Characterization of the Proton/Glutamate Symport Protein of *Bacillus subtilis* and Its Functional Expression in *Escherichia coli*

BEREND TOLNER, TREES UBBINK-KOK, BERT POOLMAN, AND WIL N. KONINGS*

Department of Microbiology and Groningen Biomolecular Science and Biotechnology Institute, University of Groningen, Haren, The Netherlands

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Transport of acidic amino acids in *Bacillus subtilis* is an electrogenic process in which L-glutamate or L-aspartate is symported with at least two protons. This is shown by studies of transport in membrane vesicles in which a proton motive force is generated by oxidation of ascorbate-phenazine methosulfate or by artificial ion gradients. An inwards-directed sodium gradient had no (stimulatory) effect on proton motive force-driven L-glutamate uptake. The transporter is specific for L-glutamate and L-aspartate. L-Glutamate transport is inhibited by β -hydroxyaspartate and cysteic acid but not by α -methyl-glutamate. The gene encoding the L-glutamate transport protein of *B. subtilis* (gltP_{Bsu}) was cloned by complementation of *Escherichia coli* JC5412 for growth on glutamate as the sole source of carbon, energy, and nitrogen, and its nucleotide sequence was determined. Putative promoter, terminator, and ribosome binding site sequences were found in the flanking regions. UUG is most likely the start codon. gltP_{Bsu} encodes a polypeptide of 414 amino acid residues and is homologous to several proteins that transport glutamate and/or structurally related compounds such as aspartate, fumarate, malate, and succinate. Both sodium- and proton-coupled transporters belong to this family of dicarboxylate transporters. Hydropathy profiling and multiple alignment of the family of carboxylate transporters spans the cytoplasmic membrane 12 times with both the amino and carboxy termini on the inside.

The amino acid transporters in the thermophile *Bacillus* stearothermophilus studied to date facilitate an electrogenic symport reaction in which Na⁺ is used as the coupling ion. The apparent affinity constants for Na⁺ are in the range of 0.5 to 1 mM (14). The transport of glutamate and aspartate is driven by the proton motive force (Δp) but also by an inwardly directed Na⁺ gradient (Δp Na). The transport of glutamate occurs most likely in symport with one H⁺ and one Na⁺ (7); the apparent affinity constant for Na⁺ is <10 μ M. So far, sodium/proton/glutamate transporters have been found in the thermophiles *Bacillus* sp. strain IS1 (*gltT*_{Bi}) (42), *B. stearothermophilus* (*gltT*_{Bs}), and *Bacillus caldotenax* (*gltT*_{Bc}). The genes encoding GltT_{Bs} and GltT_{Bc} have been cloned and functionally expressed in *Escherichia coli* (43).

Studies on the transport of L-glutamate and L-aspartate in whole cells of B. subtilis W23, 60015, 6GM, and 8G5 suggested that Δp Na is not involved as a driving force in this mesophilic Bacillus species (41). The glutamate transporter of B. subtilis is likely to differ from those of thermophilic bacilli with respect to not only cation selectivity but also thermostability. In order to compare the sodium/proton/glutamate symport protein of the thermophile B. stearothermophilus with the glutamate transport protein of the closely related mesophile B. subtilis, the latter system was studied at the molecular level. This study confirms that glutamate uptake in B. subtilis is indeed coupled to the Δp . The primary sequence of the glutamate transporter of B. subtilis is highly similar to that of the glutamate transport proteins of B. stearothermophilus and B. caldotenax. In addition, the substrate specificity of these proteins is similar but the cation selectivity is different.

MATERIALS AND METHODS

Bacterial strains, plasmids, and growth conditions. The bacterial strains, plasmids, and phages used are listed in Table 1. *B. subilis* 6GM was grown at 37°C with vigorous aeration in Luria-Bertani medium (LB) adjusted to pH 7.0 (33). *E. coli* strains were grown at 37°C with vigorous aeration in LB, M9, M9G (M9 in which ammonium chloride was replaced by L-glutamate at a final concentration of 10 mM), or M9CA medium (33, 43). The mineral media were supplemented with essential nutrients as indicated by the auxotrophic markers. When needed, carbenicillin and isoproyPi- β -D-thiogalactopyranoside (IPTG) were added to a final concentration of 100 μ g/ml and 1000 μ M, respectively.

DNA manipulations. Mini- and large-scale preparations of plasmid DNA were obtained by the alkaline lysis method (4, 15). Chromosomal DNA was isolated essentially as described previously (25), except that mutanolysine was omitted. The strains were transformed after rubidium chloride treatment of the cells (33) or by electrotransformation (8). Other DNA techniques were performed as described previously (33).

Cloning of the glutamate transport gene. The *gltP*_{Bsu} gene was cloned essentially as described previously (43). Partially *Eco*RI-, *Hin*dIII-, *PstI*-, or *Sau3*A-digested chromosomal DNA of *B. subtilis* was fractionated by agarose gel (1%, wt/vol) electrophoresis. Fragments of 2 to 10 kb were electroeluted from the gel and ligated into linearized and dephosphorylated pKK223-3. The resulting hybrid plasmids were used to transform *E. coli* JC5412 by electrotransformation. This strain does not grow on glutamate as the sole source of energy, nitrogen, and carbon. Transformants able to grow on M9G plates (supplemented with carbenicillin and IPTG) were analyzed with respect to their plasmid content. Purified plasmids were used to retransform *E. coli* JC5412 in order to distinguish between Glu⁺ revertants and true transformatis.

Sequence determination. The nucleotide sequences of both strands of the *Hind*III fragment of pGTU100, or subclones derived thereof in pUC18/19 or M13mp18/19 (*AccI, AluI, Hae*III, *Hinc*II, *Hind*III, *PstI, RsaI, Sau3A*, and *SphI* fragments), were determined by using the dideoxy-chain termination method (34). Single- or double-stranded DNA was sequenced with a T7 sequencing kit (Pharmacia). Micro Genie (release 5.0; Beckman, Palo Alto, Calif.) and PCGene (release 6.26; Genofit, Geneva, Switzerland) were used for computer-assisted sequence analysis. Amino acid sequences homologous to GltP_{Bsu} in the EMBL data bank were located with the TBLASTN program (1). Transport assays with whole cells. Cells (15 ml) of strain JC5412 harboring

Transport assays with whole cells. Cells (15 ml) of strain JCS412 harboring plasmid pKK223-3 or pGTU100, grown for 14 h in LB (supplemented with carbenicillin and IPTG), were harvested, washed three times in 50 mM potassium phosphate (pH 6.0) plus 5 mM MgSO₄, and resuspended to a final A_{660} of approximately 10 in the same buffer. Uptake of L-[¹⁴C]glutamate by the *E. coli* cells was assayed at 37°C, upon 100-fold dilution of the cells into 200 µl of 50 mM potassium phosphate (pH 6.0)–5 mM MgSO₄–10 mM glucose. This mixture was incubated for 1 min at 37°C under continuous aeration. To initiate the uptake

^{*} Corresponding author. Mailing address: Department of Microbiology, Groningen Biomolecular Science and Biotechnology Institute, University of Groningen, Kerklaan 30, 9751 NN Haren, The Netherlands. Phone: 31 50 632150. Fax: 31 50 632154.

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TABLE 1.	Bacterial	strains.	plasmids.	and	phages used
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Strain, plasmid, or phage	Relevant characteristics	Source or reference
Bacteria		
B. stearothermophilus		ATCC 7954
B. subtilis 6GM		Laboratory collection
E. coli		2
JM101	$\Delta(lac-proAB)$ F' $lacI^{q} \Delta M15$	50
JC5412	No growth on L-glutamate as the sole source of carbon, nitrogen, and energy	49
BK9MDG	GltP ⁻	47
Plasmids		
pUC18/19	Ap ^r	
pKK223-3	Ap ^r , expression vector	Pharmacia
pGTU100	pKK223-3 carrying gltP of B. subtilis on a 2,122-bp HindIII-HindIII fragment	This study
pGTU2000	pUC18 carrying gltP of B. subtilis on a 2,122-bp HindIII-HindIII fragment	This study
Phage M13mp18/19		50

experiment, L-[¹⁴C]glutamate was added to a final concentration of 1.9 μ M. The uptake reactions were terminated by adding a 10-fold excess of ice-cold 0.1 M potassium chloride and immediately filtering over cellulose nitrate filters (pore size, 0.45 μ m). The filters were washed once with 2 ml of ice-cold potassium chloride.

Isolation of membrane vesicles. For studies of transport in membrane vesicles, cells of *B. subtilis* 6GM were grown in LB (33) to an A_{660} of 1.0. Cells were harvested and membrane vesicles were isolated as described previously by Konings et al. (23).

Cells of *E. coli* BK9MDG harboring plasmid pKK223-3 or pGTU100 were grown to an A_{660} of 1.0 in LB (supplemented with 100 µg of carbenicillin per ml and 100 µM IPTG) and membrane vesicles were isolated as described previously by Kaback (18). Cytoplasmic membranes of *B. subtilis* and *E. coli* were finally resuspended to 15 mg of protein per ml in 50 mM potassium phosphate, pH 6.0, and stored in liquid nitrogen.

