ProtParam

ProtParam

A0A7P0T8P5_HUMAN (A0A7P0T8P5)

Amino acid transporter
Homo sapiens (Human)

The computation has been carried out on the complete sequence (**133** amino acids).

Warning: All computation results shown below do **not** take into account any annotated post-translational modification.
References and documentation are available.

Number of amino acids: 133

Molecular weight: 15368.47

Theoretical pI: 10.06

Amino acid composition: CSV format

Ala (A)	4	3.0%
Arg (R)	9	6.8%
Asn (N)	3	2.3%
Asp (D)	2	1.5%
Cys (C)	2	1.5%
Gln (Q)	4	3.0%
Glu (E)	7	5.3%
Gly (G)	8	6.0%
His (H)	0	0.0%
Ile (I)	7	5.3%
Leu (L)	17	12.8%
Lys (K)	11	8.3%
Met (M)	7	5.3%
Phe (F)	10	7.5%
Pro (P)	5	3.8%
Ser (S)	9	6.8%
Thr (T)	9	6.8%
Trp (W)	2	1.5%
Tyr (Y)	4	3.0%
Val (V)	13	9.8%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Total number of negatively charged residues (Asp + Glu): 9
Total number of positively charged residues (Arg + Lys): 20

Atomic composition:

Carbon	C	709
Hydrogen	H	1138
Nitrogen	N	180
Oxygen	O	181
Sulfur	S	9

Formula: $C_{709}H_{1138}N_{180}O_{181}S_9$
Total number of atoms: 2217

Extinction coefficients:

Extinction coefficients are in units of M^{-1} cm^{-1}, at 280 nm measured in water.

Ext. coefficient 17085
Abs 0.1% (=1 g/l) 1.112, assuming all pairs of Cys residues form cystines

Ext. coefficient 16960
Abs 0.1% (=1 g/l) 1.104, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is M (Met).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).
>20 hours (yeast, in vivo).
>10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 38.10
This classifies the protein as stable.

Aliphatic index: 101.73

Grand average of hydropathicity (GRAVY): 0.249