

## 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 KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTP  
 1 KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTP  
 GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR 147  
 GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR 129

2

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHI	147	XP_014705584	<a href="#">XP_014705584</a>	148	2.3e-32	150	48.0	na
gk MRSLLTILVL--CFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNVWCAAKFESNFNTQATN-RNTDG ::: 1 MRSTLIISLLSCFFAVYE-AKVFSKCELAHKLKAQEMDGFGGYS LANVWCMAEYESNFNTRAFNGKNANG  STDYGILQINSRWWCNDGRTPGSRLNCNI PCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTD :::: SSDYGLFQLNNKWCKDNKR-SSSNACNIMCSKLLDDNIDDDISC AKRVVRDPKGMSAWKAWVKHCKDKD  VQAWIRGCR 147 . . . LSEYLASCN 148								

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	FNTQATNRNTDGSTDYGI-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 CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCND DPQVGTHI-----CRGTTX SXQPGGC 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 GRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMN 125</p> <p>28 GCCSGVRS LNN---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 CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCND DPQVGTHI-----CRGTTSPQP GGC 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 CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCND DPQVGTHI-----CRGTTSPQP GGC 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 CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCND DPQVGTHI-----CRGTTSPQP GGC 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 GSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNA--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 GSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNA--WVAWRNRCKGTD 138</p> <p>30 GIRNINNL---AKTTADRQTACNCLKQLSASVPGVNANNAALPGKC-GVN 77</p>								

14

[illegible]

15

[illegible]

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
973 ILQINSRWWCNDGRTPGSRNLCNIPCSAL 101								
232 IKKINDRLGCTN-KVIGSRTL CVFDCDKL 259								

17

[illegible]

18

[illegible]

19

[illegible]

20

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHI	147	L7TV12_ACTDE	<a href="#">L7TV12</a>	189	8.3	53	24.5	16.23
GK4 CNIPCSALLSSDITASVNC AKKI VSDGNGMNAWVAWRNRCKGT DVQAWIRGC	146							
:::~::~:								
4     CNGPCRDL--NDCDGOLICIEGKCND DPEVGTHI-----CRGTTPSQPGGC	49							

21

[illegible]

22

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

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

23

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

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

24

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

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

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

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

## Exact word and sliding window results

Shown per ORF

### Exact word results:

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

18  
KVFGRCELAAMKRGHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGS TDY GILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI  
TASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG CRL 147

Name	Accession ID	Description	Species	No exact words	Hit %
0					
KVFGRCELAAMKRGHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGS TDY GILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI					
TASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG CRL 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 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  MRSLLILVLCLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTD
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
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, milk is 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
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   GRTPGSRNLNLC 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
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   RTPGSRNLNIPCS 100
   .: : : : :
   KR-SSSNACNIMCS 100
```

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

```

21 FGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPG
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
22 FSKCELAHKLKAQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSS

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 SKCELAHKLKAQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SS

RNLCNIPCSALLSS 105
: : : : : : : : : :
SNACNIMCSKLLDD 105

```

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

```

26 LAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLC
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
27 LAHKLKAQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSS-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 AHKLKAQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACN

IPCSALLSSDITAS 110
: : : : : : : : : :
IMCSKLLDDNIDDD 110

```

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

```

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

   ALLSSDITASV 111
   : : : : : :
   KLLDDNIDDDI 111
  
```

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

```

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

   LLSSDITASVNCAK 115
   : : : : : : : : : :
   LLDDNIDDDISCAK 115
  
```

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

```

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

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

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

```

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

   ITASVNCAKKIVSD 120
   : : . . . : :
   IDDDISCAKRVVRD 120
  
```

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

```
41 YSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITAS
   ::::::::::: ::::::::::: : ::::::::::: ::::::::::: : : :: :: :: :: :: :: ::
42 YSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDDNIDDD
   V NCAKKIVSDG 121
   . :: :: :: ::
   I SCAKRVVRDP 121
```

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

```
42 SLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASV
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
43 SLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDI
   NCAKKIVSDGNGMN 125
   . :: :: :: ::
   SCAKRVVRDPKGMS 125
```

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

```
46 WVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAK
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
47 WVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDDNIDDDISCAK
   KIVSDGNGMNA 126
   . : : . :: ::
   RVVRDPKGMSA 126
```

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

```
47 VCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKK
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
48 VCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKR
   IVSDGNGMNAVAV 130
   . : : . :: ::
   VVRDPKGMSAWKAW 130
```

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

```

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

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

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

```

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

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

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

```

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

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

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

```

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

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

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

60 ATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNMNAWVAWRNRCKGTDVQ 140  
 . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :  
 62 FNGKNANGSSDYGLFQLNNKWCKDNKR-SSSNACNIMCSKLDDNIDDDISCAKRVRDPKGMSAWKAWVKHCKDKDLS 140

