

## 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     |

**96**

|   |  |
|---|--|
| 1 | KVFGRCELAAAMKRHGLDNYRGYS LGNWVCAAKFESNFNTQATNRNTDGSTDY GILQINSRWWCNDGRTP<br>.....<br>KVFGRCELAAAMKRHGLDNYRGYS LGNWVCAAKFESNFNTQATNRNTDGSTDY GILQINSRWWCNDGRTP<br><br>GSRNLCNI PCSALLSSDITASVNCAKKIVSDGNMGNAWVAWRNRCKGTDVQAWIRGCR   147<br>.....<br>GSRNLCNI PCSALLSSDITASVNCAKKIVSDGNMGNAWVAWRNRCKGTDVQAWIRGCR   129 |
|---|--|

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-STEYGLFQINNKIWCKDDQNPSSN |   |             |           |        |         |         |          |        |
| LCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAW                       | 142   |             |           |        |         |         |          |        |
| ICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLAKALCS-EKLQW                         | 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> |        |            |                        |        |         |         |          |        |

14

| ID   | Length | Hit ID       | Accession | Length | E-value | Overlap | Identity | Recalc |
|--|--------|--------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI<br>89 GSRNL  | 147    | E7CLQ2_PRUAV | E7CLQ2    | 91     | 3.9     | 52      | 30.8     | 20.02  |
| CNIPCSALLSSDITASVNCAKKIVSDGNGMNA--WVAWRNRCKGTD 138<br>.:.:. . :.:.:. .<br>30 GIRNINNL---AKTTADROTACNCLKQLSASVPGVNANNAALPGKC-GVN 77 |        |              |           |        |         |         |          |        |

15

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16

| ID                                    | Length | Hit ID       | Accession | Length | E-value | Overlap | Identity | Recalc |
|---------------------------------------|--------|--------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI                             | 147    | E7BQV5_PERAM | E7BQV5    | 331    | 4.5     | 29      | 41.4     | 15.01  |
| 9% ILQINSRWWCNDGRTPGSRNLCNIPCSAL 101  |        |              |           |        |         |         |          |        |
| : : : : : : : : : : : : : : : :       |        |              |           |        |         |         |          |        |
| 232 IKKINDRLGCTN-KVIGSRTLGVFDCDKL 259 |        |              |           |        |         |         |          |        |

17

| ID  | Length | Hit ID              | Accession | Length | E-value | Overlap | Identity | Recalc |
|---|--------|---------------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI   | 147    | L7TUJ3_ACTER        | L7TUJ3    | 190    | 5.1     | 52      | 26.9     | 17.48  |
| <hr/>   |        |                     |           |        |         |         |          |        |
| GK CNIPCSALLSSDITASVNC AKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG  | 145    | :: :: : . . . . : : | :         | ::     | :       | :       | :        | :      |
| 5 CNGPCRDL--NDCDGQLICIKGKCND DPQVGTHI----CRGTT PSPQP GG | 49     |                     |           |        |         |         |          |        |

18

| ID                          | Length | Hit ID                          | Accession | Length | E-value | Overlap | Identity | Recalc |
|-----------------------------|--------|---------------------------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI                   | 147    | L7TRW9_ACTER                    | L7TRW9    | 189    | 6       | 52      | 26.9     | 17.48  |
| 94 CNIPCSALLSSDITASVNC      |        | AKKIVSDGNGMNAVAVRNRCKGTDVQAWIRG |           | 145    |         |         |          |        |
| 4 CNGPCRDL--NDCDGLICIKGKCND |        | DPEVGTHI----CRGTTSPQPGG         |           | 48     |         |         |          |        |

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20

| ID        | Length                    | Hit ID                            | Accession | Length | E-value | Overlap | Identity | Recalc |
|-----------|---------------------------|-----------------------------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147                       | L7TV12_ACTDE                      | L7TV12    | 189    | 8.3     | 53      | 24.5     | 16.23  |
| 94        | CNIPCSALLSSDITASVNC       | AKKIVSDGNGMNAVVAWRNRCKGTDVQAWIRGC | 146       |        |         |         |          |        |
| 4         | CNGPCRDL--NDCDGLICIEGKCND | DPEVGTHI----CRGTTSPQPGGC          | 49        |        |         |         |          |        |

