1APH

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A.E.M: 8412

Fasta sequence

>sp|P01317|INS_BOVIN Insulin OS=Bos taurus GN=INS PE=1 SV=2

MALWTRLRPLLALLALWPPPPARAFVNQHLCGSHLVEALYLVCGERGFFYTPKARREVEG
PQVGALELAGGPGAGGLEGPPQKRGIVEQCCASVCSLYQLENYCN

ProtParam

User-provided sequence:

```
        10         20         30         40         50         60
MALWTRLRPL LALLALWPPP PARAFVNQHL CGSHLVEALY LVCGERGFFY TPKARREVEG

        70         80         90        100
PQVGALELAG GPGAGGLEGP PQKRGIVEQC CASVCSLYQL ENYCN
```

References and documentation are available.

```
Number of amino acids: 105

Molecular weight: 11393.2

Theoretical pI: 7.60
```

CSV format

```
Amino acid composition:
Ala (A)  11     10.5%
Arg (R)   7      6.7%
Asn (N)   3      2.9%
Asp (D)   0      0.0%
Cys (C)   6      5.7%
Gln (Q)   5      4.8%
Glu (E)   8      7.6%
Gly (G)  12     11.4%
His (H)   2      1.9%
Ile (I)   1      1.0%
Leu (L)  16     15.2%
Lys (K)   2      1.9%
Met (M)   1      1.0%
Phe (F)   3      2.9%
Pro (P)  10      9.5%
```

```
Ser (S)   3       2.9%
Thr (T)   2       1.9%
Trp (W)   2       1.9%
Tyr (Y)   4       3.8%
Val (V)   7       6.7%
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): 8
Total number of positively charged residues (Arg + Lys): 9

Atomic composition:

```
Carbon      C         512
Hydrogen    H         800
Nitrogen    N         142
Oxygen      O         139
Sulfur      S           7
```

Formula: $C_{512}H_{800}N_{142}O_{139}S_{7}$
Total number of atoms: 1600

Extinction coefficients:

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

```
Ext. coefficient    17335
Abs 0.1% (=1 g/l)   1.522, assuming all pairs of Cys residues form
cystines


Ext. coefficient    16960
Abs 0.1% (=1 g/l)   1.489, 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 37.18
This classifies the protein as stable.

Aliphatic index: 92.95

Grand average of hydropathicity (GRAVY): 0.062

ProDom

database: multiple alignments

Program: ncbi-blastp

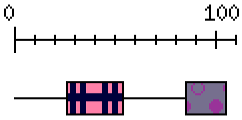
Matrix: BLOSUM62

Expect: 0.01

Filter: seg

Graphical results and forms to other applications

The following is the graphical representation of the HSP found by BLAST.
Please note that HSPs are sorted from highest to lowest scores, so that lower scoring HSPs may be hidden.



Align subsequence with ProDom domains, using Multalin

Domain ID	BEGIN	END	
PD000491	26	53	Submit
PDB892H1	33	53	Submit
PDB2H9G3	85	104	Submit

Domain 3D modelling using Swiss-Model

Domain ID	BEGIN	END	
PD000491	26	53	Submit
PDB892H1	33	53	Submit

PDB2H9G3	85	104	Submit

Domain 3D modelling using Geno3D

Domain ID	BEGIN	END	
PD000491	26	53	Submit
PDB892H1	33	53	Submit
PDB2H9G3	85	104	Submit

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HSP Results

Warning: Original output has been filtered to yield non-redundant similarities

```
blastp 2.2.26 [Sep-21-2011]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
_quot;Gapped BLAST and PSI-BLAST: a new generation of protein database
search
programs_quot;,  Nucleic Acids Res. 25:3389-3402.

Query: unkwown
         (105 letters)

Database: prodom2010.1 multiple alignments
        45,292,438 sequences; 2,147,483,647 total letters



ProDom domains producing High-scoring Segment Pairs:

  Position  ProDom domain                                       Score E value

     26-53  #PD000491                                             142 2e-10
     33-53  #PDB892H1                                             107 2e-05
    85-104  #PDB2H9G3                                             100 0.0002


>PD000491 (Closest domain: INS_TRASC 2-29)
Number of domains in family: 272
Commentary (automatic):
GROWTH SECRETED FACTOR SUBNAME: FULL=INSULIN-LIKE RECNAME: FULL=INSULIN
METABOLISM CONTAINS: CHAIN
Length = 28
```

```
Score = 142  (59.3 bits), Expect = 2e-10
Identities = 26/28 (92%), Positives = 27/28 (96%)

 Query:     26 VNQHLCGSHLVEALYLVCGERGFFYTPK 53
                NQHLCGSHLVEALYLVCGERGFFY+PK
 Sbjct:      2 ANQHLCGSHLVEALYLVCGERGFFYSPK 29
```

