**Comparing 2 crystal structures and 12 AlphaFold2-predicted human membrane glucose transporters and their water-soluble QTY variants**

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**Supplementary Materials**

**Table S1. Prediction confidence for GLUT1native, GLUT1QTY, GLUT3native, and GLUT3QTY.** “Protein” column represents native and QTY versions of GLUT1 and GLUT3. “Model” column defines the model ID (PDB-files of all models have the names as mentioned in this column). “Rank” column shows how good the model is (the better pLDDT score is, the higher the model rank is). Models are sorted by their rank. We use the models with the highest rank (rank 1). Confidence in models based on pLDDT values: very low (pLDDT < 50), low (pLDDT = 60), OK (pLDDT = 70), confident (pLDDT = 80), very high (pLDDT > 90).

| Protein | Model | Rank | pLDDT | pTMscore |
| --- | --- | --- | --- | --- |
| GLUT1 native | 3 | 1 | 89.45 | 0.8859 |
| GLUT1 native | 5 | 2 | 89.31 | 0.8937 |
| GLUT1 native | 2 | 3 | 87.44 | 0.8507 |
| GLUT1 native | 4 | 4 | 86.64 | 0.8632 |
| GLUT1 native | 1 | 5 | 86.54 | 0.8383 |
| GLUT1 QTY | 3 | 1 | 88.24 | 0.8670 |
| GLUT1 QTY | 5 | 2 | 87.45 | 0.8716 |
| GLUT1 QTY | 1 | 3 | 86.91 | 0.8516 |
| GLUT1 QTY | 2 | 4 | 86.15 | 0.8399 |
| GLUT1 QTY | 4 | 5 | 86.12 | 0.8523 |
| GLUT3 native | 5 | 1 | 89.71 | 0.8972 |
| GLUT3 native | 3 | 2 | 88.69 | 0.8849 |
| GLUT3 native | 1 | 3 | 87.39 | 0.8445 |
| GLUT3 native | 2 | 4 | 86.87 | 0.8481 |
| GLUT3 native | 4 | 5 | 86.50 | 0.8726 |
| GLUT3 QTY | 3 | 1 | 86.42 | 0.8573 |
| GLUT3 QTY | 1 | 2 | 86.32 | 0.8407 |
| GLUT3 QTY | 5 | 3 | 84.97 | 0.8528 |
| GLUT3 QTY | 2 | 4 | 83.27 | 0.8089 |
| GLUT3 QTY | 4 | 5 | 81.34 | 0.7756 |

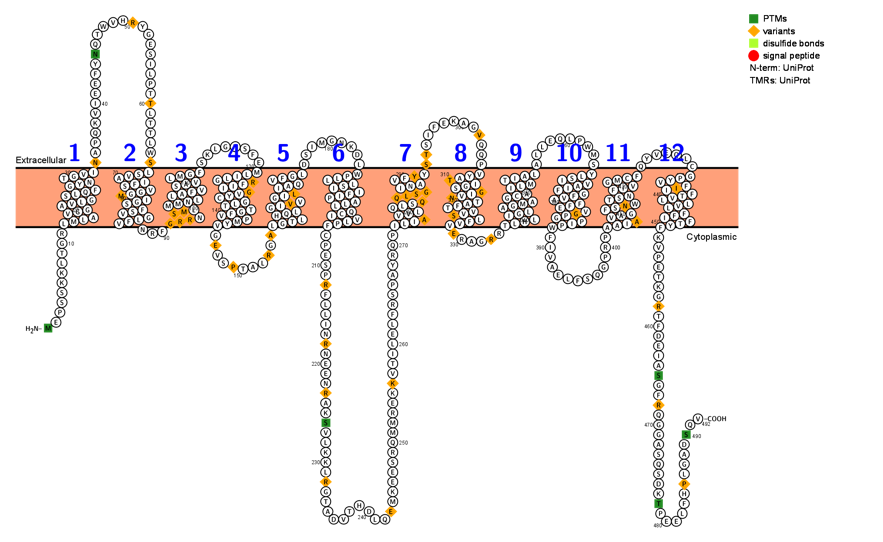
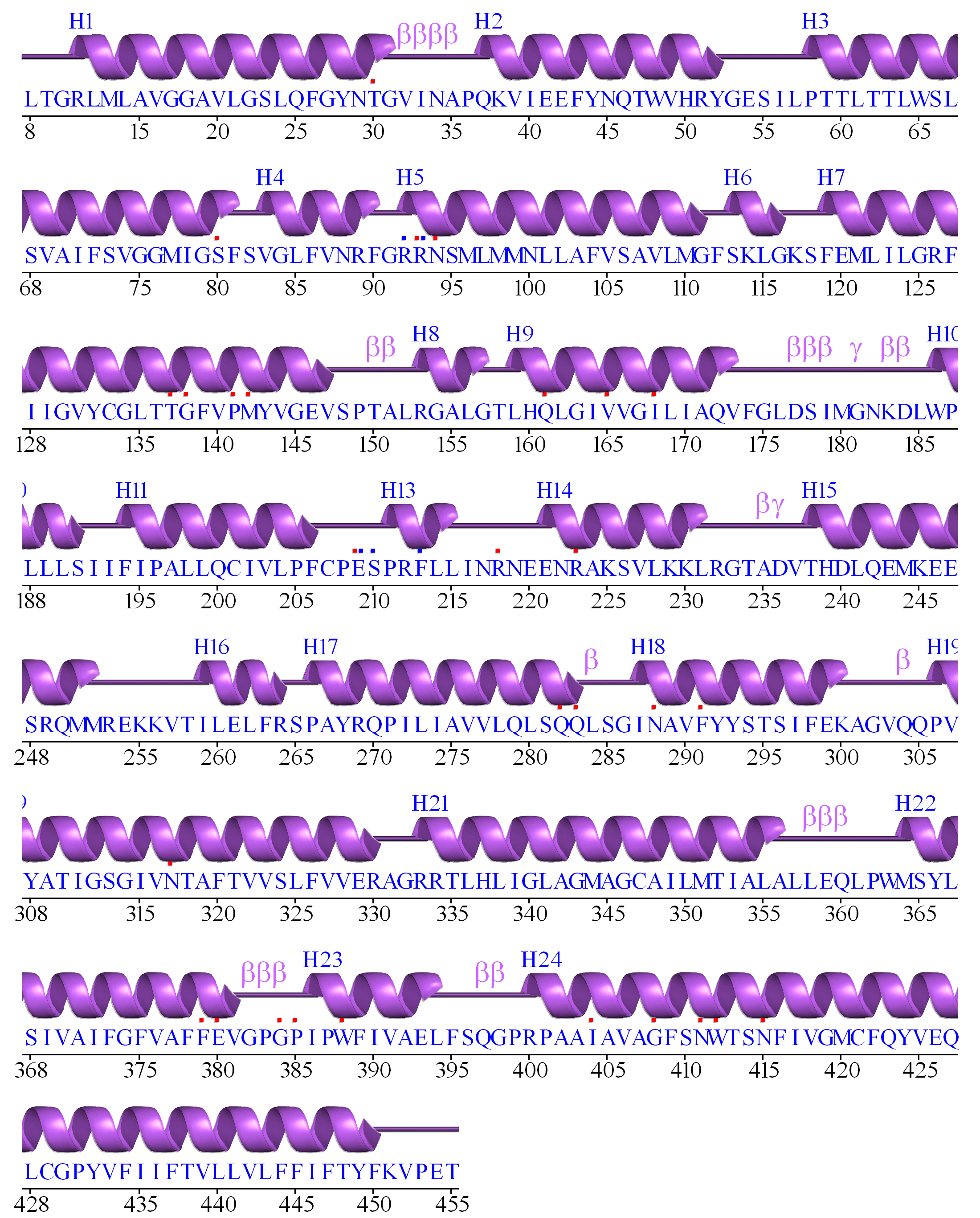
**Table S2. Prediction confidence for native glucose transporters, GLUT2QTY, and GLUT4QTY-14QTY.** “Protein” column represents native and QTY versions of GLUT2 and GLUT4-14. “Model” column defines the model ID (PDB-files of all models have the names as mentioned in this column). Confidence in models based on pLDDT values: very low (pLDDT < 50), low (pLDDT = 60), OK (pLDDT = 70), confident (pLDDT = 80), very high (pLDDT > 90). You can find information about other models in the GitHub Repository: <https://github.com/eva-smorodina/glucose-transporters>.

