

Σοφία Μαργαρίτη ΑΕΜ:8411

Ζωή Ποζίδου ΑΕΜ:8441

Πρωτεΐνη: 3LYM(P00698)

Fasta sequence:

```
>sp|P00698|LYSC_CHICK Lysozyme C OS=Gallus gallus GN=LYZ PE=1 SV=1
MRSLLILVLCFLPLAALGKVFGRCELAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQA
TNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDG
NGMNAWVAWRNRCKGTDVQAWIRGRL
```

ProtParam

User-provided sequence:

```
      10      20      30      40      50      60
MRSLLILVLC FLPLAALGKV FGRCELAAM KRHGLDNYRG YSLGNWVCAA KFESNFNTQA
      70      80      90     100     110     120
TNRNTDGSTD YGILQINSRW WCNDGRTPGS RNLNIPCSA LLSSDITASV NCAKKIVSDG
     130     140
NGMNAWVAWR NRCKGTDVQA WIRGRL
```

References and documentation are available.

Number of amino acids: 147

Molecular weight: 16238.6

Theoretical pI: 9.36

Amino acid composition:

CSV format

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

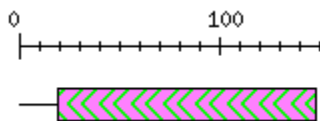
Matrix: BLOSUM62

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	<input type="text" value="19"/>	<input type="text" value="147"/>	<input type="button" value="Submit"/>
PDC5E2N9	<input type="text" value="45"/>	<input type="text" value="145"/>	<input type="button" value="Submit"/>
PDC1J6J2	<input type="text" value="42"/>	<input type="text" value="134"/>	<input type="button" value="Submit"/>

Domain 3D modelling using Swiss-Model

Domain ID	BEGIN	END	
PD000577	<input type="text" value="19"/>	<input type="text" value="147"/>	<input type="button" value="Submit"/>

Domain 3D modelling using Geno3D

Domain ID	BEGIN	END
PD000577	19	147
<input type="button" value="Submit"/>		



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
(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
RWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDV 138

RWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDV
Sbjct: 79
RWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDV 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 TWVCIAYHESRFNTSAEGRNLNADGSGDHGLFQISDIYWCS---
PPGNGWACGVSCDALKD 422

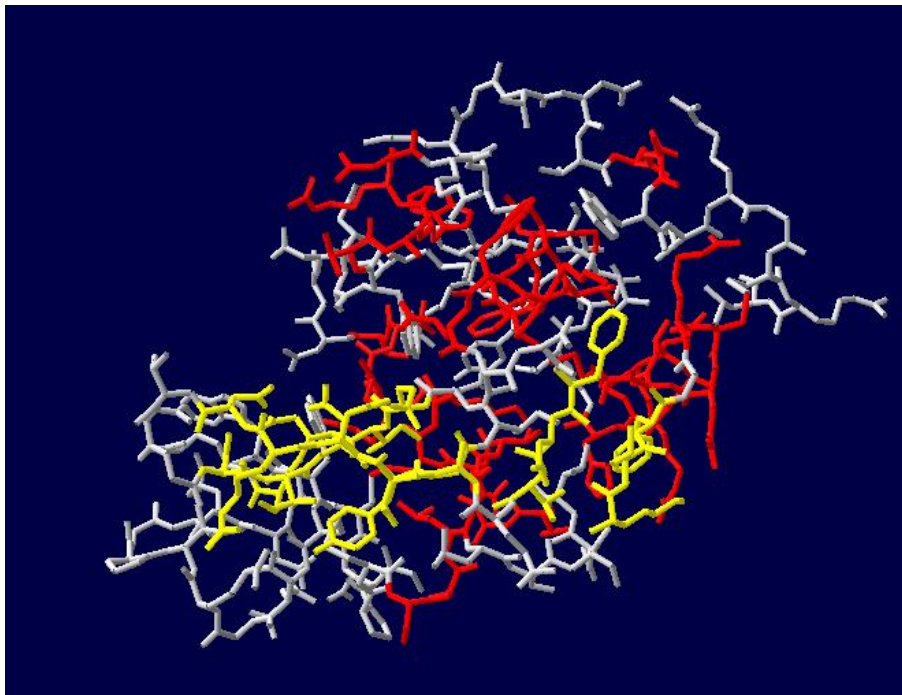
Query: 104 SDITASVNCAKKIVSD-----GNGMNAWVAWRNRCKGTDVQAWIRGC 145
SDI+ V C K I + G+G NAW ++ C+ V ++RGC
Sbjct: 423 SDISDDVQCVKTIYEEHQRLSGDGFNAWSVYKPYCQRDAVDTFVRGC 469

