Table S1: Screening for fructose-negative strains

Strains Name	Fructose fermentation*	PCR for *fru*E gene
B. longum DCP-1	+	+
B. longum DCP-2	+	+
B. longum DCP-3	+	+
B. longum DCP-4	+	+
B. longum DCP-5	+	+
B. longum DCP-6	+	+
B. longum DCP-7	+	+
B. longum DCP-8	+	+
B. longum DCP-9	+	+
B. longum DCP-10	+	+
B. longum DCP-11	+	+
B. longum DCP-12	+	+
B. longum DCP-13	+	+
B. longum DCP-14	+	+
B. longum DCP-15	+	+
B. longum DCP-16	+	+
B. longum DCP-17	+	+
***B. longum* DCP-18**	**-**	**-**
B. longum DCP-19	+	+
B. longum DCP-20	+	+
B. longum DCP-21	+	+
B. longum DCP-22	+	+
B. longum DCP-23	+	+
B. longum DCP-24	+	+

B. longum DCP-25	+	+
B. longum DCP-26	+	+
B. longum DCP-27	+	+
B. longum DCP-28	+	+
B. longum DCP-29	+	+
B. longum DCP-30	+	+
B. longum DCP-31	+	+
B. longum DCP-32	+	+
B. longum DCP-33	+	+
B. longum DCP-34	+	+
B. longum DCP-35	+	+
B. longum DCP-36	+	+
B. longum DCP-37	+	+
B. longum DCP-38	+	+
B. longum DCP-39	+	+
B. longum DCP-40	+	+
B. longum DCP-41	+	+
B. longum DCP-42	+	+
B. longum DCP-43	+	+
B. longum DCP-44	+	+
B. longum DCP-45	+	+

*: The fructose fermentation of all strains was determined by using the GEN III MicroPlate™ test panel (Biolog, Hayward) and API 20A system (bioMérieux). The substrates tested were L-arabinose, D-cellobiose, cellulose, D-fructose, D-galactose, D-glucose, lactose, maltose, D-mannose, D-raffinose, starch, sucrose, xylan, D-xylose, glycerol, D-mannitol, rhamnose, D-ribose, D-sorbitol, trehalose, peptone (0.1%, w/v) and yeast extract. All substrates were examined at a final concentration of 0.2%, with the exception of peptone (0.1%, w/v), xylan (1%, w/v) and cellulose (1%, w/v).

Supplemental Table 2 Proteins identified by ESI-MS/MS

NCBInr accession no.	Locus	Protein Description	Total Score[b]	Matched Peptide number	Peptide sequence	Sequence Coverage %	% Identify[a]	Delta
gi|23464661	BL0033	ABC-type sugar transport system, periplasmic component	768	20(10)	TANEKDIQK	46	100	0.0033
					VKIITIDGTK		100	-0.0026
					NVDVKDAEAK		100	-0.0079
					EALDNNTRAY		100	0.0003
					TVTAGLLDKYK		100	-0.0142
					TVEKDIEIESK(2)		100	-0.0016
					TVGFVAVGPEGGFR		100	-0.0743
					AAEAEIPVFTVDR		100	-0.0136
					ETAQAVKDYLDGK		100	-0.0331
					TFDAASAKEALDNNTR(3)			-0.0009
					AAEAEIPVFTVDRNVDVK(2)			-0.0041
					NFPDGANGFILEGPAGLSVVK(4)			-0.0035
					AFEDAGFDLTYSPTQNNDQQK(2)			-0.0143
gi|23464661	BL0033	COG1879: ABC-type sugar transport system, periplasmic component	1052	33(18)	IITIDGTK	58	100	-0.0008
					TANEKDIQK		100	-0.0009
					NVDVKDAEAK		100	-0.0131
					TVEKDIEIESK(3)		100	-0.0052
					AAEAEIPVFTVDR(2)		100	-0.0086

