

## Allergen Results

**Allergen database.**

The Allermatch database (AllergenDB) was constructed combining three different external sources: UniProt (SwissProt) allergens (<https://www.uniprot.org/docs/allergen>), COMPARE (Comprehensive Protein Allergen Resource) (<http://db.comparedatabase.org/>) and the WHO/IUIS Allergen database (<http://www.allergen.org/>). Overlap between the three database sources were removed using the order: UniProt > WHO/IUIS > COMPARE. If possible, the GenBank accessions were converted to UniProt accessions. This resulted in the AllergenDB with the size of 2277.

Last database update: 02/14/2021

**FASTA.**

For homology search Allermatch uses FASTA(v36.3.8h) with default the parameters(matrix = BLOSUM50(15:-5), open = -10, extend = -2, ktup = 2)

**Identity search to known allergens.**

Each of the ORF sequences has been compared with the AllergenDB using three different in-silico similarity search methods:

- A full FASTA alignment, where each ORF is compared to the AllergenDB, and the top hits are retained. All the hits are sorted on E-value and the top 100 with the lowest E-value are shown. For alignments shorter than 80 amino acids, a recalculated identity(Recalc) has been calculated to a hypothetical 80-amino-acid window.
- An 80-mer sliding window search, where each ORF is chopped up in 80-amino-acid windows with steps of a single residue. Each 80-amino-acid window is compared with all sequences in the AllergenDB. Each 80-amino-acid window with a identity of >35% is shown. For alignments shorter than 80 amino acids, a recalculated identity score over a hypothetical 80 amino acid window has been calculated. For example, 40% identity on a stretch of 40 aa converts to 20% identity on an 80 aa window.
- An 6-mer search, will look for an exact hit of >6 or more contiguous amino acids to a sequence in the AllergenDB.

## Top 100 full-FASTA search results

Based on E-Value

| ID        | Length | Hit ID     | Accession              | Length | E-value | Overlap | Identity | Recalc |
|-----------|--------|------------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147    | LYSC_CHICK | <a href="#">P00698</a> | 129    | 2.3e-61 | 129     | 100.0    | na     |

[illegible]

Jul-28-2021  
WFSR  
Report: test

2

[illegible]

3

[illegible]

4

| ID   | Length  | Hit ID      | Accession | Length | E-value | Overlap | Identity | Recalc |
|--|---|-------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI  | 147   | LALBA_BOVIN | P00711    | 123    | 1.4e-18 | 120     | 40.0     | na     |
| 93 RCELA   | AAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRN |             |           |        |         |         |          |        |
| 5 KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKDDQNPHSSN |   |             |           |        |         |         |          |        |
| LCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAW                        | 142   |             |           |        |         |         |          |        |
| ICNISCDKFLLDDLTDDIMCVKKIL-DKVGINYWLAKALCS-EKLQDW                         | 119   |             |           |        |         |         |          |        |

5

| ID        | Length   | Hit ID    | Accession | Length | E-value | Overlap | Identity | Recalc |
|-----------|--|-----------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147  | TLP_ACTCC | P83958    | 201    | 1.8     | 60      | 31.7     | 23.77  |
| 56        | FNTQATNRNTDGDSTDYGI-LQINSRWWC-NDGRTPGSRNLCNIPCSALLSSDITA-SVN | 112       |           |        |         |         |          |        |
| 103       | FNVAMEFSPTSGGCTRGIKCTANINEQCPNELRAPGG--CNNPCTVFKTDQYCCNSGN   | 159       |           |        |         |         |          |        |

6

| ID  | Length | Hit ID | Accession              | Length | E-value | Overlap | Identity | Recalc |
|---|--------|--------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI   | 147    | 4X9U_A | <a href="#">4X9U_A</a> | 189    | 2.3     | 53      | 26.4     | 17.49  |
| <p>9/4 CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCNDPQVGTHI-----CRGTTXSPQPGGC 49</p> |        |        |                        |        |         |         |          |        |

7

| ID  | Length | Hit ID    | Accession              | Length | E-value | Overlap | Identity | Recalc |
|---|--------|-----------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI   | 147    | TLP_ACTDE | <a href="#">P81370</a> | 201    | 2.4     | 62      | 32.3     | 25.03  |
| <p>5/6 FNTQATNRNTDGSTDYGI---LQINSRWWC-NDGRTPGSRNLCNIPCSALLSSDITA-SVNC 112</p> <p>103 FNVAMEFSPTSGGCTRGIKCTADINGQ--CPNELRAPGG---CNNPCTVFKTDQYCCNSGNC 159</p> |        |           |                        |        |         |         |          |        |

8

| ID  | Length | Hit ID     | Accession              | Length | E-value | Overlap | Identity | Recalc |
|---|--------|------------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI   | 147    | NLTP_MAIZE | <a href="#">P19656</a> | 93     | 2.5     | 41      | 34.1     | 17.48  |
| <p>8/5 GRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMN 125</p> <p>28 GCCSGVRSNN---AARTTADRRACNCLKNAAAGVSGLN 65</p> |        |            |                        |        |         |         |          |        |

9

| ID   | Length | Hit ID       | Accession              | Length | E-value | Overlap | Identity | Recalc |
|--|--------|--------------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI  | 147    | L7TY87_ACTDE | <a href="#">L7TY87</a> | 189    | 3.1     | 53      | 26.4     | 17.49  |
| <p>9/4 CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCNDPQVGTHI-----CRGTTSPQPGGC 49</p> |        |              |                        |        |         |         |          |        |

10

| ID   | Length | Hit ID      | Accession              | Length | E-value | Overlap | Identity | Recalc |
|--|--------|-------------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI  | 147    | KIWEL_ACTDE | <a href="#">P84527</a> | 189    | 3.1     | 53      | 26.4     | 17.49  |
| <p>9/4 CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCNDPQVGTHI-----CRGTTSPQPGGC 49</p> |        |             |                        |        |         |         |          |        |

11

| ID   | Length | Hit ID       | Accession              | Length | E-value | Overlap | Identity | Recalc |
|--|--------|--------------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI  | 147    | L7TUI7_ACTDE | <a href="#">L7TUI7</a> | 189    | 3.7     | 53      | 26.4     | 17.49  |
| <p>9/4 CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCNDPQVGTHI-----CRGTTSPQPGGC 49</p> |        |              |                        |        |         |         |          |        |

12

| ID   | Length | Hit ID       | Accession              | Length | E-value | Overlap | Identity | Recalc |
|--|--------|--------------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI  | 147    | E7CLQ1_PRUAV | <a href="#">E7CLQ1</a> | 91     | 3.9     | 52      | 30.8     | 20.02  |
| <p>8/9 GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNA--WVAWRNRCKGTD 138</p> <p>30 GIRNINNL---AKTTADRQTACNCLKQLSASVPGVNANNAALPGKC-GVN 77</p> |        |              |                        |        |         |         |          |        |

13

| ID   | Length | Hit ID     | Accession              | Length | E-value | Overlap | Identity | Recalc |
|--|--------|------------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI  | 147    | NLTP_PRUAV | <a href="#">Q9M5X8</a> | 91     | 3.9     | 52      | 30.8     | 20.02  |
| <p>8/9 GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNA--WVAWRNRCKGTD 138</p> <p>30 GIRNINNL---AKTTADRQTACNCLKQLSASVPGVNANNAALPGKC-GVN 77</p> |        |            |                        |        |         |         |          |        |

| ID   | Length | Hit ID      | Accession | Length | E-value | Overlap | Identity | Recalc |
|--|--------|-------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI  | 147    | KIWEL_ACTCC | P85261    | 189    | 8.3     | 53      | 24.5     | 16.23  |
| 94 CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC |        |             |           |        |         | 146     |          |        |
| 4 CNGPCRDL--NDCDGQLICIEGKCND DPEVGTHI-----CRGTTSPQPGGC   |        |             |           |        |         | 49      |          |        |

22

| ID        | Length | Hit ID     | Accession              | Length | E-value | Overlap | Identity | Recalc |
|-----------|--------|------------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147    | AMP1_FAGES | <a href="#">P0DKH7</a> | 40     | 8.6     | 24      | 37.5     | 11.25  |

978 SRW-WCNDGRTPGSRNLCNIPCS 100  
 : : : : : : : : : :  
 19 SQWGWG--GSTP--KYCGAGCQ 37

23

| ID        | Length | Hit ID     | Accession | Length | E-value | Overlap | Identity | Recalc |
|-----------|--------|------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147    | AMP2_FAGES | P0DKH8    | 40     | 8.6     | 24      | 37.5     | 11.25  |

978 SRW-WCNDGRTPGSRNLCNIPCS 100  
 : : : : : : : : : :  
 19 SQWGWG--GSTP---KYCGAGCQ 37

24

| ID        | Length | Hit ID    | Accession              | Length | E-value | Overlap | Identity | Recalc |
|-----------|--------|-----------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147    | VA5_VESMG | <a href="#">P86870</a> | 202    | 9.1     | 36      | 33.3     | 14.98  |

**92** NLCNI PCSA---LLSSDITASVNCAKKIVSDGNG **123**

: : : : : : : : : : : : : : : :

**2** NYCKIKCRSGIHTLCKFGISTKPNCGKNVVK-GSG **36**

## Exact word and sliding window results

Shown per ORF

### Exact word results:

| Name       | Accession ID | Description | Species       | No exact words | Hit % |
|------------|--------------|-------------|---------------|----------------|-------|
| LYSC_CHICK | P00698       | Lysozyme C  | Gallus gallus | 124            | 87.32 |

18

KVFGRCCELAAMKRGHGLDNYRGYS LGNWVCAAKFESNFNTQATNRNTDGS TDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI  
TASVNCACKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR L 147

.....

| Name  | Accession ID | Description | Species | No exact words | Hit % |
|---|--------------|-------------|---------|----------------|-------|
| 0   |              |             |         |                |       |
| KVFGRCCELAAMKRGHGLDNYRGYS LGNWVCAAKFESNFNTQATNRNTDGS TDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI |              |             |         |                |       |
| TASVNCACKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR L 129  |              |             |         |                |       |

52 ESNFNT 58  
.....  
34 ESNFNT 40

| Name         | Accession ID | Description                              | Species      | No exact words | Hit % |
|--------------|--------------|--|--------------|----------------|-------|
| XP_014705584 | XP_014705584 | PREDICTED: lysozyme C, mi<br>lk isozyeme | Equus asinus | 1              | 0.7   |