|  |  |  |  |
| --- | --- | --- | --- |
| **Protein** | **Model** | **pLDDT** | **pTMscore** |
| GLUT2 native | 5 | 86.01 | 0.8658 |
| GLUT2 QTY | 3 | 85.01 | 0.8256 |
| GLUT4 native | 5 | 87.86 | 0.8770 |
| GLUT4 QTY | 3 | 84.95 | 0.8423 |
| GLUT5 native | 3 | 89.39 | 0.8960 |
| GLUT5 QTY | 3 | 87.63 | 0.8799 |
| GLUT6 native | 3 | 82.12 | 0.8231 |
| GLUT6 QTY | 3 | 82.03 | 0.8173 |
| GLUT7 native | 3 | 87.99 | 0.8655 |
| GLUT7 QTY | 3 | 86.84 | 0.8513 |
| GLUT8 native | 3 | 81.88 | 0.8293 |
| GLUT8 QTY | 3 | 83.85 | 0.8365 |
| GLUT9 native | 1 | 83.30 | 0.8137 |
| GLUT9 QTY | 1 | 81.94 | 0.8009 |
| GLUT10 native | 3 | 74.64 | 0.7586 |
| GLUT10 QTY | 3 | 74.08 | 0.7429 |
| GLUT11 native | 3 | 88.51 | 0.8772 |
| GLUT11 QTY | 3 | 87.85 | 0.8665 |
| GLUT12 native | 3 | 73.04 | 0.7404 |
| GLUT12 QTY | 1 | 72.98 | 0.7193 |
| GLUT13 native | 3 | 80.02 | 0.7751 |
| GLUT13 QTY | 3 | 79.70 | 0.7733 |
| GLUT14 native | 5 | 87.30 | 0.8700 |
| GLUT14 QTY | 3 | 84.25 | 0.8344 |

**Figure S1. 14 human glucose transporter and their water-soluble QTY variants:**

**protein sequences, predicted 2D structures, and hydrophobic profiles**

GTR1=GLUT1=SLC2A1= facilitated glucose transporter member 1, [P11166](https://www.uniprot.org/uniprot/P11166), 492aa

>sp|P11166| GTR1=GLUT1 Solute carrier family 2, facilitated glucose transporter member 1

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ELFHPLGADSQV

The QTY variant GTR1QTY

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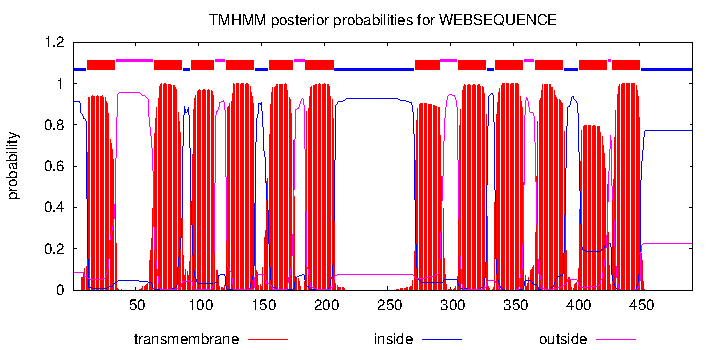
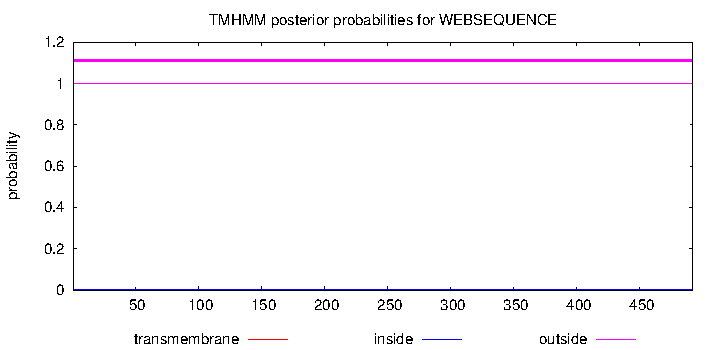
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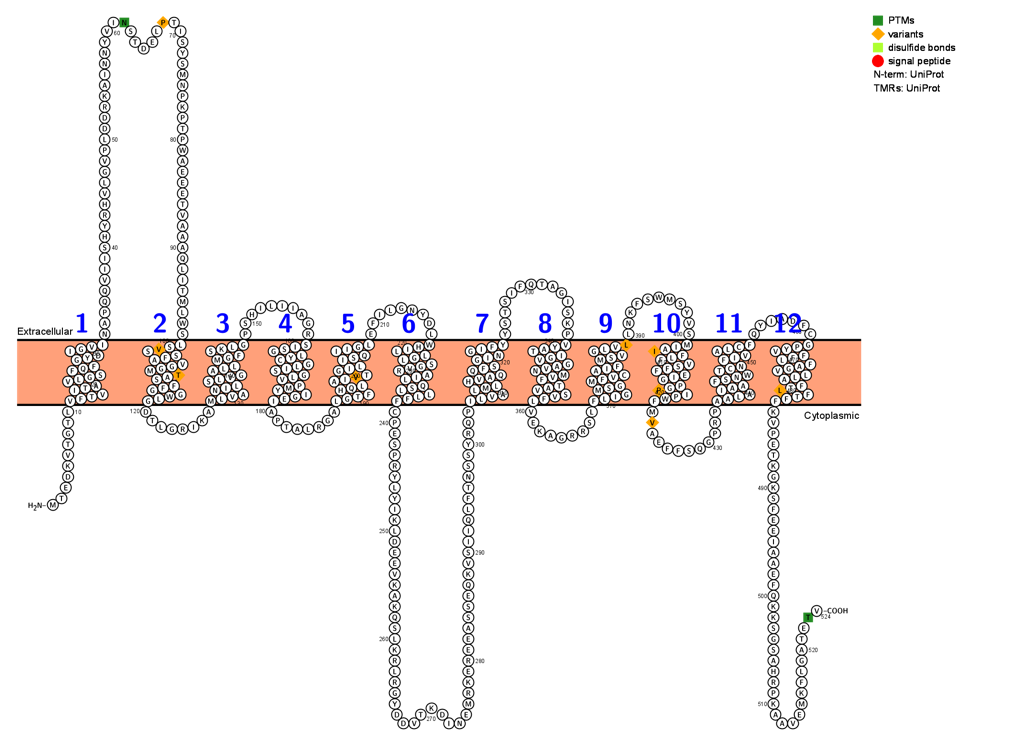
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Native GTR1 GTR1QTY

GTR2=Glut2=SLC2A2= facilitated glucose transporter member 2, [P11168](https://www.uniprot.org/uniprot/P11168), 524aa



[P11168](https://www.uniprot.org/uniprot/P11168)|GTR2 Solute carrier family 2, facilitated glucose transporter member 2