					ETAQAVKDYLDGK(5)		100	0.0003
					KAAEAEIPVFTVDR		100	-0.0326
					VLESQSANWSTDEAK		100	-0.0067
					TFDAASAKEALDNNTR(3)		100	-0.0045
					AAEAEIPVFTVDRNVDVK(3)		100	-0.0025
					NFPDGANGFILEGPAGLSVVK(6)		100	-0.0044
					AFEDAGFDLTYSPTQNNDQQK(2)		100	-0.0027
					NALQALVDGDLSYVIEYNPIFGK		100	-0.0110
					SDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)](3)		100	0.0180
gi|23464661	BL0033	ABC-type sugar transport system, periplasmic component	520	10(8)	NVDVKDAEAK	23	100	0.0029
					TVEKDIEIESK(3)		100	-0.0026
					TVGFVAVGPEGGFR		100	0.0065
					AAEAEIPVFTVDR		100	-0.0042
					ETAQAVKDYLDGK		100	-0.0081
					KTVGFVAVGPEGGFR		100	0.0055
					TFDAASAKEALDNNTR		100	-0.0058
					AAEAEIPVFTVDRNVDVK		100	-0.0015
gi|23464661	BL0033	ABC-type sugar transport system, periplasmic component	1222	37(22)	DIEIESK	62	100	-0.0615
					TANEKDIQK		100	0.0037
					VKIITIDGTK		100	-0.0066
					NVDVKDAEAK		100	0.0009

					TVTAGLLDKYK		100	-0.0020
					TVEKDIEIESK(3)		100	0.0006
					TVGFVAVGPEGGFR(2)		100	0.0011
					AAEAEIPVFTVDR(3)		100	0.0018
					ETAQAVKDYLDGK(4)		100	0.0001
					KAAEAEIPVFTVDR		100	-0.0062
					TFDAASAKEALDNNTR(2)		100	0.0092
					AAEAEIPVFTVDRNVDVK(2)		100	0.0010
					NFPDGANGFILEGPAGLSVVK(4)		100	0.0032
					NFPDGANGFILEGPAGLSVVKDR(4)		100	0.0040
					AFEDAGFDLTYSPTQNNDQQK		100	-0.0097
					FVNDEVDAIILSSTEDSGWDDSLKK		100	0.0337
					SDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)](3)		100	0.0077
					YKSDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)]		100	0.0139
gi|23464661	BL0033	ABC-type sugar transport system, periplasmic component	1307	36(24)	DIEIESK	60	100	-0.0366
					TANEKDIQK		100	-0.0005
					VKIITIDGTK		100	-0.0064
					NVDVKDAEAK		100	-0.0051
					TVEKDIEIESK(4)		100	0.0016
					TVGFVAVGPEGGFR(2)		100	0.0053

					AAEAEIPVFTVDR(2)		100	0.0020
					ETAQAVKDYLDGK(3)		100	0.0019
					KAAEAEIPVFTVDR		100	-0.0096
					TFDAASAKEALDNNTR(3)		100	-0.0051
					AAEAEIPVFTVDRNVDVK(2)		100	-0.0017
					NFPDGANGFILEGPAGLSVVK(2)		100	0.0004
					NFPDGANGFILEGPAGLSVVKDR(4)		100	-0.0020
					AFEDAGFDLTYSPTQNNDQQK		100	-0.0154
					FVNDEVDAIILSSTEDSGWDDSLKK(2)		100	0.0175
					SDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)](3)		100	0.0167
					SDNPQFIFAQNDEMGLGAAQAVDAAGLKGK[Oxidation (M)](2)		100	0.0129
					YKSDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)]		100	0.0181
gi|23464661	BL0033	ABC-type sugar transport system, periplasmic component	1359	41(26)	TANEKDIQK	65	100	-0.0009
					VKIITIDGTK		100	-0.0026
					NVDVKDAEAK		100	0.0065
					TVEKDIEIESK(4)		100	0.0006
					TVGFVAVGPEGGFR(2)		100	0.0063
					AAEAEIPVFTVDR(2)		100	-0.0048
					ETAQAVKDYLDGK(4)		100	0.0011