52 ESNFNT 58  
.....  
53 ESNFNT 59

### Sliding window results:

| Name       | Accession ID | Description | Species       | No windows | Hit % |
|------------|--------------|-------------|---------------|------------|-------|
| LYSC_CHICK | P00698       | Lysozyme C  | Gallus gallus | 68         | 100.0 |

### Alignments containing 68 window(s):

(1:81-1:62) 77.5% identity  
(2:82-1:63) 78.8% identity  
(3:83-1:64) 80.0% identity  
(4:84-1:65) 81.2% identity  
(5:85-1:66) 82.5% identity  
(6:86-1:67) 83.8% identity  
(7:87-1:68) 85.0% identity  
(8:88-1:69) 86.2% identity  
(9:89-1:70) 87.5% identity  
(10:90-1:71) 88.8% identity  
(11:91-1:72) 90.0% identity  
(12:92-1:73) 91.2% identity  
(13:93-1:74) 92.5% identity  
(14:94-1:75) 93.8% identity  
(15:95-1:76) 95.0% identity  
(16:96-1:77) 96.2% identity  
(17:97-1:78) 97.5% identity  
(18:98-1:79) 98.8% identity  
(19:99-1:80) 100.0% identity  
(20:100-2:81) 100.0% identity  
(21:101-3:82) 100.0% identity  
(22:102-4:83) 100.0% identity  
(23:103-5:84) 100.0% identity  
(24:104-6:85) 100.0% identity  
(25:105-7:86) 100.0% identity  
(26:106-8:87) 100.0% identity  
(27:107-9:88) 100.0% identity  
(28:108-10:89) 100.0% identity  
(29:109-11:90) 100.0% identity  
(30:110-12:91) 100.0% identity  
(31:111-13:92) 100.0% identity  
(32:112-14:93) 100.0% identity  
(33:113-15:94) 100.0% identity  
(34:114-16:95) 100.0% identity  
(35:115-17:96) 100.0% identity

(36:116-18:97) 100.0% identity  
(37:117-19:98) 100.0% identity  
(38:118-20:99) 100.0% identity  
(39:119-21:100) 100.0% identity  
(40:120-22:101) 100.0% identity  
(41:121-23:102) 100.0% identity  
(42:122-24:103) 100.0% identity  
(43:123-25:104) 100.0% identity  
(44:124-26:105) 100.0% identity  
(45:125-27:106) 100.0% identity  
(46:126-28:107) 100.0% identity  
(47:127-29:108) 100.0% identity  
(48:128-30:109) 100.0% identity  
(49:129-31:110) 100.0% identity  
(50:130-32:111) 100.0% identity  
(51:131-33:112) 100.0% identity  
(52:132-34:113) 100.0% identity  
(53:133-35:114) 100.0% identity  
(54:134-36:115) 100.0% identity  
(55:135-37:116) 100.0% identity  
(56:136-38:117) 100.0% identity  
(57:137-39:118) 100.0% identity  
(58:138-40:119) 100.0% identity  
(59:139-41:120) 100.0% identity  
(60:140-42:121) 100.0% identity  
(61:141-43:122) 100.0% identity  
(62:142-44:123) 100.0% identity  
(63:143-45:124) 100.0% identity  
(64:144-46:125) 100.0% identity  
(65:145-47:126) 100.0% identity  
(66:146-48:127) 100.0% identity  
(67:147-49:128) 100.0% identity  
(68:148-50:129) 100.0% identity

```

1  MRSLLIILVLCFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTD
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1  -----KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTD

```

YGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQA  
:  
YGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQA

```
WIRGCRL 148
:::
WIRGCRL 129
```

| Name         | Accession ID | Description                                | Species      | No windows | Hit % |
|--------------|--------------|--|--------------|------------|-------|
| XP_014705584 | XP_014705584 | PREDICTED: lysozyme C,<br>milk is<br>ozyme | Equus asinus | 68         | 100.0 |

**Alignments containing 2 window(s):**

**(1:81-1:82) 51.8% identity**

**(2:82-2:83) 51.8% identity**

```

1  MRSLILVL--CFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDG
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1  MRSTLIISLLSCFFAVYE-AKVFSKCELAHKLKAQEMDGGYSLANWVCMAEYESNFNTRAFNGKNANG

STDYGILQINSRWW 82
::::::::::
SSDYGLFQLNNKWW 83

```

**Alignments containing 1 window(s):**

**(3:83-4:84) 51.2% identity**

```

3  SLLILVL-CFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTD
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
4  TLIISLLSCFFAVYE-AKVFSKCELAHKLKAQEMDGGYSLANWVCMAEYESNFNTRAFNGKNANGSSD

YGILQINSRWWC 83
::::::::::
YGLFQLNNKWWC 84

```

**Alignments containing 8 window(s):**

**(4:84-6:85) 49.4% identity**

**(5:85-7:86) 50.6% identity**

**(6:86-8:87) 50.6% identity**

**(7:87-9:88) 50.6% identity**

**(8:88-10:89) 49.4% identity**

**(9:89-11:90) 49.4% identity**

**(10:90-12:91) 49.4% identity**

**(11:91-13:92) 49.4% identity**

```

4  LLILVLCFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYG
   ..  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
6  IISLLSCFFAVYE-AKVFSKCELAHKLKAQEMDGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYG

ILQINSRWWCNDGRTPGS 91
::::::::::
LFQLNNKWWCKDNKRSSS 92

```



**Alignments containing 3 window(s):**

**(12:92-13:93) 48.1% identity**

**(13:93-14:94) 48.1% identity**

**(14:94-15:95) 48.1% identity**

```

12 LPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRW
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
13 FFAVYEAKVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKW
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   WCNDGRTPGSRNL 94
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   WCKDNKRSSSNAC 95

```

**Alignments containing 1 window(s):**

**(15:95-16:95) 50.6% identity**

```

15 AALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCN
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
16 VYEAKVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCK
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   DGRTPGSRNLC 95
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   DNKR-SSSNAC 95

```

**Alignments containing 1 window(s):**

**(16:96-17:96) 51.9% identity**

```

16 ALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCND
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
17 YEAKVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKD
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   GRTPGSRNLNC 96
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   NKRSSS-NACN 96

```

**Alignments containing 4 window(s):**

**(17:97-18:97) 53.1% identity**

**(18:98-19:98) 53.1% identity**

**(19:99-20:99) 54.3% identity**

**(20:100-21:100) 54.3% identity**

```

17 LGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDG
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
18 EAKVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDN
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   RTPGSRNLCNIPCS 100
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   KR-SSSNACNIMCS 100

```

**Alignments containing 1 window(s):**  
**(21:101-22:101) 53.1% identity**

```
21 FGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPG
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
22 FSKCELAHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSS
   SRNLCNIPCSA 101
   : : : : : :
   S-NACNIMCSK 101
```

**Alignments containing 4 window(s):**  
**(22:102-23:102) 53.1% identity**  
**(23:103-24:103) 54.3% identity**  
**(24:104-25:104) 54.3% identity**  
**(25:105-26:105) 53.1% identity**

```
22 GRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGS
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
23 SKCELAHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SS
   RNLCNIPCSALLSS 105
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   SNACNIMCSKLLDD 105
```

**Alignments containing 1 window(s):**  
**(26:106-27:106) 51.9% identity**

```
26 LAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLC
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
27 LAHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSS-NAC
   NIPCSALLSSD 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   NIMCSKLLDDN 106
```

**Alignments containing 4 window(s):**  
**(27:107-28:107) 51.9% identity**  
**(28:108-29:108) 50.6% identity**  
**(29:109-30:109) 50.6% identity**  
**(30:110-31:110) 50.6% identity**

```
27 AAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCN
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
28 AHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACN
   IPCSALLSSDITAS 110
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   IMCSKLLDDNIDDD 110
```

**Alignments containing 1 window(s):**  
**(31:111-32:111) 50.6% identity**

```

31 KRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCS
   . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
32 KAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCS

   ALLSSDITASV 111
   : : : : : :
   KLLDDNIDDDI 111

```

**Alignments containing 4 window(s):**  
**(32:112-33:112) 49.4% identity**  
**(33:113-34:113) 50.6% identity**  
**(34:114-35:114) 51.9% identity**  
**(35:115-36:115) 53.1% identity**

```

32 RHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSA
   . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
33 AQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSK

   LLSSDITASVNCAK 115
   : : : : : :
   LLDDNIDDDISCAK 115

```

**Alignments containing 1 window(s):**  
**(36:116-37:116) 53.1% identity**

```

36 DNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSS
   . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
37 DGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDD

   DITASVNCAKK 116
   . : . . . :
   NIDDDISCAKR 116

```

**Alignments containing 4 window(s):**  
**(37:117-38:117) 51.9% identity**  
**(38:118-39:118) 53.1% identity**  
**(39:119-40:119) 53.1% identity**  
**(40:120-41:120) 54.3% identity**

```

37 NYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSD
   . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
38 GFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDN

   ITASVNCAKKIVSD 120
   : : . . . : :
   IDDDISCAKRVVRD 120

```

**Alignments containing 1 window(s):**  
**(41:121-42:121) 53.1% identity**

```

41 YSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITAS
   ::::::::::: ::::::::::: : ::::::::::: ::::::::::: : : :: :: :: :: :: :: ::
42 YSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDDNIDDD

VNC AKKIVSDG 121
:: :: :: :: :: ::
ISC AKRVVRDP 121
  
```

**Alignments containing 4 window(s):**  
**(42:122-43:122) 51.9% identity**  
**(43:123-44:123) 51.9% identity**  
**(44:124-45:124) 51.9% identity**  
**(45:125-46:125) 51.9% identity**

```

42 SLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASV
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
43 SLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDI

NCA KKI VSDGNGMN 125
:: :: :: :: :: ::
SCA KRVVRDPKGMS 125
  
```

**Alignments containing 1 window(s):**  
**(46:126-47:126) 51.9% identity**

```

46 WVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAK
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
47 WVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDDNIDDDISCAK

KIVSDGNGMNA 126
.: : .:::
RVVRDPKGMSA 126
  
```

**Alignments containing 4 window(s):**  
**(47:127-48:127) 51.9% identity**  
**(48:128-49:128) 50.6% identity**  
**(49:129-50:129) 50.6% identity**  
**(50:130-51:130) 51.9% identity**

```

47 VCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKK
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
48 VCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKR

IVSDGNGMNAVAV 130
.: : .:::
VVRDPKGMSAWKAW 130
  
