ProtParam

ProtParam

User-provided sequence:

```
        10         20         30         40         50         60
MTKSNGEEPK MGGRMERFQQ GVRKRTLLAK KKVQNITKED VKSYLFRNAF VLLTVTAVIV

        70         80         90        100        110        120
GTILGFTLRP YRMSYREVKY FSFPGELLMR MLQMLVLPLI ISSLVTGMAA LDSKASGKMG

       130        140        150        160        170        180
MRAVVYYMTT TIIAVVIGII IVIIIHPGKG TKENMHREGK IVRVTAADAF LDLIRNMFPP

       190        200        210        220        230        240
NLVEACFKQF KTNYEKRSFK VPIQANETLV GAVINNVSEA METLTRITEE LVPVPGSVNG

       250        260        270        280        290        300
VNALGLVVFS MCFGFVIGNM KEQGQALREF FDSLNEAIMR LVAVIMWYAP VGILFLIAGK

       310        320        330        340        350        360
IVEMEDMGVI GGQLAMYTVT VIVGLLIHAV IVLPLLYFLV TRKNPWVFIG GLLQALITAL

       370        380        390        400        410        420
GTSSSSATLP ITFKCLEENN GVDKRVTRFV LPVGATINMD GTALYEALAA IFIAQVNNFE

       430        440        450        460        470        480
LNFGQIITIS ITATAASIGA AGIPQAGLVT MVIVLTSVGL PTDDITLIIA VDWFLDRLRT

       490        500        510        520        530        540
TTNVLGDSLG AGIVEHLSRH ELKNRDVEMG NSVIEENEMK KPYQLIAQDN ETEKPIDSET


KM
```

References and documentation are available.

Number of amino acids: 542

Molecular weight: 59572.31

Theoretical pI: 8.52

Amino acid composition: CSV format

```
Ala (A)  41       7.6%
Arg (R)  24       4.4%
Asn (N)  26       4.8%
Asp (D)  16       3.0%
Cys (C)   3       0.6%
Gln (Q)  15       2.8%
Glu (E)  33       6.1%
Gly (G)  42       7.7%
His (H)   5       0.9%
Ile (I)  49       9.0%
Leu (L)  56      10.3%
Lys (K)  28       5.2%
Met (M)  26       4.8%
Phe (F)  25       4.6%
Pro (P)  19       3.5%
Ser (S)  24       4.4%
Thr (T)  40       7.4%
Trp (W)   3       0.6%
Tyr (Y)  12       2.2%
Val (V)  55      10.1%
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): 49
Total number of positively charged residues (Arg + Lys): 52

Atomic composition:

```
Carbon      C         2694
Hydrogen    H         4374
Nitrogen    N          696
Oxygen      O          758
Sulfur      S           29
```

Formula: $C_{2694}H_{4374}N_{696}O_{758}S_{29}$
Total number of atoms: 8551

Extinction coefficients:

Extinction coefficients are in units of M^{-1} cm^{-1}, at 280 nm measured in water.

```
Ext. coefficient    34505
Abs 0.1% (=1 g/l)   0.579, assuming all pairs of Cys residues form cystines


Ext. coefficient    34380
Abs 0.1% (=1 g/l)   0.577, 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 27.78
This classifies the protein as stable.
```

Aliphatic index: 112.55

Grand average of hydropathicity (GRAVY): 0.377