Expasy

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

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ProtParam - Results

A0A7P0TAF5_HUMAN (https://www.uniprot.org/uniprotkb/A0A7P0TAF5) (A0A7P0TAF5)

Description:

Solute carrier family 1 member 3 (Fragment)

Organism:

Homo sapiens (Human)

The computation has been carried out on the complete sequence (37 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: 37

Molecular weight: 4277.05
Theoretical pI: 11.10

Amino acid composition: `CSV format`
```
Ala (A)    1       2.7%
Arg (R)    4      10.8%
Asn (N)    2       5.4%
Asp (D)    0       0.0%
Cys (C)    0       0.0%
Gln (Q)    3       8.1%
Glu (E)    3       8.1%
Gly (G)    4      10.8%
His (H)    0       0.0%
Ile (I)    1       2.7%
Leu (L)    2       5.4%
Lys (K)    6      16.2%
Met (M)    3       8.1%
Phe (F)    1       2.7%
Pro (P)    1       2.7%
Ser (S)    1       2.7%
Thr (T)    3       8.1%
Trp (W)    0       0.0%
Tyr (Y)    0       0.0%
Val (V)    2       5.4%
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): 3
Total number of positively charged residues (Arg + Lys): 10

Atomic composition:
```
Carbon      C          181
Hydrogen    H          316
Nitrogen    N           60
Oxygen      O           53
Sulfur      S            3
```

Formula: $C_{181}H_{316}N_{60}O_{53}S_3$
Total number of atoms: 613

Extinction coefficients:
As there are no Trp, Tyr or Cys in the region considered, your protein
should not be visible by UV spectrophotometry.

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 52.61
This classifies the protein as unstable.

Aliphatic index: 50.00
Grand average of hydropathicity (GRAVY):-1.208

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