

[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

**[A0A7P0T7Q9\\_HUMAN](https://www.uniprot.org/uniprotkb/A0A7P0T7Q9) (<https://www.uniprot.org/uniprotkb/A0A7P0T7Q9>) (A0A7P0T7Q9)**

**Description:**

Solute carrier family 1 member 3

**Organism:**

Homo sapiens (Human)

---

The computation has been carried out on the complete sequence (71 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:** 71

**Molecular weight:** 8108.43

**Theoretical pI:** 9.90

**Amino acid composition:**

[CSV format](#)

Ala (A)	3	4.2%
Arg (R)	5	7.0%
Asn (N)	3	4.2%
Asp (D)	3	4.2%
Cys (C)	0	0.0%
Gln (Q)	4	5.6%
Glu (E)	5	7.0%
Gly (G)	4	5.6%
His (H)	1	1.4%
Ile (I)	2	2.8%
Leu (L)	7	9.9%
Lys (K)	8	11.3%
Met (M)	3	4.2%
Phe (F)	3	4.2%
Pro (P)	2	2.8%
Ser (S)	4	5.6%
Thr (T)	6	8.5%
Trp (W)	0	0.0%
Tyr (Y)	1	1.4%
Val (V)	7	9.9%
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):** 8

**Total number of positively charged residues (Arg + Lys):** 13

**Atomic composition:**

Carbon	C	356
Hydrogen	H	593
Nitrogen	N	103
Oxygen	O	106
Sulfur	S	3

**Formula:** C<sub>356</sub>H<sub>593</sub>N<sub>103</sub>O<sub>106</sub>S<sub>3</sub>

**Total number of atoms:** 1161

**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 1490

Abs 0.1% (=1 g/l) 0.184

**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 47.12

This classifies the protein as unstable.

**Aliphatic index:** 82.25

**Grand average of hydropathicity (GRAVY):**-0.541



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>)