1H6M

ΜΟΥΝΤΑΝΕΑ ΟΛΓΑ

Α.Ε.Μ: 8344

FASTA sequence

```
>sp|P00698|LYSC_CHICK Lysozyme C OS=Gallus gallus GN=LYZ PE=1 SV=1
MRSLLILVLCFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQA
TNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDG
NGMNAWVAWRNRCKGTDVQAWIRGCRL
```

ProtParam

User-provided sequence:

10 20 30 40 50 60

MRSLLILVLC FLPLAALGKV FGRCELAAAM KRHGLDNYRG YSLGNWVCAA KFESNFNTQA

70 80 90 100 110 120

TNRNTDGSTD YGILQINSRW WCNDGRTPGS RNLCNIPCSA LLSSDITASV NCAKKIVSDG

130 140

NGMNAWVAWR NRCKGTDVQA WIRGCRL

References and documentation are available.

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Number of amino acids: 147

Molecular weight: 16238.6

Theoretical pI: 9.36

Amino acid composition:

Ala (A)	14	9.5%
Arg (R)	12	8.2%
Asn (N)	14	9.5%
Asp (D)	7	4.8%
Cys (C)	9	6.1%
Gln (Q)	3	2.0%
Glu (E)	2	1.4%
Gly (G)	13	8.8%
His (H)	1	0.7%
Ile (I)	7	4.8%
Leu (L)	15	10.2%
Lys (K)	6	4.1%
Met (M)	3	2.0%
Phe (F)	4	2.7%
Pro (P)	3	2.0%
Ser (S)	11	7.5%
Thr (T)	7	4.8%
Trp (W)	6	4.1%
Tyr (Y)	3	2.0%
Val (V)	7	4.8%
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): 9

Total number of positively charged residues (Arg + Lys): 18

Atomic composition:

Carbon	C	705
Hydrogen	H	1116
Nitrogen	N	214
Oxygen	O	204
Sulfur	S	12

Formula: C705H1116N214O204S12

Total number of atoms: 2251

Extinction coefficients:

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

Ext. coefficient 37970

Abs 0.1% (=1 g/l) 2.338, assuming all pairs of Cys residues form cystines

Ext. coefficient 37470

Abs 0.1% (=1 g/l) 2.307, 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 19.86

This classifies the protein as stable.

Aliphatic index: 81.70

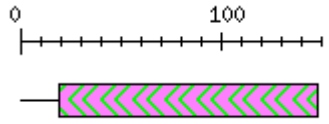
Grand average of hydropathicity (GRAVY): -0.150

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	
PD000577	19	147	Submit
PDC5E2N9	45	145	Submit
PDC1J6J2	42	134	Submit

Domain 3D modelling using Swiss-Model

Domain ID	BEGIN	END	
PD000577	19	147	Submit

Domain 3D modelling using Geno3D

Domain ID	BEGIN	END	
PD000577	19	147	Submit

Top

HSP Results

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

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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
```

(147 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
19-147	#PD000577	678	3e-89
42-134	#PDC1J6J2	180	2e-14
45-145	#PDC5E2N9	202	1e-17

>**PD000577** (Closest domain: LYSC_CHICK 19-147)
Number of domains in family: 566
Commentary (automatic):
DISULFIDE BOND SUBNAME: FULL=LYSOZYME C RECNAME: ALTNAME: EC=3.2.1.17
GLYCOSIDASE PRECURSOR
Length = 129
Score = 678 (265.8 bits), Expect = 3e-89
Identities = 129/129 (100%), Positives = 129/129 (100%)

```
 Query:     19
KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINS 78

KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINS
 Sbjct:     19
KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINS 78

 Query:     79
RWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDV 138

RWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDV
 Sbjct:     79
RWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDV 138

 Query:    139 QAWIRGCRL 147
             QAWIRGCRL
 Sbjct:    139 QAWIRGCRL 147
```

>**PDC5E2N9** (Closest domain: Q7Q6R2_ANOGA 366-501)
Number of domains in family: 2
Commentary (automatic):
SUBNAME: DISULFIDE BOND FULL=LYSOZYME FULL=AGAP005717-PA REFERENCE C-6
Length = 136
Score = 202 (82.4 bits), Expect = 1e-17
Identities = 44/107 (41%), Positives = 59/107 (55%), Gaps = 9/107 (8%)

```
 Query:     45 NWVCAAKFESNFNTQATNR-
NTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLS 103
               WVC A  ES FNT A  R N DGS D+G+ QI+  +WC+    PG+   C +
C AL
 Sbjct:    366 TWVCIAYHESRFNTSAEGRLNADGSGDHGLFQISDIYWCS---
PPGNGWACGVSCDALKD 422