GTR2=GLUT2

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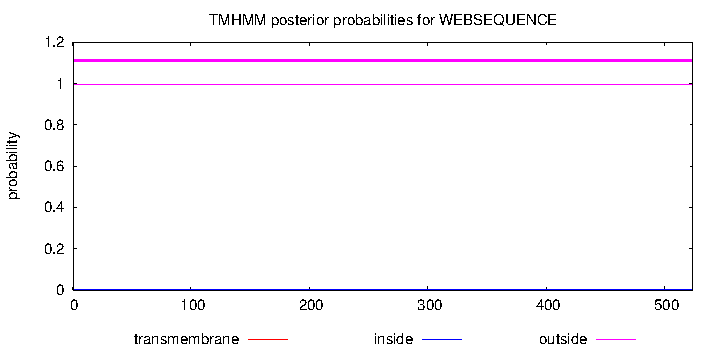
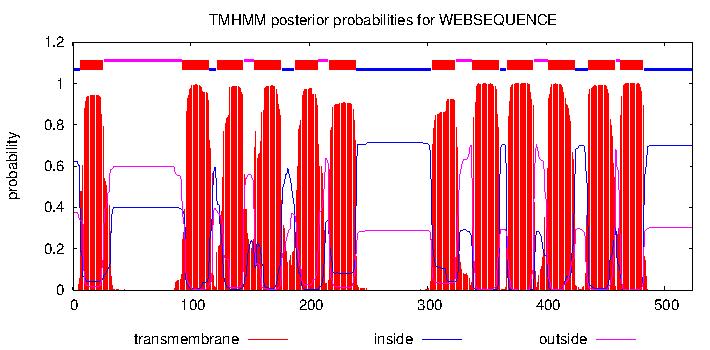
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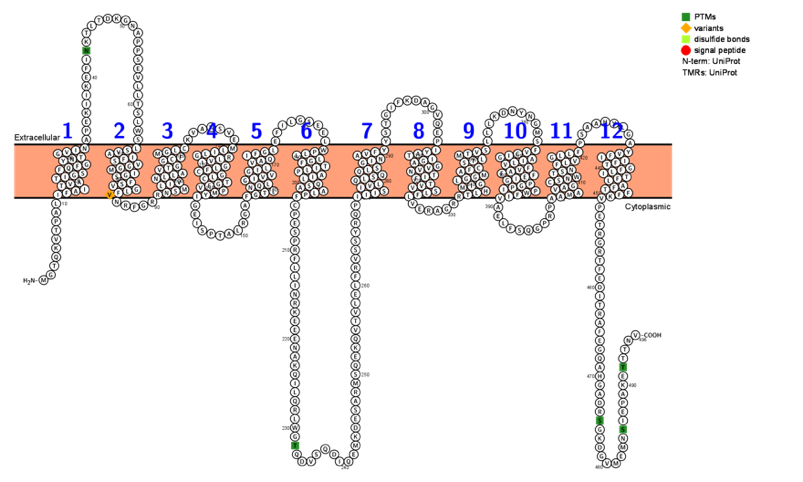
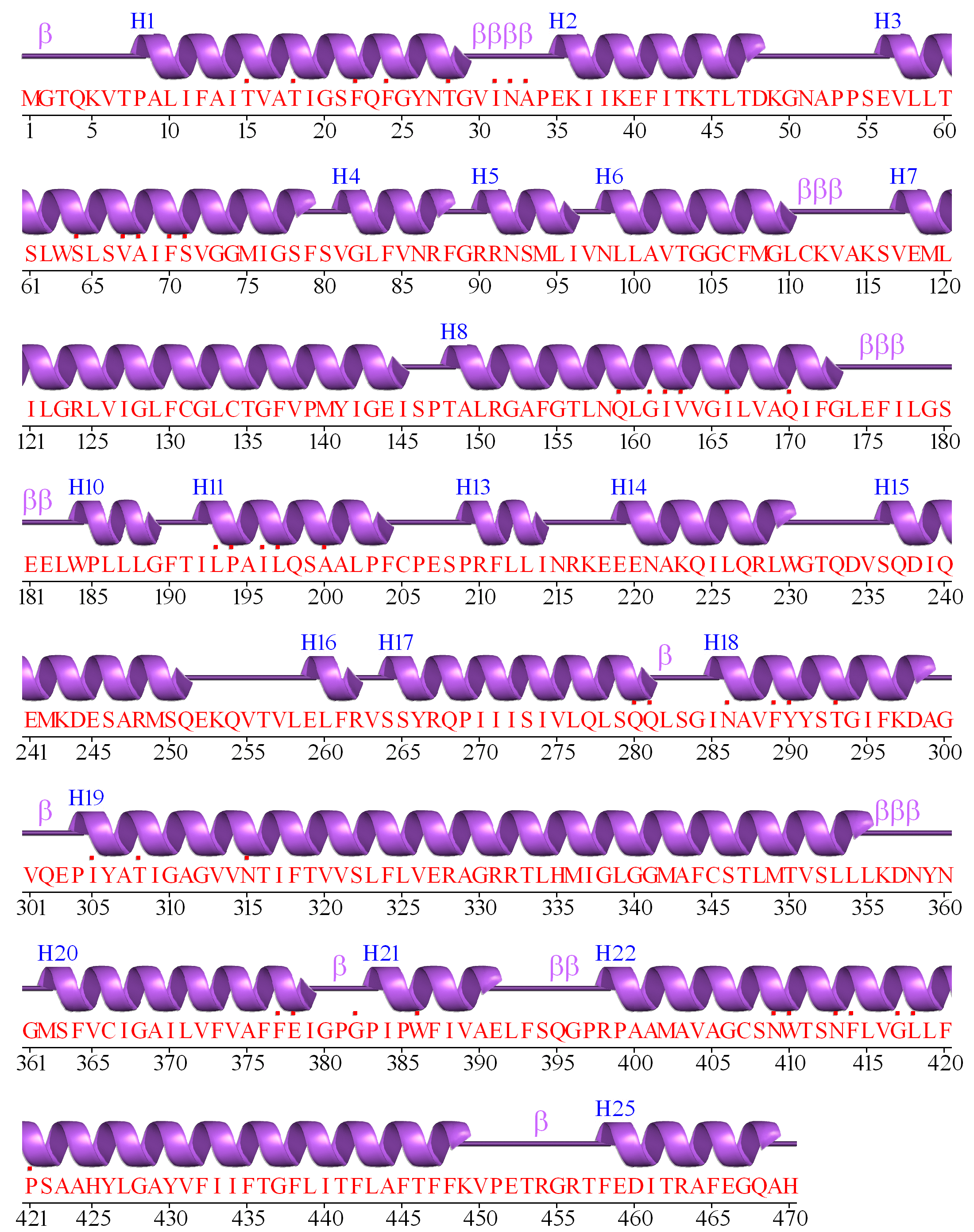
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GTR3=GLUT3=SLC2A3= facilitated glucose transporter member 3, [P11169](https://www.uniprot.org/uniprot/P11169), 496aa

TM8-9

GTR3=GLUT3

[P11169](https://www.uniprot.org/uniprot/P11169)|GTR3 HUMAN Solute carrier family 2, facilitated glucose transporter member 3