```

**Alignments containing 1 window(s):**  
**(51:131-52:131) 50.6% identity**

```

51 KFESNFTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSD
   ..... : ..... : ..... : ..... : ..... : ..... : ..... : ..... :
52 EYESNFTNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDDNIDDDISCAKRVVRD

   NGMNAWVAWR 131
   ..... :
   PKGMSAWKAWV 131
  
```

**Alignments containing 4 window(s):**  
**(52:132-53:132) 50.6% identity**  
**(53:133-54:133) 50.6% identity**  
**(54:134-55:134) 50.6% identity**  
**(55:135-56:135) 50.6% identity**

```

52 FESNFTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDG
   ..... : ..... : ..... : ..... : ..... : ..... : ..... : ..... :
53 YESNFTNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDP

   NGMNAWVAWRNRCK 135
   ..... : ..... :
   KGMSAWKAWVKHCK 135
  
```

**Alignments containing 1 window(s):**  
**(56:136-57:136) 49.4% identity**

```

56 FNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMN
   ..... : ..... : ..... : ..... : ..... : ..... : ..... : ..... :
57 FNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDDNIDDDISCAKRVVRDPKGMS

   AWWAWRNRCKG 136
   .. : .. : .. :
   AWKAWVKHCKD 136
  
```

**Alignments containing 3 window(s):**  
**(57:137-58:137) 48.1% identity**  
**(58:138-59:138) 48.1% identity**  
**(59:139-60:139) 46.9% identity**

```

57 NTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNA
   ..... : ..... : ..... : ..... : ..... : ..... : ..... : ..... :
58 NTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSA

   WVAWRNRCKGTDV 139
   : .. : .. : .. :
   WKAWVKHCKDKDL 139
  
```

**Alignments containing 1 window(s):  
(60:140-62:140) 45.0% identity**

60 ATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQ 140  
 . . . . . :  
 62 FNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVRDPKGMSAWKAWVKHCKDKDLS 140

**Alignments containing 1 window(s):  
(61:141-63:141) 45.0% identity**

61 TNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNMGNAWVAWRNRCKGTDVQA 141  
... : .. : . :  
63 NGKNANGSSDYGLFQLNNKWCKDNKRSSS-NAC NIMCSKLDDNIDDDISCAKRVRDPKGMSAWKA WKHKCDKDLSE 141

---

(c) NCBI/NLM/NIH/DHAP; accession number F07891-1.

**Alignments containing 4 window(s):**  
**(62:142-64:142) 45.0% identity**  
**(63:143-65:143) 45.0% identity**  
**(64:144-66:144) 45.0% identity**  
**(65:145-67:145) 43.8% identity**

```

62 NRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRN
64 GKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVK
RCKGTDVQAWIRG 145
HCKDKDLSEYLAS 145

```

**Alignments containing 1 window(s):  
(66:146-68:146) 45.0% identity**

66 DGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146  
 :::::::::::::::::::: : :::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: :  
 68 NGSSDYGLFQLNNKWWCKDNKRSS-NACNIMCSKLDDNIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLSEYLASC 146

**Alignments containing 2 window(s):**  
**(67:147-69:147) 45.0% identity**  
**(68:148-70:148) 45.0% identity**

```

67  GSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDGNGMNAWVAWRNRCKGT
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : : : : :
69  GSSDYGLFQLNNKWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVRDPKGMSAWKAWVKHCKDK
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : : : : :
   DVQAWIRGCRLL 148
   :::::::::::::::
   DLSEYLASCNLL 148

```

| Name        | Accession ID | Description              | Species        | No windows | Hit % |
|-------------|--------------|--------------------------|----------------|------------|-------|
| LYSC1_HORSE | P11376       | Lysozyme C, milk isozyme | Equus caballus | 68         | 100.0 |

**Alignments containing 14 window(s):**

(1:81-1:63) 43.2% identity  
(2:82-1:64) 44.4% identity  
(3:83-1:65) 45.7% identity  
(4:84-1:66) 45.7% identity  
(5:85-1:67) 46.9% identity  
(6:86-1:68) 46.9% identity  
(7:87-1:69) 46.9% identity  
(8:88-1:70) 46.9% identity  
(9:89-1:71) 46.9% identity  
(10:90-1:72) 46.9% identity  
(11:91-1:73) 48.1% identity  
(12:92-1:74) 48.1% identity  
(13:93-1:75) 48.1% identity  
(14:94-1:76) 48.1% identity

```

1  MRSLILVLCLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGST
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1  -----KVFSKCELAHKLKAQEMDGGYSLANWVCMAYESNFNTRAFNGKNANGSS

   DYGILQINSRWWCNDGRTPGSRNL 94
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DYGLFQLNNKWWCKDNKRSSSNAC 76

```

**Alignments containing 1 window(s):**  
**(15:95-1:76) 50.6% identity**

```

15  AALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCN
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1  ----KVFSKCELAHKLKAQEMDGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCK

   DGRTPGSRNLC 95
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DNKR-SSSNAC 76

```

**Alignments containing 1 window(s):**  
**(16:96-1:77) 51.9% identity**

```

16  ALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCND
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1  ---KVFSKCELAHKLKAQEMDGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKD

   GRTPGSRNLN 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   NKRSSS-NACN 77

```

**Alignments containing 4 window(s):**

(17:97-1:78) 53.1% identity  
(18:98-1:79) 53.1% identity  
(19:99-1:80) 54.3% identity  
(20:100-2:81) 54.3% identity

```
17 LGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDG
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1  --KVFSKCELAHKLKAQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDN

RTPGSRNLCNIPCS 100
. : : : : :
KR-SSSNACNIMCS 81
```

**Alignments containing 1 window(s):**

(21:101-3:82) 53.1% identity

```
21 FGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPG
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
3  FSKCELAHKLKAQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSS

SRNLCNIPCSA 101
: : : : :
S-NACNIMCSK 82
```

**Alignments containing 4 window(s):**

(22:102-4:83) 53.1% identity  
(23:103-5:84) 54.3% identity  
(24:104-6:85) 54.3% identity  
(25:105-7:86) 53.1% identity

```
22 GRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGS
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4  SKCELAHKLKAQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SS

RNLCNIPCSALLSS 105
: : : : : : : :
SNACNIMCSKLLDE 86
```

**Alignments containing 1 window(s):**

(26:106-8:87) 51.9% identity

```
26 LAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLC
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8  LAHKLKAQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NAC

NIPCSALLSSD 106
: : : : : :
NIMCSKLLDEN 87
```



**Alignments containing 4 window(s):**

(27:107-9:88) 51.9% identity  
(28:108-10:89) 50.6% identity  
(29:109-11:90) 50.6% identity  
(30:110-12:91) 50.6% identity

```
27 AAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCN
   : . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
9  AHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACN

   IPCSALLSSDITAS 110
   : : : : : : :
   IMCSKLLDENIDDD 91
```

**Alignments containing 1 window(s):**

(31:111-13:92) 50.6% identity

```
31 KRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCS
   : . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
13 KAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCS

   ALLSSDITASV 111
   : : . : . :
   KLLDENIDDDI 92
```

**Alignments containing 4 window(s):**

(32:112-14:93) 49.4% identity  
(33:113-15:94) 50.6% identity  
(34:114-16:95) 51.9% identity  
(35:115-17:96) 53.1% identity

```
32 RHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSA
   . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
14 AQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSK

   LLSSDITASVNCAK 115
   : : . : . : : :
   LLDENIDDDISCAK 96
```

**Alignments containing 1 window(s):**

(36:116-18:97) 53.1% identity

```
36 DNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSS
   : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
18 DGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDE

   DITASVNCAKK 116
   . : . : : : .
   NIDDDISCAKR 97
```

**Alignments containing 4 window(s):**

(37:117-19:98) 51.9% identity

(38:118-20:99) 53.1% identity

(39:119-21:100) 53.1% identity

(40:120-22:101) 54.3% identity

```

37 NYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSD
.. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
19 GFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDEN

ITASVNCAKKIVSD 120
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
IDDDISCAKRVVRD 101

```

**Alignments containing 1 window(s):**

(41:121-23:102) 53.1% identity

```

41 YSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITAS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
23 YSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDD

VNCAKKIVSDG 121
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
ISCAKRVVRDP 102

```

**Alignments containing 4 window(s):**

(42:122-24:103) 51.9% identity

(43:123-25:104) 51.9% identity

(44:124-26:105) 51.9% identity

(45:125-27:106) 51.9% identity

```

42 SLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
24 SLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDI

NCAKKIVSDGNGMN 125
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
SCAKRVVRDPKGMS 106

```

**Alignments containing 1 window(s):**

(46:126-28:107) 51.9% identity

```

46 WVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAK
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
28 WVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDDISCAK

KIVSDGNGMNA 126
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RVVRDPKGMSA 107

```

**Alignments containing 4 window(s):**

(47:127-29:108) 51.9% identity  
(48:128-30:109) 50.6% identity  
(49:129-31:110) 50.6% identity  
(50:130-32:111) 51.9% identity

```
47 VCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACK
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
29 VCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKR

   IVSDGNGMNAVVAW 130
   .: : .: : : : :
   VVRDPKGMSAWKAW 111
```

**Alignments containing 1 window(s):**

(51:131-33:112) 50.6% identity

```
51 KFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSD
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
33 EYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDDISCAKRVVRD

   GNGMNAVVAWR 131
   .: : : : :
   PKGMSAWKAWV 112
```

**Alignments containing 4 window(s):**

(52:132-34:113) 50.6% identity  
(53:133-35:114) 50.6% identity  
(54:134-36:115) 50.6% identity  
(55:135-37:116) 50.6% identity

```
52 FESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDG
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
34 YESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDP

   NGMNAVVAWRNRCK 135
   .: : : : :
   KGMSAWKAWVKHCK 116
```

**Alignments containing 1 window(s):**

(56:136-38:117) 49.4% identity

```
56 FNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDGNGMN
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
38 FNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDDISCAKRVVRDPKGMS

   AWVAWRNRCKG 136
   :: : : : :
   AWKAWVKHCKD 117
```