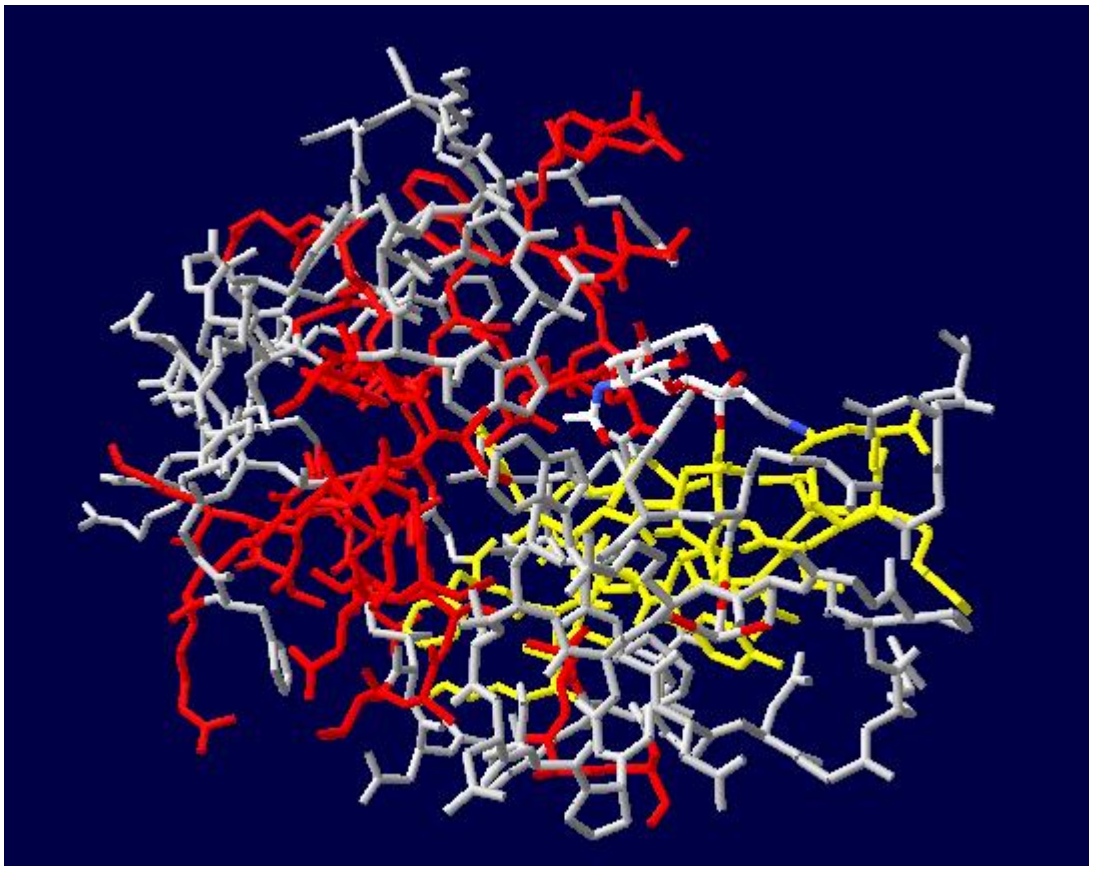
 Query:    104 SDITASVNCAKKIVSD-----GNGMNAWVAWRNRCKGTDVQAWIRGC 145
             SDI+  V C K I  +     G+G NAW  ++  C+   V  ++RGC
 Sbjct:    423 SDISDDVQCVKTIYEEHQRLSGDGFNAWSVYKPYCQRDAVDTFVRGC 469
```

>**PDC1J6J2** (Closest domain: B4IWP9_DROGR 949-1127)
Number of domains in family: 3
Commentary (automatic):
SUBNAME: DISULFIDE BOND FULL=GI13315 FULL=GH16162
