

ProtParam - Results

User-provided sequence:

```
      10      20      30      40      50      60
MIFGCFALFE LLASLVFGNY LVHIGAKFMF VAGMFVSGGV TILFGVLDRV PDGPVFIAMC

      70      80      90     100     110     120
FLVRVMDAVS FAAAMTASSS ILAKAFPNNV ATVLGSLETF SGLGLILGPP VGGFLYQSFG

     130     140     150     160     170     180
YEVPFIVLGC VLLLMVPLNM YILPNYESDP GEHSFWKLIA LPKVGLIAFV INSLSSCFGF

     190     200     210     220     230     240
LDPTLSLFVL EKFNLPAGYV GLVFLGMALS YAISSPLFGL LSDKRPLRK WLLVFGNLIT

     250     260     270     280     290     300
AGCYMLLGPV PILHIKSLQW LLVLILVVSF LSAGMSIIPT FPEILSCAHE NGFEEGLSTL

     310     320     330     340     350     360
GLVSGLFSAM WSIGAFMGPT LGGFLYEKIG FEWAAAIQGL WALISGLAMG LFYLLLEYSRR

     370     380
KRSKSNILS TEEERTTLLP NET
```

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

Number of amino acids: 383

Theoretical pI: 5.62

Molecular weight: 41388.24

Amino acid composition:

[CSV format](#)

Ala (A)	28	7.3%
Arg (R)	8	2.1%
Asn (N)	11	2.9%
Asp (D)	6	1.6%
Cys (C)	6	1.6%
Gln (Q)	4	1.0%
Glu (E)	17	4.4%
Gly (G)	40	10.4%
His (H)	4	1.0%
Ile (I)	24	6.3%
Leu (L)	64	16.7%
Lys (K)	11	2.9%
Met (M)	14	3.7%
Phe (F)	32	8.4%
Pro (P)	21	5.5%
Ser (S)	33	8.6%
Thr (T)	13	3.4%
Trp (W)	6	1.6%
Tyr (Y)	11	2.9%
Val (V)	30	7.8%
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): 23

Total number of positively charged residues (Arg + Lys): 19

Total number of positively charged residues (Arg + Lys): 19

Atomic composition:

Carbon	C	1950
Hydrogen	H	3009
Nitrogen	N	447
Oxygen	O	502
Sulfur	S	20

Formula: C₁₉₅₀H₃₀₀₉N₄₄₇O₅₀₂S₂₀

Total number of atoms: 5928

Extinction coefficients:

Extinction coefficients are in units of M⁻¹ cm⁻¹, at 280 nm measured in water.

Ext. coefficient 49765

Abs 0.1% (=1 g/l) 1.202, assuming all pairs of Cys residues form cystines

Ext. coefficient 49390

Abs 0.1% (=1 g/l) 1.193, assuming all Cys residues are reduced

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 44.50

This classifies the protein as unstable.

Aliphatic index: 119.63

Grand average of hydropathicity (GRAVY):0.860



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