					KTVGFVAVGPEGGFR		100	-0.0105
					KAAEAEIPVFTVDR		100	0.0008
					VLESQSANWSTDEAK		100	0.0061
					TFDAASAKEALDNNTR		100	-0.0128
					AAEAEIPVFTVDRNVDVK(2)		100	0.0127
					NFPDGANGFILEGPAGLSVVK(4)		100	0.0016
					NFPDGANGFILEGPAGLSVVKDR(4)		100	0.0010
					AFEDAGFDLTYSPTQNNDQQK(2)		100	0.0056
					FVNDEVDAIILSSTEDSGWDDSLKK		100	0.0322
					SDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)](6)		100	-0.0031
					SDNPQFIFAQNDEMGLGAAQAVDAAGLKGK[Oxidation (M)](2)		100	-0.0009
					YKSDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)]		100	0.0208
gi|23464661	BL0033	ABC-type sugar transport system, periplasmic component	1612	44(27)	QIQAFNK	67	100	-0.0039
					TANEKDIQK		100	0.0007
					VKIITIDGTK		100	-0.0016
					NVDVKDAEAK		100	-0.0027
					EALDNNTRAY		100	-0.0033
					TVEKDIEIESK(4)		100	0.0002
					TVGFVAVGPEGGFR(2)		100	0.0073

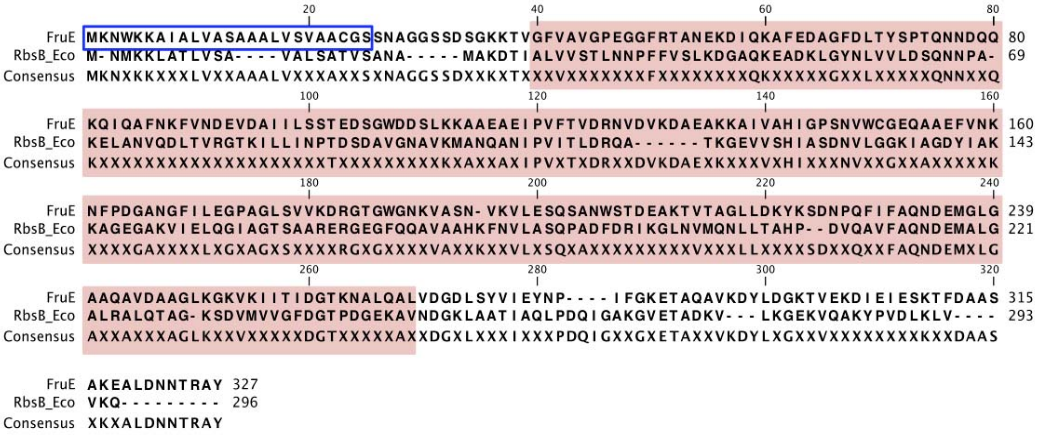
					AAEAEIPVFTVDR(2)		100	0.0038
					ETAQAVKDYLDGK(4)		100	-0.0011
					KTVGFVAVGPEGGFR		100	-0.0453
					KAAEAEIPVFTVDR		100	-0.0360
					VLESQSANWSTDEAK(3)		100	-0.0103
					TFDAASAKEALDNNTR(2)		100	-0.0360
					AAEAEIPVFTVDRNVDVK(2)		100	0.0040
					NFPDGANGFILEGPAGLSVVK(3)		100	0.0120
					NFPDGANGFILEGPAGLSVVKDR(5)		100	-0.0077
					AFEDAGFDLTYSPTQNNDQQK(3)		100	-0.0018
					FVNDEVDAIILSSTEDSGWDDSLKK		100	0.0214
					SDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)](3)		100	-0.0004
					SDNPQFIFAQNDEMGLGAAQAVDAAGLKGK[Oxidation (M)](2)		100	0.0126
					YKSDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)]		100	0.0244
gi|23464661	BL0033	ABC-type sugar transport system, periplasmic component	934	25(14)	DIEIESK	48	100	-0.0279
					IITIDGTK		100	-0.0058
					NVDVKDAEAK(2)		100	-0.0001
					TVEKDIEIESK		100	-0.1194
					TVGFVAVGPEGGFR		100	-0.0325

