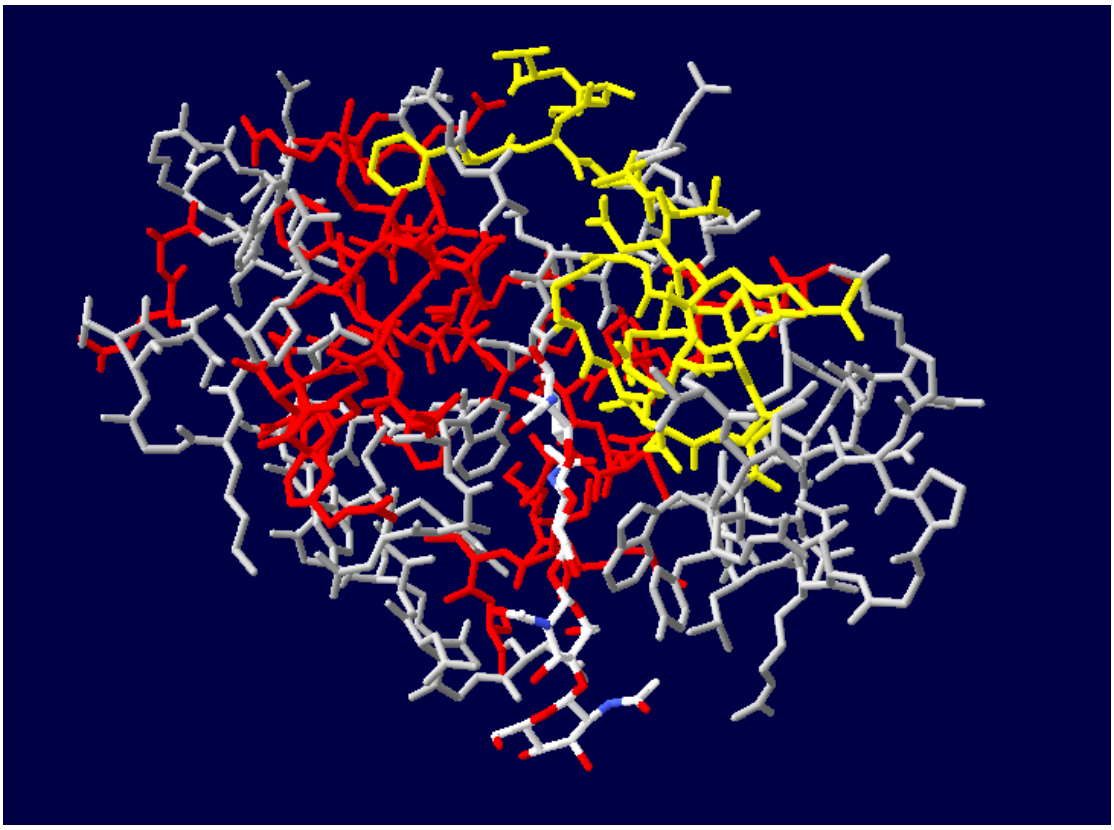
Marina-Tzouliana Daskalopoulou

AEM: 8145

1LZE (P00698)



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.

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: $C_{705}H_{1116}N_{214}O_{204}S_{12}$
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

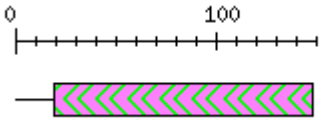
Matrix: BLOSUM62

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

```
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%)

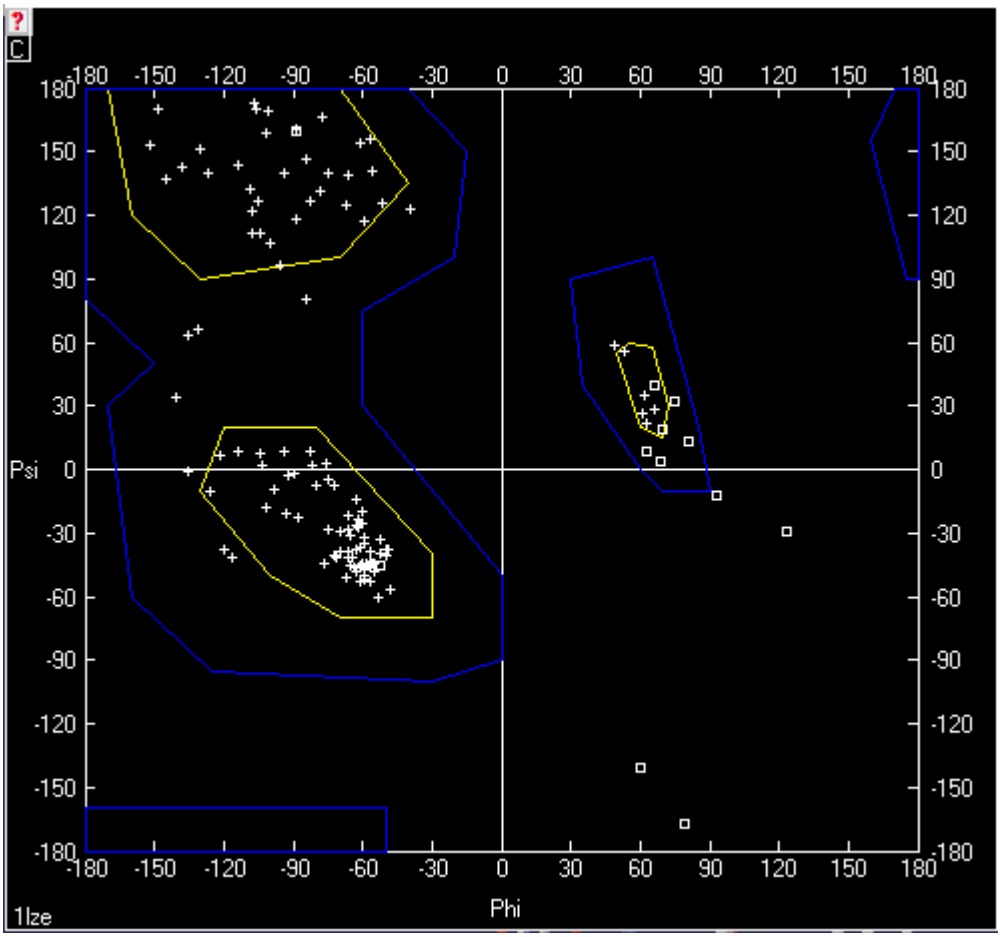
```
 Query:     45 NWVCAAKFESNFNTQATNR-
NTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLS 103
                WVC A  ES FNT A  R N DGS D+G+ QI+  +WC+    PG+   C +
C AL
 Sbjct:    366 TWVCIAYHESRFNTSAEGRLNADGSGDHGLFQISDIYWCS---
PPGNGWACGVSCDALKD 422

 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
```



Τα αμινοξέα που βρίσκονται εκτός των επιτρεπτών κινήσεων είναι :

A Gly49 ,A s Gly54 , A Gly102, A Gly104