**Alignments containing 3 window(s):**

**(57:137-39:118) 48.1% identity**

**(58:138-40:119) 48.1% identity**

**(59:139-41:120) 46.9% identity**

```
57 NTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNMNA
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
39 NTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVRDPKGMSA

WVAWRNRCKGTDV 139
: : : : : : : :
WKAUVKHCKDKDL 120
```

**Alignments containing 1 window(s):**

**(60:140-43:121) 45.0% identity**

```
60 ATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNMNAWVAWRNRCKGTDVQ 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
43 FNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVRDPKGMSAWKAWVKHCKDKDLS 121
```

**Alignments containing 1 window(s):**

**(61:141-44:122) 45.0% identity**

```
61 TNRTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNMNAWVAWRNRCKGTDVQA 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
44 NGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDDISCAKRVRDPKGMSAWKAWVKHCKDKDLSE 122
```

**Alignments containing 4 window(s):**

**(62:142-45:123) 45.0% identity**

**(63:143-46:124) 45.0% identity**

**(64:144-47:125) 45.0% identity**

**(65:145-48:126) 43.8% identity**

```
62 NRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNMNAWVAWRN
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
45 GKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVRDPKGMSAWKAWVK

RCKGTDVQAWIRG 145
: : : : : : : :
HCKDKDLSEYLAS 126
```

**Alignments containing 1 window(s):**

**(66:146-49:127) 45.0% identity**

```
66 DGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNMNAWVAWRNRCKGTDVQAWIRGC 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
49 NGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDDISCAKRVRDPKGMSAWKAWVKHCKDKDLSEYLASC 127
```

**Alignments containing 2 window(s):**

**(67:147-50:128) 45.0% identity**

**(68:148-51:129) 45.0% identity**

```
67 GSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNMNAWVAWRNRCKGT
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
50 GSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVRDPKGMSAWKAWVKHCKDK

DVQAWIRGCRL 148
: : : : : : : :
DLSEYLASCNL 129
```

| Name        | Accession ID | Description       | Species    | No windows | Hit % |
|-------------|--------------|-------------------|------------|------------|-------|
| LALBA_BOVIN | P00711       | Alpha-lactalbumin | Bos taurus | 59         | 86.76 |

**Alignments containing 1 window(s):**  
**(9:89-3:67) 36.2% identity**

```

9  LCFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGDSTDYGILQINSRWWCNDGRTP 89
   :               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
3  LT-----KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNN--STEYGLFQINNKIWCKDDQNP 67

```

**Alignments containing 1 window(s):**  
**(11:91-2:69) 37.5% identity**

```

11  FLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGDSTDYGILQINSRWWCNDGRTPGS 91
   :               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2  QLT-----KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNN--STEYGLFQINNKIWCKDDQNP 69

```

**Alignments containing 3 window(s):**  
**(12:92-1:70) 37.5% identity**  
**(13:93-2:71) 38.8% identity**  
**(14:94-3:72) 38.8% identity**

```

12  LPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGDSTDYGILQINSRWW
   :               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1  EQLT-----KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNN--STEYGLFQINNKIW
   CNDGRTPGSRNL 94
   : : : : : : :
   CKDDQNP 72

```

**Alignments containing 3 window(s):**  
**(15:95-1:73) 41.2% identity**  
**(16:96-2:74) 42.5% identity**  
**(17:97-3:75) 43.8% identity**

```

15  AALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGDSTDYGILQINSRWWCND
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1  EQLTK---CEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNN--STEYGLFQINNKIWCKD
   GRTPGSRNLCNI 97
   : : : : : : :
   DQNP 75

```

**Alignments containing 1 window(s):**  
**(18:98-1:76) 41.2% identity**

```

18  GKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGDSTDYGILQINSRWWCNDGRTPGSRNLCNIP 98
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1  EQLT-KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNN--STEYGLFQINNKIWCKDDQNP 76

```

**Alignments containing 7 window(s):**

(19:99-1:77) 42.5% identity  
(20:100-2:78) 42.5% identity  
(21:101-3:79) 42.5% identity  
(22:102-4:80) 42.5% identity  
(23:103-5:81) 43.8% identity  
(24:104-6:82) 43.8% identity  
(25:105-7:83) 42.5% identity

```

19  KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTP
   . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1   EQLTKCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKDDQNP

   GSRNLCNIPCSALLSS 105
   : : : : : : : : : :
   HSSNICNISCDKFLDD 83
  
```

**Alignments containing 17 window(s):**

(26:106-6:84) 41.2% identity  
(27:107-7:85) 41.2% identity  
(28:108-8:86) 42.5% identity  
(29:109-9:87) 42.5% identity  
(30:110-10:88) 42.5% identity  
(31:111-11:89) 42.5% identity  
(32:112-12:90) 42.5% identity  
(33:113-13:91) 43.8% identity  
(34:114-14:92) 43.8% identity  
(35:115-15:93) 45.0% identity  
(36:116-16:94) 45.0% identity  
(37:117-17:95) 46.2% identity  
(38:118-18:96) 46.2% identity  
(39:119-19:97) 45.0% identity  
(40:120-20:98) 45.0% identity  
(41:121-21:99) 43.8% identity  
(42:122-22:100) 43.8% identity

```

26  LAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCN
   . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
6   CEVFRELKDLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKDDQNP HSSNICN

   IPCSALLSSDITASVNC AKKIVSDGN 122
   : : : : : : : : : : : : : : : :
   ISCDKFLDDDLTDDIMCVKKILDKVG 100
  
```

**Alignments containing 16 window(s):**

(43:123-23:100) 45.0% identity  
(44:124-24:101) 43.8% identity  
(45:125-25:102) 45.0% identity  
(46:126-26:103) 45.0% identity  
(47:127-27:104) 45.0% identity  
(48:128-28:105) 43.8% identity  
(49:129-29:106) 43.8% identity  
(50:130-30:107) 43.8% identity  
(51:131-31:108) 43.8% identity  
(52:132-32:109) 43.8% identity  
(53:133-33:110) 43.8% identity  
(54:134-34:111) 45.0% identity  
(55:135-35:112) 43.8% identity  
(56:136-36:113) 43.8% identity  
(57:137-37:114) 43.8% identity  
(58:138-38:115) 43.8% identity

```

43  LGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC
   . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
23  LPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKDDQNP HSSNICNISCDKFLDDDLTDDIMC

   AKKIVSDGNGMNAWVAWRNRCKGTD 138
   . . . . . : : : : : : : : : : :
   VKKIL-DKVGINYWLAHKALCSEKL 115
  
```

**Alignments containing 1 window(s):**  
**(59:139-39:117) 43.2% identity**

```

59 QATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVA
   ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
39 QAI VQNND-STEYGLFQINNKIWCKDDQNP HSSNICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLA

   WRNRC-KGTDV 139
       :  :
   HKALCSEKLDQ 117

```

**Alignments containing 2 window(s):**  
**(60:140-40:117) 42.5% identity**  
**(61:141-41:118) 41.2% identity**

```

60 ATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAW
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
40 AIVQNND-STEYGLFQINNKIWCKDDQNP HSSNICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLAH

   RNRCKGTDVQA 141
       :  :
   KALCSEKLDQW 118

```

**Alignments containing 3 window(s):**  
**(62:142-42:118) 41.2% identity**  
**(63:143-43:119) 41.2% identity**  
**(64:144-44:120) 41.2% identity**

```

62 NRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRN
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
42 VQNND-STEYGLFQINNKIWCKDDQNP HSSNICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLAHKA

   RCKGTDVQAWIR 144
       :  :  :
   LCS-EKLDQWLC 120

```

**Alignments containing 1 window(s):**  
**(65:145-44:121) 38.8% identity**

```

65 TDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG 145
   ..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
44 NNDSTEYGLFQINNKIWCKDDQNP HSSNICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLAHKALCS-EKLDQWLCE 121

```

**Alignments containing 3 window(s):**  
**(66:146-45:120) 40.0% identity**  
**(67:147-46:121) 40.0% identity**  
**(68:148-47:122) 40.0% identity**

```

66 DGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKG
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
45 NDSTEYGLFQINNKIWCKDDQNP HSSNICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLAHKALCS-

   TDVQAWIRGCR L 148
       :  :  :
   EKLDQWL--CEK 122

```

## Celiac Results

### Celiac database.

The epitope database is constructed by the combination of three different sources. Epitopes from Sollid and coauthors (<https://pubmed.ncbi.nlm.nih.gov/31735991/>), ProPepper (<https://www.propepper.net/epitope>) and AllergenOnline (<http://www.allergenonline.org/celiacbrowse.shtml>) were combined and duplicates were removed.

Last database update: 02/14/2021

### FASTA.

For homology search Allermatch uses FASTA(v36.3.8h) with default the parameters(matrix = BLOSUM50(15:-5), open = -10, extend = -2, ktup = 2)

### Identity search to known celiac epitopes.

Each of the ORF sequences has been compared with the epitope database using three different in-silico similarity search methods:

- A partial epitope match, where each epitope from the epitope database is compared to each ORF and the top hits are retained. All the hits are sorted on E-value and the top 100 with the lowest E-value are shown.
- An identical epitope match, where each epitope from the epitope database is compared to each ORF and only 100% hits are retained.
- A Q/E-X1-P-X2 motif search, where each of the possible 50 motif combinations is matched to each ORF. Additional a motif occurrence is calculated, which indicates how many times a certain motif is present in the epitope database.

