEKLPKNVVVNHKAPAL   682
ADE19785.1|MCRO_0158              NTPFA-HELSYYNKPEILTKIKIEG-----   683
                                  .
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ECOLI, *E. coli* ; MAU, *M. auris,* MBVG*, M. bovigenitalium;* MCRO*, M. crocodyli*

7) Amino acid permease

Lactobacillus crispatus used as reference. No known active site.

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EST03631.1|Lc367_0497_LACR        -------------MDNKLKRSIGFGSAFSIVIGTIIGSGIFFKQASVLDS-AGSTTMALL    46
ADR24969.1|MBOVPG45_0533          ------MSKKSDAIADNNSKKISFISAMLITVGSSFGAGIFFKSKSVLDSSHGSLILAIF    54
NP_109996.1|MPN308                --------------MKQQKPKISFIAAMLIVIGSSIGAGIFFKSSTVLENSQASLVLAIF    46
ENY68956.1|MBVG_6250              ---MTEQNSQSNFKNAPKHKKMGFFSAMLIVMGSSIGAGIFFKSEEVLNNSRGNLVLAII    57
AAP56893.2|MGA_0287               MPIIRMNKKNRSLKDAPKSKKIGFFSGITIAIGSSIGAGIFFKAQAVLQNSHYSLAFAIF    60
                                                        .:.* :.: *.:*: :*:*****   **:.   .  :*::

EST03631.1|Lc367_0497_LACR        AWIFGGLITLAAGLTIAEIGAQMPYTGGLYVYIENLYGR-----ILGFMAGW------MQ    95
ADR24969.1|MBOVPG45_0533          AWIIASVAVICIALALVEISSTHSDNLSLTSWNKVFNNRFVYNVSKDFNTYVCLPLVFFF   114
NP_109996.1|MPN308                NWLVASVAVIAMALALIEIASVRNDNLSIISWVKVFNRRWLYHGCKNFMTYLYLPLTFFF   106
ENY68956.1|MBVG_6250              CWIIASFSVISMAMAIIEVAGVKNDNLSLIGWNRIFNSRWVHQASKNFMVYLTLPLTFFY   117
AAP56893.2|MGA_0287               SWLFAAFSVTSMALALVEISSGRNDNLSIIGWCQTFNNHYVYKTCKNFMVYIYVPLTYFF   120
                                   *:.... . . .::: *:..    . .:  : . :  :        * .        :

EST03631.1|Lc367_0497_LACR        IIVYG-PAIIAAVAGFMSIMMTNFFGLNHSWRIPLALITVLAIG--IMNFFENKVGAIFS   152
ADR24969.1|MBOVPG45_0533          IPLYSFISLQDGLKFLT-NKT--GFGTGHDWVIWMFISLALTLYFLTAPALYSKVGDIQN   171
NP_109996.1|MPN308                MPLYFICSIQDGFRGLLGLETGAHFNTSVDWLIWLALALIITTYFLTIPPLYAKVGNIQN   166
ENY68956.1|MBVG_6250              MPVYTIMVLQDGLGALA-NKEALTFGTNNDWLIWLAITTFIGLYFLTIPTLISKIGNIHN   176
AAP56893.2|MGA_0287               MPFFFLLSIQDGIRGFNENYH--GLNTKADWAILMLVSVGISAYFIVVSGISSSAANFQN   178
                                  : .:    :  ..  :        :    .* * : :   :         :  . . : .

EST03631.1|Lc367_0497_LACR        VITTIAKMIPIAVITICGICWGQQDAINQTVAK-----------------------VSQH   189
ADR24969.1|MBOVPG45_0533          IISLAIKLVPLIFITFLGFILVATGKGGASEVSLLVTK------NHSYIEFIKQGKGIEH   225
NP_109996.1|MPN308                MVVSAVKFIPLVFVPIIGFIVAGTGNGELKNVKALVQPPQINGATASFTQLVQAGYGITR   226
ENY68956.1|MBVG_6250              IIVLCIKFLPLVFIIIIGIVLAVTGKGGTDSVKILEFE------KN---YNIKTGSSIIH   227
AAP56893.2|MGA_0287               LIISVVKFLPLLLAIILGFVIFNHNGSKPVNPKIGL------GFQNSATTDLA---TKYS   229
                                  ::    *::*: .  : *:             .