Transport assays. (i) Sodium- and proton motive force-driven uptake. The electron donor system potassium-ascorbate (K-asc)-phenazine methosulfate (PMS) was used to generate a Δp . Membrane vesicles were diluted 100-fold into 50 mM potassium phosphate (pH 6.0)-5 mM MgSO₄-10 mM K-asc-100 μ M PMS. The effect of the sodium motive force (Δs) was assessed by adding 10 mM NaCl to the assay buffer. When appropriate, valinomycin (2 nmol per mg of protein), nigericin (1 μ M), or cabonyl cyanide *m*-chlorophenylhydrazone (10 μ M) (CCCP) was added to abolish the transmembrane electrical potential ($\Delta \Psi$), the transmembrane proton gradient (Δp H), or the Δp , respectively. After a 1-min incubation, uptake was initiated by adding L-[¹⁴C]glutamate to a final concentration of 1.9 μ M. The uptake reaction was terminated as described above.

(ii) Artificial ion gradients. The buffers used to generate artificial gradients are listed in Table 2. Membrane vesicles were washed twice in buffer 1 and subsequently incubated for 2 h at 4°C in the same buffer. After centrifugation for 5 min

TABLE 2. Buffers used to generate artificial ion gradients and resulting forces

	Com	position ^b		
Buffer ^a	MES (mM)	Other ingredient(s) ^{d}	Valinomycin ^c	Force(s)
1^e	20	HAc, KOH	_	None
2^e	120	Mglu	+	Δp
3^e	20	HĂc, Mglu	+	$\Delta \Psi$
4^e	120	KOH	+	ΔpH
5	20	HAc,	_	Δp Na
		NaOH		-
6	20	HAc,	+	$\Delta p Na + \Delta \Psi$
		NaOH		-
7	120	NaOH	_	$\Delta p \text{Na} + \Delta p \text{H}$
8	120	NaOH	+	$\Delta p Na + \Delta p$

 $^{\it a}$ Adjusted to pH 6.0 with methylglucamine or H_2SO4; 5 mM MgSO4 was present in all cases.

^b MES, morpholineethanesulfonic acid; Mglu, methylglucamine.

^c Final concentration, 2 nmol/mg of protein.

^d 100 mM each.

^{*e*} Sodium ion contamination, $\leq 10 \mu$ M.

at 200,000 × g the membranes were resuspended in buffer 1 to a concentration of approximately 40 mg of protein per ml. Uptake driven by specific ion gradients was initiated by diluting the membrane vesicles 100-fold into the appropriate buffer (Table 2) containing $t-1^{14}$ C]glutamate (1.9 µM). The reaction was terminated as described above. Care was taken to avoid contamination of buffers with sodium ions; disposable plastic materials and ultrapure chemicals were used in all experiments. The uptake experiments were performed at 37°C unless stated otherwise. The kinetic parameters for transport, apparent K_m and V_{max} , were estimated from the initial rates of uptake of the labeled amino acid determined after 10 s. Results were analyzed by fitting the data to the Michaelis equation.

Protein determination. Protein was measured by the method of Lowry et al. (26), using bovine serum albumin as the standard.

Nomenclature. In order to discriminate between Na⁺/glutamate, H⁺/glutamate and Na⁺/H⁺/glutamate transport proteins, the gene designations *gltS*, *gltP*, and *gltT* are used. Additionally, the subscripts Bs, Bc, Bsu, and Ec (B or K-12) are used to discriminate between the genes or proteins of *B. stearothermophilus*, *B. caldotenax*, *B. subtilis*, and *E. coli* (B or K-12), respectively.

Nucleotide sequence accession numbers. The nucleotide sequence accession numbers for the proteins discussed in this article are as follows: GltP_{Bsu}, U15147; GltT_{Bs}, M86508 (43); GltT_{Bc}, M86509 (43); GltP_{Ec}, M84805 (44); DctA_{Rm}, J03683 (48), M26399 (10), and M26531 (16); DctA_{Rlp}, S38912 (45); DctA_{Rl}, Z11529 (31); ASCT1_{Hs}, L14595 (3); SATT_{Hs}, L19444 (36); GluA_{Hs}, U03504 (2); GLAST (GLUT-1), X63744 (38) and S59158 (39); GLT-1, X67857 (29); EAAC1, L12411 (20).

RESULTS

Glutamate transport. (i) Effects of ionophores on glutamate transport. Membrane vesicles of B. subtilis accumulate L-glutamate at a high rate and at high steady-state levels in the presence of K-asc-PMS (Fig. 1). L-Glutamate in/out ratios of approximately 700 are reached when a specific internal volume of 3 µl/mg of protein is assumed (22, 24). Nigericin, which dissipates the transmembrane pH gradient (electroneutral K^+/H^+ exchange), inhibited the uptake of L-glutamate partially. Valinomycin, which dissipates the membrane potential (K⁺ ionophore), decreased the uptake of L-glutamate even further (Fig. 1). Complete inhibition of glutamate uptake was observed in the presence of nigericin and valinomycin (Fig. 1). These findings, and the observation that NaCl (10 mM) did not affect transport (Fig. 1), suggest that L-glutamate is transported in B. subtilis by an electrogenic process in symport with protons. Similar results were obtained with membrane vesicles of E. coli BK9MDG/pGTU2000 in which the glutamate transport protein of B. subtilis was functionally expressed (data not shown).

(ii) Artificial gradients. Since L-glutamate is an anionic species at a physiological pH, the electrogenic nature of the transport process suggests that at least two cations are symported with the substrate. To specify the nature of the cotransported cations more precisely, experiments in which glutamate uptake



FIG. 1. Effects of ionophores and sodium ions on the uptake of L-glutamate in membrane vesicles of *B. subtilis*. Uptake of L-glutamate (1.9 μ M) was measured at 37°C in oxygen-saturated 50 mM potassium phosphate (pH 6.0) plus 5 mM MgSO₄. Uptake was performed in the absence (\bigcirc) or presence (\bullet) of the electron donor system K-asc-PMS either without ionophores or in the presence of nigericin (1 μ M) (\bigtriangledown), valinomycin (2 nmol/mg of protein) (\triangle), nigericin plus valinomycin (\Box), or 10 mM NaCl (\blacksquare).

was driven by artificial ion gradients were carried out. The Δp as well as its components $\Delta \Psi$ and ΔpH were able to drive L-glutamate uptake (Fig. 2). A sodium gradient, whether or not in addition to an artificially generated Δp , $\Delta \Psi$, or ΔpH , had no effect on glutamate uptake (data not shown). The sodium gradients were generated by varying the external sodium concentration among 0, 0.2, 0.5, 1, 5, 10, 50, and 100 mM; the initial internal concentrations were less than 10 μ M. These data strongly suggest that only protons are cotransported with glutamate.



FIG. 2. Uptake of L-glutamate in membrane vesicles of *B. subtilis* driven by artificially imposed ion gradients. Glutamate uptake was performed in the presence of a Δp (\bigcirc), Δp plus Δp Na (\bullet), ΔP (\bigcirc), $\Delta \Psi$ (\bigtriangledown), or sodium motive force (\Box) as described in Materials and Methods. Control experiments were performed by diluting the membrane vesicles 100-fold into the buffer in which the membranes were resuspended (\blacksquare).

TABLE 3. Inhibition of the initial uptake rate of L-glutamate in membrane vesicles of *B. subtilis* and *E. coli* BK9MDG/pGTU2000

T 1'1', <i>A</i>	% Inhibition			
Inhibitor	B. subtilis	BK9MDG/pGTU2000		
L-Glutamate	91	64		
D-Glutamate	27	19		
L-Glutamine	12	8		
L-Aspartate	84	86		
L-Asparagine	5	18		
β-Hydroxyaspartate	84	83		
Cysteic acid	80	64		
α-methyl-Glutamate	1	0		

^a Added in a 50-fold excess. Final L-[¹⁴C]glutamate concentration, 1.9 µM.

(iii) Substrate specificity. The substrates used to examine the substrate specificity of the L-glutamate transporter are listed in Table 3. The effects of a 50-fold excess of unlabeled substrates on the initial rate of L-glutamate uptake indicate that the transport system is specific for L-glutamate, L-aspartate, β -hydroxyaspartate, and cysteic acid but not for D-glutamate, α -methyl-glutamate, L-glutamine, or L-asparagine (Table 3).

Cloning of the glutamate transport gene of B. subtilis. The $gltP_{Bsu}$ gene was cloned as outlined in Materials and Methods. A Glu⁺ transformant, originating from the HindIII chromosomal digest, was grown in liquid M9G medium, and plasmid DNA was isolated. The isolated plasmid pGTU100 (pKK223-3 harboring a 2.1-kb HindIII insert) conferred upon retransformation a Glu⁺ phenotype on E. coli JC5412. Uptake of Lglutamate by whole cells (E. coli JC5412) harboring pGTU100 (GltP_{Bsu}) was severalfold higher than that in cells harboring pKK223-3 (data not shown). Membrane vesicles derived from strain BK9MDG/pGTU100 also showed significantly higher L-glutamate uptake than membrane vesicles derived from strain BK9MDG/pKK223-3 (data not shown). The kinetics of glutamate uptake in membrane vesicles of E. coli BK9MDG/ pGTU100 and BK9MDG/pKK223-3 as well as that of B. sub*tilis* 6GM was determined. The apparent K_m and V_{max} for glutamate uptake in membrane vesicles of *B. subtilis* 6GM were 9 μ M and 65 nmol \cdot min⁻¹ \cdot mg of protein⁻¹, respectively (Fig. 3). The data for *E. coli* BK9MDG/pGTU100 were 9 µM and 12.4 nmol \cdot min⁻¹ \cdot mg of protein⁻¹, respectively (Fig. 3, inset).