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

61 TNRNTDGSTDYGILQINSRWWCNDGRTPGSRLNCNIPCSALLSSDITASVNC AKKIVSDGNMGMAWVAWRNRCKGTDVQA 141  
... : ... : ... : ... : ... : ... : ... : ... : ... : ... :  
63 NGKNANGSSDYGLFQLNNKWCKDNKRSSS-NACNIMCSKLDDNIDDISCAKRVRDPKGMSAWKAWVKHCKDKDLSE 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-SSSNACNIMCSKLLDDNIDDDISCAKRVRDPKGMSAWKAWVK  
RCKGTDVQAWIRG 145  
HCKDKDLSEYLAS 145

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

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

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

67 GSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDGNMGNAWVAWRNRCKGT  
:::  
69 GSSDYGLFQLNNKWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVKHKCDK  
  
DVQAWIRGCRL 148  
:. . . : :  
DLSEYLASCNL 148

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

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

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

```

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

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

```

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

```

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

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

```

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

```

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

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

```

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

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

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

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

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

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

```
36 DNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSS
   . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
18 DFGGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-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 GFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDEN

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

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

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

```
41 YSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITAS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
23 YSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-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 SLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDI

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

```
57 NTQATN-RNTDGYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNA
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
39 NTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSA

WVAWRNRCKGTDV 139
: : : : : : :
WKAWVKHCKDKDL 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  LCFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTP 89
   :               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
3  LT-----KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNN--STEYGLFQINNKIWCKDDQNP 67

```

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

```

11  FLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGS 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  LPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWW
   :               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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  AALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCND
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1  EQLTK----CEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNN--STEYGLFQINNKIWCKD
   GRTPGSRNLCNI 97
   : : : : : : :
   DQNP 75

