<center>**Supplementary data**</center>

Figure S1: Molecular mass determination of YeSlc26A2 calculated from the distribution coefficient K_{av} and the calibration curve obtained from standard proteins (See Fig. 2D). K_{av} were calculated from the equation $K_{av} = (V_e - V_0)/(V_t - V_0)$ where V_e is the elution volume of each protein, V_0 column void volume and V_t total bed volume.

Figure S2: Trypsin proteolysis/Mass spectrometry analysis of *Yersinia enterocolotica* Slc26A2. YeSlc26A2 was purified to homogeneity and separated from trace impurities by SDS-PAGE, the resulting band was digested with trypsin overnight and the resulting peptides detected by mass spectrometry (nLC-MS-MS on an LTQ Orbitrap Velos) . The *Yersinia enterocolotica* Slc26A2 amino acid sequence is aligned to that of the *Synechococcus* Slc26 protein BicA using Clustal W, "*",":", and "." under sequences mark positions of complete sequence conservation, conserved substitutions and semi-conserved substitutions respectively. The YeSlc26A2 peptides detected are defined by green bars with the trypsin cleavage sites indicated by red arrowheads. BicA (Shelden, M. C., Howitt, S. M., and Price, G. D. (2010) *Mol Membr Biol* 27, 12-23) transmembrane α-helices are highlighted in cyan. All the sites at which trypsin cleaves YeSlc26A2 are within predicted exposed loops or the soluble STAS domain, suggesting the detergent micelle protects the transmembrane region from trypsinolysis.

Figure S3: Amino acid sequence alignment of *Yersinia enterocolotica* Slc26A2 and *Mus musculus* SLC26A6 generated using Clustal W. The glutamate residues in red have been proposed to be functionally essential. "*",":", and "." under sequences mark positions of complete sequence conservation, conserved substitutions and semi-conserved substitution respectively.
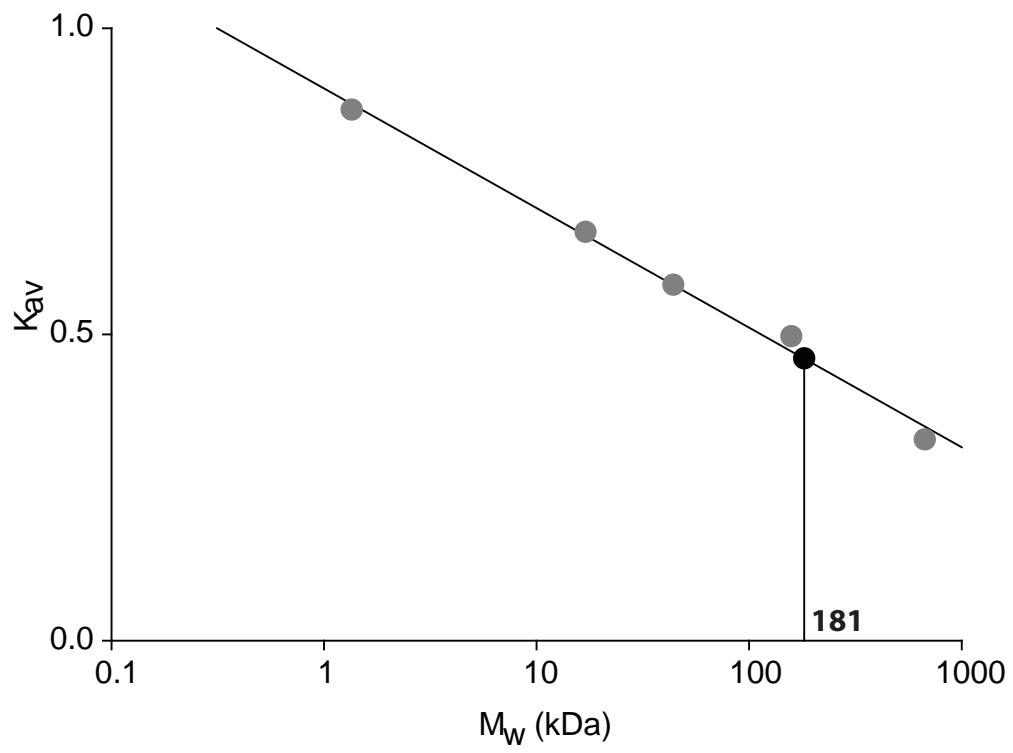
<center>1</center>