## Top 100 epitope match results

Based on E-Value

1

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Glt-156 minimal epitope in considered Deamidated form | 15     | 0.0088  | 7       | 57.1     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |   |        |         |         |          |            |                |

```
53 ESNFNTQ 59
   :: ::
7  ESPFSQQ 13
```

2

| ID  | Length | Hit ID                  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Glt-156 minimal epitope | 15     | 0.018   | 7       | 57.1     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |                         |        |         |         |          |            |                |

```
53 ESNFNTQ 59
   :: ::
9  ESPFSQQ 15
```



3

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Glt-156 minimal epitope in considered Deamidated form | 15     | 0.018   | 7       | 57.1     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |   |        |         |         |          |            |                |

53 ESNFNTQ 59  
:: :: ::  
8 ESPFSQQ 14

4

| ID  | Length | Hit ID                              | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | LMW glutenin-glt-156 (p40-p59; E51) | 20     | 0.027   | 7       | 57.1     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |                                     |        |         |         |          |            |                |

53 ESNFNTQ 59  
:: :: ::  
12 ESPFSQQ 18

5

| ID  | Length | Hit ID                | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|-----------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | alpha gliadin 123-132 | 10     | 0.028   | 3       | 100.0    | 100.0      | ProPepper |
| <a href="https://www.iedb.org/epitope/51376">https://www.iedb.org/epitope/51376</a> |        |                       |        |         |         |          |            |           |

96 IPC 98  
:: ::  
3 IPC 5

6

| ID  | Length | Hit ID                          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | gamma5-gliadin (p227-237; E232) | 11     | 0.028   | 4       | 75.0     | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15972656">https://pubmed.ncbi.nlm.nih.gov/15972656</a> |        |                                 |        |         |         |          |            |                |

72 GILQ 75  
:: ::  
1 GIIQ 4

7

| ID  | Length | Hit ID                                      | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | LMW glutenin-glt-156 (p40-p59; E48 and E51) | 20     | 0.028   | 7       | 57.1     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |   |        |         |         |          |            |                |

53 ESNFNTQ 59  
:: :: ::  
12 ESPFSQQ 18

8

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Wheat peptide W09 | 14     | 0.032   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

11 FLP 13  
:::  
5 FLP 7

9

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Wheat peptide W09 | 12     | 0.033   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

11 FLP 13  
:::  
4 FLP 6

10

| ID  | Length | Hit ID                             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | alpha-Glia AG11 (p78<br>-p95; E86) | 17     | 0.034   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/19299713">https://pubmed.ncbi.nlm.nih.gov/19299713</a> |        |                                    |        |         |         |          |            |                |

11 FLP 13  
:::  
6 FLP 8

11

| ID  | Length | Hit ID                       | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | alpha-gliadin(p123-p<br>132) | 10     | 0.036   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12594302">https://pubmed.ncbi.nlm.nih.gov/12594302</a> |        |                              |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/18395083">https://pubmed.ncbi.nlm.nih.gov/18395083</a> |        |                              |        |         |         |          |            |                |

96 IPC 98  
:::  
3 IPC 5

12

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | gamma5-gliadin (p227<br>-p237) ; gamma-II ep<br>itope | 11     | 0.037   | 4       | 75.0     | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15972656">https://pubmed.ncbi.nlm.nih.gov/15972656</a> |        |   |        |         |         |          |            |                |

72 GILQ 75  
:::  
1 GIIQ 4

13

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Wheat peptide W09 | 14     | 0.038   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

11 FLP 13  
:::  
5 FLP 7

14

| ID  | Length | Hit ID               | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|----------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | DQ2-gamma-II peptide | 11     | 0.039   | 4       | 75.0     | 100.0      | ProPepper |
| <a href="https://www.iedb.org/epitope/20305">https://www.iedb.org/epitope/20305</a> |        |                      |        |         |         |          |            |           |

72 GILQ 75  
:::  
1 GILQ 4

15

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|-------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | alpha gliadin P11 | 15     | 0.04    | 3       | 100.0    | 100.0      | ProPepper |
| <a href="https://www.iedb.org/epitope/139589">https://www.iedb.org/epitope/139589</a> |        |                   |        |         |         |          |            |           |

11 FLP 13  
:::  
5 FLP 7

16

| ID  | Length | Hit ID                      | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|-----------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | alpha gliadin 78-95<br>AG11 | 17     | 0.041   | 3       | 100.0    | 100.0      | ProPepper |
| <a href="https://www.iedb.org/epitope/109723">https://www.iedb.org/epitope/109723</a> |        |                             |        |         |         |          |            |           |

11 FLP 13  
:::  
6 FLP 8

17

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | gamma gliadin 1 | 9      | 0.048   | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/32728397">https://pubmed.ncbi.nlm.nih.gov/32728397</a> |        |                 |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/22726570">https://pubmed.ncbi.nlm.nih.gov/22726570</a> |        |                 |        |         |         |          |            |                |

53 ESNFNTQ 59  
:::  
2 EQSFPQQ 8

18

| ID  | Length | Hit ID        | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | gamma gliadin | 9      | 0.05    | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/32728397">https://pubmed.ncbi.nlm.nih.gov/32728397</a> |        |               |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/22726570">https://pubmed.ncbi.nlm.nih.gov/22726570</a> |        |               |        |         |         |          |            |                |

53 ESNFNTQ 59  
: : : : :  
2 EQSFPQQ 8

19

| ID  | Length | Hit ID                    | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | alpha-Glia AG11 (p78-p95) | 17     | 0.052   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/19299713">https://pubmed.ncbi.nlm.nih.gov/19299713</a> |        |                           |        |         |         |          |            |                |

11 FLP 13  
: : :  
6 FLP 8

20

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Wheat peptide W36 | 15     | 0.055   | 9       | 44.4     | 88.9       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

1 MRSLILVL 9  
: : : : :  
5 IRSLVLRTL 13

21

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Wheat peptide W36 | 15     | 0.056   | 9       | 44.4     | 88.9       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

1 MRSLILVL 9  
: : : : :  
5 IRSLVLRTL 13

22

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Wheat peptide W36 | 16     | 0.061   | 9       | 44.4     | 88.9       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

1 MRSLILVL 9  
: : : : :  
5 IRSLVLRTL 13

23

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | W09    | 20     | 0.064   | 3       | 100.0    | 100.0      | ProPepper |
| <a href="https://www.iedb.org/epitope/238729">https://www.iedb.org/epitope/238729</a> |        |        |        |         |         |          |            |           |

11 FLP 13  
:::  
10 FLP 12

24

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Wheat peptide W09 | 20     | 0.064   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

11 FLP 13  
:::  
10 FLP 12

25

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Rye peptide R12 | 12     | 0.064   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                 |        |         |         |          |            |                |

12 LPL 14  
:::  
10 LPL 12

26

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Glt-156 minimal epitope in considered native form | 15     | 0.067   | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |   |        |         |         |          |            |                |

53 ESNFNTQ 59  
:::  
7 QSPFSQQ 13

27

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Glia-gamma30-gliadin (p222-236; E225 and E231) | 15     | 0.07    | 4       | 75.0     | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |  |        |         |         |          |            |                |

72 GILQ 75  
:::  
5 GIQ 8

28

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | DQ2-y -II y-Glia (p<br>222-p236; E229) | 15     | 0.073   | 4       | 75.0     | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/19299713">https://pubmed.ncbi.nlm.nih.gov/19299713</a> |        |  |        |         |         |          |            |                |

72 GILQ 75  
:::  
3 GIIQ 6

29

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Rye peptide R12 | 12     | 0.073   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                 |        |         |         |          |            |                |

12 LPL 14  
:::  
10 LPL 12

30

| ID  | Length | Hit ID                           | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|----------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | DQ2-y -II y-Glia (p<br>222-p236) | 15     | 0.074   | 4       | 75.0     | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/19299713">https://pubmed.ncbi.nlm.nih.gov/19299713</a> |        |                                  |        |         |         |          |            |                |

72 GILQ 75  
:::  
3 GIIQ 6

31

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Rye peptide R09 | 12     | 0.078   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                 |        |         |         |          |            |                |

12 LPL 14  
:::  
2 LPL 4

32

| ID  | Length | Hit ID                                   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Glia-gamma30-gliadin<br>(p222-236; E231) | 15     | 0.079   | 4       | 75.0     | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |  |        |         |         |          |            |                |

72 GILQ 75  
:::  
5 GIIQ 8

33

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | W36s   | 16     | 0.081   | 9       | 44.4     | 88.9       | ProPepper |
| <a href="https://www.iedb.org/epitope/238963">https://www.iedb.org/epitope/238963</a> |        |        |        |         |         |          |            |           |

1 MRSLLILVL 9  
.:...:.  
5 IRSVLRLTL 13

34

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Wheat peptide W36 | 20     | 0.081   | 9       | 44.4     | 88.9       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

1 MRSLLILVL 9  
.:...:.  
9 IRSVLRLTL 17

35

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Wheat peptide W37 | 12     | 0.082   | 8       | 37.5     | 62.5       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

119 DNGMNAW 126  
.:...:.  
3 DPSGQVQW 10

36

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | R12E   | 12     | 0.085   | 3       | 100.0    | 100.0      | ProPepper |
| <a href="https://www.iedb.org/epitope/238932">https://www.iedb.org/epitope/238932</a> |        |        |        |         |         |          |            |           |

12 LPL 14  
.:...:  
10 LPL 12

37

| ID  | Length | Hit ID                              | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Glia-gamma30-gliadin<br>(p222-p236) | 15     | 0.086   | 4       | 75.0     | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |                                     |        |         |         |          |            |                |

72 GILQ 75  
.:...:  
5 GIHQ 8

38

| ID  | Length | Hit ID                                   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Glia-gamma30-gliadin<br>(p222-236; E225) | 15     | 0.087   | 4       | 75.0     | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |  |        |         |         |          |            |                |

72 GILQ 75  
:::  
5 GIIQ 8

39

| ID  | Length | Hit ID                            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Sec-gammal in Deamid<br>ated form | 14     | 0.087   | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/14517794">https://pubmed.ncbi.nlm.nih.gov/14517794</a> |        |                                   |        |         |         |          |            |                |

53 ESNFNTQ 59  
:::  
5 EQSFPEQ 11

40

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | LMW glutenin-glt-156<br>(p40-p59; E48) | 20     | 0.088   | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |  |        |         |         |          |            |                |

53 ESNFNTQ 59  
:::  
12 QSPFSQQ 18

41

| ID  | Length | Hit ID               | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|----------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Rye peptide R01, R09 | 20     | 0.088   | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                      |        |         |         |          |            |                |

12 LPL 14  
:::  
3 LPL 5

42

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | LMW glutenin-glt-156<br>(p46-p54; E48 and E<br>51) | 9      | 0.089   | 4       | 75.0     | 75.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/16091925">https://pubmed.ncbi.nlm.nih.gov/16091925</a> |        |  |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |  |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/32728397">https://pubmed.ncbi.nlm.nih.gov/32728397</a> |        |  |        |         |         |          |            |                |

53 ESNF 56  
:::  
6 ESPF 9



43

| ID  | Length | Hit ID                         | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | HMW glutenin-glt04 (p707-p742) | 36     | 0.091   | 29      | 13.8     | 62.1       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/10540324">https://pubmed.ncbi.nlm.nih.gov/10540324</a> |        |                                |        |         |         |          |            |                |