EST03631.1|Lc367_0497_LACR        TSNFG------VAVLATLFGYDGWILIANLGGEMKNPQKLLPRAIIAGITAVLAIYTLIT   243
ADR24969.1|MBOVPG45_0533          FNHIGAGLGMFLAIASIFYAYDGFYVSAGIQSEMKEPKKT-PMALFLGLSLTTLIYLIIA   284
NP_109996.1|MPN308                FTGIGAGMGSFISIAAIFFAYDGFYVTAGLQSEMREPKKT-PWALFLGLLITTLFYLILA   285
ENY68956.1|MBVG_6250              YGGFGGFIGIFLSIGAIFFAYDGFYIAAGMQSEMKNPKKT-SLALSLGLIIITIIYLLIA   286
AAP56893.2|MGA_0287               FSNLSPGFGLFISVGGIYFAYDGFYYAAGIQTEMKKPQKT-PLAILIGLLFVTSVYLIMA   288
                                     :.      ::: .  :.***:   * :  **::*:*    *:  *:     .* :::

EST03631.1|Lc367_0497_LACR        IGIFRFIPANQIHQLGENTTTYLANAVFGAIGGKILSIGIIISMMGTLNGKMLTFPRIVY   303
ADR24969.1|MBOVPG45_0533          ISMSINGGSFS--KMHAYSINLMGL-KATNIIFGIMNIFIAIGVLGIANGFAMWMPRYIE   341
NP_109996.1|MPN308                VALSINGGLFS--GMEESMGKLFNNKRAGQIVFGVVNLMIGIGVLGIINGFALWAPRFVE   343
ENY68956.1|MBVG_6250              ISMSINGGSFS--QMRQFIENIMGN-KTGRIIFGLINIAIAIGVIGVINGFSMWMPRYIE   343
AAP56893.2|MGA_0287               IAMSLGSTDGSPFGFKAYFA-----RNDLLPLYAVFQITIGVGILGIINGLSLWANRFME   343
                                  :.:       .   :                   :..: * :.::*  **  :   * :
```

```
EST03631.1|Lc367_0497_LACR      AMAKRGDLPFSKYLAYVTPKGKSPVVATLFIVLLALLMMIFFDP----------------     347
ADR24969.1|MBOVPG45_0533        DLLIKGDLPFWEKLAPKVNP-RKPVVGIIYSSIISVPLIIIFTLIGALGYIDTSSYGTVY     400
NP_109996.1|MPN308              DLLAQGDLPFWKQVQGRLNP-NKPVVGVIYCLVLSLTVQVLFTVIGALAYLPTVADYKNY     402
ENY68956.1|MBVG_6250            SLLAEGELPFWRLTIKKLNP-NRPVIGVIYSLIIGLSANIIFTIIGAKLYLPTNDIYLKY     402
AAP56893.2|MGA_0287             DLIKKFELPFSMKLINKISP-NKVVVGMQYNLILAVPVVIIASLIGGLGYIDNSYSDADY     402
                                 :  . :***           .  *:.  :  ::.:   ::

EST03631.1|Lc367_0497_LACR      ------------------DHLSDLCVFTVYCFYLLAFFGIFILRKKNKAERPFSTPLYPF     389
ADR24969.1|MBOVPG45_0533        -----DSTMSMAKLYSFADLMANWNALGCFLLVALAIYGGIRNRKTNKVEIPSKKKYFLP     455
NP_109996.1|MPN308              VNTEIDKLNSMQWLYSFSDLMATWTSLFTFAFIACAIFGAIVNRKTKKITIANPKRYFLP     462
ENY68956.1|MBVG_6250            -----G--TDMASIYSFTDLIANWITVFTFVFIALAIIGALRNRKTKKVPISNPKKSFKF     455
AAP56893.2|MGA_0287             -------GTGVGRIYSFSDLMANWTSVIAFVYIVIAIMGGLANRKTNKIKVN-KSKIFVP     454
                                                  * ::    .  :     *: * :  **.:*      .  :

EST03631.1|Lc367_0497_LACR      VPIIAILGGLFVLISELINDPAGVLL----------------------------------     415
ADR24969.1|MBOVPG45_0533        TAWISILFVASAIFISILVPIINLFLLIGIDRSL---ISN-------VEFTQLLVGRLML     505
NP_109996.1|MPN308              AAWIAVVVNCISVFVTIIEPFINLFLLFGYDETVAHTVL----GNDFIELNELVIGRVML     518
ENY68956.1|MBVG_6250            FAYCTIIFVSLAMLAQILVPILDFALIFVFDIKQYAIEKNVSYEQAQNFFISLAISRSML     515
AAP56893.2|MGA_0287             SAVCAIFTMVVSVSLTFFQPMADALLLYNIPF-------N-------DQYKNVYISRILL     500
                                    ::.     :   ::       *

