

ProtParam

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A0A7P0T9Z4_HUMAN (A0A7P0T9Z4)

Amino acid transporter (Fragment)
Homo sapiens (Human)

The computation has been carried out on the complete sequence (123 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: 123

Molecular weight: 12791.61

Theoretical pI: 4.52

Amino acid composition:

[CSV format](#)

Ala (A)	13	10.6%
Arg (R)	1	0.8%
Asn (N)	1	0.8%
Asp (D)	4	3.3%
Cys (C)	0	0.0%
Gln (Q)	3	2.4%
Glu (E)	2	1.6%
Gly (G)	13	10.6%
His (H)	1	0.8%
Ile (I)	16	13.0%
Leu (L)	17	13.8%
Lys (K)	2	1.6%
Met (M)	4	3.3%
Phe (F)	4	3.3%
Pro (P)	5	4.1%
Ser (S)	5	4.1%
Thr (T)	11	8.9%
Trp (W)	2	1.6%
Tyr (Y)	3	2.4%
Val (V)	15	12.2%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%

(B)	0	0.0%
(Z)	0	0.0%
(X)	1	0.8%

Total number of negatively charged residues (Asp + Glu): 6

Total number of positively charged residues (Arg + Lys): 3

Atom composition:

As there is at least one ambiguous position (B,Z or X) in the sequence considered, the atomic composition cannot be computed.

Extinction coefficients:

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

Ext. coefficient	15470
Abs 0.1% (=1 g/l)	1.209

Estimated half-life:

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

Due to the presence of an N-terminal ambiguity, the estimated half-life can not be computed.

Instability index:

The instability index (II) is computed to be 19.09
This classifies the protein as stable.

Aliphatic index: 150.57

Grand average of hydropathicity (GRAVY): 1.307



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