>**PDB892H1** (Closest domain: Q7LZN0_POLSP 9-29)

```
Number of domains in family: 52
Commentary (automatic):
RECNAME: FULL=INSULIN METABOLISM CHAIN CONTAINS: CARBOHYDRATE DISULFIDE BOND
GLUCOSE A
Length = 21
Score = 107  (45.8 bits), Expect = 2e-05
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 1/21 (4%)

 Query:     33 SHLVEALYLVCGERGFFYTPK 53
               SHLVEALYLVCGERGFFYTP
 Sbjct:      9 SHLVEALYLVCGERGFFYTPN 29
```

>**PDB2H9G3** (Closest domain: INS_CAMDR 31-50)

```
Number of domains in family: 123
Commentary (automatic):
FULL=INSULIN RECNAME: METABOLISM CHAIN CONTAINS: CARBOHYDRATE DISULFIDE BOND
GLUCOSE HORMONE
Length = 20
Score = 100  (43.1 bits), Expect = 0.0002
Identities = 20/20 (100%), Positives = 20/20 (100%), Gaps = 1/20 (5%)

 Query:     85 GIVEQCCASVCSLYQLENYC 104
               GIVEQCCASVCSLYQLENYC
 Sbjct:     31 GIVEQCCASVCSLYQLENYC 50
```