Length = 179
Score = 180 (73.9 bits), Expect = 2e-14
Identities = 38/100 (38%), Positives = 55/100 (55%), Gaps = 10/100 (10%)

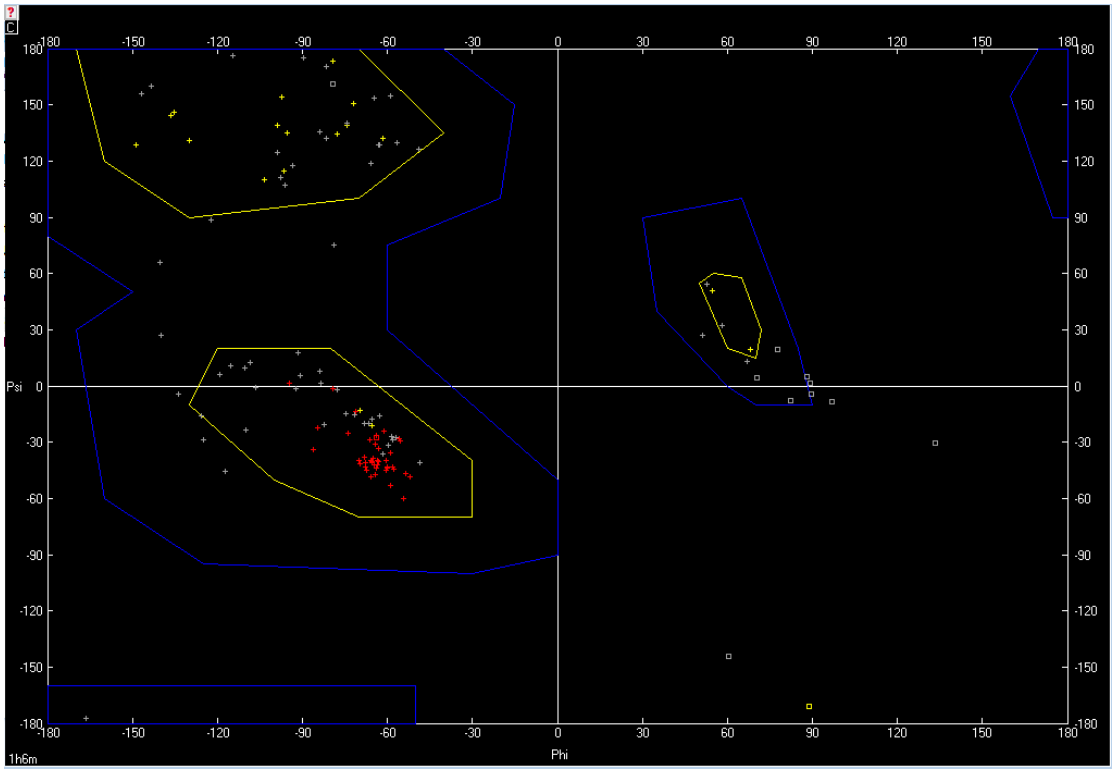
```
 Query:     42 SLGNWVCAAKFESNFNTQATNR-NTDGSTDYGILQINSRWWC-
NDGRTPGSRNLCNIPCS 99
               +  WVC A+ ES+++T A  R NTD S D+G+ QI+  +WC +DG    S
C+I C
 Sbjct:    960 EIPTWVCIAQHESSYSTAAVGRLNTDSSEDHGLFQISDLYWCTHDG---
SSGKACHIECD 1016