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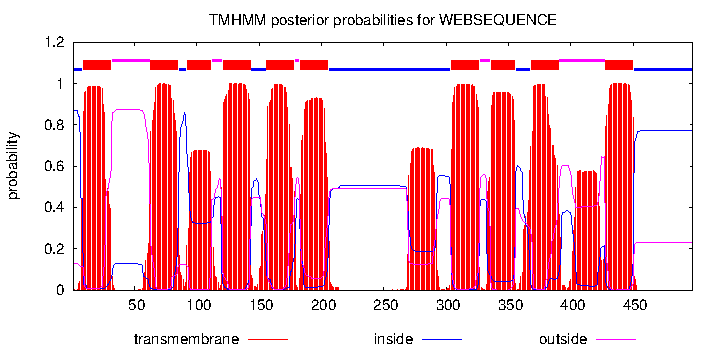
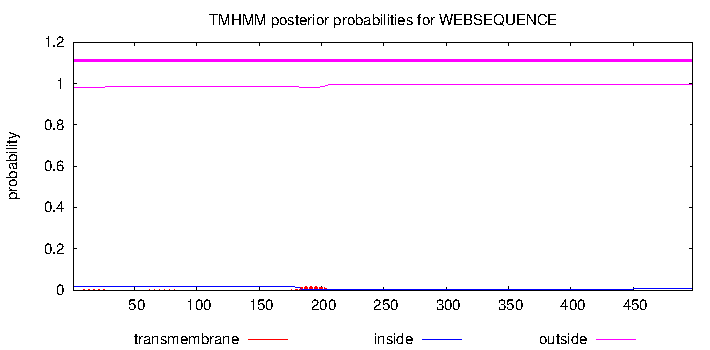
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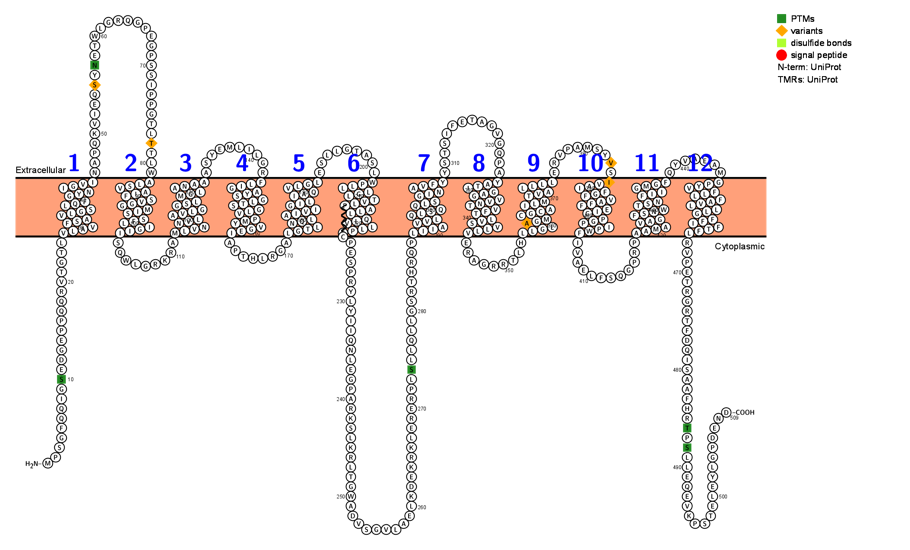
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GTR4=GLUT4=SLC2A4= facilitated glucose transporter member 4, [P14672](https://www.uniprot.org/uniprot/P14672), 509aa



GTR4=GLUT4

P14672|GLUT4 HUMAN Solute carrier family 2, facilitated glucose transporter member 4

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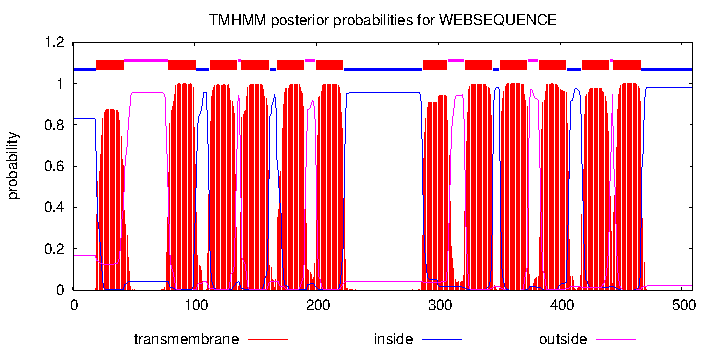
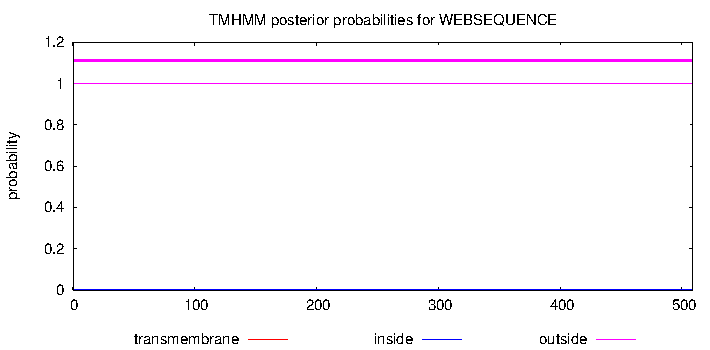
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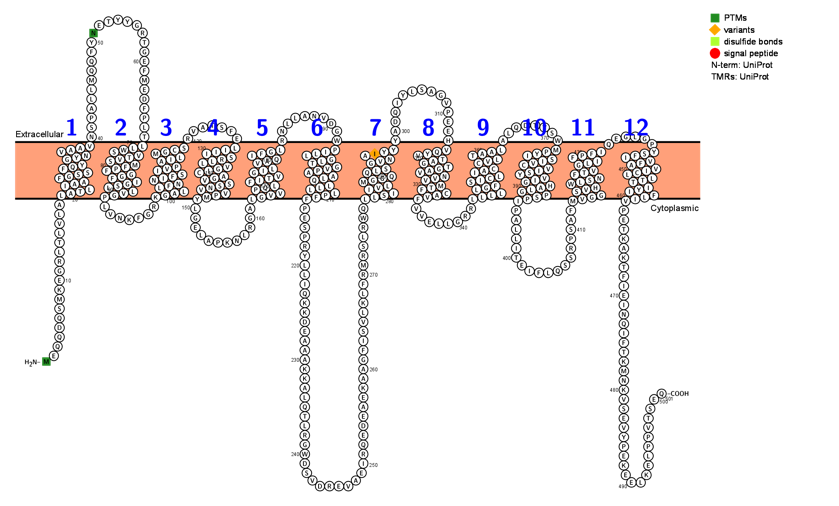
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GTR5=GLUT5=SLC2A5= facilitated glucose transporter member 5, [P22732](https://www.uniprot.org/uniprot/P22732), 501aa



[P22732](https://www.uniprot.org/uniprot/P22732)| GTR5=GLUT5 Solute carrier family 2, facilitated glucose transporter member 5

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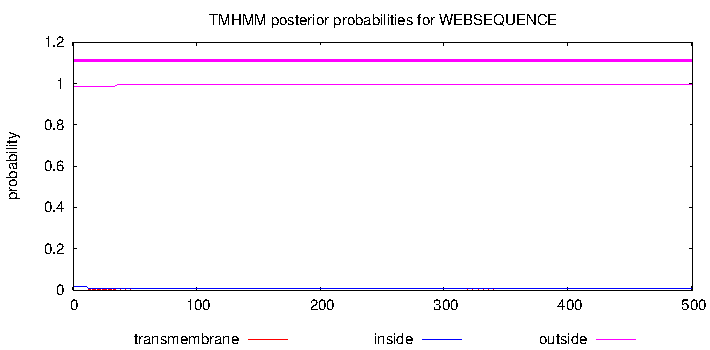
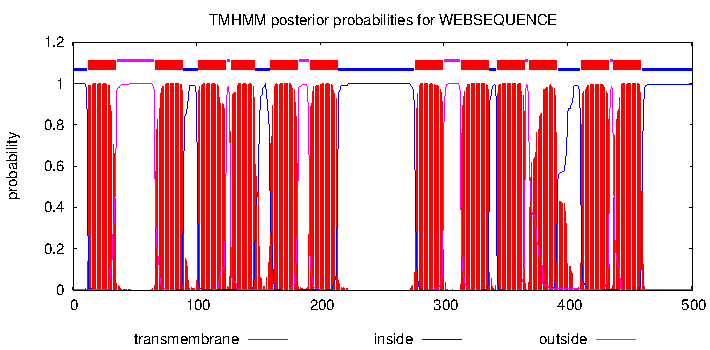
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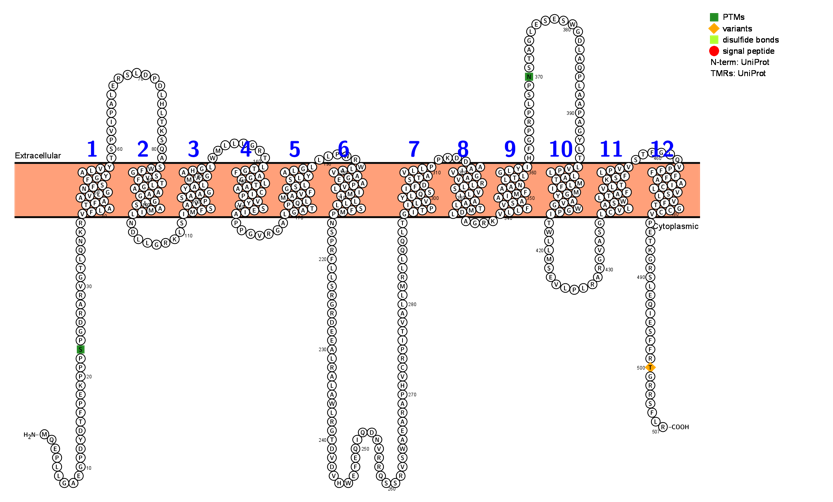
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GTR6=GLUT6=SLC2A6= facilitated glucose transporter member 6, [Q9UGQ3](https://www.uniprot.org/uniprot/Q9UGQ3), 507aa