	AAEAEIPVFTVDR	100	-0.0438
	ETAQAVKDYLDGK(3)	100	0.0015
	TFDAASAKEALDNNTR(2)	100	-0.0171
	AAEAEIPVFTVDRNVDVK(2)	100	-0.0119
	NFPDGANGFILEGPAGLSVVK(2)	100	-0.0040
	NFPDGANGFILEGPAGLSVVKDR(4)	100	0.0012
	AFEDAGFDLTYSPTQNNDQQK(2)	100	-0.0053
	SDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)](2)	100	0.0017
	YKSDNPQFIFAQNDEMGLGAAQAVDAAGLK[Oxidation (M)]	100	0.0118

a) Percentage of identity between the amino acids present in MS/MS tag and the sequences in databases.

b) Ion scores greater than 44 are significant (*p*<0.05), total score is the sum of every ion score.

Figure S1A



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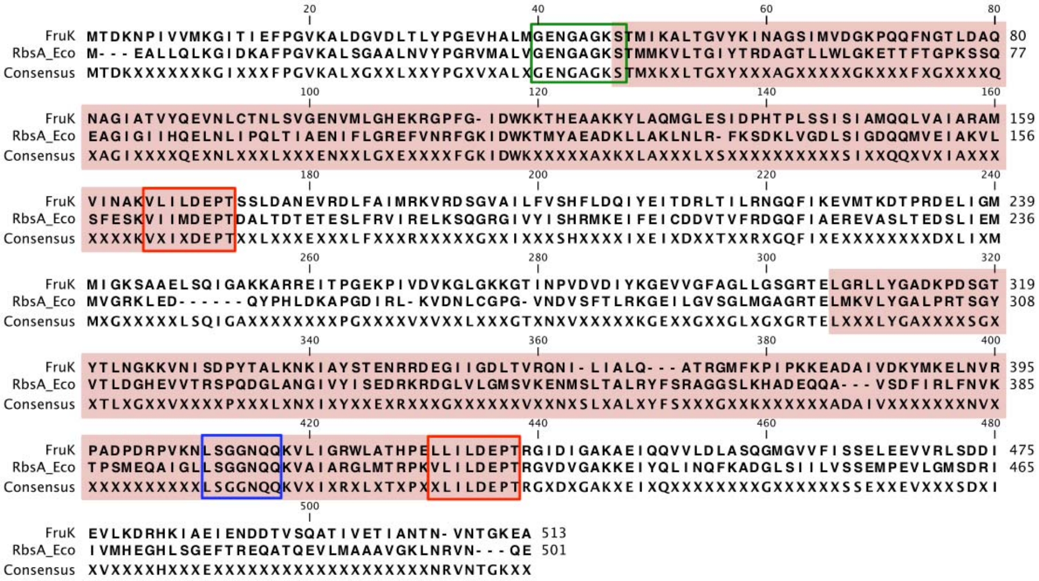
                            20                  40                  60                  80
     FruE MKNWKKAIALVASAAALVSVAACGSSNAGGSSDSGKKTVGFVAVGPEGGFRTANEKDIQKAFEDAGFDLTYSPTQNNDQQ 80
 RbsB_Eco M-NMKKLATLVSA----VALSATVSANA-----MAKDTIALVVSTLNNPFFVSLKDGAQKEADKLGYNLVVLDSQNNPA- 69
Consensus MKNXKKXXXLVXXAAALVXXXAXXSXNAGGSSDXXKXTXXXVXXXXXXXFXXXXXXXXQKXXXXXGXXLXXXXXQNNXXQ