Nucleotide sequence and coding regions. From sequencing data of the 3' and 5' ends of the cloned DNA fragment, it became clear that the multiple cloning site of pKK223-3 had been partly duplicated, resulting in its presence at both ends of the cloned DNA fragment. Southern blot analysis revealed that the 1,820-bp *SphI-Hind*III fragment, together with a 275-bp fragment upstream of the *SphI* site of pGTU100, originates from *B. subtilis* 6GM. The sequencing strategy for this 2,095-bp fragment is presented in Fig. 4; the sequence is shown in Fig. 5 (the duplicated 27-bp vector sequence GCATGCAAGCTT GGCTGCAGGTCGACG upstream of the *B. subtilis* sequence is not included in this figure). Between positions 499 and 1741 an open reading frame of 1,242 bp was found. The deduced polypeptide contains 414 amino acid residues (molecular mass, 44,707 Da).

Amino acid composition and hydropathy. The amino acid composition of GltP_{Bsu} is typical of an integral membrane protein; it contains 68.9% nonpolar and 31.1% polar residues (5). Of the 414 residues, 31 (7.5%) are basic (His residues not taken into account) and 27 (6.5%) are acidic. The hydropathy



FIG. 3. Saturation kinetics of glutamate transport in membrane vesicles of *B. subtilis* 6GM and *E. coli* BK9MDG/pTU100 (inset). The kinetic parameters for transport, apparent K_m and V_{max} , were estimated from the Michaelis-Menten equation that was used to fit the experimental data. Uptakes were performed at 37°C by diluting membrane vesicles 100-fold into 50 mM potassium phosphate (pH 6.0)–5 mM MgSO₄–10 mM K-asc–100 μ M PMS. After a 1-min incubation, L-[¹⁴C] glutamate (0 to 100 μ M) was added, and initial rates of uptake were determined after 10 s. Samples were further handled as described in Materials and Methods.

profile of GltP_{Bsu} , calculated by the method of Eisenberg et al. (9), predicts a minimum of 10 membrane-spanning regions (data not shown).

DISCUSSION

The studies of uptake in *B. subtilis* membrane vesicles demonstrate that L-glutamate is transported electrogenically in symport with at least two protons. This is shown by the effect of ionophores on K-asc–PMS-energized transport as well as Lglutamate transport in the presence of artificially imposed ion gradients. The $\Delta\Psi$ and Δ pH alone can drive transport but not an inwardly directed Na⁺ gradient. Also, Δp Na does not stimulate Δp -, Δp H-, or $\Delta \Psi$ -driven uptake. Our results are in accordance with previous observations of L-glutamate transport in whole cells of *B. subtilis* (41). Thus, it appears that L-glutamate transport in *B. subtilis* is coupled to protons whereas sodium ions and protons are used in the related thermophiles *B. stearothermophilus* and *B. caldotenax* (7, 14).

Studies in membrane vesicles of B. subtilis and E. coli

BK9MDG/pGTU2000, in which GltP_{Bsu} was functionally expressed, revealed that the L-glutamate transporter is specific for the substrates L-glutamate and L-aspartate. L-Glutamate transport is inhibited by the inhibitors β -hydroxyaspartate and cysteic acid, which also inhibit the H⁺/glutamate symport protein (GltP) of *E. coli* (35). The inhibitor of the Na⁺/glutamate symporter (GltS) of *E. coli*, α -methyl-glutamate (35), did not affect GltP_{Bsu}.

GltP_{Bsu} is homologous to various carboxylate transport proteins (see below). On the basis of the similarities between GltP_{EcK12}, GltT_{Bs}, and GltT_{Bc}, the putative start codon is located at positions 499 to 501, which correspond to the leucine codon UUG. UUG is not commonly used as a translation initiation codon, but its use has been described before (11). A putative ribosome binding site is located upstream of the UUG codon, which shows extensive similarity to the 3' end of *B. subtilis* 16S rRNA (13, 28). The stop codon (positions 1741 to 1743) is immediately followed by an inverted repeat (ΔG° , -23.4 kcal [ca. -97.9 kJ]/mol, calculated by the method of Tinoco et al. [40]) and has features typical of a putative



FIG. 4. Sequencing strategy. Part of the vector sequence (open box), the cloned fragment (shaded box), and the position and direction of transcription of the putative gene upstream of $glrP_{Bsu}$ and $glrP_{Bsu}$ are shown. ORF, open reading frame. The regions sequenced are indicated below (arrows). Sp. *SphI*; S, *StuI*; Sa, *SalI*, B, *BalI*; H, *HindIII*; A, *AccI*; Hd, *HindIII*; P, *PstI*.

D Q V F S E K M M G E G F A I I P S E	G G
AAAGTCGTTGCACCTGCGGACGGCGAGATCGTCTCGATTTTTCCGACAAAACACGC K V V A P A D G E I V S I F P T K H A	CATC 120
GGCTTTATGAGCGCCGGCGCGCGCGCACCGAAATCCTGATTCATGTCGGCGATCGAT	CAAA 180 K
CTGAATGGGGAAGGCTTTGAAGCACATGTCACAAGCGGACAAGCCGTCAAACAAGG L N G E G F E A H V T S G Q A V K Q G	CGAA 240 E
CTGCTTCTCACCTTTGATCTCAATTACATCAAGCAGCATGCCGCTTCAGCCATAACCLL L L T F D L N Y I K Q H A A S A I T	ACCG 300 P
STOP GTTATTTTCACAAATACCTCTGAAGAAGATCTAAAGCACATTCAAATGAACAATGAAA V I F T N T S E E D L K H I Q M K	AAGT 360
TERMINATOR CCCCCCCTGCTGCGGGGGGGGCTTTTTCCGCCAACATGAAAGCGCTGTCAAAAATAAA <	ATAA 420
-35 -10 CTTGAAAAAAGGTG TTTGCA TTTGAATCACGAATGA TATGAA TATGCCTACATTCTM	ATCG 480
RBS START TTCT <u>AAAGGGGGATTCATTTGAAAAAATTAATCGCGTTTCAAATTTTAATCGCTTT</u>	GGCT 540
	A
V G A V I G H F F P D F G M A L R P V	GGA 600 G
GATGGATTTATCCGCCTGATTAAAATGATTGTTGTGCCGATTGTATTTTCTACCAT D G F I R L I K M I V V P I V F S T I	IGTC 660 V
ATTGGAGCCGCAGGAAGCGGAAGCATGAAAAAATGGGCAGTCTCGGCATCAAGAC I G A A G S G S M K K M G S L G I K T	JATC 720 I
ATTTGGTTCGAAGTGATTACAACGTTGGTATTAGGGCTTGGACTTTATTAGCGAAC I W F E V I T T L V L G L G L L L A N	IGTC 780 V
TTAAAACCAGGTGTCGGGCTTGACCTCTCCCATTTGGCAAAAAAAGATATTCATGA L K P G V G L D L S H L A K K D I H E	ACTT 840 L
TCCGGCTACACAGACAAAGTTGTTGATTTCAAGCAAATGATCCTGGATATTATCCC S G Y T D K V V D F K Q M I L D I I P	TACA 900 T
AACATTATTGATGTCATGGCCAGAAATGATTTGCTTGCCGTTATTTTCTTCGCCAT N I I D V M A R N D L L A V I F F A I	ITTA 960 L
TTTGGTGTCGCCGCAGCTGGTATCGGCAAAGCTTCTGAACCAGTAATGAAGTTTTT F G V A A A G I G K A S E P V M K F F	IGAA 1020 E
TCTACAGCTCAGATTATGTTCAAGCTCACGCAAATCGTCATGGTCACTGCTCCTATG S T A Q I M F K L T Q I V M V T A P I	CGGC 1080 G
GTGTTAGCCCTGATGGCTGCTTCTGTAGGCCAATATGGCATTGAACTCCTCCCCC V L A L M A A S V G Q Y G I E L L L P	FATG 1140 M
TTTAAGCTGGTTGGCACCGTATTCCTTGGCCTGTTCCTGATCCTCTTTGTCCTCTT. F K L V G T V F L G L F L I L F V I, F	FCCG 1200
CTTGTCGGTCTCATCTTTCGAGATTAGGAAGTATTGGAAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATATGGAAATGGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAGTGAATGGAATGGAATGGAATGGAAGTGAATGGAAATGGAATGGAAGTGAATGGAATGGAAGTGAATGGAAGTGATGGAAGTGAATGGAAGTGAAGTGATGGAAGTGAAGTGAATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	FCTG 1260
TTTTTAATTGCATTTCCACCACCACCACCACTCACCCTCCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCA	TAGA 1320
ATGAGAAAATACGGCTGCCCCAAACGAGTGGTATCATTTGTCGTCCCCCCCC	3TCA 1380
TTGAACTGTGACGGCTCCAGCTTATATTATCGGTTTCTTGTATCTTTCTCGCACAC	3GCC 1440
TTTCAAGTAGACATGACATTGTCCCAGCAGCTGCTCATGATGCTTGTGCTTGTGATC	A 3ACC 1500
F Q V D M T L S Q Q L L M M L V L V M AGTAAAGGCATTGCAGCTGTACCCTCAGGATCGCTTGTAGTTCTTCTGGCGACTGC	T CAAT 1560
S K G I A A V P S G S L V V L L A T A GCTGTAGGACTGCCGGGTGAAGGGGTTGCCATTATCGCGGGGTGTTGACCGCGGCTGAA	N BGAC 1620
A V G L P A E G V A I I A G V D R V M ATGGCGAGAACAGGCGTGAACGTACCGGGACATGCGATCGCCTGTATCGTGGTATC2	D AAAA 1680
M A R T G V N V P G H A I A C I V V S TGGGAAAAGGCCTTCCGCCAAACAGGCAAACAGCCAAACTGAAAGG	K CATA 1740
WEKAFRQKEWVSANSQTES STOD	I
TAGAAAAAAAGAACACCTCAATACGAGGGGTGTTCTTTTTTTATTCAGCAGCAGCGTG4	ATCT 1800
TCTGTTTCAATCGCTGCCAGTCTTGCGTTTACTTCTTCTGTCATATTATGCTCT	CTTC 1860
ACATACGGGTTTCTTGGGTTCGTGCCGGCATTCGTGGCTGCAGCTGCGCATATATT	TATA 1920
CTCATTTTCCGGTGTGCATATCATTTTTTTTTTGCAAGATGGATTTGGCGCAGTTC	ACAT 1980
AACGCTCACACGGTTCTCCTGTAAAGTAGTCCTTGCCACAATCACATGCTCGACAAC	CGGT 2040
TGACAGGCACGCTGATTCTTTCATCAAATACGTAGCACTGGCCGTCCCAAAGCTT	2095