[Q9UGQ3](https://www.uniprot.org/uniprot/Q9UGQ3)| GTR6=GLUT6 Solute carrier family 2, facilitated glucose transporter member 6

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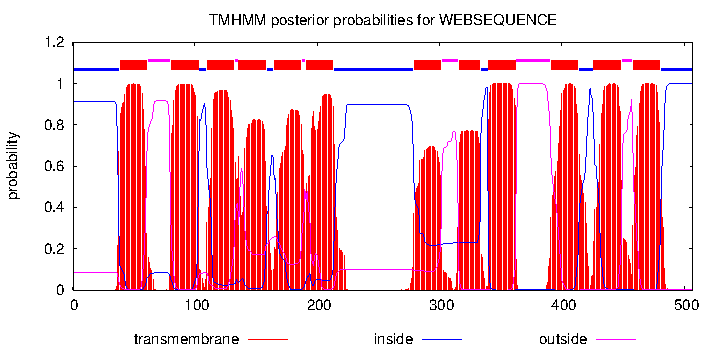
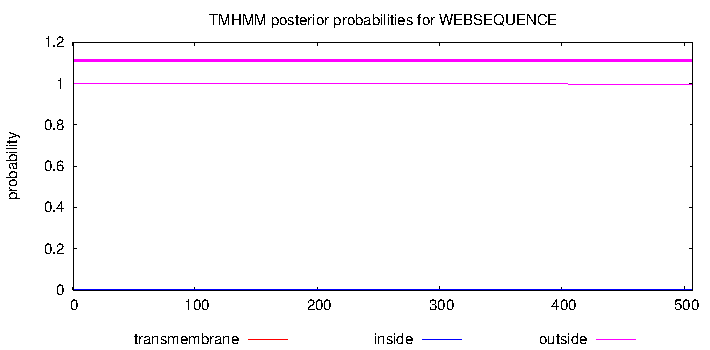
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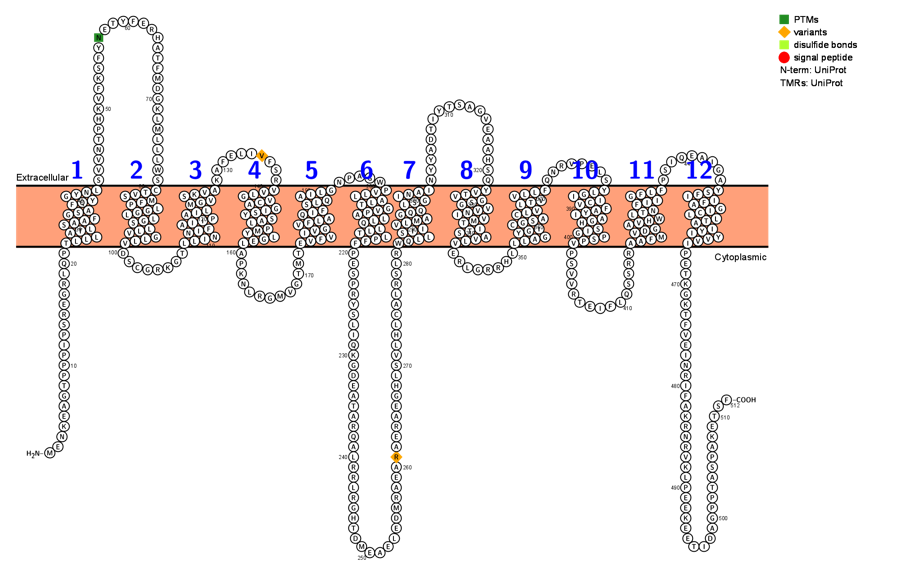
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MSEVLPLRARGVASGQCTQASWQTAYTQTKSYQPTTSTFGLQVPYYYYAATCQTSQTYTG

CCTPETKGRSLEQIESFFRTGRRSFLR

GTR7=GLUT7=SLC2A7= facilitated glucose transporter member 7, [Q6PXP3](https://www.uniprot.org/uniprot/Q6PXP3), 512aa



[Q6PXP3](https://www.uniprot.org/uniprot/Q6PXP3)| GTR7=GLUT7 Solute carrier family 2, facilitated glucose transporter member 7

MENKEAGTPPPIPSREGRLQPTLLLATLSAAFGSAFQYGYNLSVVNTPHKVFKSFYNETY

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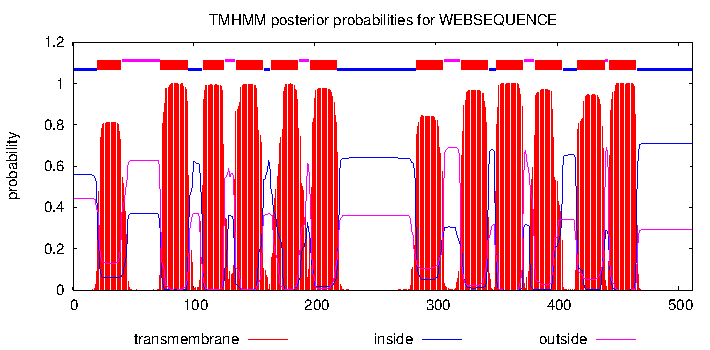
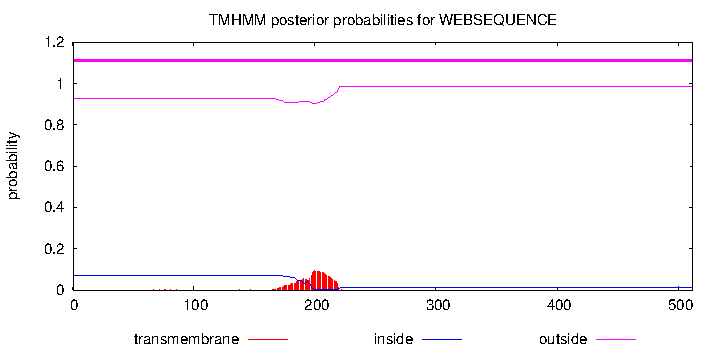
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GLUT7QTY

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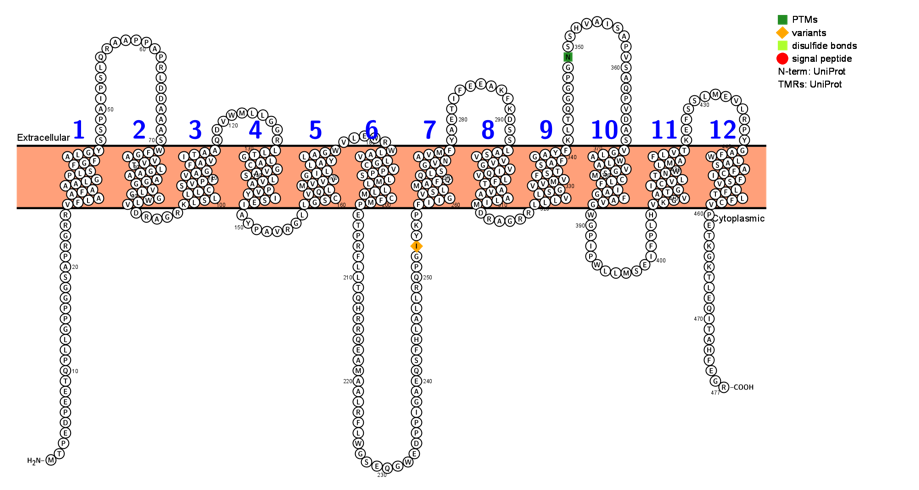
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FAKRNRVKLPEEKEETIDAGPPTASPAKETSF

