

CLUSTAL O(1.2.4) multiple sequence alignment

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PvSUT1.5 -----MEPSSSSLQVETGERQQPSPLRKMFAVSSIGAGIQFGWALQLSLLTPY      48
PvSUT1.1 --MEPLSATKHHNNLAKPSSLHMEAPPEPSPLRKIMVVASIAAGVQFGWALQLSLLTPY      58
AtSUC2    MVSHPMKAA--NGA--SALETQTGELDQPERLRKIISVSSIAAGVQFGWALQLSLLTPY      56
          :          :*  ***:  *:*:*****
          :          :*  ***:  *:*:*****

PvSUT1.5 VQILGVPHAWSSFIWLCGPISGLLVQPIVGYSSDRCTSRFGRRRPFILSGAVAVAIIVFL      108
PvSUT1.1 VQLLGIPIHTWAAFIWLCGPISGLLVQPIVGYHSDHCTSRFGRRRPFIAAGALAVAIIVFL      118
AtSUC2    VQLLGIPIHKWASLIWLCGPISGLLVQPIVGYHSDRCTSRFGRRRPFIVAGAGLVTVAVFL      116
          ** **:*  *::*****:***** **:***** :** *::***

PvSUT1.5 IGYAADIGHATGDDITKKTRPRAVAIFVVGFWILDVANMMLQGPCRAFLGDLAAGDQKKT      168
PvSUT1.1 IGYAADLGHMFGDSLAKKTRPRAIAIFVVGFWILDVANMMLQGPCRALADLSAGDHRKT      178
AtSUC2    IGYAADIGHSMGDQLDKPKTRAI AIFALGFWILDVANNTLQGPCRAFLADLSAGNAKKT      176
          *****:*** ** : * : **:*:***** *****:*.**:*: :**

PvSUT1.5 RTANAFYSFFMAIGNVLGYAAGSYDKLHHLFRFTETEACGVFCANLKSCHFFSIVLLLVL      228
PvSUT1.1 RNANAFSFFMAVGNVLGYAAGSYGLHHVFPFTKACDVYCANLKSCHFFLSIALLLTL      238
AtSUC2    RTANAFSFFMAVGNVLGYAAGSYRNLYKVVFPFTMTESCDLYCANLKTCHFFLSITLLLV      236
          *.*:*:*****:***** *::. ** *:*:*****:***.*** :

PvSUT1.5 CAIVLTCVDDPQFTPDVCNANNP---QTGSWYSCFGEGLGIAFKGLQKPMMLMLVTAIINW      285
PvSUT1.1 ATIALTYVKEERVSSEKSSANVAEEDGSRGMPFCFGLFGAFRELKRPWILLVTCINW      298
AtSUC2    TFVSLCYVKEKFWTPEP-----TADGKASNVFFGEIFGAFKELKRPWMLLVITALNW      290
          : * *.: : : . . **:*  **:*  *:*:*** :*:*:***

PvSUT1.5 VAWFPYVLYDIDWVGREYVGGVVG-----SNAYDNGVHAGSLGLMLNSVVLAVMSLVV      338
PvSUT1.1 IAWFPFLLFDIDWVGHEVYGGTVG-----EGNAYDRGVRAGALGLMLNSVLGATSLGV      352
AtSUC2    IAWFPFLLFDIDWVGREYVGGNSDATATAASKKLYNDGVRAGALGLMLNAIVLGFMSLVG      350
          :****:*.*****:***** . : *:*:***:*****:***. ** *

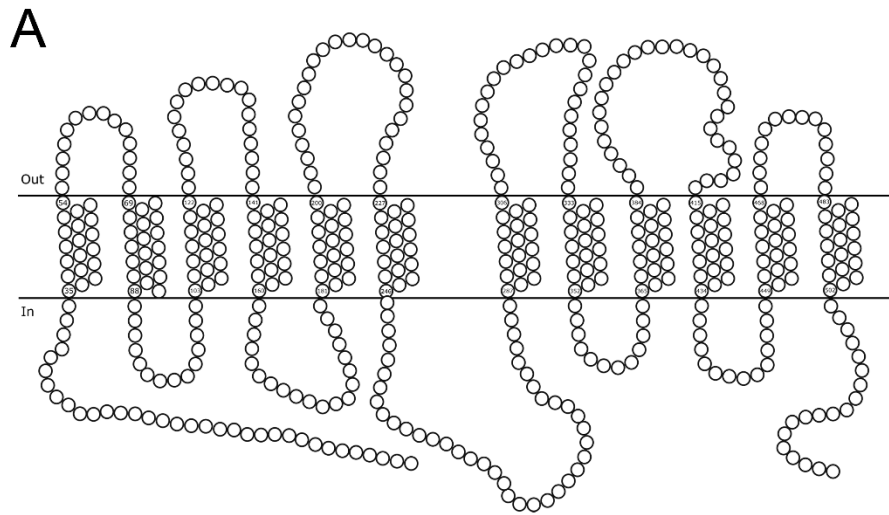
PvSUT1.5 EPLGRIVGGVKWLWAAVNVILAVCMAMTVVITKAARHERNHGVL-----VGHPSFGVKA      393
PvSUT1.1 DVLARGVGGVKRLWGIWNFLLAICLAMTVLITKMAQHSRQYTVLPNGHQEPLPPPSGVKA      412
AtSUC2    EWIGRKLGGAKRLWGIWNFILAI CLAMTVVVTKQAEHRRDH-----GGAKTGPPGNVTA      405
          :.* :**.* ** .**:*:*****:*** *.: * . * .**

PvSUT1.5 GAMSFFSILGIPLAITYSVFFALASIYSTSGAGQGLSLGLLNVAIVVPQMIVSAISGFW      453
PvSUT1.1 GALALFSVLGVPLAITYSIPFALASIFSTTSGAGQGLSLGVLNLAIVIPQMVVSVISGFW      472
AtSUC2    GALTFLAILGIPQAITFSIPFALASIFSTNSGAGQGLSLGVLNLAIVVPQMIVSVGGGPF      465
          **::*:*:***:***:*****:*.*****:***:***:***:*. ** :

PvSUT1.5 DSWFGGGLNPAFVLGAVAAVSAVLAVVMLPSPKPADVSKASSVTVGNFH      503
PvSUT1.1 DALFGGGLNPAFVVGAVAAAASGILSIIILLSPPPDL-AKAATATGGGFH      521
AtSUC2    DELFGGGLNIPAFVLGAIAAAVSGVLALTVLPSPPPDA-PAFKAT--MGFH      512
          * *****:*****:***.***.***: :**** * :. .**

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Supplemental Figure S1. Peptide alignment of Arabidopsis SUC2 and common bean SUT1.1 and SUT1.5 transporters.



B

OsSUT1	R ¹⁸⁸	QGPALMAD
AtSUC2	R ¹⁶²	QGPCRAFLGD
PvSUT1.1	R ¹⁶⁴	QGPCRAFLAD
PvSUT1.5	R ¹⁵⁴	QGPCRALAD

Supplemental Figure S2. PvSUT1.1 cartoon model showing (A) transmembrane regions and (B) conserved arginine residue.