FIG. 5. Nucleotide sequence of the 2,095-bp fragment comprising the *gltP*_{Bsu} gene of *B. subtilis* and flanking regions. The start and stop codons, a putative promoter (-35/-10), a possible ribosome binding site (RBS), and possible terminator sequences (--><--) are indicated. The amino acid sequence deduced from the DNA sequence of the *gltP*_{Bsu} gene and the putative open reading frame upstream of *gltP*_{Bsu} are shown below the DNA sequence.

rho-independent transcription terminator sequence (32). A transcription termination sequence is also found at positions 352 to 384, i.e., immediately upstream of $gltP_{\rm Bsu}$. Several promoter elements can be identified between this terminator sequence and the start codon. For none of the sequences is the expected distance of 16 to 18 bp observed (13, 28). A putative promoter with a 15-bp spacing between the -35 and -10 regions is indicated in Fig. 5. Upstream of the $gltP_{\rm Bsu}$ gene the 3' end of a putative open reading frame was found (Fig. 5). This region encodes 117 amino acid residues of a polypeptide which is homologous to IIA proteins of several phosphoenol-pyruvate-sugar-phosphotransferase systems as well as the IIA domain of the lactose transport protein (LacS) of *Streptococcus thermophilus* (30).

Sequence comparison of the H⁺/glutamate symport protein of B. subtilis and sequences in the EMBL data bank revealed a number of homologous proteins. All these proteins transport one or more of the structurally related compounds glutamate, aspartate, fumarate, malate, and/or succinate. The systems comprise sodium as well as proton-coupled transporters. Extensive similarity was found between $\mbox{GltP}_{\rm Bsu}$ and the thermophilic Na⁺/H⁺/glutamate symport proteins of *B. stearothermophilus* and *B. caldotenax* (43) and between GltP_{Bsu} and the mesophilic H⁺/glutamate symport protein of E. coli K-12 (44) (in each case the identity was approximately 44%). The similarity between GltP_{Bsu} and the C₄-dicarboxylate carriers of Rhizobium meliloti (10, 16, 48) and Rhizobium leguminosarum (31, 45) corresponds to approximately 34% identical residues. GltP_{Bsu} also is approximately 26% identical with a third group of proteins: the Homo sapiens Na+/alanine/serine/cysteine/ threonine transporter (ASCT1_{Hs} [adult motor brain]) (3), Na⁺/alanine/serine/cysteine transporter (SATT_{Hs} [hippocampus]) (36), excitatory glutamate transporters 1 to 3 (motor cortex) (2, 21, 37), and glutamate transporter (GLTRpa1 [brain and pancreas]) (27); the Rattus norvegicus Na⁺/glutamate/aspartate transporters GLAST (brain) (38) and GLUT-1 (brain) (39) and Na⁺/glutamate transporter GLT-1 (brain glial cells) (29); and the Oryctolagus cuniculus Na⁺/glutamate transporter (EAAC1 [rabbit small intestine]) (20). On the other hand, no significant similarity exists between ${\rm GltP}_{\rm Bsu}$ and the $Na^+/glutamate symport proteins of E. coli B (6) and K-12 (19)$ (data not shown).

Alignment of the homologous proteins reveals that identical and similar residues are distributed along the entire amino acid sequence (Fig. 6). Also, when the proton- and sodium-dependent symporters are compared, it appears that differences are not confined to one or a few regions, making it difficult to predict whether a given residue or protein segment determines the cation selectivity. Moreover, changes such as substituting a single amino acid may already alter the cation selectivity, as has been observed for the melibiose transport protein of Klebsiella pneumoniae (12). The number of membrane-spanning helices of the proteins indicated in Fig. 6 as predicted according to the method of Eisenberg et al. (9) ranges from 9 to 12. In the case of the C_4 -dicarboxylate carrier of *R. meliloti*, the secondarystructure predictions are substantiated by a limited number of PhoA and LacZ gene fusions, and the number of membranespanning helices was proposed to be 12 (17). In addition, indicative of similar secondary and tertiary structures are the gene fusions between $gltP_{\rm Ec}$ and $gltT_{\rm Bs}$ that result in fully functional glutamate transport proteins (41). On the basis of the similarity between the proteins, the hydropathy profiles of the individual sequences, and the topology rules proposed by Von Heijne (46), we propose that the transporters shown in Fig. 6 may have a similar secondary structure with 12 putative transmembrane-spanning α -helices. The locations of these putative

