E**x**pasy

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

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ProtParam - Results

A0A7P0T8R2_HUMAN (https://www.uniprot.org/uniprotkb/A0A7P0T8R2) (A0A7P0T8R2)

Description:

Solute carrier family 1 member 3 (Fragment)

Organism:

Homo sapiens (Human)

The computation has been carried out on the complete sequence (47 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: 47

Molecular weight: 5264.02
Theoretical pI: 7.16

Amino acid composition: [CSV format]
```
Ala (A)   3       6.4%
Arg (R)   1       2.1%
Asn (N)   3       6.4%
Asp (D)   1       2.1%
Cys (C)   4       8.5%
Gln (Q)   2       4.3%
Glu (E)   1       2.1%
Gly (G)   5      10.6%
His (H)   6      12.8%
Ile (I)   1       2.1%
Leu (L)   1       2.1%
Lys (K)   1       2.1%
Met (M)   1       2.1%
Phe (F)   2       4.3%
Pro (P)   4       8.5%
Ser (S)   5      10.6%
Thr (T)   0       0.0%
Trp (W)   2       4.3%
Tyr (Y)   2       4.3%
Val (V)   1       2.1%
Pyl (O)   0       0.0%
Sec (U)   0       0.0%

 (B)      0       0.0%
 (Z)      0       0.0%
 (X)      1       2.1%
```

Total number of negatively charged residues (Asp + Glu): 2
Total number of positively charged residues (Arg + Lys): 2

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   14230
Abs 0.1% (=1 g/l)   2.703, assuming all pairs of Cys residues form cystines

Ext. coefficient   13980
Abs 0.1% (=1 g/l)   2.656, 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 49.75
This classifies the protein as unstable.

Aliphatic index: 29.15
Grand average of hydropathicity (GRAVY):−0.713

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