>**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%)

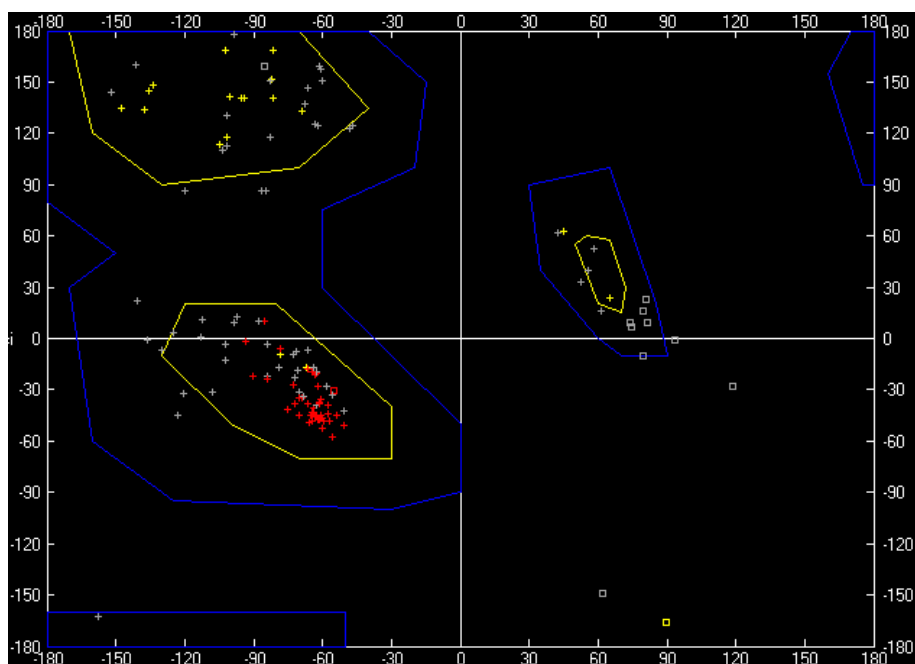
Query: 42 SLGNWVCAAKFESNFNTQATNR-NTDGSTDYGILQINSRWWC-
NDGRTPGSRNLCNIPCS 99
+ WVC A+ ES+++T A R NTD S D+G+ QI+ +WC +DG S
C+I C
Sbjct: 960 EIPTWVCIAQHESYSTAAVGRNLNTDSSEDHGLFQISDLYWCTHDG---
SSGKACHIECD 1016

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

Rendered by 3D/colored by secondary structure



Ramachandran Plot



Τα αμινοξέα που εμφανίζονται εκτός των επιτρεπτών στερεοτακτικών δομών είναι τα:
GLY102 GLY104 GLY 54 GLY49

Η πλευρική αλυσίδα της γλυκίνης είναι αρκετά μικρή αφού έχει ένα μόνο άτομο υδρογόνου, η γλυκίνη μπορεί να συμμετέχει σε πολλές διαμορφώσεις μη αποδεκτές για άλλα αμινοξέα και να κάνει πολλές κινήσεις.

Τα αμινοξέα της γλυκίνης στο πρωτεϊνικό μόριο της 3LYM.