GTR8=GLUT8= SLC2A8= facilitated glucose transporter member 8, [Q9NY64](https://www.uniprot.org/uniprot/Q9NY64), 477aa



Q9NY64|GTR8=GLUT8 Solute carrier family 2, facilitated glucose transporter member 8, 477aa

MTPEDPEETQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPP

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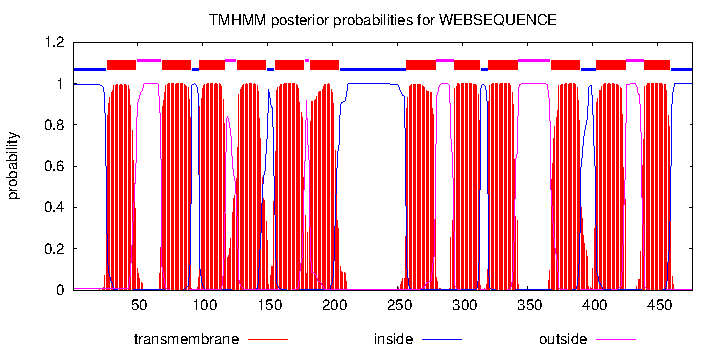
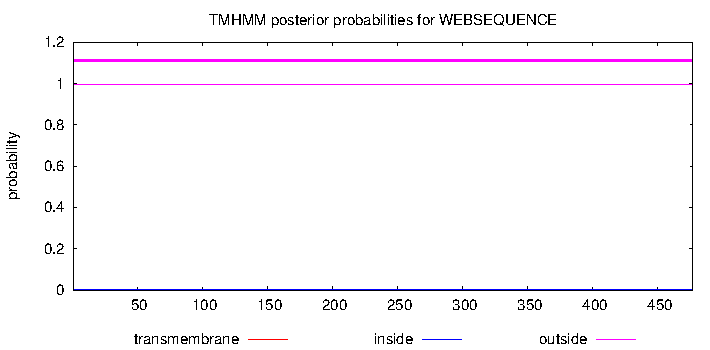
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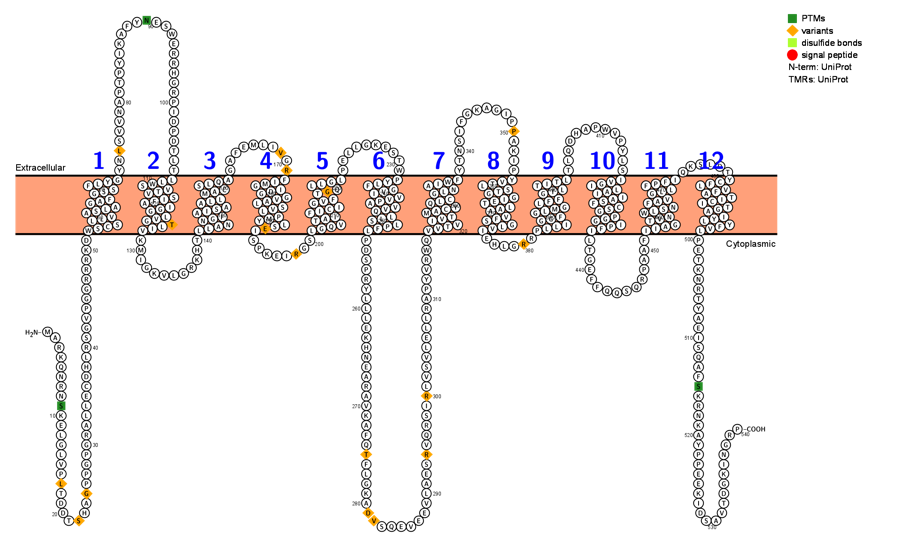
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GTR9=GLUT9=SLC2A9= facilitated glucose transporter member 9, [Q9NRM0](https://www.uniprot.org/uniprot/Q9NRM0), 540aa



[Q9NRM0](https://www.uniprot.org/uniprot/Q9NRM0) | GTR9=GLUT9 Solute carrier family 2, facilitated glucose transporter member 9

MARKQNRNSKELGLVPLTDDTSHAGPPGPGRALLECDHLRSGVPGGRRRKDWSCSLLVAS

LAGAFGSSFLYGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTVSIFAIG

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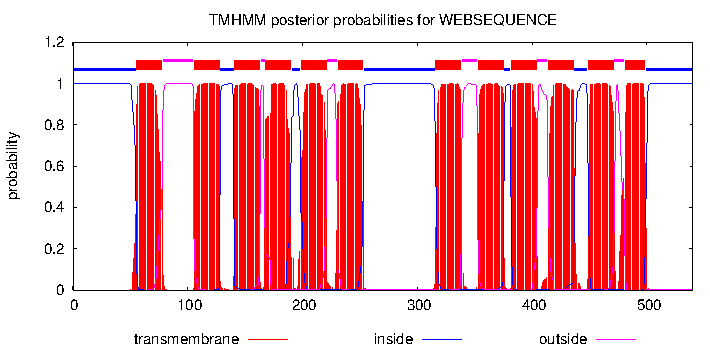
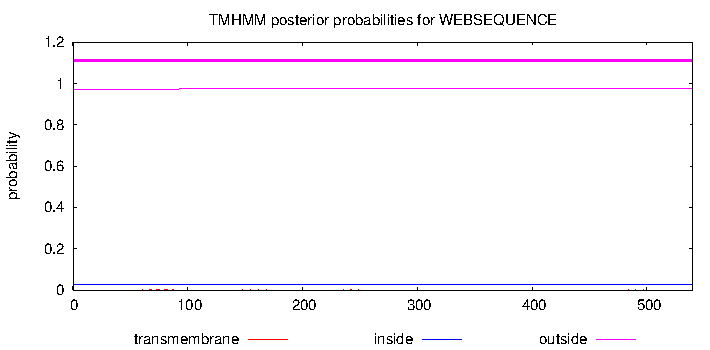
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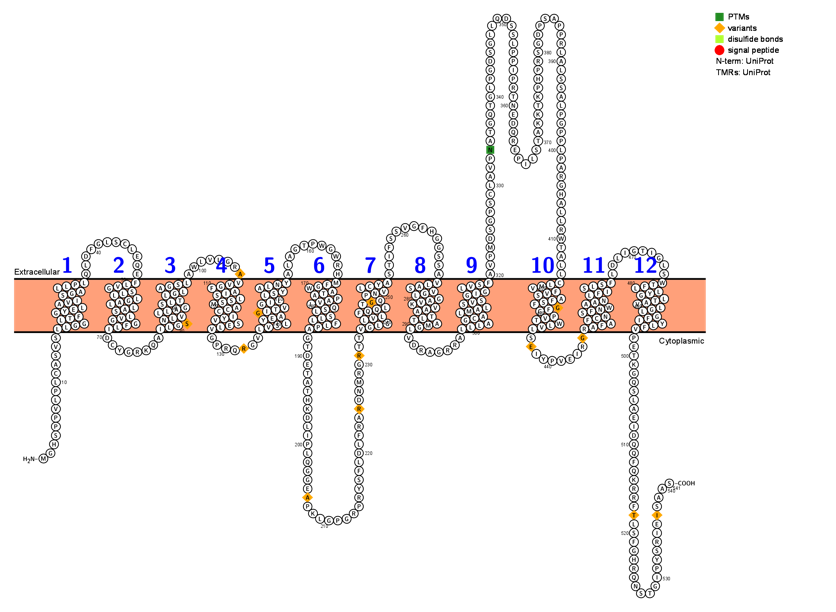
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GTR10=GLUT10=SLC2A10= facilitated glucose transporter member 10, [O95528](https://www.uniprot.org/uniprot/O95528), 541aa