Figure S1

```
BicA     MQITNKIHFRNIRGDIFGGLTAAVIALPMALAFGVASGAGAEAGLWGAVLVGFFAALFGG 60
YeSulP2  -MWQVLKSPKLMTRECLAGVVTALALVPEVISFSVIAGVDPKVSLIASIVLCFTLSILGG 59
                :  :  : :.*:.:*:  :*  .::*.* :*....:..*  .:::: *   :::**


BicA     TPTLISEPTGPMTVVMTAVIAHFTASAATPEEGLAIAFTVVMMAGVFQIIFGSLKLGKYV 120
YeSulP2  RPAMVSAAAGSVALVIGPMVH---------AHGVEYILPAVILAGIVQILFGLTGLSRMM 110
          *:::*  .:*.:::*: .::        .*:   :..*::**:.**:** *.: .


BicA     TMMPYTVISGFMSGIGIILVILQLAPFLGQASPGGGVIGTLQNLPTLLSNIQPGETALAL 180
YeSulP2  RYIPRSVMIGFVNALGILIFFAQVPHIWGHSS--------------------LVWVMF 148
           :* :*: **:..:**::.: *:. : *::*                      . : :


BicA     GTVAIIWFMPEKFKKVIPPQLVALVLGTVIAFFVFP--PEVSDLRRIGEIRAGFPELVRP 238
YeSulP2  AVTLIIVLLLPRILKSVPSPLIAIIVVTLVAILMGYRLPNVGDEGAMSADLPSFTQLLVP 208
         ... ** :: :: * :*. *:*::: *::*:::   *:*.*   :.   ..*.:*: *


BicA     SFSPVEFQRMILDAAVLGMLGCIDALLTSVVADSLTRTEHNSNKELIGQGLGNLFSGLFG 298
YeSulP2  -LNWQTFQIVVWPTALSVAFVGLMESLLTAKLVDDITDTQSSKRRESWGLGVGNILAGFYG 267
          :.   ** :    * :.::* :::***: :*.:* *: ...:*   * *:**:::*::*


BicA     GIAGAGATMGTVVNIQSG-GRTALSGLVRAFVLLVVILGAASLTATIPLAVLAGIAFKVG 357
YeSulP2  GIAGCAMIGQTIVNVELGKARSVSTVAAAVVLLVLVTGLSKLLAQIPMVVLAGIMMVVA 327
         ****..   *:**:: * .*: :* :. *.****:: * :.* .**:.***** : *.


BicA     VDIIDWSFLKRAHEISP--KGALIMYGVILLTVLVD-LIVAVGVGVFVANVLTIERMSNL 414
YeSulP2  VKTVNWHSLQPATLKRMPWSETLVMVLTVLVTVWTSNLALGVLAGVIVAMILFARRIAHV 387
         *. .:*   *: *      . .:*:*  .:*:**  .. * :.* .**:** :*:. .*::::


                                                         start of
                                                         STAS domain
BicA     QSEKVQTVSDADDNIRLTTTEKRWLDEGQGRVLLFQLSGPMIFGVAKAIAREHNAMGDCD 474
YeSulP2  IYAERTLSDD------------------GKSVRYTVHGPLFFASSNDLFEHFDYAHDPK 428
          :   .*              *: : : : **::*. :: : ...:   *. .


BicA     ALVFDIGEVPHMGVTASLALENAIEEALDKERQVYIVGAAGQTRRRLEKLKLFKRVPPDK 534
YeSulP2  RVIIDLTHAQIWDASTVAALDGIEYRYQRYGAEVIIEGLDTRSSDFHSRLSGNLRGSENL 483
          :::*:  ..  ..:: **:.  .  :* * * ::    .:*.   *


BicA     CLMSREEALKNAVLGIYPHLADGVTAPSSEMG 566
YeSulP2
```