21

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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 | <a href="#">P0DKH8</a> | 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  
KVFGRCELAAMKRGHGLDNYRGYS LGNWVCAAKFESNFNTQATNRNTDGS TDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI  
TASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL 147

| Name   | Accession ID | Description | Species | No exact words | Hit % |
|--|--------------|-------------|---------|----------------|-------|
| 0  |              |             |         |                |       |
| KVFGRCELAAMKRGHGLDNYRGYS LGNWVCAAKFESNFNTQATNRNTDGS TDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI |              |             |         |                |       |
| TASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL 129   |              |             |         |                |       |
| 52 ESNFNT 58   |              |             |         |                |       |
| 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  
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 MRSLLILVL--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):**  
**(51:131-52:131) 50.6% identity**

```
51 KFESNFTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSD
   ..... : ..... : ..... : ..... : ..... : ..... : ..... : ..... :
52 EYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-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 YESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDP

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

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

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

AWVAWRNRCKG 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
```

Jul-28-2021  
WFSR  
Report: test

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

60 ATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNMGNAWVAWRNRCKGTDVQ 140  
 . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :  
 62 FNGKNANGSSDYGLFQLNNKWCKDNKR-SSSNACNIMCSKLDDNIDDDISCAKRVVRDPKGMSAWKAVVKHCKDKDLS 140

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

61 TNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLNIPCSALLSSDITASVNC AKKIVSDGNMGMAWVAWRNRCKGTDVQA 141  
 ... :  
 63 NGKNANGSSDYGLFQLNNKWCKDNKRSSS-NACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKA WKHKCDKDLSE 141

**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 GKNANGSSDYGLFQLNNKWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVK  
RCKGTDVQAWIRG 145  
HCKDKDLSEYLAS 145

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

66 DGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGN GMNAWVAWRNRCKGTDVQAWIRGC 146  
.: : . :  
68 NGSSDYGLFQLNNKWCKDNKRSS-NACNIMCSKLDDNIDDDISCAKRVVRDPKGMSAWKA VKHCKDKDLSEYLASC 146

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

[illegible]

| 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

RNLNIPCSALLSS 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 VCAAKFESNFTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKK
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
29 VCMAYESNFTNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKR

   IVSDGNGMNAWVAW 130
   .: : .: : : : :
   VVRDPKGMSAWKAW 111
```

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

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

```
51 KFESNFTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSD
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
33 EYESNFTNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDDISCAKRVVRD

   GNGMNAWVAWR 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 FESNFTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDG
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
34 YESNFTNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDP

   NGMNAWVAWRNRCK 135
   .: : : : :
   KGMSAWKAWVKHCK 116
```

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

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

```
56 FNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMN
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
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-RNTDGYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNA
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
39 NTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSA

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

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

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

```
60 ATNRNTDGYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQ 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
43 FNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLS 121
```

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

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

```
61 TNRTDGYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQA 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
44 NGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLSE 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 NRNTDGYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRN
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
45 GKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVK

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

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

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

```
66 DGYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
49 NGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLSEYLASC 127
```

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

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

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

```
67 GSDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGT
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
50 GSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVKHCKDK

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 QATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVA
   .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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 ATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAW
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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 NRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRN
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
42 VQNND-STEYGLFQINNKIWCKDDQNP HSSNICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLAHKA

   RCKGTDVQAWIR 144
       : : : :
   LCS-EKLDQWLC 120

```

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

```

65 TDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG 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 DGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKG
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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     | 0.015   | 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     | 0.016   | 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     | 0.016   | 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    | gamma5-gliadin (p227-237; E232) | 11     | 0.024   | 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

5

| ID  | Length | Hit ID                | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|-----------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | alpha gliadin 123-132 | 10     | 0.029   | 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    | Wheat peptide W09 | 14     | 0.03    | 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

7

| ID  | Length | Hit ID                              | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | LMW glutenin-glt-156 (p40-p59; E51) | 20     | 0.03    | 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   | 147    | alpha-gliadin(p123-p132) | 10     | 0.031   | 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

9

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | gamma5-gliadin (p227-p237) ; gamma-II epitope | 11     | 0.032   | 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

10

| ID  | Length | Hit ID                                      | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | LMW glutenin-glt-156 (p40-p59; E48 and E51) | 20     | 0.032   | 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

11

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Wheat peptide W09 | 12     | 0.034   | 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

12

| ID  | Length | Hit ID                         | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | alpha-Glia AG11 (p78-p95; E86) | 17     | 0.035   | 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

13

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|-------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | alpha gliadin P11 | 15     | 0.038   | 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

14

| ID  | Length | Hit ID                    | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | alpha-Glia AG11 (p78-p95) | 17     | 0.038   | 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

15

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 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

16

| ID  | Length | Hit ID               | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|----------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | DQ2-gamma-II peptide | 11     | 0.043   | 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 GIIQ 4