GltPBsu			01 · PP		
(4) ET 80	LКК	3	GitPBsu	KLTQIVMVTAPIGVLALMAASVGQYGIELLL - PMFKLVGTVFLGLFLIL	229
GICIDO	MKR	3	GIUTBC	YVTNQIMKFAPFGVFALIGVTVSKFGVESLIPLSKLVIVVYATMLFFI	237
GITTBs	MKR	3	GITTBS	YVTNQIMKFAPFGVFALIGVTVSKFGVESLIPLSKLVIVVYATMVFFI	237
GltPEc	MKNIK	5	GITPEC	KVTHMVMRYAPVGVFALIAVTVANFGFSSLWPLAKLVLLVHFAILFFA	245
DctARl	MIAAPLDAVAGSKGKKPFY	19	DctAR1	KLVAILMKAAPIGAFGAMAFTIGKYGVGSIANLAMLIGTFYITSLLFV	247
DctARm	MHPDWACHVEDI-MIIEHSAEVRGKTPLY	28	DctARm	RLVAILMKAAPIGAFGAMAFTIGKYGIASIANLAMLIGTFYLTSFLFV	256
DctARlp	MILIVENLAEVRGKTPHY	31	DetARlp	RLVAILMKAAPIGAFGAMAFTIGKYGVASIANLAMLIGTFYLTSFLFV	258
SATTHS	MEKSNETNGYLDSAQAGPARRPGAPGPRRDARRCAASCG	39	SAT THS	VLVSWIMWYVPVGIMFLVGSKIVEMKDIIVLVTSLGKYIFASILGHVIHG	306
ASCT1Hs	MEKSNETNGYLDSAQAGPAAGPGAPGTAAGRARRCARFLRR	41	ASCT1Hs	VLVSWIMWYVPVGIMFLVGSKIVEMKDIIVLVTSLGKYIFASILGHVING	309
GLT-1	MASTEGANNMPKQVEVRMHDSHLSSEEPKHRNLGMRMCD-KLGK	43	GLT-1	EVSDHDHVVFPAGIACLICGKIIAIKDLEVVARQLGMYMITVIVGLIIHG	328
GluBHs	MASTEGANNMPKQVEVRMPDSHLGSEEPKHRHLGLRLCD-KLGK	43	GluBHs	KLVIMIMWYSPLGIACLICGKIIAIKDLEVVARQLGMYMVTVIIGLIIHG	328
GLAST	MTKSNGEEPRMGSRMERFQQGVRKRTLLAKKKVQNITKEDVKSYL-FR	47	GLAST	RLVAVIMWYAPLGILFLIAGKILEMEDMGVIGGQLAMYTVTVIVGLLIHA	329
GluAHs	MTKSNGEEPKMGGRMERFQQGVRKRTLLAKKKVQNITKEDVKSYL-FR	47	GluAHs	RLVAVIMWYAPVGILFLIAGKIVEMEDMGVIGGOLAMYTVTVIVGLLTHA	329
EAAC1	MGKPARKGCDS-KRFLKN	17	EAAC1	KIVQIIMCYMPLGILFLIAGKIIEVEDWEIFR-KLGLYMVTVLSGLAIHS	297
GluCHs	MGKPARKGCPSWKRFLKN	18	GluCHs	KIVOLIMCYMPLGILFLIAGKIIEVEDWEIFR-KLGLYMATVLTGLATHS	297
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GITPBSU	-LIAFQILIADAVGAVIGHFFPDFGMALR-PVGDGFIRLIKM	4.5	GILPBSU	FVLFPLVGL-IFQIKYFEVLKMIWDLFLIAFSTTSTETILPQLMDRME-K	277
GITTBC	IGLAWQIFIGLILGIIVGAIFYGNPKVAAYLQ-PIGDIFLRLIKM	47	GITTBC	FAVLGGVAK-LFGINIFHIIKILKDELILAYSTASSETVLPRIMDKME-K	285
GITIBS	IGLAWQDF1GL1LG11VGA1FYGNPKVATYLQ-PIGD1FLRL1KM	47	GITTBS	FVVLGGVAK-LFGINIFHIIKILKDELILAYSTASSETVLPKIMEKME-N	285
GITPEC	FSLAWQILFAMVLGILLGSYLHYHSDSRDWLVVNLLS-PAGDIFIHLIKM	54	GITPEC	LVVLGIVAR-LCGLSVWILIRILKDELILAYSTASSESVLPRIIEKME-A	293
DetARI	SHLYVQVLVAIAAGILLGHFYPELGTQLK-PLGDAFIKLVKM	60	DCLARI	FIVLGAVAR-YNGFSIVALLRYIKEELLLVLGTSSSEAALPGLMNKME-K	295
DCTARM	RHLYVQVLAATAAGILLGHFYPDIGTELK-PLGDAFIRLVKM	69	DecARII	FLVLGAVAR-YNGFSILSLIRYIKEELLLVLGTSSSEAALPGLMNKME-K	304
DctARIp	RHLYVQVLAAIAVGILLGYFYPDVGSKMK-PLGDAFIMLVKM	72	DCTARID	FMVLGAVAR - YNGFSIVALIRYIKEELLLVLGTSSSEAALPGLMNKME - K	306
SATTHS	AKLVLLTVSGVLAGAGLGAALRGLSLSRTQVTYLAFP-GEMLLRIVRM	86	SATTHS	GIVLPLIYFVFTRKNPFRFLLGLLAPFATAFATCSSSATLPSMMKCIEEN	356
ASCT1Hs	QALVLLTVSGVLAGAGLGAALRGLSLSRTQVTYLAFP-GEMLLRMLRM	88	ASCTINS	GIVLPLIYFVFTRKNPFRFLLGLLAPFATAFATCSSSATLPSMMKCIEEN	359
GLT-1	NLLLSLTVFGVILGAVCGGLLR-LAAPIHPDVVMLIAFP-GDILMRMLKM	91	GLT-1	GIFLPLIYFVVTRKNPFSFFAGIFQAWITALGTASSAGTLPVTFRCLEDN	378
GluBHs	NLLLTLTVFGVILGAVCGGLLR-LASPIHPDVVMLIAFP-GDILMRMLKM	91	GIUBHS	GIFLPLIYFVVTRKNPFSLFAGIFQAWITALGTASSAGTLPVTFRCLEEN	378
GLAST	NAFVLLTVSAVIVGTILGFALR-PYKMSYREVK-YFSFP-GELLMRMLQM	94	GLAST	VIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSSSSATLPITFKCLEEN	379
GluAHs	NAFVLLTVTAVIVGTILGFTLR-PYRMSYREVK-YFSFP-GELLMRMLQM	94	GIUAHS	VIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSSSSATLPITFKCLEEN	379
EAAC1	NWLLLSTVVAVVLGIVIGVLVREYSNLSTLDKF-YFAFP-GEILMRMLKL	65	EAAC1	IVILPLIYFIVVRKNPFRFAMGMTQALLTALMISSSSATLPVTFRCAEEK	347
GluCHs	NWVLLSTVAAVVLGITTGVLVREHSNLSTLEKF-YFAFP-GEILMRMLKL	66	GluCHs	IVILPLIYFIVVRKNPFRFAMGMAQALLTALMISSSSATLPVTFRCAEEN	347
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GltPRov		00	GltPRen	VCCDKRIN/SEIN/DSCI.SI.NCDCCCI VI OVOCI BI ACA BOUDART COOT	205
Glimpa	TVTPTVFSTTVTGAAGS-GSMKKMGSH-GT-KTTTWFEVTTTDVDGDGHE	90	Clempa	FOODEN INCENTION POODEN AND AND AND AND AND AND AND AND AND AN	327
GLUBC	IVIPIVISSEVVGVASV-GDEKKEGKE-GG-KILIPEEIIIIAIVVGEE	94	GICIBC .	FGCFKATISFVIFIGISFNLDGSTBYQALAAIFIAQLYGIDMSVSQQISL	335
GITTBS	IVIPIVISSLVVGVASV-GDLKKLGKL-GG-KTTIYFEITTTTALVVGLG	94	GILIBS	FGCPRAITSFVIPTGYSFNLDGSTLYQALAAIFIAQLYGIDMPISQQISL	335
GITPEC	IVVPIVISTLVVGIAGV-GDAKQLGRI-GA-KTIIYFEV-FITVAIILGIT	101	GITPEC	YGAPVSITSFVVPTGYSFNLDGSTLYQSIAAIFIAQLYGIDLSIWQEIIL	343
DctARI	IIAPVIFLTVATGIAGM-SDLQKVGRVAGKAMLYFLTFSTLALIIGLI	107	DCtARI	AGCKRSVVGLVIPTGYSFNLDGTNIYMTLAALFIAQATGIHLSWGDQILL	345
DctARm	IIAPVIFLTVATGIAGM-TDLAKVGRVAGKAMIYFLAFSTLALVVGLV	116	DetARm	AGCKRSVVGLVIPTGYSFNLDGTNIYMTLAALFIAQATDTPLSYGDQILL	354
DctARlp	IIAPVIFLTVATGIAGM-TDLAKVGRVAGKAMIYFLAFSTLALLVGLV	119	DetARIp	AGCKRSVVGLVIPTGYSFNLDGTNIYMTLAALFIAQGTDTPISYGDQILL	356
SATTHS	IILPLVVCSLVSARLARCQLPRASGRHRVAYFGLTTLTASALAVA	131	SATTHS	NGVDKRISRFILPIGATVNMDGAAIFQCVAAVFIAQLNNVELNAGQIFTI	406
ASCT1Hs	IILPLVVCSLVSGAASLDASCLGRL-GGIR-VAYFGLTTLSASALAVA	134	ASCT1Hs	NGVDKRISRFILPIGATVNMDGAAIFQCVAAVFIAQLNNIELNAGQIFTI	409
GLT-1	LILPLIISSLITGLSGLDAKASGRL-GT-RAMVYYMSTTIIAAVLGVI	137	GLT-1	LGIDKRVTRFVLPVGATINMDGTALYEAVAAIFIAQMNGVILDGGQIVTV	428
GluBHs	LILPLIISSLITGLSGLDAKASGRL-GT-RAMVYYMSTTIIAAVLGVI	137	GluBHs	LGIDKRVTRFVLPVGATINMDGTALYEAVAAIFIAOMNGVVLDGGQIVTV	428
GLAST	LVLPLIISSLVTGMAALDSKASGKM-GM-RAVVYYMTTTIIAVVIGII	140	GLAST	NGVDKRITRFVLPVGATINMDGTALYEALAAIFIAQVNNFDLNFGQIITI	429
GluAHs	LVLPLIISSLVTGMAALDSKASGKM-GM-RAVVYYMTTTIIAVVIGII	140	GluAHs	NGVDKRVTRFVLPVGATINMDGTALYEALAAIFIAQVNNFELNFGQIITI	429
EAAC1	VILPLIVSSMITGVAALDSNVSGKI-GL-RAVLYYFCTTIIAVILGIV	111	EAAC1	NRVDKRITRFVLPVGATINMDGTALYEAVAAVFIAQLNDMDLSIGQIITI	397
GluCHs	IILPLIISSMITGVAALDSNVSGKI-GL-RAVVYYFCTTLIAVILGIV	112	GluCHs	NQVDKRITRFVLPVGATINMDGTALYEAVAAVFIAQLNDLDLGIGQIITI	397
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GltPBsu GltTBc GltTBs GltPEc DctARl DctARm DctARlp SATTHs ASCT1HS	><000000000000000000000000000000000000	135 143 143 150 153 162 165 179 182	GltPEsu GltTEc GltTEs GltPEc DctARl DctARm DctARm DctARlp SATTHS ASCTIHS	10	376 384 392 395 404 406 455 458
GltPBsu GltTBc GltTBs GltPEc DctARl DctARn DctARm DctARm ASCTIHS GLT-1	<pre>>cococococococococococococococococococ</pre>	135 143 143 150 153 162 165 179 182 179	GltPBsu GltTBc GltTBs GltPEc DctARl DctARm DctARhp SATTHs ASCTIHS GLT-1	10	376 384 392 395 404 455 458 477
GltPBsu GltTBc GltTBs GltPEc DctAR1 DctARm DctAR1p SATTHs ASCT1Hs GLT-1 GluBHs	<pre>>cococococococococococococococococococ</pre>	135 143 143 150 153 162 165 179 182 179 182	GltPBsu GltTBc GltTBs GltPEc DctARl DctARm DctARlp SATTHs ASCT1Hs GLT-1 GluBHs	10> <iiiiiii><11><coooooo MLVLVMTSKGIAAVPSGSLVVLLATANAV-GLPAEGVAIIAGVDRVMDMA LLVLWMTSKGIAGVPGSFVVLLATLGTV-GLPVEGLAFIAGIDRILDMA LLVLMVTSKGIAGVPGVSFVVLLATLGTV-GIPIEGLAFIAGIDRILDMA VLTLMVTSKGIAGVPGVSFVVLLATLGTV-GIPIEGLAFIAGIDRILDMA LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALLGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALLGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALLGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALLGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALLGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVPSVPVAGMALLGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVPSVPVAGMALLGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVPSVPVAGMALLGIDRFMSEC LJVTATASSVGAAGVPAFGVLITIAIILEAI-GLPTHDLPLILAVDWIVDRT SLTATLASVGAAGIPAGGLVTIAIILEAI-GLPTHDISLLVAVDWLDRM SLTATLASVGAASIPSAGLVTMLLILTAV-GLPTEDISLLVAVDWLLDRM</coooooo </iiiiiii>	376 384 392 395 404 406 455 458 477 477
