

ProtParam

User-provided sequence:

102030405060

XYAPVGILFL IAGKIVEMED MGVIGGQLAM YTVTVIVGLL IHAVIVLPLL YFLVTRKNPW

708090100110120

VFIGGLLQAL ITALGTSSRD RLRTTTNVLG DSLGAGIVEH LSRHELKNRD VEMGNSVIEE

130140

NEMKKPYQLI AQDNETEKPI DSETKM

[References](#) and [documentation](#) are available.

Number of amino acids: 146

Molecular weight: 16089.03

Theoretical pI: 5.34

Amino acid composition:

CSV format

Ala (A)	8	5.5%
Arg (R)	6	4.1%
Asn (N)	6	4.1%
Asp (D)	6	4.1%
Cys (C)	0	0.0%
Gln (Q)	4	2.7%
Glu (E)	11	7.5%
Gly (G)	13	8.9%
His (H)	3	2.1%
Ile (I)	13	8.9%
Leu (L)	19	13.0%
Lys (K)	7	4.8%
Met (M)	6	4.1%
Phe (F)	3	2.1%
Pro (P)	5	3.4%
Ser (S)	6	4.1%
Thr (T)	10	6.8%
Trp (W)	1	0.7%
Tyr (Y)	4	2.7%
Val (V)	14	9.6%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	1	0.7%

Total number of negatively charged residues (Asp + Glu): 17
Total number of positively charged residues (Arg + Lys): 13

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	11460
Abs 0.1% (=1 g/l)	0.712

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 31.18
This classifies the protein as stable.

Aliphatic index: 118.77

Grand average of hydropathicity (GRAVY): 0.234



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