39 RGYSLGNWVCAAKFESNFNTQATNRNTDGS 67  
 3 QGQRPQWLQPGQGQGYPTSPQQSGQGQ 31

44

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | W36    | 20     | 0.092   | 9       | 44.4     | 88.9       | ProPepper |
| <a href="https://www.iedb.org/epitope/238943">https://www.iedb.org/epitope/238943</a> |        |        |        |         |         |          |            |           |

1 MRSLILVL 9  
 9 IRSLVLR TL 17

45

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | LMW glutenin-glt-156 (p45-p54; E48, E49 and E51) minimal epitope | 10     | 0.092   | 4       | 75.0     | 75.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |  |        |         |         |          |            |                |

53 ESNF 56  
 7 ESPF 10

46

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Glt-156 minimal epitope in considered native form | 15     | 0.096   | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |   |        |         |         |          |            |                |

53 ESNFNTQ 59  
 8 QSPFSQQ 14

47

| ID  | Length | Hit ID                    | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|---------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | gliadin-gamma30 (222-236) | 15     | 0.097   | 4       | 75.0     | 100.0      | ProPepper |
| <a href="https://www.iedb.org/epitope/70564">https://www.iedb.org/epitope/70564</a> |        |                           |        |         |         |          |            |           |

72 GILQ 75  
 5 GIQ 8

48

| ID  | Length | Hit ID             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | alpha-gliadin 4037 | 17     | 0.097   | 9       | 44.4     | 66.7       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/21091908">https://pubmed.ncbi.nlm.nih.gov/21091908</a> |        |                    |        |         |         |          |            |                |

71 YGILQINSR 79  
 . . . . .  
 9 FGIFGTNYR 17

49

| ID  | Length | Hit ID                        | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Sec-gammal in Deamidated form | 14     | 0.098   | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/14517794">https://pubmed.ncbi.nlm.nih.gov/14517794</a> |        |                               |        |         |         |          |            |                |

53 ESNFNTQ 59  
 . . . . .  
 5 EQSFPEQ 11

50

| ID  | Length | Hit ID                | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|-----------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | alpha gliadin 251-270 | 20     | 0.099   | 9       | 44.4     | 66.7       | ProPepper |
| <a href="https://www.iedb.org/epitope/72058">https://www.iedb.org/epitope/72058</a> |        |                       |        |         |         |          |            |           |

71 YGILQINSR 79  
 . . . . .  
 12 FGIFGTNYR 20

51

| ID  | Length | Hit ID                             | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | gamma gliadin 222-236 DQ2-gamma-II | 15     | 0.1     | 4       | 75.0     | 100.0      | ProPepper |
| <a href="https://www.iedb.org/epitope/109223">https://www.iedb.org/epitope/109223</a> |        |                                    |        |         |         |          |            |           |

72 GILQ 75  
 . . . . .  
 3 GIIQ 6

52

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | 1448   | 15     | 0.1     | 14      | 28.6     | 71.4       | ProPepper |
| <a href="https://www.iedb.org/epitope/22327">https://www.iedb.org/epitope/22327</a> |        |        |        |         |         |          |            |           |

55 NFNTQATNRNTDGS 68  
 . . . . .  
 2 SFQPSQQNPQAQGS 15

53

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | R01    | 20     | 0.1     | 3       | 100.0    | 100.0      | ProPepper |
| <a href="https://www.iedb.org/epitope/238942">https://www.iedb.org/epitope/238942</a> |        |        |        |         |         |          |            |           |

12 LPL 14  
:::  
3 LPL 5

54

| ID  | Length | Hit ID                             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | alpha2-gliadin 1448<br>(p231-p245) | 15     | 0.1     | 14      | 28.6     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/16878175">https://pubmed.ncbi.nlm.nih.gov/16878175</a> |        |                                    |        |         |         |          |            |                |

55 NFNTQATNRNTDGS 68  
:::  
2 SFQPSQQNPQAQGS 15

55

| ID  | Length | Hit ID                               | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Glt-156 minimal epitope<br>(p41-p55) | 15     | 0.1     | 5       | 60.0     | 80.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |                                      |        |         |         |          |            |                |

53 ESNFN 57  
:::  
11 ESPFS 15

56

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | alpha-gliadin CAB769<br>61 (p251-p270) | 20     | 0.11    | 9       | 44.4     | 66.7       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/17629515">https://pubmed.ncbi.nlm.nih.gov/17629515</a> |        |  |        |         |         |          |            |                |

71 YGILQINSR 79  
:::  
12 FGIFGTNYR 20

57

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | CAUTION 100% match to<br>o Archaea protein lower<br>to others and to gamma5<br>(p63-p71; E63, E68 and E71) | 9      | 0.11    | 7       | 42.9     | 57.1       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15972656">https://pubmed.ncbi.nlm.nih.gov/15972656</a> |        |  |        |         |         |          |            |                |

53 ESNFNTQ 59  
:::  
1 EQPFPEQ 7

58

| ID  | Length | Hit ID                            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | LMW glutenin-glt-156<br>(p40-p59) | 20     | 0.11    | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |                                   |        |         |         |          |            |                |

53 ESNFNTQ 59  
 . . . . .  
 12 QSPFSQQ 18

59

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | LMW glutenin-glt-156<br>(p46-p54; E51) | 9      | 0.11    | 4       | 75.0     | 75.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/16091925">https://pubmed.ncbi.nlm.nih.gov/16091925</a> |        |  |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |  |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/32728397">https://pubmed.ncbi.nlm.nih.gov/32728397</a> |        |  |        |         |         |          |            |                |

53 ESNF 56  
 . . . . .  
 6 ESPF 9

60

| ID  | Length | Hit ID                      | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | glt04 (p723-p735; E7<br>24) | 13     | 0.11    | 7       | 42.9     | 57.1       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/22342873">https://pubmed.ncbi.nlm.nih.gov/22342873</a> |        |                             |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/10540324">https://pubmed.ncbi.nlm.nih.gov/10540324</a> |        |                             |        |         |         |          |            |                |

84 DGRTPGS 90  
 . . . . .  
 2 EGYPTS 8

61

| ID  | Length | Hit ID                            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Sec-gammal in Deamid<br>ated form | 14     | 0.11    | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/14517794">https://pubmed.ncbi.nlm.nih.gov/14517794</a> |        |                                   |        |         |         |          |            |                |

53 ESNFNTQ 59  
 . . . . .  
 5 EQSFPQQ 11

62

| ID  | Length | Hit ID                            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Sec-gammal in Deamid<br>ated form | 14     | 0.11    | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/14517794">https://pubmed.ncbi.nlm.nih.gov/14517794</a> |        |                                   |        |         |         |          |            |                |

53 ESNFNTQ 59  
 . . . . .  
 5 EQSFPQQ 11

63

| ID  | Length | Hit ID        | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|---------------|--------|---------|---------|----------|------------|----------|
| >LYSC_CHICK<br>K  | 147    | DQ2.5-glut-L2 | 9      | 0.11    | 4       | 75.0     | 75.0       | Sollid   |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |               |        |         |         |          |            |          |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |               |        |         |         |          |            |          |

53 ESNF 56  
:::  
6 ESPF 9

64

| ID  | Length | Hit ID                            | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|-----------------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | DQ2.2-glut-L-1 containing peptide | 20     | 0.12    | 7       | 42.9     | 71.4       | ProPepper |
| <a href="https://www.iedb.org/epitope/52130">https://www.iedb.org/epitope/52130</a> |        |                                   |        |         |         |          |            |           |

53 ESNFNTQ 59  
:::  
12 QSPFSQQ 18

65

| ID  | Length | Hit ID                         | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | gamma-gliadin 1383 (p141-p160) | 20     | 0.12    | 6       | 50.0     | 83.3       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/16878175">https://pubmed.ncbi.nlm.nih.gov/16878175</a> |        |                                |        |         |         |          |            |                |

97 PCSALL 102  
:::  
10 PCKNFL 15

66

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Glt-156 minimal epitope in considered Deamidated form | 15     | 0.12    | 5       | 60.0     | 80.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |   |        |         |         |          |            |                |

53 ESNFN 57  
:::  
10 ESPFS 14

67

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | LMW glutenin-glt-156 (p45-p54; E48 and E51) minimal epitope | 10     | 0.12    | 4       | 75.0     | 75.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |   |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |   |        |         |         |          |            |                |

53 ESNF 56  
:::  
7 ESPF 10

68

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | LMW glutenin-glt-156<br>(p45-p54; E49 and E<br>49) minimal epitope | 10     | 0.12    | 4       | 75.0     | 75.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |  |        |         |         |          |            |                |

53 ESNF 56  
:::  
7 ESPF 10

69

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Rye peptide R12 | 20     | 0.12    | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                 |        |         |         |          |            |                |

12 LPL 14  
:::  
16 LPL 18

70

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHIC<br>K   | 147    | R12    | 20     | 0.13    | 3       | 100.0    | 100.0      | ProPepper |
| <a href="https://www.iedb.org/epitope/238384">https://www.iedb.org/epitope/238384</a> |        |        |        |         |         |          |            |           |

12 LPL 14  
:::  
16 LPL 18

71

| ID  | Length | Hit ID                                | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|---------------------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHIC<br>K   | 147    | DQ2.2-glut-L-1 conta<br>ining peptide | 20     | 0.13    | 7       | 42.9     | 71.4       | ProPepper |
| <a href="https://www.iedb.org/epitope/167143">https://www.iedb.org/epitope/167143</a> |        |                                       |        |         |         |          |            |           |

53 ESNFNTQ 59  
:::  
12 QSPFSQQ 18

72

| ID  | Length | Hit ID                          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | alpha-gliadin p19 (p<br>21-p40) | 20     | 0.13    | 12      | 25.0     | 66.7       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/8315377">https://pubmed.ncbi.nlm.nih.gov/8315377</a> |        |                                 |        |         |         |          |            |                |

12 LPLAALGKVFGR 23  
:::  
2 VPLVQQQQLGQ 13

73

| ID  | Length | Hit ID                             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | gamma5 (p62-p72; E68, E63 and E71) | 11     | 0.13    | 7       | 42.9     | 57.1       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15972656">https://pubmed.ncbi.nlm.nih.gov/15972656</a> |        |                                    |        |         |         |          |            |                |

