Expasy

ProtParam (https://web.expasy.org/protparam)

ProtParam - Results

A0A7P0T8H5_HUMAN (https://www.uniprot.org/uniprotkb/A0A7P0T8H5) (A0A7P0T8H5)

Description:

Solute carrier family 1 member 3 (Fragment)

Organism:

Homo sapiens (Human)

The computation has been carried out on the complete sequence (25 amino acids).

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

[Documentation (/protparam/protparam-doc.html) / Reference (/protparam/protpar-ref.html)]

Number of amino acids: 25

Molecular weight: 2799.33
Theoretical pI: 6.73

Amino acid composition: [CSV format]

Ala (A)	1	4.0%
Arg (R)	0	0.0%
Asn (N)	2	8.0%
Asp (D)	0	0.0%
Cys (C)	2	8.0%
Gln (Q)	1	4.0%
Glu (E)	1	4.0%
Gly (G)	0	0.0%
His (H)	1	4.0%
Ile (I)	0	0.0%
Leu (L)	1	4.0%
Lys (K)	1	4.0%
Met (M)	1	4.0%
Phe (F)	2	8.0%
Pro (P)	2	8.0%
Ser (S)	6	24.0%
Thr (T)	1	4.0%
Trp (W)	1	4.0%
Tyr (Y)	0	0.0%
Val (V)	1	4.0%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	1	4.0%

Total number of negatively charged residues (Asp + Glu): 1
Total number of positively charged residues (Arg + Lys): 1

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   5625
Abs 0.1% (=1 g/l)   2.009, assuming all pairs of Cys residues form cystines

Ext. coefficient   5500
Abs 0.1% (=1 g/l)   1.965, assuming all Cys residues are reduced

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 112.41
This classifies the protein as unstable.

Aliphatic index: 31.20
Grand average of hydropathicity (GRAVY): -0.336

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