 Query:    100 ALLSSDITASVNCAKKIVSD-----GNGMNAWVAWRNRCK 134
                LL SDI+  + C K I  +     G+G  AW  +   C+
 Sbjct:   1017 RLLDSDISDDIECIKTIYKEHTRISGDGFTAWTVYNGHCR 1056
```

1H6M (render by 3D/colored by secondary structure)

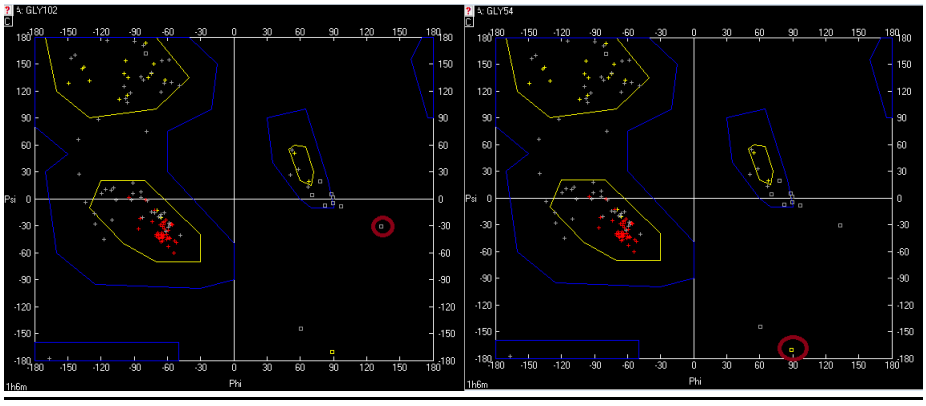


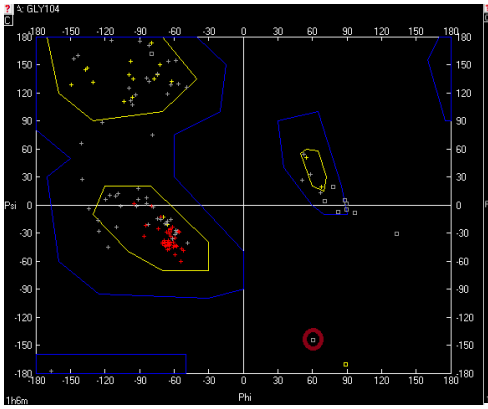
Ramachandran Plot

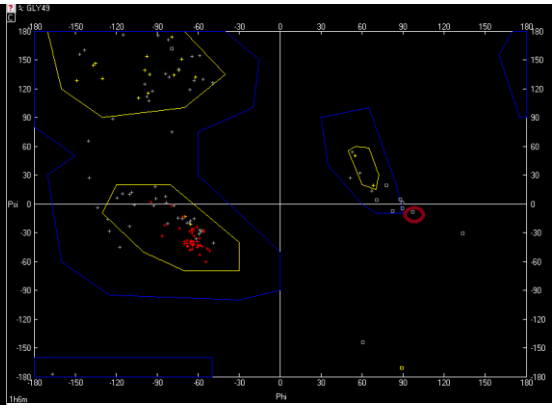


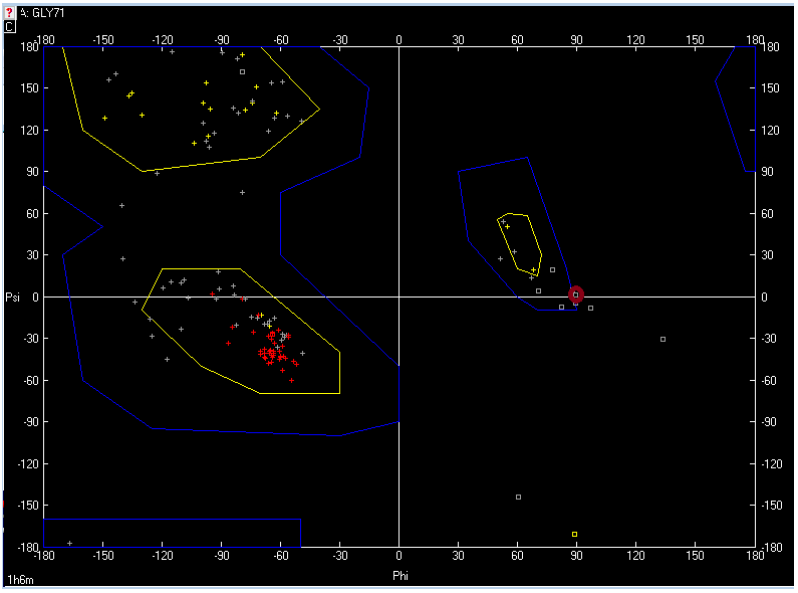
Αμινοξέα που εμφανίζονται εκτός των επιτρεπτών στερεοτακτικών δομών :GLY102, GLY54 ,GLY104 , GLY 49 και GLY71.

Εκτός αυτού , όπως θα παρατηρήσουμε στο Ramachandran Plot υπάρχουν 2 αμινοξέα τα οποία βρίσκονται ακριβώς πάνω στις γραμμές του μπλε κύκλου τα οποία είναι με σειρά από πάνω προς τα κάτω τα : GLY22 ΚΑΙ GLY126.Η γλυκίνη έχει μόνο ένα άτομο υδρογόνου για πλευρική αλυσίδα , με μια πολύ μικρότερη ακτίνα van der Waals από τις CH3, CH2, ή CH ομάδες που ξεκινούν την πλευρική αλυσίδα όλων των άλλων αμινοξέων. Ως εκ τούτου, είναι λιγότερο περιορισμένη , και αυτό είναι εμφανές στο Ramachandran Plot.









Παραπάνω παρατίθενται τα αμινοξέα με την ίδια σειρά όπως αναφέρθηκαν δηλαδή GLY102, GLY54 ,GLY104 , GLY 49 και GLY71 κυκλωμένα με κόκκινο χρώμα.

<u>Τα αμινοξέα της γλυκίνης στο πρωτεϊνικό μόριο της 1H6M τα παρατηρούμε με μαύρο χρώμα στην παρακάτω δομή</u>