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ProtParam - Results

[A0A7P0Z4F7_HUMAN](https://www.uniprot.org/uniprotkb/A0A7P0Z4F7) (<https://www.uniprot.org/uniprotkb/A0A7P0Z4F7>) (A0A7P0Z4F7)

Description:

Solute carrier family 1 member 3 (Fragment)

Organism:

Homo sapiens (Human)

The computation has been carried out on the complete sequence (23 amino acids).

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

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Number of amino acids: 23

Molecular weight: 2683.39

Theoretical pI: 9.51

Amino acid composition:

[CSV format](#)

Ala (A)	2	8.7%
Arg (R)	3	13.0%
Asn (N)	1	4.3%
Asp (D)	2	8.7%
Cys (C)	0	0.0%
Gln (Q)	0	0.0%
Glu (E)	0	0.0%
Gly (G)	0	0.0%
His (H)	0	0.0%
Ile (I)	2	8.7%
Leu (L)	5	21.7%
Lys (K)	0	0.0%
Met (M)	1	4.3%
Phe (F)	0	0.0%
Pro (P)	0	0.0%
Ser (S)	1	4.3%
Thr (T)	3	13.0%
Trp (W)	1	4.3%
Tyr (Y)	0	0.0%
Val (V)	1	4.3%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%

(B)	0	0.0%
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(Z)	0	0.0%
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(X)	1	4.3%
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Total number of negatively charged residues (Asp + Glu): 2

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 5500

Abs 0.1% (=1 g/l) 2.050

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 50.35

This classifies the protein as unstable.

Aliphatic index: 140.00

Grand average of hydropathicity (GRAVY):0.430



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