53 ESNFNTQ 59  
:::  
2 EQPFPEQ 8

74

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Wheat peptide W37 | 20     | 0.13    | 8       | 37.5     | 62.5       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

119 DGNMNAW 126  
:::  
8 DPSGQVQW 15

75

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Wheat peptide W05 | 20     | 0.13    | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

53 ESNFNTQ 59  
:::  
11 EQPFSQQ 17

76

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Rye peptide R12 | 16     | 0.13    | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                 |        |         |         |          |            |                |

12 LPL 14  
:::  
12 LPL 14

77

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Rye peptide R21 | 12     | 0.13    | 8       | 37.5     | 62.5       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                 |        |         |         |          |            |                |

122 GMNAWVAW 129  
:::  
3 GPSGQVEW 10

78

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHIC<br>K   | 147    | W37s   | 16     | 0.14    | 8       | 37.5     | 62.5       | ProPepper |
| <a href="https://www.iedb.org/epitope/238519">https://www.iedb.org/epitope/238519</a> |        |        |        |         |         |          |            |           |

119 DGNGMNAW 126  
: : : : :  
5 DPSGQVQW 12

79

| ID  | Length | Hit ID                       | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|------------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHIC<br>K   | 147    | gamma gliadin peptid<br>1383 | 20     | 0.14    | 6       | 50.0     | 83.3       | ProPepper |
| <a href="https://www.iedb.org/epitope/52318">https://www.iedb.org/epitope/52318</a> |        |                              |        |         |         |          |            |           |

97 PCSALL 102  
: : : : :  
10 PCKNFL 15

80

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHIC<br>K   | 147    | R21E   | 12     | 0.14    | 8       | 37.5     | 62.5       | ProPepper |
| <a href="https://www.iedb.org/epitope/238962">https://www.iedb.org/epitope/238962</a> |        |        |        |         |         |          |            |           |

122 GMNAWVAW 129  
: : : : :  
3 GPSGQVEW 10

81

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | LMW glutenin-glt-156<br>(p45-p54; E51) mini<br>mal epitope | 10     | 0.14    | 4       | 75.0     | 75.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a> |        |  |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |  |        |         |         |          |            |                |

53 ESNF 56  
: : : : :  
7 ESPF 10

82

| ID  | Length | Hit ID        | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|---------------|--------|---------|---------|----------|------------|----------|
| >LYSC_CHIC<br>K   | 147    | DQ8.5-glut-H1 | 9      | 0.14    | 6       | 50.0     | 50.0       | Sollid   |
| <a href="https://pubmed.ncbi.nlm.nih.gov/22013116">https://pubmed.ncbi.nlm.nih.gov/22013116</a> |        |               |        |         |         |          |            |          |

85 GRTPGS 90  
: : : : :  
2 GYYPTS 7



83

| ID  | Length | Hit ID                              | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | alpha-gliadin (proline-rich domain) | 16     | 0.15    | 7       | 42.9     | 42.9       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/1720424">https://pubmed.ncbi.nlm.nih.gov/1720424</a> |        |                                     |        |         |         |          |            |                |

48 CAAKFES 54  
: : :  
1 CPQPFPS 7

84

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | gamma-gliadin M23 M36999 (221-240) homologous to DQ2-gamma-I | 20     | 0.15    | 10      | 40.0     | 70.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12198706">https://pubmed.ncbi.nlm.nih.gov/12198706</a> |        |  |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/16878175">https://pubmed.ncbi.nlm.nih.gov/16878175</a> |        |  |        |         |         |          |            |                |

13 PLAALGKVFVG 22  
: : : : :  
3 PLFQLAQGLG 12

85

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Naturally occurring glutenins (p722-p736) (homolog of glt04) | 15     | 0.15    | 7       | 57.1     | 57.1       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/10540324">https://pubmed.ncbi.nlm.nih.gov/10540324</a> |        |  |        |         |         |          |            |                |

97 PCSALLS 103  
: : : : :  
7 PTSPQLS 13

86

| ID  | Length | Hit ID                     | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|----------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | DQ8-glut-H1, DQ8.5-glut-H1 | 9      | 0.16    | 6       | 50.0     | 50.0       | ProPepper |
| <a href="https://www.iedb.org/epitope/161144">https://www.iedb.org/epitope/161144</a> |        |                            |        |         |         |          |            |           |

85 GRTPGS 90  
: : : : :  
2 GYYPTS 7

87

| ID  | Length | Hit ID                             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | alpha-gliadin CAB76960 (p253-p272) | 20     | 0.16    | 4       | 50.0     | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/17629515">https://pubmed.ncbi.nlm.nih.gov/17629515</a> |        |                                    |        |         |         |          |            |                |

93 LCNI 96  
: : : : :  
2 MCNV 5

88

| ID  | Length | Hit ID                             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | gamma5 (p62-p74; E63, E68 and E71) | 13     | 0.16    | 7       | 42.9     | 57.1       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15972656">https://pubmed.ncbi.nlm.nih.gov/15972656</a> |        |                                    |        |         |         |          |            |                |

53 ESNFNTQ 59  
: : :  
2 EQPFPEQ 8

89

| ID  | Length | Hit ID                   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | HMW glutenin (p724-p734) | 11     | 0.16    | 6       | 50.0     | 50.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/16091925">https://pubmed.ncbi.nlm.nih.gov/16091925</a> |        |                          |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/10540324">https://pubmed.ncbi.nlm.nih.gov/10540324</a> |        |                          |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/22013116">https://pubmed.ncbi.nlm.nih.gov/22013116</a> |        |                          |        |         |         |          |            |                |

85 GRTPGS 90  
: : :  
2 GYYPTS 7

90

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Naturally occurring glutenins (p722-p736) (homolog of glt04) | 15     | 0.16    | 7       | 57.1     | 57.1       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/10540324">https://pubmed.ncbi.nlm.nih.gov/10540324</a> |        |  |        |         |         |          |            |                |

97 PCSALLS 103  
: : : :  
7 PTSPLQS 13

91

| ID  | Length | Hit ID             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Barley peptide B03 | 16     | 0.16    | 13      | 30.8     | 46.2       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                    |        |         |         |          |            |                |

85 GRTPGSRNLCNIP 97  
: : : :  
1 GQQPFPQPEQPIPI 13

92

| ID  | Length | Hit ID      | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------|--------|---------|---------|----------|------------|----------|
| >LYSC_CHICK   | 147    | DQ8-glut-H1 | 9      | 0.16    | 6       | 50.0     | 50.0       | Sollid   |
| <a href="https://pubmed.ncbi.nlm.nih.gov/10540324">https://pubmed.ncbi.nlm.nih.gov/10540324</a> |        |             |        |         |         |          |            |          |

85 GRTPGS 90  
: : :  
2 GYYPTS 7

93

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | gamma-gliadin I391 (p231-p250) ; gamma-gliadin M24 M36999 (231-250) identical to DQ2-gamma-II | 20     | 0.17    | 6       | 50.0     | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12198706">https://pubmed.ncbi.nlm.nih.gov/12198706</a> |        |   |        |         |         |          |            |                |
| <a href="https://pubmed.ncbi.nlm.nih.gov/16878175">https://pubmed.ncbi.nlm.nih.gov/16878175</a> |        |   |        |         |         |          |            |                |

1 MRSLLI 6  
.:...:  
15 IRSLVL 20

94

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Wheat peptide W11 | 15     | 0.17    | 7       | 42.9     | 71.4       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

53 ESNFNTQ 59  
.:...:  
8 EQTFPHQ 14

95

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Glutenin-Glt-17 (p50-p58; E52 and E53) | 9      | 0.17    | 2       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/16091925">https://pubmed.ncbi.nlm.nih.gov/16091925</a> |        |  |        |         |         |          |            |                |

13 PL 14  
.:  
8 PL 9

96

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Glutenin-Glt-17 (p50-p58; E53 and E55) | 9      | 0.17    | 2       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/16091925">https://pubmed.ncbi.nlm.nih.gov/16091925</a> |        |  |        |         |         |          |            |                |

13 PL 14  
.:  
8 PL 9

97

| ID  | Length | Hit ID                               | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | G4-9A gliadin (p62-p75; E65 and A70) | 14     | 0.18    | 5       | 60.0     | 60.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/12524402">https://pubmed.ncbi.nlm.nih.gov/12524402</a> |        |                                      |        |         |         |          |            |                |

12 LPLAA 16  
.:  
5 LPYPA 9

98

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Glutenin-Glt-17 (p50<br>-p58; E52, E53 and E<br>55) | 9      | 0.18    | 2       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/16091925">https://pubmed.ncbi.nlm.nih.gov/16091925</a> |        |   |        |         |         |          |            |                |

13 PL 14  
::  
8 PL 9

99

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Deamidated Glt-156 m<br>inimal epitope (p40-<br>p59) | 15     | 0.18    | 4       | 75.0     | 75.0       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/15714306">https://pubmed.ncbi.nlm.nih.gov/15714306</a> |        |  |        |         |         |          |            |                |

53 ESNF 56  
:::  
12 ESPF 15

100

| ID  | Length | Hit ID        | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|---------------|--------|---------|---------|----------|------------|----------|
| >LYSC_CHIC<br>K   | 147    | DQ2.2-glia-a1 | 9      | 0.18    | 4       | 50.0     | 100.0      | Sollid   |
| <a href="https://pubmed.ncbi.nlm.nih.gov/25261484">https://pubmed.ncbi.nlm.nih.gov/25261484</a> |        |               |        |         |         |          |            |          |

56 FNTQ 59  
:::  
2 FSVQ 5



Jul-28-2021  
WFSR  
Report: test

## Toxin Results

### Toxin database.

For the toxin database sequences have been retrieved from Swiss-Prot's animal toxin annotation project(<https://www.uniprot.org/program/Toxins>). If annotated, signal- and propeptides are removed. This results in a database with a size of 7452.

Last database update: 01/28/2021

### FASTA.

For homology search Allermatch uses FASTA(v36.3.8h) with default the parameters(matrix = BLOSUM50(15:-5), open = -10, extend = -2, ktup = 2)

### Identity search to known toxins.

A full FASTA alignment search has been performed, where each ORF is compared to the sequences in the toxin database. For each ORF the top hits are retained. All the hits are sorted on E-value and the top 100 with the lowest E-value are shown.