17

| ID  | Length | Hit ID                   | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | alpha gliadin 78-95 AG11 | 17     | 0.044   | 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

18

| ID  | Length | Hit ID        | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | gamma gliadin | 9      | 0.046   | 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_CHIC<br>K   | 147    | gamma gliadin 1 | 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

20

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Wheat peptide W36 | 15     | 0.051   | 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  
: : : : :  
5 IRSVLRLTL 13

21

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Wheat peptide W09 | 20     | 0.053   | 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

22

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Wheat peptide W36 | 15     | 0.058   | 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  
: : : : :  
5 IRSVLRLTL 13

23

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Rye peptide R12 | 12     | 0.06    | 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

24

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 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 MRSLLILVL 9  
:::  
5 IRSVLRLTL 13

25

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 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

26

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Wheat peptide W37 | 12     | 0.065   | 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

27

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Rye peptide R12 | 12     | 0.067   | 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

28

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Glia-gamma30-gliadin<br>(p222-236; E225 and<br>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 GIIQ 8

29

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Glt-156 minimal epitope in considered native form | 15     | 0.073   | 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

30

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHIC<br>K   | 147    | W36s   | 16     | 0.074   | 9       | 44.4     | 88.9       | ProPepper |
| <a href="https://www.iedb.org/epitope/238963">https://www.iedb.org/epitope/238963</a> |        |        |        |         |         |          |            |           |

1 MRSLILVL 9  
:::  
5 IRSVLRLTL 13

31

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHIC<br>K   | 147    | R12E   | 12     | 0.076   | 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

32

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Rye peptide R09 | 12     | 0.079   | 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

33

| ID  | Length | Hit ID                                   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Glia-gamma30-gliadin<br>(p222-236; E225) | 15     | 0.08    | 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

34

| ID  | Length | Hit ID                                   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Glia-gamma30-gliadin<br>(p222-236; E231) | 15     | 0.08    | 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

35

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Wheat peptide W36 | 20     | 0.082   | 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  
:::  
9 IRSVLRLTL 17

36

| 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     | 0.083   | 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

37

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | LMW glutenin-glt-156<br>(p45-p54; E48, E49<br>and E51) minimal epi<br>tope | 10     | 0.084   | 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

38

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | LMW glutenin-glt-156<br>(p46-p54; E48 and E<br>51) | 9      | 0.085   | 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

39

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Glt-156 minimal epit<br>ope in considered na<br>tive form | 15     | 0.086   | 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

40

| ID  | Length | Hit ID                             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | alpha2-gliadin 1448<br>(p231-p245) | 15     | 0.089   | 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

41

| ID  | Length | Hit ID               | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|----------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Rye peptide R01, R09 | 20     | 0.089   | 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_CHIC<br>K   | 147    | Sec-gammal in Deamid<br>ated form | 14     | 0.09    | 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



43

| ID  | Length | Hit ID             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | alpha-gliadin 4037 | 17     | 0.091   | 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

44

| ID  | Length | Hit ID                       | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | DQ2-y -II y-Glia (p222-p236) | 15     | 0.092   | 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

45

| ID  | Length | Hit ID                           | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|----------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Glia-gamma30-gliadin (p222-p236) | 15     | 0.093   | 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

46

| ID  | Length | Hit ID                        | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Sec-gammal in Deamidated form | 14     | 0.097   | 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 EQSFPPQ 11

47

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 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

48

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | W36    | 20     | 0.1     | 9       | 44.4     | 88.9       | ProPepper |
| <a href="https://www.iedb.org/epitope/238943">https://www.iedb.org/epitope/238943</a> |        |        |        |         |         |          |            |           |

1 MRSLLILVL 9  
.:...:.  
9 IRSLLVRLTL 17

49

| ID  | Length | Hit ID                    | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|---------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | gliadin-gamma30 (222-236) | 15     | 0.1     | 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 GLIQ 8

50

| ID  | Length | Hit ID                        | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Sec-gammal in Deamidated form | 14     | 0.1     | 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

51

| ID  | Length | Hit ID                        | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Sec-gammal in Deamidated form | 14     | 0.1     | 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

52

| ID  | Length | Hit ID        | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|---------------|--------|---------|---------|----------|------------|----------|
| >LYSC_CHICK   | 147    | DQ2.5-glut-L2 | 9      | 0.1     | 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

53

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | gamma gliadin 222-23<br>6 DQ2-gamma-II | 15     | 0.11    | 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