                           100                 120                 140                 160
     FruE KQIQAFNKFVNDEVDAIILSSTEDSGWDDSLKKAAEAEIPVFTVDRNVDVKDAEAKKAIVAHIGPSNVWCGEQAAEFVNK 160
 RbsB_Eco KELANVQDLTVRGTKILLINPTDSDAVGNAVKMANQANIPVITLDRQA------TKGEVVSHIASDNVLGGKIAGDYIAK 143
Consensus KXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXKXAXXAXIPVXTXDRXXDVKDAEXKXXXVXHIXXXNVXXGXXAXXXXXK
                           180                 200                 220                 240
     FruE NFPDGANGFILEGPAGLSVVKDRGTGWGNKVASN-VKVLESQSANWSTDEAKTVTAGLLDKYKSDNPQFIFAQNDEMGLG 239
 RbsB_Eco KAGEGAKVIELQGIAGTSAARERGEGFQQAVAAHKFNVLASQPADFDRIKGLNVMQNLLTAHP--DVQAVFAQNDEMALG 221
Consensus XXXXGAXXXXLXGXAGXSXXXXRGXGXXXXVAXXKXXVLXSQXAXXXXXXXXXVXXXLLXXXXSDXXQXXFAQNDEMXLG
                           260                 280                 300                 320
     FruE AAQAVDAAGLKGKVKIITIDGTKNALQALVDGDLSYVIEYNP----IFGKETAQAVKDYLDGKTVEKDIEIESKTFDAAS 315
 RbsB_Eco ALRALQTAG-KSDVMVVGFDGTPDGEKAVNDGKLAATIAQLPDQIGAKGVETADKV---LKGEKVQAKYPVDLKLV---- 293
Consensus AXXAXXXAGLKXXVXXXXXDGTXXXXXAXXDGXLXXXIXXXPDQIGXXGXETAXXVKDYLXGXXVXXXXXXXXKXXDAAS

