ProtParam

ProtParam

User-provided sequence:

```
3<u>0</u>
                                                              5<u>0</u>
                      20
                                                 4<u>0</u>
XIGFFIAFGI AMGKMGDQAK LMVDFFNILN EIVMKLVIMI MWYSPLGIAC LICGKIIAIK
                      80
                                    90
                                                100
                                                             110
DLEVVARQLG MYMVTVIIGL IIHGGIFLPL IYFVVTRKNP FSFFAGIFQA WITALGTASS
                     14<u>0</u>
                                   15<u>0</u>
                                                16<u>0</u>
                                                             17<u>0</u>
AGTLPVTFRC LEENLGIDKR VTRFVLPVGA TINMDGTALY EAVAAIFIAQ MNGVVLDGGQ
                     20<u>0</u>
                                   21<u>0</u>
                                                22<u>0</u>
                                                             23<u>0</u>
IVTVSLTATL ASVGAASIPS AGLVTMLLIL TAVGLPTEDI SLLVAVDWLL DRMRTSVNVV
                                  270
                                                280
                     26<u>0</u>
                                                             290
GDSFGAGIVY HLSKSELDTI DSQHRVHEDI EMTKTQSIYD DMKNHRESNS NQCVYAAHNS
                     320
                                   330
VIVDECKVTL AANGKSADCS VEEEPWKREK
```

References and documentation are available.

```
Number of amino acids: 330

Molecular weight: 35816.19
```

Theoretical pI: 5.27

```
Amino acid composition: CSV format
Ala (A) 30
                 9.1%
Arg (R) 10
                 3.0%
Asn (N) 12
                 3.6%
Asp (D) 17
                 5.2%
Cys (C)
                 1.8%
        6
Gln (Q)
        8
                 2.4%
Glu (E)
        15
                 4.5%
Gly (G)
                 7.9%
        26
His (H)
                 1.8%
        6
Ile (I)
        33
                10.0%
                9.4%
Leu (L) 31
                 4.2%
        14
Lys (K)
                 4.2%
Met (M)
        14
Phe (F)
        15
                 4.5%
Pro (P)
        8
                 2.4%
Ser (S)
        20
                 6.1%
Thr (T)
        20
                 6.1%
Trp (W)
         4
                 1.2%
         7
Tyr (Y)
                 2.1%
Val (V)
        33
                10.0%
Pyl (0)
         0
                 0.0%
Sec (U)
                 0.0%
                 0.0%
(B)
      0
 (Z)
      0
                 0.0%
(X)
                 0.3%
```

```
Total number of negatively charged residues (Asp + Glu): 32
Total number of positively charged residues (Arg + Lys): 24
```

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 $\,\mathrm{M}^{-1}$ cm $^{-1}$, at 280 nm measured in water.

Ext. coefficient 32805

Abs 0.1% (=1 g/l) 0.916, assuming all pairs of Cys residues form cystines

Ext. coefficient 32430

Abs 0.1% (=1 g/l) 0.905, assuming all Cys residues are reduced

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 $28.85\,$ This classifies the protein as stable.

Aliphatic index: 113.73

Grand average of hydropathicity (GRAVY): 0.533



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