GltPBsu GltTBc GltTBc DctARl DctARl DctARlp SATTHs ASCT1Hs GLT-1 GluBHs GLAST	<pre>>cococococococococococococococococococ</pre>	135 143 150 153 162 165 179 182 179 181	GltPBsu GltTBc GltTBs GltPEc DctARl DctARlp DctARlp SATTHS ASCT1HS GLT-1 GluBHS GLAST	10	376 384 392 395 404 455 458 477 477 478
GltPBsu GltTBc GltTBc DctARl DctARm DctARm DctARm SATTHS ASCTIHS GLT-1 GluBHS GLAST GluAHS	<pre>>cococococococococococococococococococ</pre>	135 143 150 153 162 165 179 182 179 181 181	GltPBsu GltTBc GltTBs GltPEc DctAR1 DctARm DctARm DctARlp SATTHS ASCT1Hs GLT-1 GluBHs GLAHS GLAHS	10> <iiiiiii><11><coocooco MLVLVMTSKGIAAVPSGSLVVLLATANAV-GLPAEGVAIIAGVDRVMDMA LLVLMVTSKGIAGVPGVSFVVLLATLGTV-GIPVEGLAFIAGIDRILDMA LLVLMVTSKGIAGVPGVSFVVLLATLGTV-GIPVEGLAFIAGIDRILDMA VLTLMVTSKGIAGVPGVSFVVLLATLGSV-GIPVEGLAFIAGIDRILDMA LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LLVAMLSSKGAAGVPAGVLITAIILEAI-GLPTHDLPLILAVDWIVDRT SUTATLASIGAAGVPAGGUVTMVILLTAV-GLPTDDISLLVAVDWLLDRM SUTATLASVGAASIFPAGUVTMVIVLTSV-GLPTDDITLIIAVDWFLDRL SITATAASIGAAGIPQAGUVTMVIVLTSV-GLPTDDITLIIAVDWFLDRL SITATAASIGAAGIPQAGUVTMVIVLTSV-GLPTDDITLIIAVDWFLDRL</coocooco </iiiiiii>	376 384 392 395 404 455 458 477 477 478 478
GltPBsu GltTBs GltTBs GltPEc DctAR1 DctAR1p SATTHS ASCTIHS GLT-1 GluBHS GLAST GluBHS ELAST GluAHS	><000000000000000000000000000000000000	135 143 143 150 153 162 165 179 182 179 182 179 181 181 153	GltPBsu GltTBc GltTBs GltPEc DctARM DctARM DctARMP SATTHS ASCTIHS GLT-1 GluBHS GLAST GluAHS EAAC1	10	376 384 392 395 404 455 458 477 477 478 478 478
GltPBsu GltTBc GltTBs GltPEc DctARl DctARlp SATTHs ASCTIHS GLT-1 GLUBHS GLAST GluAHS EAAC1 GluCHS	<pre>>cococococococococococococococococococ</pre>	135 143 150 153 165 179 182 179 182 179 181 181 153 154	GltPEsu GltTEc GltDEc DctARI DctARM DctARM DctARM GLT-1 GluBHS GLAST GLAST GLAST GluCHS		376 384 392 395 404 406 458 477 478 478 478 478 446
GltPBsu GltTBc GltTBc GltPBc DctARl DctARlp SATTHS ASCTIHS GLT-1 GluBHS GLAST GluAHS EAAC1 GluCHS	<pre>>cococococococococococococococococococ</pre>	135 143 150 153 165 179 182 179 182 179 181 181 153 154	GltPEsu GltTBc GltTBs GltPEc DctAR1 DctARm DctARp SATTHs ASCTIHS GLT-1 GluBHS GLAST GluAHS EAAC1 GluCHS	10	376 384 392 395 404 405 458 477 478 478 478 446 446
GltPBsu GltTBc GltTBc GltPEc DctARl DctARl DctARlp SATTHS ASCTIHS GLT-1 GluBHS GLAST GluAHS EAAC1 GluCHS	<pre>>cococococococococococococococococococ</pre>	135 143 153 150 162 165 179 182 179 179 181 153 154	GltPEsu GltTEc GltTEs GltPEc DctARl DctARh DctARh ASCTIHS GLT-1 GluBHS GLAST GluBHS GluCHS	10	376 384 392 392 404 4558 477 478 478 478 446
GltPBsu GltTBc GltTBs GltPEc DctARl DctARlp SATTHs ASCTIHS GLT-1 GluBHS GLAST GluAHS EAAC1 GluCHS	<pre>>cococococococococococococococococococ</pre>	135 143 150 153 162 165 179 182 179 181 181 153 154	GltPEsu GltTEc GltTEs GltPEc DctARI DctARIp SATTHS ASCTIHS GLT-1 GluBHS GLAST GluAHS EAAC1 GluCHS	<pre></pre>	376 384 392 395 404 455 455 455 455 477 478 477 478 446 446
GltPBsu GltTBc GltTBc GltPBc DctARl DctARlp SATTHS ASCTIHS GLT-1 GluBHS GLAST GluAHS EAAC1 GluCHS GltPBsu GltPBsu GltPBsu	<pre>>cococococococococococococococococococ</pre>	135 143 143 153 162 165 179 182 179 181 153 154	GltPEsu GltTEc GltTEs GltPEc DctAR1 DctARm DctARm DctARp SATTHS ASCTIHS GLT-1 GluBHS GLAST GluAHS EAAC1 GluCHS GltPEsu GltPEsu GltPEsu	<pre>10><iiiiiii><11><000000 MLVUVMTSKGIAAVPSGSLVVLLATANAV-GLPAEGVAIIAGVDRVMDMA LVUMVTSKGIAGVPGVSFVVLLATLGTV-GLPUEGLAFIAGIDRILDMA LVUMVTSKGIAGVPGVSFVVLLATLGTV-GIPLEGLAFIAGUDRILDMA VUTLWATSKGIAGVGVSFVVLLATLGSV-GIPLEGLAFIAGUDRILDMA LLVAMUSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LUVAMUSSKGAAGITGAGFITLAATLSVVPSVVAGMALILGIDRFMSEC LUVAMUSSKGAAGITGAGFITLAATLSVVPSVVAGMALILGIDRFMSEC LUVAMUSSKGAAGITGAGFITLAATLSVVPSVVAGMALILGIDRFMSEC LUVAMUSSKGAAGITGAGFITLAATLSVVPSVVAGMALILGIDRFMSEC LUTATASSVGAAGVPAGGVLITAIILEAI-GLPTHDLPLILAVDMVDRT LVTATASSVGAAGVPAGGVLTIAIILEAI-GLPTHDLPLILAVDMVDRT SUTATLASIGAAGIPSAGUVTMULLITAV-GLPTEDISLLVAVDWLDDRM SUTATLASIGAAGIPSAGUVTMVIVLTSV-GLPTEDISLLVAVDWLDDRM SITATAASIGAAGIPQAGLVTMVIVLTSV-GLPTEDITLIIAVDWLDDRF STATASASIGAAGVPAGULTWIVLTSV-GLPTEDITLIIAVDWLDDRF STATASSIGAAGVPAGULTWIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUTMVIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUTVVIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUTVVIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUTVVIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUTVVIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUTVVIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUTVVIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUTVVIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUTVVIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUSTVVIVLSAV-GLPAEDVTLIIAVDWLDDRF STATASSIGAAGVPAGUSTVVIVLSAV-GLPAEDVTLIAVDWLDDRF STATASSIGAAGVPAGUSTVVIVLSAV-GLPAEDVTLIAVDWLDDRF STATASSIGAAGVPAGUSTVVIVLSAV-GLPAEDVTLIAVDWLDDRF STATASSIGAAGVPAGUSTVVIVLSAV-GLPAEDVTLIAVDWLDDRF STATASSIGAAGVPAGUSTVVIVLSAV-GLPAEDVTLIAVDWLDRF STATASSIGAAGVPAGUSTVVIVLSAV-GLPAEDVTLIAVVUNATIANGUSTASIGAAGVPAGUSTVVIVLSAV-GLPAEDVTLIAVVUNATIANGUSTASIGAAGVPAGUSTVVIVLSAV-GLPAEDVTLIAVVUNATAGUSTASIGAAGVPAGUSTSI</iiiiiii></pre>	376 384 384 395 404 406 455 458 477 478 478 446 446 414
GltPBsu GltTBc GltTBs GltPEc DctARl DctARlp SATTHS ASCTIHS GLAST GluBHS GLAST GluCHS GltPBsu GltPBsu GltPBsu GltTBc GltTBs	<pre>>cococococococococococococococococococ</pre>	135 143 143 153 162 165 179 182 179 181 181 181 181 154 154	GltPEsu GltTBc GltTBc GltDEc DctARL DctARL DctARM DctARLS GLT-1 GluEHs GLAST GluAHS EAAC1 GluCHS GltPBsu GltPBsu GltPBsu GltPBsu	<pre>10</pre>	376 384 392 395 404 458 477 478 446 446 414 421
GltPBsu GltTBc GltTBc GltPEc DctAR1 DctARm DctARlp SATTHS ASCTIHS GLF-1 GluBHS GLF-1 GluAHS EAAC1 GluCHS GltPBsu GltTBc GltTBc GltTBc GltPBc	<pre>>cococococococococococococococococococ</pre>	135 143 153 162 165 179 179 179 181 181 153 154 142 150 157	GltPEsu GltTEc GltTEc DctARI DctARIp SATTHS ASCTIHS GLT-1 GluBHS GLAST GLAST GLAST GLAST GLAST GLUCHS GltPEsu GltTEc GltTES GltPEsc	<pre>10</pre>	376 384 392 395 404 405 458 477 477 478 476 446 414 421 421 421