     FruE AKEALDNNTRAY 327
 RbsB_Eco VKQ--------- 296
Consensus XKXALDNNTRAY
```

Fig. S1A: Alignment of the amino acid sequences of FruE (BL0033) and RbsB of E. coli K-12 MG1655 with predicted signal peptide (blue box) and the residues of the conserved periplasmatic sugar binding (light red background). The two proteins show an identity of 28.6% and a similarity of 45.5%.

Figure S1B



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                            20                  40                  60                  80
     FruK MTDKNPIVVMKGITIEFPGVKALDGVDLTLYPGEVHALMGENGAGKSTMIKALTGVYKINAGSIMVDGKPQQFNGTLDAQ 80
 RbsA_Eco M---EALLQLKGIDKAFPGVKALSGAALNVYPGRVMALVGENGAGKSTMMKVLTGIYTRDAGTLLWLGKETTFTGPKSSQ 77
Consensus MTDKXXXXXXKGIXXXFPGVKALXGXXLXXYPGXVXALXGENGAGKSTMXKXLTGXYXXXAGXXXXXGKXXXFXGXXXXQ
                           100                 120                 140                 160
     FruK NAGIATVYQEVNLCTNLSVGENVMLGHEKRGPFG-IDWKKTHEAAKKYLAQMGLESIDPHTPLSSISIAMQQLVAIARAM 159
 RbsA_Eco EAGIGIIHQELNLIPQLTIAENIFLGREFVNRFGKIDWKTMYAEADKLLAKLNLR-FKSDKLVGDLSIGDQQMVEIAKVL 156
Consensus XAGIXXXXQEXNLXXXLXXXENXXLGXEXXXXFGKIDWKXXXXXAXKXLAXXXLXSXXXXXXXXXXSIXXQQXVXIAXXX
                           180                 200                 220                 240
     FruK VINAKVLILDEPTSSLDANEVRDLFAIMRKVRDSGVAILFVSHFLDQIYEITDRLTILRNGQFIKEVMTKDTPRDELIGM 239
 RbsA_Eco SFESKVIIMDEPTDALTDTETESLFRVIRELKSQGRGIVYISHRMKEIFEICDDVTVFRDGQFIAEREVASLTEDSLIEM 236
Consensus XXXXKVXIXDEPTXXLXXXEXXXLFXXXRXXXXXGXXIXXXSHXXXXIXEIXDXXTXXRXGQFIXEXXXXXXXXDXLIXM
                           260                 280                 300                 320
     FruK MIGKSAAELSQIGAKKARREITPGEKPIVDVKGLGKKGTINPVDVDIYKGEVVGFAGLLGSGRTELGRLLYGADKPDSGT 319
 RbsA_Eco MVGRKLED------QYPHLDKAPGDIRL-KVDNLCGPG-VNDVSFTLRKGEILGVSGLMGAGRTELMKVLYGALPRTSGY 308
Consensus MXGXXXXXLSQIGAXXXXXXXXPGXXXXVXVXXLXXXGTXNXVXXXXXKGEXXGXXGLXGXGRTELXXXLYGAXXXXSGX
                           340                 360                 380                 400
     FruK YTLNGKKVNISDPYTALKNKIAYSTENRRDEGIIGDLTVRQNI-LIALQ---ATRGMFKPIPKKEADAIVDKYMKELNVR 395
 RbsA_Eco VTLDGHEVVTRSPQDGLANGIVYISEDRKRDGLVLGMSVKENMSLTALRYFSRAGGSLKHADEQQA---VSDFIRLFNVK 385
Consensus XTLXGXXVXXXXPXXXLXNXIXYXXEXRXXXGXXXXXXVXXNXSLXALXYFSXXXGXXKXXXXXXADAIVXXXXXXXNVX
                           420                 440                 460                 480
     FruK PADPDRPVKNLSGGNQQKVLIGRWLATHPELLILDEPTRGIDIGAKAEIQQVVLDLASQGMGVVFISSELEEVVRLSDDI 475
 RbsA_Eco TPSMEQAIGLLSGGNQQKVAIARGLMTRPKVLILDEPTRGVDVGAKKEIYQLINQFKADGLSIILVSSEMPEVLGMSDRI 465
Consensus XXXXXXXXXXLSGGNQQKVXIXRXLXTXPXXLILDEPTRGXDXGAKXEIXQXXXXXXXXGXXXXXXSSEXXEVXXXSDXI
                           500
     FruK EVLKDRHKIAEIENDDTVSQATIVETIANTN-VNTGKEA 513
 RbsA_Eco IVMHEGHLSGEFTREQATQEVLMAAAVGKLNRVN---QE 501
Consensus XVXXXXHXXXEXXXXXXXXXXXXXXXXXXXNRVNTGKXX
```

