

[Home \(/protparam/\)](/protparam/)[Documentation \(/protparam/protparam-doc.html\)](/protparam/protparam-doc.html)[Reference \(/protparam/protpar-ref.html\)](/protparam/protpar-ref.html)[Contact \(/contact\)](/contact)

---

## ProtParam - Results

**[A0A7P0T9P1\\_HUMAN](https://www.uniprot.org/uniprotkb/A0A7P0T9P1) (<https://www.uniprot.org/uniprotkb/A0A7P0T9P1>) (A0A7P0T9P1)**

**Description:**

Solute carrier family 1 member 3 (Fragment)

**Organism:**

Homo sapiens (Human)

---

The computation has been carried out on the complete sequence (34 amino acids).

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

---

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

---

**Number of amino acids:** 34

**Molecular weight:** 4006.94

**Theoretical pI:** 8.25

**Amino acid composition:**

CSV format

Ala (A)	0	0.0%
Arg (R)	2	5.9%
Asn (N)	0	0.0%
Asp (D)	0	0.0%
Cys (C)	0	0.0%
Gln (Q)	1	2.9%
Glu (E)	2	5.9%
Gly (G)	1	2.9%
His (H)	0	0.0%
Ile (I)	2	5.9%
Leu (L)	7	20.6%
Lys (K)	1	2.9%
Met (M)	4	11.8%
Phe (F)	2	5.9%
Pro (P)	2	5.9%
Ser (S)	4	11.8%
Thr (T)	1	2.9%
Trp (W)	0	0.0%
Tyr (Y)	2	5.9%
Val (V)	3	8.8%
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):** 2

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

**Atomic composition:**

Carbon	C	186
Hydrogen	H	302
Nitrogen	N	42
Oxygen	O	47
Sulfur	S	4

**Formula:** C<sub>186</sub>H<sub>302</sub>N<sub>42</sub>O<sub>47</sub>S<sub>4</sub>

**Total number of atoms:** 581

**Extinction coefficients:**

This protein does not contain any Trp residues. Experience shows that this could result in more than 10% error in the computed extinction coefficient. Extinction coefficients are in units of M<sup>-1</sup> cm<sup>-1</sup>, at 280 nm measured in water.

Ext. coefficient 2980

Abs 0.1% (=1 g/l) 0.744

**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 36.46

This classifies the protein as stable.

**Aliphatic index:** 128.82

**Grand average of hydropathicity (GRAVY):**0.821



Expasy (<https://www.expasy.org>) is operated by the [SIB Swiss Institute of Bioinformatics \(https://sib.swiss\)](https://sib.swiss)

[Terms of Use \(https://www.expasy.org/terms-of-use\)](https://www.expasy.org/terms-of-use) | [Privacy policy \(https://www.sib.swiss/privacy-policy\)](https://www.sib.swiss/privacy-policy)