GltPBsu GltTBc GltTBs GltPEc DctARl DctARlp SATTHS ASCTIHS GLWHS GLAST GluBHS GLAST GluCHS GltPBsu GltPBsu GltTBc GltTBc GltPBsu GltPBsu GltPBsu	<pre>>cococococccccccccccccccccccccccccccc</pre>	135 143 153 162 165 179 182 179 181 181 153 154 142 150 150 150 150	GltPEsu GltTBc GltTBc GltPEc DctARL DctARm DctARm CltARM GLT-1 GluBHs GLAST GluBHs GluCHs GluCHs GltPEsu GltPEsu GltPEsu GltPEsu GltPEc DctARL	<pre>10</pre>	376 384 392 395 404 455 455 455 4777 478 478 446 421 421 421 421 421
GltPBsu GltTBc GltTBs GltPBc DctARl DctARlp SATTHS ASCTIHS GLF-1 GluBHS GLAST GluBHS GluBHS GluCHS GltPBsu GltTBc GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu	<pre>>=cococococococococococococococococococ</pre>	135 143 143 153 162 179 189 179 181 153 154 142 150 157 160	GltPEsu GltTEc GltTEs GltPEc DctARI DctARI DctARIP SATTHS ASCTIHS GLAST GluAHS EAAC1 GluCHS CltPEsu GltTEc GltPEsu GltPEc DctARM	<pre>10</pre>	3764 38423954 4065454 455874778 47784784 446 41214 42214 4337443
GltPBsu GltTBs GltTBs GltPEc DctARl DctARlp SATTHS ASCT1HS GLT-1 GluCHS GluCHS GluCHS GluCHS GluCHS GltTBs GltTBs GltTBs GltTBs GltTBs GltTBs GltPBsu DctARlp DctARlp	<pre>>=cococococococococococococococococococ</pre>	135 143 153 162 165 179 182 179 181 153 154 142 150 150 157 160 160 169 171	GltPBsu GltTBs GltTBs GltPEc DctARl DctARm DctARlp SATTHS ASCT1HS GLT-1 GluEHS GluCHS GluCHS GluCHS GltTBs GltTBs GltTBs GltTBs GltTBs GltPBsu DctARlp DctARlp	<pre>10</pre>	376 384 392 395 404 455 458 477 478 477 478 446 446 414 421 421 421 421 421 421 423 444
GltPBsu GltTBc GltTBs GltPEc DctARl DctARlp SATTHS ASCTIHS GluBHS GluBHS GluBHS GluCHS GltPBsu GltPBsu GltPBsu GltPBsu GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs Gl	<pre>>cococococococococococococococococococ</pre>	135 143 153 165 179 182 179 181 153 154 142 150 150 157 160 157 169 171	GltPEsu GltTBc GltDEc DctARI DctARIp SATTHS ASCTIHS GLAST GluAHS EAAC1 GluCHS CltPBsu GltTBc GltPEsu GltPEsu GltPEsu GltPEsu SATTHS	<pre></pre>	376 384 392 395 458 456 477 478 446 477 478 446 446 414 421 421 421 437 453 456 502
GltPBsu GltTBc GltTBc GltPBc DctARl DctARlp SATTHS ASCTIHS GLT-1 GluBHS GLT-1 GluBHS GLAST GluAHS EAAC1 GluCHS GltPBsu GltTBc GltTBc GltTBc GltPBc DctARlp SATTHS ASCTIHS	<pre>>=cococococococococococococococococococ</pre>	135 143 1450 153 165 179 179 179 179 179 181 181 153 154 142 150 157 160 157 160 157 160 157	GltPEsu GltTBc GltTBc GltPEc DctARI DctARIp SATTHS ASCTIHS GLJ-1 GluBHS GLJ-1 GluBHS GLJ-1 GluBHS GLJ-1 GluBHS GLJ-1 GluCHS GltPEsu GltTBc GltTBc GltTBc GltDBsu GltPEc DctARI DctARIP SATTHS ASCTIHS	<pre>10><iiiiiii><11><000000 MLVUVMTSKGIAAVPSGSLVVLLATANAV-GLPAEGVAIIAGVDRVMDMA LVUMVTSKGIAGVPGVSFVVLLATLGTV-GIPVEGLAFIAGIDRILDMA LVUMVTSKGIAGVPGVSFVVLLATLGTV-GIPVEGLAFIAGIDRILDMA LLVLMVTSKGIAGVGVSFVVLLATLGSV-GIPVEGLAFIAGIDRILDMA LLVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVPSVPVAGMALILGIDRFMSEC LUTATASSVGAAGVPAGVLTIAIILEAI-GLPTHDLPLILAVDMVDRT LVTATASSVGAAGVPAGVLTIAIILEAI-GLPTHDLPLILAVDMVDRT SLTATLASIGAAGIPAGUTMVIVLTSV-GLPTEDISLLVAVDMLDRM SITATASIGAAGIPAGGUTMVIVLTSV-GLPTEDISLLVAVDMLDRM SITATASIGAAGVPAGLVTMVIVLTSV-GLPTEDITLIIAVDWLDRT SVTATASIGAAGVPAGLVTMVIVLSAV-GLPAEDVTLIIAVDMLDRF ************************************</iiiiiii></pre>	376 384 392 395 455 477 477 478 478 478 478 478 476 446 446 414 421 421 421 421 421 425 505
GltPBsu GltTBc GltTBs GltPEc DctARl DctARlp SATTHS ASCTIHS GLAST GluBHS GlAST GluCHS GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu	<pre>>cococococococococococococococococococ</pre>	135 143 150 153 165 179 181 181 153 154 142 150 150 150 150 169 171 208 211	GltPEsu GltTBc GltTBc GltDEc DctARI DctARIp SATTHs ASCT1Hs GLAST GluAHS EAAC1 GluCHS GltPBsu GltPBsu GltPBsu GltPEc DctARI DctARIP DctARIP SATTHS ASCT1HS GLTS	$\label{eq:second} 10 > < 1i iiii < < - + 11 > < < > < < < > < < > < < > < < > < < > < < > < < > < < < < < < < < < < < < < < < < < < < <$	3764 384 392 395 406 455 477 478 446 446 414 421 421 437 444 453 456 502 502 502
GltPBsu GltTBc GltTBc GltPEc DctAR1 DctARm DctARh GL7-1 GluBHs GL7-1 GluBHs GL7-1 GluBHs GluT-1 GltPBsu GltTBc GltTBs GltTBs GltTBs GltPBsu DctAR1 DctAR1 DctAR1 DctAR1 GltP-1 GltPBs	<pre>>cococococococococococococococococococ</pre>	135 143 1450 153 165 179 179 179 181 181 181 185 154 142 150 157 160 157 160 157 160 157 160 211 221 229	GltPEsu GltTEc GltTEs GltPEc DctARI DctARIp SATTHS ASCTIHS GLAST GLAST GLAST GLAST GLAST GLAST GLAST GLAST GLAST GLCHS GltPEsu GltTEs GltTEs GltTEs GltTEs GltPEsu DctARIp SATTHS ASCTIHS GLT-1 GLDES	<pre>10><iiiiiii><11><000000 MLVUVMTSKGIAAVPSGSLVVLLATANAV-GLPAGGVAIIAGVDRVUDMA LVUVMTSKGIAGVPGVSFVVLLATLGTV-GLPUSGLAFIAGIDRILDMA LVUTMVTSKGIAGVPGVSFVVLLATLGTV-GLPUSGLAFIAGIDRILDMA VUTLWVTSKGIAGVPGVSFVVLLATLGSV-GLPUSGLAFIAGUDRILDMA VUTLWVTSKGIAGVPGVSFVVLLATLGSV-GLPUSGLAFIAGUDRILDMA VUTLWATSKGIAGVPGVSFVVLLATLGSV-GLPUSGLAFIAGUDRILDMA VUTLWATSKGIAGVPGVSFVVLLATLGSV-GLPUSGLAFIAGUDRILDMA VUTLWATSKGIAGVPAGVSFVLLATLSVVFSVPVAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVFSVPVAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVFSVPVAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVFSVPVAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVFSVPVAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVFSVPVAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVFSVPUAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVFSVPUAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVFSVPUAGMALILGIDRFMSEC LUVAMLSSKGAAGITGAGFITLAATLSVVFSVPUAGMALILGIDRFMSEC LVTATASSVGAAGVPAGGUVTMILILEAT-GLPTBDISLLVAVDMILDDRM SUTATLASVGAAGVPAGULTWIVUTSV-GLPTDDITLIIAVDWFLDRL SITATASIGAAGPQAGLVTWVIVLTSV-GLPTDDITLIIAVDWFLDRL STTATASIGAAGVPQAGLVTWVIVLSAV-GLPAEDVTLIIAVDMLLDRF SITATSASIGAAGVPQAGLVTWVIVLSAV-GLPAEDVTLIIAVDMLLDRF SITATSASIGAAGVPQAGLVTWVIVLSAV-GLPAEDVTLIIAVDMLLDRF</iiiiiii></pre>	376 384 384 392 395 404 406 455 477 478 478 478 478 478 478 478 421 437 421 433 456 502 505 5277
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GltPBsu GltTBc GltTBs GltPEc DctARI DctARID SATTHS ASCTIHS GLAST GluAHS EAAC1 GluCHS GltPBsu GltPBsu GltTBc GltTBc GltTBc GltTBc GltTBc GltPBsu GltTBc GltPBsu GltPBsu GltPBsu GltPBsu GltAST GluAHS EAAC1 GluBs GLT-1 GluBs GLAST GluBs GluCHS	<pre>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>></pre>	135 143 143 150 153 165 179 182 179 181 181 153 154 142 150 157 160 157 169 171 208 211 208 211 202	GltPEsu GltTBc GltTBc GltDEc DctARI DctARIp SATTHs ASCT1Hs GLAST GluAHS EAAC1 GluCHS GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu G	<pre>10</pre>	3764 384 384 392 395 404 455 458 477 478 478 446 446 414 421 437 478 446 446 453 505 5277 528 496 496