54

| ID  | Length | Hit ID                    | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|---------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | alpha gliadin 251-27<br>0 | 20     | 0.11    | 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

55

| ID  | Length | Hit ID                          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | alpha-gliadin p19 (p<br>21-p40) | 20     | 0.11    | 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 VPLVQQQQFLGQ 13

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 t<br>o Archaea protein lo<br>wer to others and to<br>gamma5 (p63-p71; E6<br>3, 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_CHIC<br>K   | 147    | gamma-gliadin 1383 (<br>p141-p160) | 20     | 0.11    | 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

59

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | LMW glutenin-glt-156<br>(p40-p59; E48) | 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

60

| 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     | 0.11    | 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

61

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 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

62

| ID  | Length | Hit ID                             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | HMW glutenin-glt04 (<br>p707-p742) | 36     | 0.11    | 29      | 13.8     | 62.1       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/10540324">https://pubmed.ncbi.nlm.nih.gov/10540324</a> |        |                                    |        |         |         |          |            |                |

39 RGYS LGNWVCAAKFESNFNTQATNRNTDGS 67  
:::  
3 QGQRPQGWLQPGQGQGYPTSPQQSGQGQ 31

63

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | W37s   | 16     | 0.12    | 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

64

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | 1448   | 15     | 0.12    | 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

65

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | R21E   | 12     | 0.12    | 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

66

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Wheat peptide W37 | 20     | 0.12    | 8       | 37.5     | 62.5       | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |                   |        |         |         |          |            |                |

119 DGNGMNAW 126  
 : : : : :  
 8 DPSGQVQW 15

67

| ID  | Length | Hit ID                            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | LMW glutenin-glt-156<br>(p40-p59) | 20     | 0.12    | 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

68

| ID  | Length | Hit ID                            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Glt-156 minimal epitope (p41-p55) | 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  
:::  
11 ESPFS 15

69

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 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

70

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 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

71

| ID  | Length | Hit ID                  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | glt04 (p723-p735; E724) | 13     | 0.12    | 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

72

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 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

73

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Rye peptide R12 | 16     | 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  
:::  
12 LPL 14

74

| ID  | Length | Hit ID          | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK   | 147    | Rye peptide R21 | 12     | 0.12    | 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

75

| ID  | Length | Hit ID                            | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|-----------------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | DQ2.2-glut-L-1 containing 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

76

| ID  | Length | Hit ID                            | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|-----------------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK   | 147    | DQ2.2-glut-L-1 containing peptide | 20     | 0.13    | 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

77

| 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

78

| 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     | 0.13    | 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

79

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Naturally occurring<br>glutenins (p722-p736<br>) (homolog of glt04) | 15     | 0.13    | 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

80

| 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

81

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | alpha-gliadin CAB769<br>60 (p253-p272) | 20     | 0.14    | 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

82

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Wheat peptide W05 | 20     | 0.14    | 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



83

| ID  | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | R12    | 20     | 0.15    | 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

84

| ID  | Length | Hit ID                              | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 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

85

| ID  | Length | Hit ID   | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 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 PTSPLQS 13

86

| ID  | Length | Hit ID      | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------|--------|---------|---------|----------|------------|----------|
| >LYSC_CHICK<br>K  | 147    | DQ8-glut-H1 | 9      | 0.15    | 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

87

| ID  | Length | Hit ID        | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|---------------|--------|---------|---------|----------|------------|----------|
| >LYSC_CHICK<br>K  | 147    | DQ8.5-glut-H1 | 9      | 0.15    | 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

88

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | gamma5 (p62-p74; E63<br>, 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_CHIC<br>K   | 147    | gamma-gliadin 1391 (p231-p250) ; gamma-gliadin M24 M36999 (231-250) identical to DQ2-gamma-II | 20     | 0.16    | 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 IRSVL 20

90

| ID  | Length | Hit ID                                      | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Glutenin-Glt-17 (p50-p58; E52, E53 and E55) | 9      | 0.16    | 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

91

| ID  | Length | Hit ID                                       | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | Deamidated Glt-156 minimal epitope (p40-p59) | 15     | 0.16    | 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

92

| ID  | Length | Hit ID                               | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC<br>K   | 147    | G4-9A gliadin (p62-p75; E65 and A70) | 14     | 0.17    | 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

93

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | gamma-gliadin M23 M3<br>6999 (221-240) homologous to DQ2-gamma-I<br>I | 20     | 0.17    | 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 PLFQLAQLG 12

94

| ID  | Length | Hit ID                       | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | HMW glutenin (p724-p<br>734) | 11     | 0.17    | 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