Fig. S1B: Alignment of the amino acid sequences of FruK (BL0034) and RbsB with motifs Walker A (GXXGXGKS, green box) and Walker B (X_4DEPT, residues 166-173 and 426-433, red boxes) as well as the conserved signature motif (LSGGNQQ/RQ, residues 406-412). The conserved ATP-binding cassette domains are marked by a light red background. The two proteins 37.5% identity and 57.7% similarity.

Figure S1C

```
                                    20                  40                  60                  80
FruF       MAE----KAKAEGNNFVKKLLSSNLTWSIVAFILLVIICTIFQHDFLALSWNSNTGGLAGPLITMLQESARYLMIATGMT 76
RbsC_Eco   MTT----QTVSGRRYFTKAWLMEQK--SLIALLVLIAIVSTLSPNFFTIN----------NLFNILQQTSVNAIMAVGMT 64
FruG       MTTATANKVKAPKKGFKLDRQMIPTLAAVVIFILMIIMGQALFGTYIRLGF----------ISSLFIDHAYLIILAVAMT 70
Consensus  MTT----KXKAXXXXFXKXXLMXXXXXSXVAFILLIIIXXXLXXXFXXLXX----------XLXXXLQXXAXXXIXAVGMT

                                    100                 120                 140                 160
FruF       LVISTAGIDLSVGSVMAVAGAAAMQTLSNGMNVWLSILIALAVGLAIGCVNGALVSFLGLQPFITTLIMMLAGRGMAKVI 156
RbsC_Eco   LVILTSGIDLSVGSLLALTGAVAASIVGIEVNALVAVAAALALGAAIGAVTGVIVAKGRVQAFIATLVMMLLLRGVTMVY 144
FruG       LPILTGGIDLSVGAIVAITAVVGLKLANAGVPAFLVMIIMLLIGAVFGLLAGTLIEEFNMQPFIATLSTMFLARGLASII 150
Consensus  LVILTXGIDLSVGSXXAXTGAVAXXXXXXGVNAXLXXXIALAXGAAIGXVXGXLVXXXXXQPFIATLXMMLLXRGXAXVI

                                    180                 200                 220                 240
FruF       TSGENT-----DASAVAGN-EPLKWFANGFILGIPANFVIAVIIVILVGLLCRKTAMGMMIEAVGINQEASRMTGIKPKK 230
RbsC_Eco   TNGSPV-----NTGFTENA-DLFGWFGIGRPLGVPTPVWIMGIVFLAAWYMLHHTRLGRYIYALGGNEAATRLSGINVNK 218
FruG       STDSLTFPQGNDFSFISNVIKIIDNPKISNDLSFNVGVIIALVVVVFGYVFLHHTRTGRTIYAIGGSRSSAELMGLPVKR 230
Consensus  TXGSXT-----DXSFXXNX-XXXXWFXIGXXLGXPXXVXIAXIVVXXXXXXLHHTRXGRXIYAXGGNXXAXRLXGIXVKK

                                    260                 280                 300                 320
FruF       ILFLVYAISGFLAAIAGLFATASVMRVDVVKTGQDLEMYAILAVVIGGTSLLGGKFSLAGSAVGAVIIAMIRKTIITLGV 310
RbsC_Eco   IKIIVYSLCGLLASLAGIIEVARLSSAQPT-AGTGYELDAIAAVVLGGTSLAGGKGRIVGTLIGALILGFLNNGLNLLGV 297
FruG       TQYIIYLTSATLAALASIVYTANIGSAKNT-VGVGWELDAVASVVIGGTIITGGFGYVLGSVLGSLVRSILDPLTSDFGV 309
Consensus  IXXIVYXXSGXLAALAGIXXTAXXXSAXXT-XGXGXELDAIAAVVIGGTSLXGGKGXXXGSXXGALIXXXLXXXXXXLGV

                                    340                 360
FruF       NAEATPAFFAVVVIVICVMQAPKIHNLSANMKRKRALKAQAKAVAA 356
RbsC_Eco   SS-----YYQMIVKAVVILLAVLVDN-----------KKQ------ 321
FruG       PAEWTTIVIGLMILVFVVLQRAVM---------------AVGGDKK 340
Consensus  XAEXTXXXXXXXVXVXVVLQAXXXXN-----------KXQXXXXXX
```

Fig. S1C: Alignment of the amino acid sequences of FruF (BL0035), FruG (BL0036) and RbsC with the conserved ABC-transporter permease domain marked by a light red background, predicted transmembrane helices are indicated by blue boxes. The Similarity and identity between the FruF and RbsC are 30.8 and 51.0% respectively. FruG and RbsC share 31.4% identical and 54.0% similar amino acid residues.