GltPBsu GltTBc GltTBc GltPBc DctARl DctARlp SATTHS ASCTIHS GLJT-1 GluBHS GLJT-1 GluBHS GLJTBC GltTBC GltTBC GltTBC GltTBS GltPSC DctARl DctARlp SATTHS ASCTIHS GLAST GluAHS EAAC1 GluAHS GLAST GluCHS	<pre>>>cocococococococococococococococococo</pre>	135 143 143 150 152 162 179 182 179 181 153 154 142 150 150 150 150 150 150 150 150 150 1208 229 231 221 231 202	GltPEsu GltTEc GltTEs GltPEc DctARI DctARIp SATTHS ASCTIHS GLAT-1 GluBHS GLAST GluCHS GltPEsu GltTEs GltTEs GltTEs GltTEs GltPEc DctARI DctARIP SATTHS ASCTIHS GLAST GluAHS ELAST GluAHS ELAST GluCHS	<pre>10</pre>	376 384 384 392 395 404 455 458 477 477 477 444 421 421 421 421 421 455 502 502 527 527 527 528 496 496 496
GltPBsu GltTBc GltTBs GltPEc DctARl DctARlp SATTHS ASCTIHS GLAST GluBHS GLAST GluCHS GltPBsu GltPBsu GltPBsu GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltBs GltPBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs GltBs	<pre>>>cocococococococococococococococococo</pre>	135 143 143 150 153 165 179 181 181 153 154 142 150 150 150 150 150 169 171 208 211 208 212 201 201 202 181 189	GltPBsu GltTBc GltTBc GltPEc DctARI DctARM DctARM GLT-1 GluBHs GLAST GluCHs GltPBsu GltPBsu GltPBsu GltPEc DctARI DctARM DctARIP SATTHS ASCTIHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluCHS	<pre></pre>	3764 3844 3844 392395 4046 4555 4588 4777 4777 477 477 477 477 478 478 446 446 4211 437 453 456 505 5277 5288 496 496 496 496
GltPBsu GltTBc GltTBc GltPEc DctARl DctARlp SATTHS ASCTIHS GLF-1 GluBHS GLAST GluBHS GluBHS GluCHS GltPBsu GltTBc GltTBc GltPBc DctARl DctARR DctARR DctARR GltPBc GltBs GltBs GltBs GluBHS GluBHS GluCHS GluCHS GltPBsu GltTBc GluCHS	<pre>>cococococococococococococococococococ</pre>	135 143 143 150 152 162 179 182 179 181 153 154 142 150 150 150 150 150 150 150 150 150 1221 228 229 231 231 202 181 189	GltPEsu GltTEc GltTEc DctARI DctARIp SATTHS ASCTIHS GLAST GluAHS EAAC1 GluCHS CltPEsu GltTEc GltPEc DctARIp DctARM DctARIP SATTHS ASCTIHS GLTES GluCHS	<pre>10</pre>	376 384 384 392 395 404 456 455 458 477 477 477 477 444 421 421 421 453 456 502 527 527 528 528 528 496 496 496
GltPBsu GltTBc GltTBs GltPEc DctARl DctARlp SATTHs ASCTIHS GLAST GluBHS GLAST GluCHS GltPBsu GltPBsu GltTBc GltTBc GltTBc GltPBc DctARlp SATTHs ASCTIHS GLAST GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLT-1 GluBHS GLTBC	<pre>>>cocococococococococococococococococo</pre>	135 143 143 150 153 165 179 181 182 179 181 183 154 142 150 150 150 150 150 150 150 150 160 160 160 160 160 1208 229 231 201 202 231 201 202 189 189 189	GltPBsu GltTBc GltTBc GltPEc DctARL DctARM DctARM GLT-1 GluBHs GLAST GluCHS GltPBsu GltPBsu GltPBsu GltPEc DctARM DctARL DctARM DctARL GluCHS GltPEs GltPEc GltBs GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu	<pre></pre>	3764 3844 3844 3923 3925 4046 4558 4777 477 477 477 477 477 474 446 446 414 4377 444 453 5025 5055 5288 496 496 496 414 421
GltPBsu GltTBc GltTBc GltPEc DctARl DctARlp SATTHS ASCTIHS GluBHS GluBHS GluBHS GluCHS GltPBsu GltPBsu GltPBsu GltPEc DctARl DctARR DctARR GltPEc GluBHS GluBHS GluBHS GluBHS GluCHS GluBHS GluCHS GluBHS GluCHS GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu	<pre>>cococococococococococococococococococ</pre>	135 143 143 150 153 165 179 182 179 181 181 153 154 142 150 157 160 157 160 157 169 171 229 231 201 202 201 202 181 189 189	GltPEsu GltTBc GltTBc GltPEc DctARI DctARIp SATTHS ASCTIHS GLAST GluCHS GltPBsu GltPBsu GltTBc GltPEsu GltPEsu GltPEsu GltPEsu GltCHS GltPHS GltPEsu GltCHS GluCHS	<pre>10</pre>	376 384 384 392 395 404 455 458 477 477 477 478 446 446 421 421 421 421 453 456 505 527 528 496 496 496 496 414 421 421 424 421 424 421 424 421 424 421 424 424
GltPBsu GltTBs GltTBs GltPEc DctARl DctARlp SATTHS ASCTIHS GLT-1 GluBHS GluAHS ENAC1 GluCHS GltTBc GltTBc GltTBc GltTBs GltPBsu GltTBc GltTBs GltPBc DctARl DctARlp SATTHS ASCTIHS GLT-1 GluBHS GLT-1 GluBHS GltTBc GltTBc GltTBs GltTBc GltTBs GltTBc GltTBs GltTBc GltTBs GltTBc GltTBs GltTBc GltTBs GltTBc GltTBs GltTBc GltTBc GltTBc GltTBc GltTBs GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc GltTBc C C C C C C C C C C C C C C C C C C C	<pre>>>cocococococococococococococococococo</pre>	135 143 143 150 153 165 179 182 179 181 153 154 142 150 157 150 157 160 157 208 211 201 228 229 231 202 189 189 189 189 189 197 199 208	Glt PBsu Glt TBs Glt TBs Glt PEc DctARL DctARL DctARM DctARL Glt PBsu Glt PBsu Glt PBsu Glt PBsu Glt PBsu Glt PBs Glt PBs Glt	<pre></pre>	3764 3824 3824 4064 4558 4777 4788 4466 446 4421 4377 478 4466 446 421 437 4565 5055 5528 5288 5288 4966 496 496 421 421 421 421 421 421 421 421 421 421
GltPBsu GltTBc GltTBs GltPEc DctARI DctARI GltPEc GltPEc GltPEc GltAST GluASS GluASS GluASS GluASS GluCHS GltPBsu GltTBc GltPBsu GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs GltPBs	<pre>>>cocococococococococococococococococo</pre>	135 143 143 150 153 165 179 182 179 181 181 153 154 142 150 157 169 171 208 211 208 221 201 202 231 201 202 181 189 189 189 199 2210	GltPBsu GltTBc GltTBs GltDEc DctARI DctARIp SATTHs ASCT1Hs GLAST GluAHS EAAC1 GluCHS GltPBsu GltPBsu GltPEc DctARI DctARN DctARN GltPEc DctARI GluCHS GLTS GluCHS	<pre>10</pre>	3763 384 384 382 392 395 404 455 458 477 477 477 477 477 477 477 477 477 47
GltPBsu GltTBs GltTBs GltPEc DctAR1 DctAR1 DctARm GlTHS GLT-1 GluCHS GluCHS GluCHS GluCHS GluCHS GltTBs GltTBs GltTBs GltTBs GltTBs GltTBs GltTBs GltTBs GltTBs GltTBs GltTARn DctAR1 DctAR1 GluCHS GltTBs GltTBs GluCHS GltTBs GluCHS GltTBs GluCHS CLAR1 DctAR1 DctAR1 DctAR1 DctAR1 DctAR1 DctAR1 CluCHS GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu GltPBsu 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FIG. 6. Alignment of the deduced amino acid sequences of 15 members of the dicarboxylate transport protein family (see Discussion). The best fit was achieved by introducing gaps in order to maximize the identity score. The membrane-spanning fragments as predicted by the method of Eisenberg et al. (9) are shaded. $\langle iii \rangle$ and $\langle ooo \rangle$, internal and external loops, respectively. The proposed transmembrane segments 1 to 12 are indicated. The positions of the transmembrane segments as predicted by the DctA-PhoA and DctA-LacZ gene fusions in the DctA protein of *R. meliloti* (17) are underlined. * and \odot , identical and similar amino acid residues, respectively.

helices coincide with those predicted by the DctA-PhoA and DctA-LacZ gene fusions in the DctA protein of *R. meliloti* (17) (Fig. 6). The proposed transmembrane segment 4 is highly amphipathic in GltP_{Bsu}, GltT_{Bc}, GltT_{Bs}, SATT_{Hs}, ASCT1_{Hs}, GLT-1, GluA_{Hs}, EAAC1, and GluC_{Hs}.

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