Figure S2

```
M.mSLC26A6    MELQRRDYHVERPLLNQEQLEDLGHWGPAAKTHQWRTWFRCSRARAHSLLLQHVPVLGWL 60
YeSlc26A2     -----------------------------------------------------------MW 2


M.mSLC26A6    PRYPVREWLLGDLLSGLSVAIMQLPQGLAYALLAGLPPMFGLYSSFYPVFIYFLFGTSRH 120
YeSlc26A2     QVLKSPKLMTRECLAGVVTALALVPEVISFSVIAGVDPKVSLIASIVLCFTLSILGGRPA 62
                :  :   : *:*: .*:   :*: ::::::::**: *  ..* :*:   *     ::*

M.mSLC26A6    ISVGTFAVMSVMVGSVTESLTADKAFVQGLNATADDARVQVAYTLSFLVGLFQVGLGLVH 180
YeSlc26A2     MVSAAAGSVALVIG----------------PMVHAHGVEYILPAVILAGIVQILFGLTG 105
              :  .:  . :::::*                  . ...   *:  .  :*.*:.*: :**.

M.mSLC26A6    FGFVVTYLSEPLVRSYTTAASVQVLVSQLKYVFGIKLSSHSGPLSVIYTVLEVCAQLPET 240
YeSlc26A2     LSRMMRYIPRSVMIGFVNALGILIFFAQVPHIWG-----HSSLVWVMFAVTLIIVLLLPR 160
              :. :: *:...:: .:..* .: ::.:*: :::*     **. : *:::* : . *

M.mSLC26A6    VPGTVVTAIVAGVALVLVKLLNEKLHRRLPLPIPGELLTLIGATGISYGVKLNDRFKVDV 300
YeSlc26A2     ILKSVPSPLIAIIVVTLVAIL---MGYRLPN---------VGDEGAMS----------- 196
              :   :* :.::* :.:.** :*   :   ***          :* *

M.mSLC26A6    VGNITTGLIPPVAPKTELFATLVGNAFAIAVVGFAIAISLGKIFALRHGYRVDSNQELVA 360
YeSlc26A2     -ADLPSFTQLLVPLNWQTFQIVWPTALSVAFVGLMESLLTAKLVDDITDTQSSKRRESWG 255
               .::.:      *. : : *  :  .*:::*.**: ::  .*:.    . : ...:*  .

M.mSLC26A6    LGLSNLIGGFFQCFPVSCSMSRSLVQESTGGN-TQVAGAVSSLFILLIIVKLGELFRDLP 419
YeSlc26A2     LGVGNILAGFYGGIAGCAMIGQTIVNVELGKARSRVSTVAAAVYLLVLVTGLSKLLAQIP 315
              **:.*::.**:  :. .. :.:::*: . *   ::*: ..::.:*:::. *.:*: ::*

M.mSLC26A6    KAVLAAVIIVNLKGMMKQFSDICSLWKAN--RVDLLIWLVTFVATILLNLDIGLAVSIVF 477
YeSlc26A2     MVVLAGIMMVVAVKTVNWHSLQPATLKRMPWSETLVMVLTVLVTVWTSNLALGVLAGVIV 375
               .***.:::*       :: .*   :  *         *:: *..:*:.   ** :*: ..:.

M.mSLC26A6    SLLLVVVRMQLPHY -491
YeSlc26A2     AMILFARRIAHVIY -389
```

Figure S3

4