Figure S1D

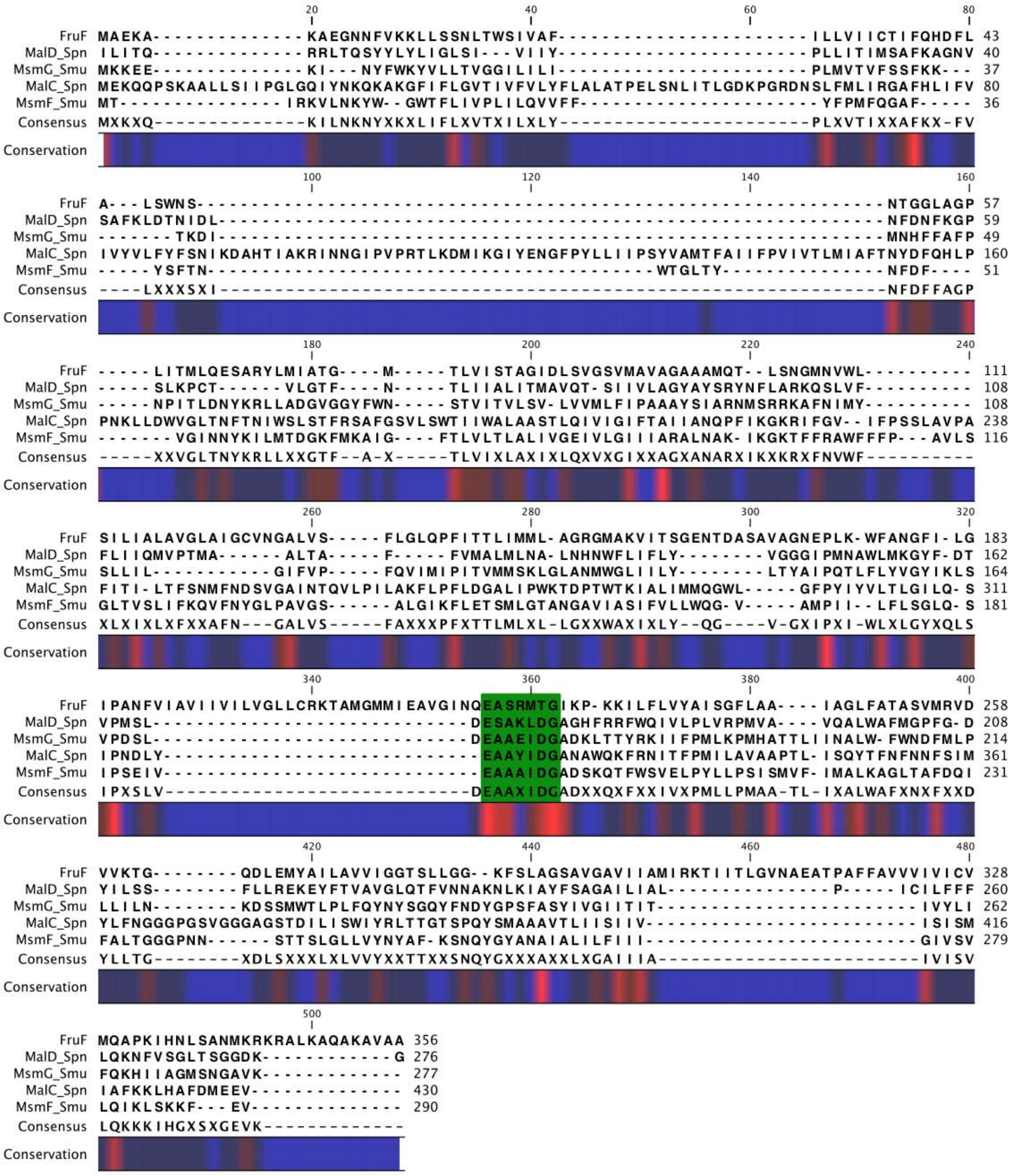

Fig. S1D: Alignment of the amino acid sequences of FruF (BL0035) with the ABC sugar transporter permeases MalC and MalD of *Streptococcus pneumoniae* (MalC_Spn and MalD_Spn) and MsmF and MsmG of *Streptococcus mutans* (MsmF_Smu and MsmG_Smu). Regions of high conservation are indicated by red colour in the conservation plot. The identified EAA motif is marked by green background color.