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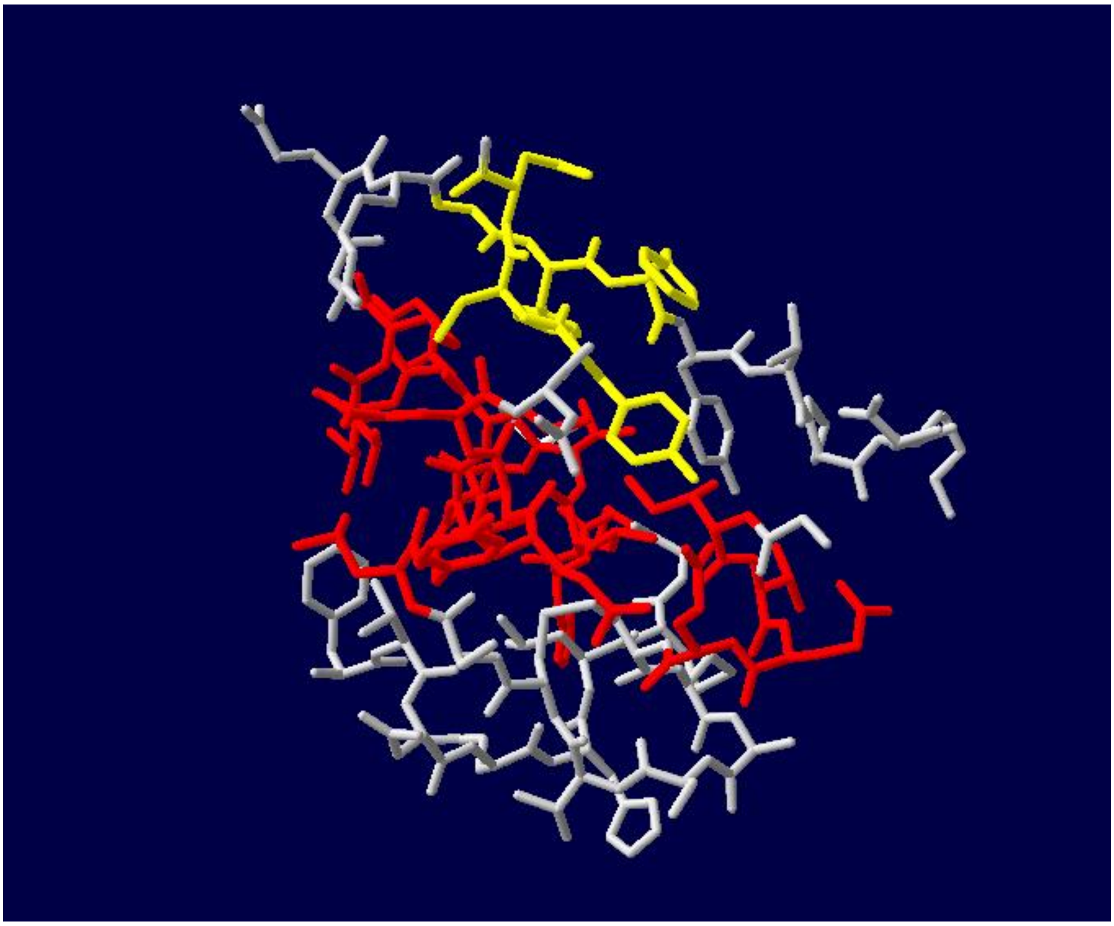
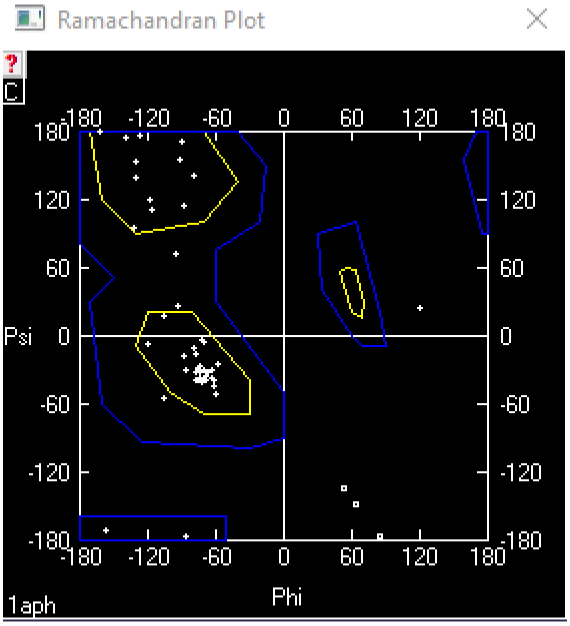
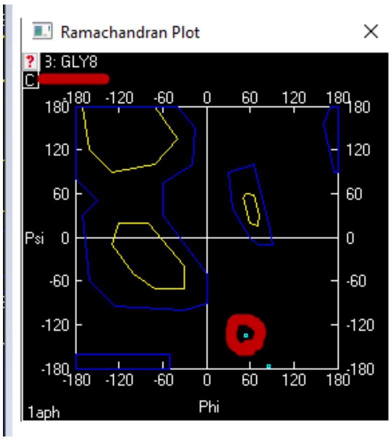
(render by 3D/colored by secondary structure)

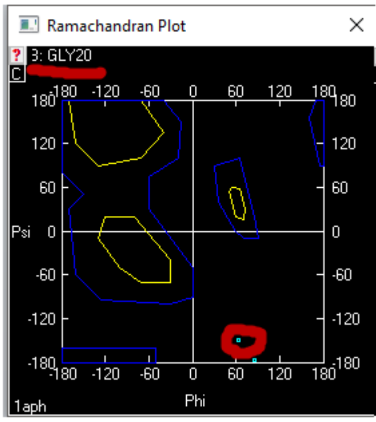


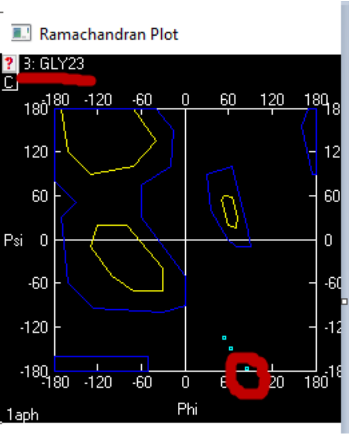
Ramachandran Plot



Αμινοξέα που εμφανίζονται εκτός των επιτρεπτών στερεοτακτικών δομών : GLY8, GLY20, GLY23







Τα αμινοξέα της γλυκίνης στο πρωτεϊνικό μόριο της 1APH