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ProtParam - Results

User-provided sequence:

10 20 30 40 50 60
MMCYSILGPF FPKEAEKKGA SNTIIGMIFG CFALFELLAS LVFGNYLVHI GAKFMFVAGM

70 80 90 100 110 120
FVSGGVVTILF GVLDRVPDGP VFIAMCFLVR VMDAVSFAAA MTASSSILAK AFPNNVATVL

130 140 150 160 170 180
GSLETFSGLG LILGPPVGGF LYQSFGYEVP FIVLGCVLL MVPLNMYILP NYESDPGEHS

190 200 210 220 230 240
FWKLIALPKV GLIAFVINSL SSCFGFLDPT LSLFVLEKFN LPAGYVGLVF LGMALSYAIS

250 260 270 280 290 300
SPLFGLLSDK RPPLRKWLLV FGNLITAGCY MLLGPVPILH IKSQWLWLLV ILVVSGLSAG

310 320 330 340 350 360
MSIIPTFPEI LSCAHENGFE EGLSTLGLVS GLFSAMWSIG AFMGPTLGGF LYEKIGFEWA

370 380 390 400
AAIQGLWALI SGLAMGLFYL LEYSRRKRSK SQNILSTEEE RTTLLPNET

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

Number of amino acids: 409

Theoretical pI: 5.86

Molecular weight: 44203.59

Amino acid composition: [CSV format](#)

Ala (A)	30	7.3%
Arg (R)	8	2.0%
Asn (N)	12	2.9%
Asp (D)	6	1.5%
Cys (C)	7	1.7%
Gln (Q)	4	1.0%
Glu (E)	19	4.6%
Gly (G)	43	10.5%
His (H)	4	1.0%
Ile (I)	27	6.6%
Leu (L)	65	15.9%
Lys (K)	14	3.4%
Met (M)	16	3.9%
Phe (F)	34	8.3%
Pro (P)	23	5.6%
Ser (S)	35	8.6%
Thr (T)	14	3.4%
Trp (W)	6	1.5%
Tyr (Y)	12	2.9%
Val (V)	30	7.3%
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): 25

Total number of positively charged residues (Arg + Lys): 22

Atomic composition:

Carbon	C	2078
Hydrogen	H	3209
Nitrogen	N	477
Oxygen	O	537
Sulfur	S	23

Formula: C₂₀₇₈H₃₂₀₉N₄₇₇O₅₃₇S₂₃

Total number of atoms: 6324

Extinction coefficients:

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

Ext. coefficient 51255

Abs 0.1% (=1 g/l) 1.160, assuming all pairs of Cys residues form cystines

Ext. coefficient 50880

Abs 0.1% (=1 g/l) 1.151, 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 43.03

This classifies the protein as unstable.

Aliphatic index: 116.33

Grand average of hydropathicity (GRAVY): 0.811

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