EST03631.1|Lc367_0497_LACR      ------FAGIVIIGLPIFYAVKRMNKHRLH------------------------------     439
ADR24969.1|MBOVPG45_0533        IVVLILFVSLSILPTIIL---NKIRTKKFGSIDKYYEYTEEKLKSLK---TRLSTIN---     556
NP_109996.1|MPN308              IVVLVFFAIISFLPVYVE---DQYHKRKFGSLANYQQYVQQHLAHST---ING-------     565
ENY68956.1|MBVG_6250            VAVLIIFHFLVFLPIPIF---DKYNKRKYGSLEAFEQYKANFIKTNL---RKNDA-----     564
AAP56893.2|MGA_0287             VLVLFVFLFIMFIPILIE---DQLMIKRYGSVSKGELAKLRIKAEVKKTSFKQELLDYIE     557
                                      *  : ::   :    .:   ::

EST03631.1|Lc367_0497_LACR      --------------------------- 439
ADR24969.1|MBOVPG45_0533        --------------------------- 556
NP_109996.1|MPN308              --------------------------- 565
ENY68956.1|MBVG_6250            --------------------------- 564
AAP56893.2|MGA_0287             TLKTKDLNDDLKAALKEVNVEVDELII 584
```

LACR, *Lactobacillus crispatus*.

8) Glycine cleavage H protein (GCSH)

Aerococcus urinae used as reference. No known active site.

```
AEA00776.1|HMPREF9243_0576_AEUR      MTKRGNYLFVEKNG--DLYTVSMTPELQDDIGTVGYAEFAQED--QVEKDDALLNIEASK 56
ADR24909.1|MBOVPG45_0459             MKKLIGKFTLEYLDGKNEYVLRLTPDAQDELISIKELKILVKENSAYSTDELFMIIHTAK 60
WP_004420912.1|MBVG_4610             MKKIVKYLIVEKLETKDQYYLRMTPEMQDDIGTVGHIQFRNTDKSMLKENDEFMAFEASK 60
ACU79130.1|MMCAP1_0466               MKKVIKFLVIEKIDDKNEYYLRMTSEMQDDIGTVSYLQFKNTDKKHLKEDDIFLALEASK 60
AGJ91024.1|MPUT9231_6310             MKKVINYLVLEKQENSNNYYLRLTAEMQDDIGTVGYVQFKNTDKKDFQKDDVFLALEASK 60
WP_046178069.1|GCSH_SDE              MKKFANYLLIEKKE--DRYTISMTPELQDDIGTIGYAEFTEND--TLAVDDIILNLEASK 56
                                     *.*    : :*     : * : :* : **:: ::   ::   :      :: :: :.::*

AEA00776.1|HMPREF9243_0576_AEUR      TVMEIQSPLKGSVVERHTEVVDQPSLLNSAKSEENWIVRLKDVDPAEFDALEEA------ 110
ADR24909.1|MBOVPG45_0459             EEKEFKMPIKASIIKINDSILAKPTLISSVYDDENWIATLKDINKEEYDKLDEFAMWDRY 120
WP_004420912.1|MBVG_4610             AILTLKMPFDAKVVEWNNAALAKPSLVSSHKDSENWIMIISDINPEILANLEDF------ 114
ACU79130.1|MMCAP1_0466               AILNLKMPLDATVVKWNQKALENPKLISSHDDNENWIMVLSDIDQNKFMSLEDF------ 114
AGJ91024.1|MPUT9231_6310             AILTLKMPLDATVVEWNQQIIENPELISSADQNNNWIMILTNIDKKTFDSLEDF------ 114
WP_046178069.1|GCSH_SDE              TVMSVLTPLAGTVVERNEAATLTPTLLNSEKADENWIVVLADVDQAAFDVLEDA------ 110
                                         .  *: ..::: .      * *:.*   .:***  : :::      *::

AEA00776.1|HMPREF9243_0576_AEUR      --------       110
ADR24909.1|MBOVPG45_0459             QSLISLIS       128
WP_004420912.1|MBVG_4610             --------       114
ACU79130.1|MMCAP1_0466               --------       114
AGJ91024.1|MPUT9231_6310             --------       114
WP_046178069.1|GCSH_SDE              --------       110
```

AEUR, *Aerococcus urinae;* MMCAP1, *M. mycoides* subsp.capri;, MPUT9231, *M. putrefaciens,* SDE, *Streptococcus dysgalactiae* subspecies *equisimilis*

Figure S1. Multiple sequence alignments of proteins (referred to in Table S2) that were assigned new enzyme annotations in this study for *M. bovis*. Multiple sequence alignments were constructed for the assigned proteins in *M. bovis* with homologous proteins identified in other mycoplasma and bacterial species using Clustal Omega at http://www.ebi.ac.uk/Tools/msa/clustalo/. Numbers on right indicate the position of the adjacent amino acid residue. An asterisk (*) indicates an amino acid that is conserved in all aligned sequences, a colon (:) indicates one substitution with a very similar amino acid, and a full stop (.) indicates at least one substitution with a similar amino acid. Dashed lines (-) indicate gaps in the amino acid sequence alignment. The active site for each enzyme is highlighted in red.