[O95528](https://www.uniprot.org/uniprot/O95528)| GTR10=GLUT10 Solute carrier family 2, facilitated glucose transporter member 10

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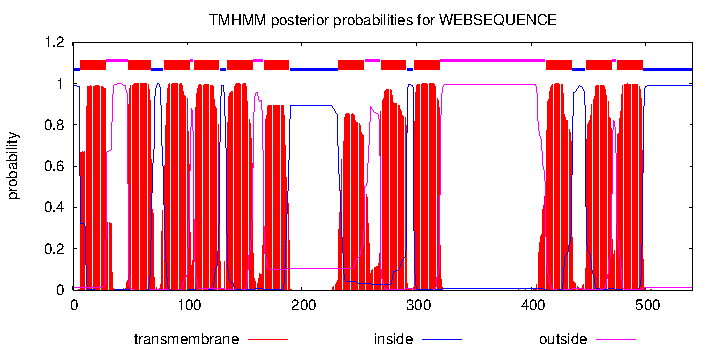
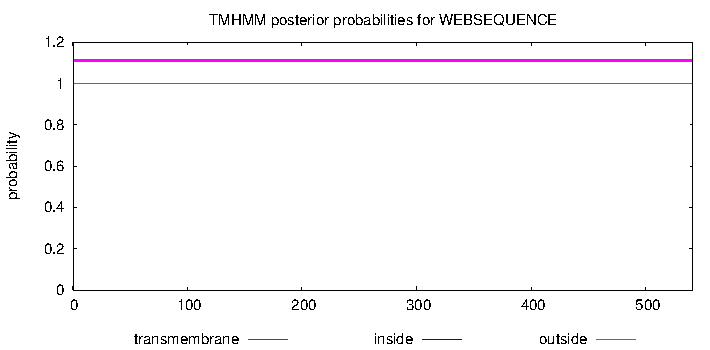
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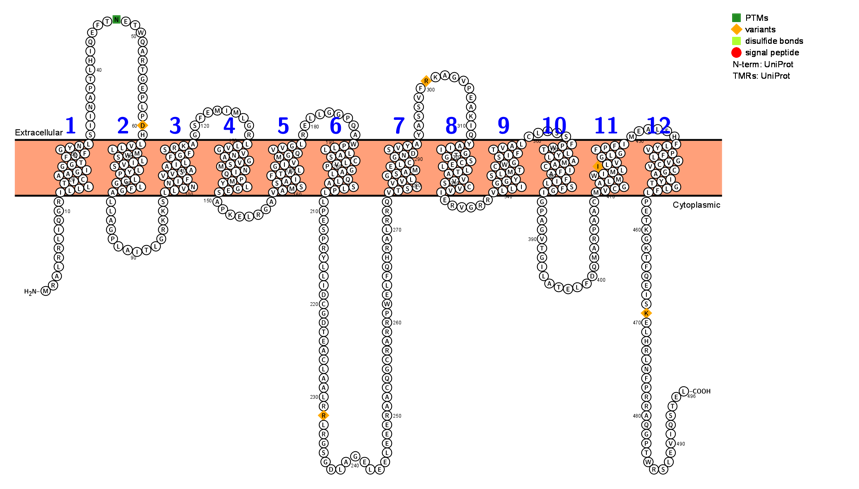
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GTR11=GLUT11=SLC2A11=, facilitated glucose transporter member 11, [Q9BYW1](https://www.uniprot.org/uniprot/Q9BYW1), 496aa



[Q9BYW1](https://www.uniprot.org/uniprot/Q9BYW1)| GTR11=GLUT11 Solute carrier family 2, facilitated glucose transporter member 11

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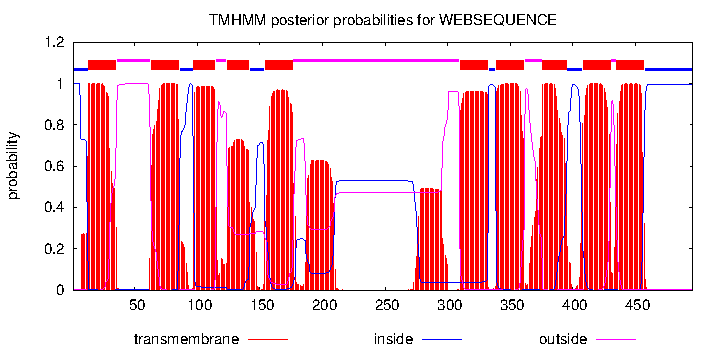
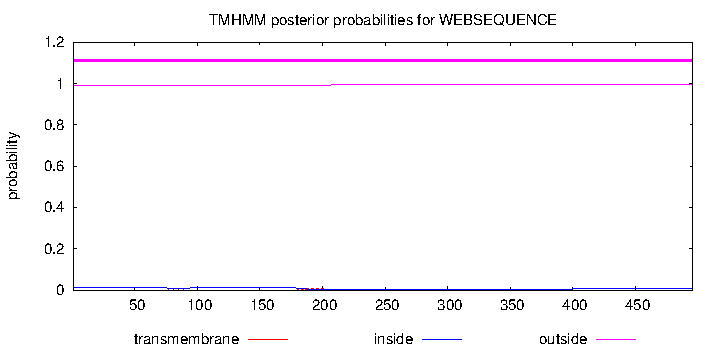
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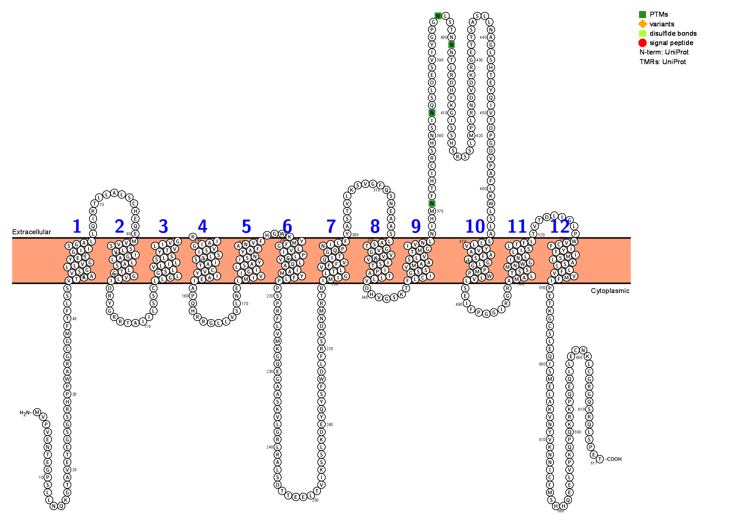
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QGPTWRSLEVIQSTEL

GLUT12=GTR12=SLC2A12= facilitated glucose transporter member 12, [Q8TD20](https://www.uniprot.org/uniprot/Q8TD20), 617aa



[Q8TD20](https://www.uniprot.org/uniprot/Q8TD20)| GLUT12=GTR12 Solute carrier family 2, facilitated glucose transporter member 12