95

| ID  | Length | Hit ID             | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Barley peptide B03 | 16     | 0.17    | 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 GQQFFPQPEQPIIP 13

96

| ID  | Length | Hit ID  | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Homolog of oat avenin-derived T cell-stimulatory peptide in Deamidated form | 15     | 0.17    | 3       | 100.0    | 100.0      | AllergenOnline |
| <a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a> |        |   |        |         |         |          |            |                |

73 ILQ 75  
: : :  
12 ILQ 14

97

| ID  | Length | Hit ID                     | Length | E-value | Overlap | Identity | Similarity | Database  |
|---|--------|----------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK<br>K  | 147    | DQ8-glut-H1, DQ8.5-glut-H1 | 9      | 0.18    | 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

98

| ID  | Length | Hit ID            | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Wheat peptide W11 | 15     | 0.18    | 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

99

| 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      | 0.18    | 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

100

| ID  | Length | Hit ID                                 | Length | E-value | Overlap | Identity | Similarity | Database       |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK<br>K  | 147    | Glutenin-Glt-17 (p50-p58; E52 and E55) | 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



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  | KRHGLDNYRGYS LGNWVCAAKFESNFNTQATNRNTD--GSTDY GILQIN 77     |             |           |        |         |         |          |
| 43        | MAALEYKHGMRNYRPH TVSHCDN QFRSCL-MNVKDR TADLVGMTYFTVLKIS 95 |             |           |        |         |         |          |

5

| 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--ESNFNTQATNRNTD GSTDY GILQI--NSRWWCNDGRTPGSRNLCNIPCSALLS   |             |           |        |         |         |          |
| 122       | YKSYRVG---CAASYCPSSSYNYFYVCQYCPAGNFAGLTATPYKSGPTCGDCPSACDNGLCTNPCS---R |             |           |        |         |         |          |
|           | SDITASVNC AKKIVSDGNGMNAWVAWRNRCKGT 136                                 |             |           |        |         |         |          |
|           | EDVF--MNC-KSLVAQSNCQDDYI--RKNCPAT 213                                  |             |           |        |         |         |          |

6

| 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--ESNFNTQATNRNTD GSTDY GILQI--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 PGSRN  | LNCNIPCSALLSSDITASVNC-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  | STDY GILQINSRWWCNDGRTPGSRNLCNIP---CSALLSSDITASVNC AKKIVSDGNGMNAWVAW   |             |           |        |         |         |          |
| 4         | QNLGSGIPHDKIKLPNGQWC---KTPG--DLCSSSSECCAKHSNSVTYASFCSRQW----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 NTQATNRNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRC 133  
 2 NCIELNND CDGSKD-DCQCCRDNAYCSCYNFFGIKSGCK--CS-VGNSGTGYSV-CLKKL--ECPNRRRAWTSWKKEC 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-DITASVNC AKKIVSDGNGMNAW-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---CSALLSSDITASVNC AKKIVSDGNGMNAWVAW  
 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-DITASVNC AKKIVSDGNGMNAW-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-DITASVNC AKKIVSDGNGMNAW-VAWRNRC 133  
 77 CNDGELTCKDN--NDECKAFICNCDRTAAICFARTPYNDAN----WNIDTKTRC 124

14

| 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     |

68 YRGYSLG--NWVCAAKFESNFNT--QATNRNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLS  
 122 YKSYRIGCAAYYCPSSLYNYFYVCQYCPAGNFAGRT---ATPYNSGPTCGDCPSACDNGLCNTPCSE--K  
 SDITASVNC AKKIVSDGNGMNAWVAWRNCKGT 136  
 NEFT---NC-NELVQQSSCQDDWI--KSNCAAT 213



15

| 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     |
| <pre> 3/8  YRGYSLGNWV--CAAKFESNFNT--QATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLS       :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  ::::: 122  YKTYRIGCAVNYCPSSEYSYFYVCQYCPSGNMRGST---ATPYKSGPTCGDCPSACDNGLCTNPCT--LY       :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::       SDITASVNC AKKIVSDGNGMNAWVAWRNRCKGT 136       :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::       NEYT---NC-DSL VKQSSCQDEWI--KSKCPAS 213 </pre> |        |            |                        |        |         |         |          |

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     |
| <pre> 8/2  CNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSD-----GNGMNAWVAWRNRC 133       :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  ::::: 19  CDCGR-PGK---CQNPCCNATTCKLTGPSQCADGLCCDQCRFKGAGTECRAA-RSEC 70 </pre> |        |             |                        |        |         |         |          |