## Top 100 full-FASTA search results

Based on E-Value

1

| ID   | Length | Hit ID      | Accession              | Length | E-value | Overlap | Identity |
|--|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI  | 147    | TX219_APOSC | <a href="#">P49272</a> | 76     | 0.036   | 82      | 26.8     |
| <pre> 878 RNTDGS TDY GILQINSRWWCNDGRTPG----SRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVA       ::::: 4  QNLGSDIPHDIIKLPNGQWC---KTPGALCSSRSEC---CKAKHSDSVTYSSGCSRQW-SDQQGL-----       :::::       WRNRCKGTDVQA 140       :::::       FINQCRTC NVES 73 </pre> |        |             |                        |        |         |         |          |

2

| ID   | Length | Hit ID      | Accession              | Length | E-value | Overlap | Identity |
|--|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI  | 147    | SCX12_CENNO | <a href="#">P63019</a> | 67     | 0.7     | 46      | 34.8     |
| <pre> 874 DGRTE GSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAW 129       ::::: 2  DGY-PLASNGCKFGCSGLGENNPTCNHVCEKKAGSDYGYCYAWTCY 46 </pre> |        |             |                        |        |         |         |          |

3

| ID  | Length | Hit ID      | Accession              | Length | E-value | Overlap | Identity |
|---|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI   | 147    | SX15F_RHOJU | <a href="#">E7CLP4</a> | 65     | 0.97    | 59      | 33.9     |
| <pre> 878 PGSRNLCNIPCSALLSSDITASVNC-AKKIVSDGNGMNAWVAWRNRCKGT----DVQAW 141       ::::: 5  PMGRNGCKIPCAI---NDNICKVEQAKWKQSDGYCY----SWGLSCYCTNLLEDAEVW 56 </pre> |        |             |                        |        |         |         |          |

4

| ID        | Length   | Hit ID      | Accession | Length | E-value | Overlap | Identity |
|-----------|--|-------------|-----------|--------|---------|---------|----------|
| >LYSC_CHI | 147  | PA2A2_HELSU | P80003    | 142    | 1       | 54      | 29.6     |
| 26 LAAAM  | KRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTD--GSTDYGILQIN 77     |             |           |        |         |         |          |
| 43        | MAALEYKHGMRNRYRPHTVSHCDNQRFRSCL-MNVKDRADLVGMTYFTVLKIS 95 |             |           |        |         |         |          |

5

| ID        | Length  | Hit ID      | Accession | Length | E-value | Overlap | Identity |
|-----------|---|-------------|-----------|--------|---------|---------|----------|
| >LYSC_CHI | 147   | CRVP1_DISTY | Q2XXQ6    | 219    | 3.3     | 103     | 25.2     |
| 98 YRGY   | SLGNWVCAAKF--ESNFNTQATNRNTDGDSTDYGILQI--NSRWWCNDGRTPGSRNLCNIPCSALLS     |             |           |        |         |         |          |
| 122       | YKSYRVG---CAASYCPPSSSYNYFYVCQYCPAGNFAGLTATPYKSGPTCGDCPSACDNGLCTNPCS---R |             |           |        |         |         |          |
|           | SDITASVNC AKKIVSDGNGMNAWVAWRNRCKGT 136                                  |             |           |        |         |         |          |
|           | EDVF--MNC-KSLVAQSNCQDDYI--RKNCPAT 213                                   |             |           |        |         |         |          |

6

| ID        | Length   | Hit ID      | Accession | Length | E-value | Overlap | Identity |
|-----------|--|-------------|-----------|--------|---------|---------|----------|
| >LYSC_CHI | 147  | CRVP2_DISTY | Q2XXQ5    | 219    | 3.3     | 103     | 25.2     |
| 98 YRGY   | SLGNWVCAAKF--ESNFNTQATNRNTDGDSTDYGILQI--NSRWWCNDGRTPGSRNLCNIPCSALLS    |             |           |        |         |         |          |
| 122       | YKSYRVG---CAASYCPSSSYNYFYVCQYCPAGNFAGLTATPYKSGPTCGDCPSACDNGLCTNPCS---R |             |           |        |         |         |          |
|           | SDITASVNC AKKIVSDGNGMNAWVAWRNRCKGT 136                                 |             |           |        |         |         |          |
|           | EDVF--MNC-KSLVAQSNCQDDYI--RKNCPAT 213                                  |             |           |        |         |         |          |

7

| ID        | Length   | Hit ID      | Accession | Length | E-value | Overlap | Identity |
|-----------|--|-------------|-----------|--------|---------|---------|----------|
| >LYSC_CHI | 147  | SX17F_RHOJU | E7CLP5    | 65     | 4.2     | 55      | 29.1     |
| 68 PGSRL  | CNIPCSALLSSDITASVNC-AKKIVSDGNGMNAWVAWRNRCKGTDVQAW 141      |             |           |        |         |         |          |
| 5         | PMGRNGCKIPCAI---NDNICKTECQAKWKQSDGYCYSPGMSYCTNLPEDA EVW 56 |             |           |        |         |         |          |

8

| ID        | Length   | Hit ID      | Accession | Length | E-value | Overlap | Identity |
|-----------|--|-------------|-----------|--------|---------|---------|----------|
| >LYSC_CHI | 147  | TX216_APOSC | P49270    | 76     | 4.4     | 81      | 22.2     |
| 63 RNTDG  | STDYGILQINSRWWCNDGRTPGSRNLCNIP---CSALLSSDITASVNC AKKIVSDGNGMNAWVAW     |             |           |        |         |         |          |
| 4         | QNLGSGIPHDKIKLPNGQWC---KTPG--DLCSSESSECKAKHSNSVTYASFCSRQW----SGQQALFI- |             |           |        |         |         |          |
|           | RNRCKGTDVQA 140  |             |           |        |         |         |          |
|           | -NQCRTCNVES 73   |             |           |        |         |         |          |

9

| ID        | Length | Hit ID      | Accession              | Length | E-value | Overlap | Identity |
|-----------|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI | 147    | TOPC5_PHONI | <a href="#">P84093</a> | 80     | 4.7     | 77      | 27.3     |

67 NTQATNRNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDGNGMNAWVAWRNRC 133  
 2 NCIELNNDGSKD-DCQCCRDNAYCSCYNFFGIKSGCK--CS-VGNSGTGYSV-CLKKL--ECPNRRATSWKKEC 71

10

| ID        | Length | Hit ID      | Accession              | Length | E-value | Overlap | Identity |
|-----------|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI | 147    | PA2A3_TROCA | <a href="#">Q45Z28</a> | 124    | 6.2     | 54      | 31.5     |

82 CNDGRTPGSRNLCNIPCSALLSS-DITASVNCACKIVSDGNGMNAW-VAWRNRC 133  
 77 CNDGELTCKDN--NDECKAFICNCDRTAAICFARTPYNDAN----WNINTKTRC 124

11

| ID        | Length | Hit ID      | Accession              | Length | E-value | Overlap | Identity |
|-----------|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI | 147    | TX214_APOSC | <a href="#">P49269</a> | 76     | 6.4     | 81      | 22.2     |

63 RNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIP---CSALLSSDITASVNCACKIVSDGNGMNAWVAW  
 4 QNLGSGIPHDRIKLPNGQWC---KTPG--DLCSSSSECCAKHSNSVTYASFCSREW-SGQQL-----F  
 RNRCKGTDVQA 140  
 INQCRTCNVE 73

12

| ID        | Length | Hit ID      | Accession              | Length | E-value | Overlap | Identity |
|-----------|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI | 147    | PA2A2_TROCA | <a href="#">Q45Z29</a> | 124    | 7.5     | 54      | 31.5     |

82 CNDGRTPGSRNLCNIPCSALLSS-DITASVNCACKIVSDGNGMNAW-VAWRNRC 133  
 77 CNDGELTCKDN--NDECKAFICNCDRTAAICFARAPYNDAN----WNIDTKTRC 124

13

| ID        | Length | Hit ID      | Accession              | Length | E-value | Overlap | Identity |
|-----------|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI | 147    | PA2A1_TROCA | <a href="#">Q45Z30</a> | 124    | 7.5     | 54      | 31.5     |

82 CNDGRTPGSRNLCNIPCSALLSS-DITASVNCACKIVSDGNGMNAW-VAWRNRC 133  
 77 CNDGELTCKDN--NDECKAFICNCDRTAAICFARTPYNDAN----WNIDTKTRC 124

14

| ID        | Length | Hit ID     | Accession              | Length | E-value | Overlap | Identity |
|-----------|--------|------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI | 147    | CRVP_OPHHA | <a href="#">Q7ZT98</a> | 221    | 8.3     | 103     | 24.3     |

68 YRGYSLGNWV--CAAKFESNFNT--QATNRNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLS  
 122 YKTYRIGCAVNYCPSEYSYFYVCQYCPSGNMRGST---ATPYKSGPTCGDCPSACDNLCTNPCT--LY  
 SDITASVNCACKIVSDGNGMNAWVAWRNCKGT 136  
 NEYT---NC-DSLVKQSSCQDEWI--KSKCPAS 213



15

| ID   | Length | Hit ID     | Accession              | Length | E-value | Overlap | Identity |
|--|--------|------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI  | 147    | CRVP_PHIOL | <a href="#">Q09GJ9</a> | 221    | 8.3     | 103     | 23.3     |
| 3/8 YRGYSLG--NWVCAAKFESNFNT--QATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLS |        |            |                        |        |         |         |          |
| 122 YKSYRIGCAAYYCPSSLYNYFYVCQYCPAGNFAGRT---ATPYNSGPTCGDCPSACDNGLCTNPCSE--K |        |            |                        |        |         |         |          |
| SDITASVNC AKKIVSDGNGMNAWVAWRNRCKGT   | 136    |            |                        |        |         |         |          |
| NEFT---NC-NELVQQSSCQDDWI--KSNCAAT  | 213    |            |                        |        |         |         |          |

16

| ID   | Length | Hit ID      | Accession              | Length | E-value | Overlap | Identity |
|--|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI  | 147    | VM3B1_BOTJA | <a href="#">Q0NZY0</a> | 166    | 9.5     | 57      | 29.8     |
| 8/2 CNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSD-----GNGMNAWVAWRNRC | 133    |             |                        |        |         |         |          |
| 19 CDCGR-PGK---CQNPCCNATTCKLTGPSQCADGLCCDQCRFKGAGTECRAA-RSEC   | 70     |             |                        |        |         |         |          |