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ISGALLQIKTLLALSCHEQEMVVSSLVIGALLASLTGGVLIDRYGRRTAIILSSCLLGLG

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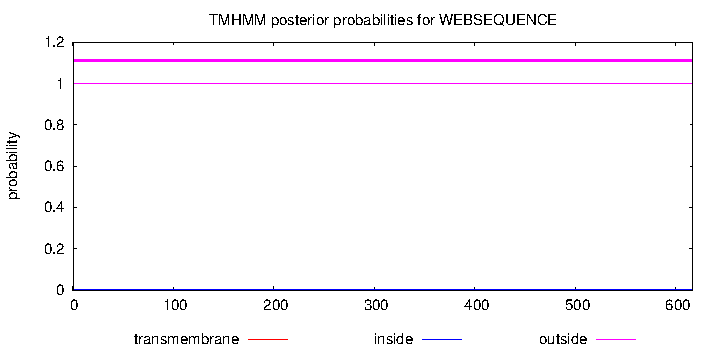
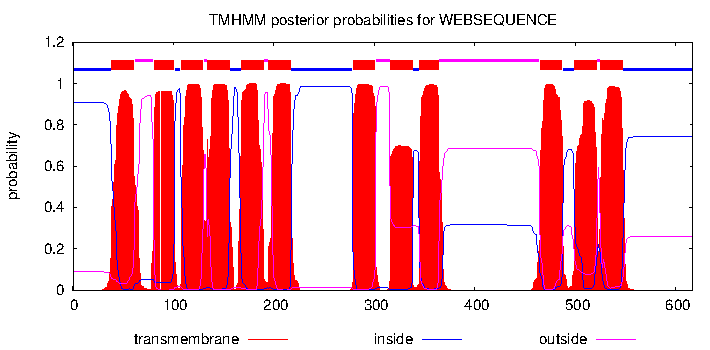
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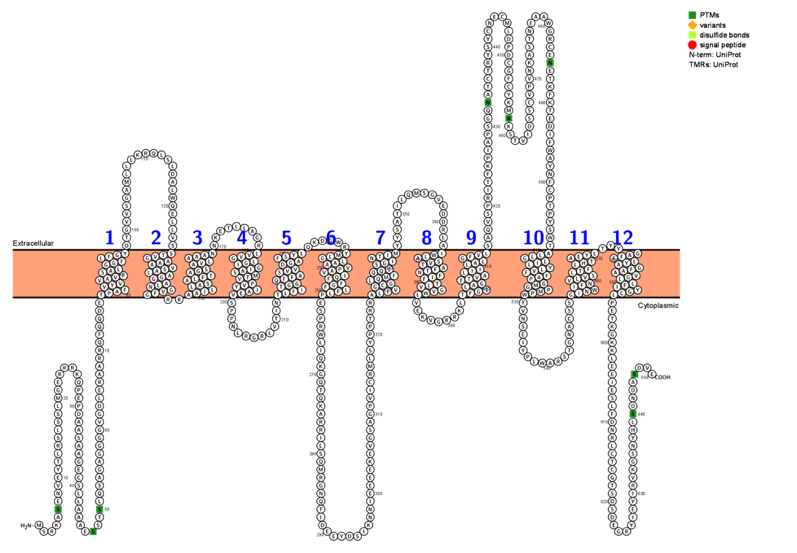
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GLUT13=SLC2A13=MYCT=HMIT, [Q96QE2](https://www.uniprot.org/uniprot/Q96QE2), 648aa



>sp|[Q96QE2](https://www.uniprot.org/uniprot/Q96QE2)|MYCT=GLUT13=SLC2A13 Proton myo-inositol cotransporter

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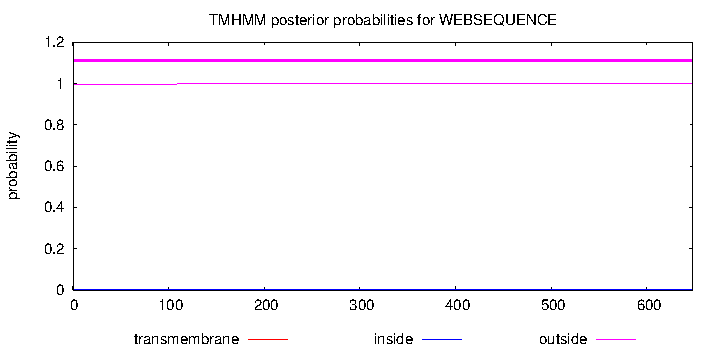
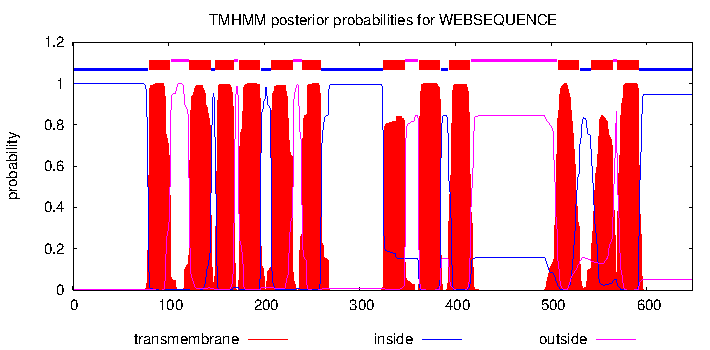
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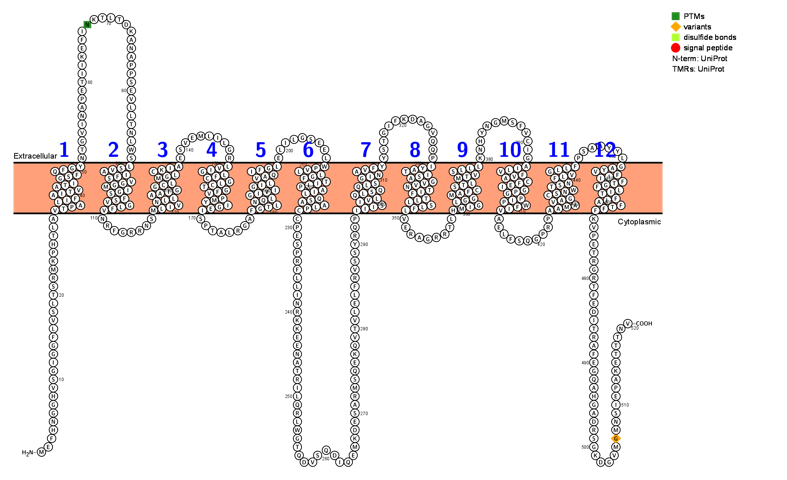
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GTR14=GLUT14=SLC2A14= facilitated glucose transporter member 14, [Q8TDB8](https://www.uniprot.org/uniprot/Q8TDB8), 520aa



[Q8TDB8](https://www.uniprot.org/uniprot/Q8TDB8)| GTR14=GLUT14 Solute carrier family 2, facilitated glucose transporter member 14

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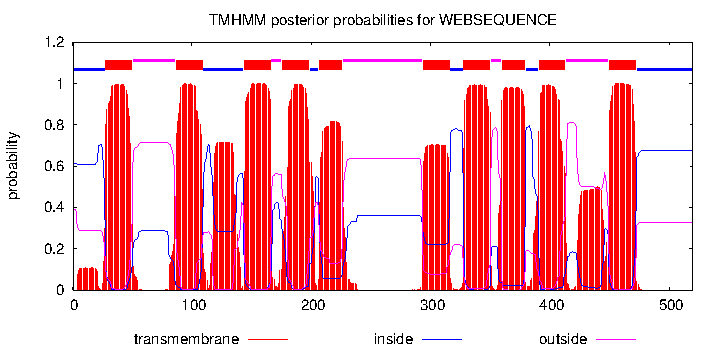
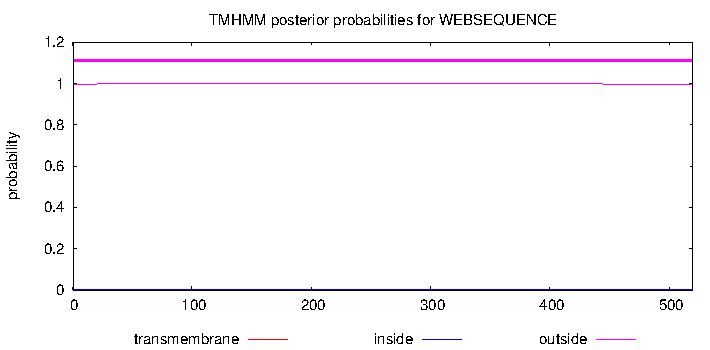
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