```

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

```

18  GKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIP 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/ceciacbrowse.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 K	147	Glt-156 minimal epitope in considered Deamidated form	15	0.012	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

2

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Glt-156 minimal epitope in considered Deamidated form	15	0.012	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



3

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope	15	0.013	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

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 GLIQ 4

5

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p40-p59; E48 and E51)	20	0.025	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

6

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

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

7

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha gliadin 123-132	10	0.03	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

8

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	alpha-gliadin(p123-p 132)	10	0.033	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_CHIC K	147	gamma5-gliadin (p227 -p237) ; gamma-II ep itope	11	0.033	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_CHIC K	147	DQ2-gamma-II peptide	11	0.038	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

11

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Wheat peptide W09	12	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  
:::  
4 FLP 6

12

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Wheat peptide W09	14	0.04	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

13

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha gliadin P11	15	0.042	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	Wheat peptide W09	14	0.044	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

15

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-Glia AG11 (p78 -p95; E86)	17	0.045	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

16

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-Glia AG11 (p78 -p95)	17	0.048	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

17

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

53 ESNFNTQ 59  
:::  
2 EQSFPQQ 8

18

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	gamma gliadin 1	9	0.049	7	42.9	71.4	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/32728397">https://pubmed.ncbi.nlm.nih.gov/32728397</a>								
<a href="https://pubmed.ncbi.nlm.nih.gov/22726570">https://pubmed.ncbi.nlm.nih.gov/22726570</a>								

53 ESNFNTQ 59  
: : : : :  
2 EQSFPQQ 8

19

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	alpha gliadin 78-95 AG11	17	0.05	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

20

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK 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 MRSLILVL 9  
: : : : :  
5 IRSVLRTL 13

21

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Rye peptide R12	12	0.058	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

22

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Wheat peptide W09	20	0.059	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

23

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Wheat peptide W36	15	0.059	9	44.4	88.9	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a>								

1 MRSLILVL 9  
.:.:.:  
5 IRSVLRLTL 13

24

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Glia-gamma30-gliadin (p222-236; E225 and E231)	15	0.063	4	75.0	100.0	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/1205577">https://pubmed.ncbi.nlm.nih.gov/1205577</a>								

72 GILQ 75  
.:.:  
5 GIIQ 8

25

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	W09	20	0.065	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 K	147	Wheat peptide W36	16	0.069	9	44.4	88.9	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a>								

1 MRSLILVL 9  
.:.:.:  
5 IRSVLRLTL 13

27

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	DQ2-y -II y-Glia (p 222-p236; E229)	15	0.071	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

28

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope in considered native form	15	0.071	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

29

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glia-gamma30-gliadin (p222-236; E225)	15	0.074	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

30

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R12	12	0.074	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

31

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W37	12	0.076	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  
: : : : :  
3 DPSGQVQW 10

32

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glia-gamma30-gliadin (p222-236; E231)	15	0.076	4	75.0	100.0	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a>								

72 GILQ 75  
: : :  
5 GIIQ 8

33

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	R12E	12	0.078	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

34

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ2-y -II y-Glia (p222-p236)	15	0.078	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

35

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	W36s	16	0.079	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 IRSVLRTL 13

36

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope in considered native form	15	0.079	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

37

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	HMW glutenin-glt04 (p707-p742)	36	0.08	29	13.8	62.1	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/10540324">https://pubmed.ncbi.nlm.nih.gov/10540324</a>								

39 RGYSLGNWVCAAKFESNFNTQATNRNTDGS 67  
:::  
3 QGQRPQGWLQPGQGQGYPTSPQQSGQGQ 31

38

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Rye peptide R09	12	0.08	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

39

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Glia-gamma30-gliadin (p222-p236)	15	0.081	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 GLIQ 8

40

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Sec-gammal in Deamid ated form	14	0.086	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

41

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Wheat peptide W36	20	0.087	9	44.4	88.9	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a>								

1 MRSLLILVL 9  
:::  
9 IRSLVLR TL 17

42

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	alpha-gliadin 4037	17	0.089	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



43

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	alpha2-gliadin 1448 (p231-p245)	15	0.09	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

44

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Rye peptide R01, R09	20	0.09	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

45

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	LMW glutenin-glt-156 (p46-p54; E48 and E 51)	9	0.092	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

46

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	R01	20	0.093	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

47

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	LMW glutenin-glt-156 (p40-p59; E48)	20	0.095	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

48

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gliadin-gamma30 (222-236)	15	0.096	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 GIIQ 8

49

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma gliadin 222-236 DQ2-gamma-II	15	0.097	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

50

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p40-p59)	20	0.097	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

51

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 EQSFPEQ 11

52

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p45-p54; E48, E49 and E51) minimal epitope	10	0.098	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

53

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

71 YGILQINSR 79  
 . . . . .  
 12 FGIFGTNYR 20

54

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

55 NFNTQATNRNTDGS 68  
 . . . . .  
 2 SFQPSQQNPQAQGS 15

55

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 MRSLILVL 9  
 . . . . .  
 9 IRSVLRLTL 17

56

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin CAB769 61 (p251-p270)	20	0.1	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	147	LMW glutenin-glt-156 (p46-p54; E51)	9	0.1	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

58

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ2.2-glut-L-1 containing peptide	20	0.11	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

59

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope (p41-p55)	15	0.11	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

60

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope in considered Deamidated form	15	0.11	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

61

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	0.11	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

62

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

53 ESNFNTQ 59  
:::  
5 EQSFPQQ 11

63

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

53 ESNFNTQ 59  
:::  
5 EQSFPQQ 11

64

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

53 ESNF 56  
:::  
6 ESPF 9

65

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

53 ESNFNTQ 59  
:::  
12 QSPFSQQ 18

66

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin p19 (p21-p40)	20	0.12	12	25.0	66.7	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/8315377">https://pubmed.ncbi.nlm.nih.gov/8315377</a>								

12 LPLAALGKVFGR 23  
:::  
2 VPLVQQQQLGQ 13

67

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma5 (p62-p72; E68, E63 and E71)	11	0.12	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

68

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	CAUTION 100% match to Archaea protein lower to others and to gamma5 (p63-p71; E63, E68 and E71)	9	0.12	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

69

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	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 DPŠGQVQW 15

70

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

53 ESNF 56  
:::  
7 ESPF 10

72

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

73

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma-gliadin 1383 (p141-p160)	20	0.13	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

74

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

53 ESNFNTQ 59  
:::  
11 EQPFSQQ 17

75

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	glt04 (p723-p735; E724)	13	0.13	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

76

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R12	20	0.13	3	100.0	100.0	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a>								

12 LPL 14  
:::  
16 LPL 18

77

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	R12	20	0.14	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

78

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma5 (p62-p74; E63, E68 and E71)	13	0.14	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

79

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glutenin-Glt-17 (p50-p58; E52, E53 and E55)	9	0.14	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

80

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R21	12	0.14	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

81

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma gliadin peptid 1383	20	0.15	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

82

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	R21E	12	0.15	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



83

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	gamma-gliadin 1391 (p231-p250) ; gamma-gliadin M24 M36999 (231-250) identical to DQ2-gamma-II	20	0.15	6	50.0	100.0	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/12198706">https://pubmed.ncbi.nlm.nih.gov/12198706</a>								
<a href="https://pubmed.ncbi.nlm.nih.gov/16878175">https://pubmed.ncbi.nlm.nih.gov/16878175</a>								

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

84

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Deamidated Glt-156 minimal epitope (p40-p59)	15	0.15	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

85

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC 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 PTSPQLS 13

86

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	W37s	16	0.16	8	37.5	62.5	ProPepper
<a href="https://www.iedb.org/epitope/238519">https://www.iedb.org/epitope/238519</a>								

119 DNGMNAW 126  
.:...:  
5 DPSGQVQW 12

87

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	alpha-gliadin CAB769 60 (p253-p272)	20	0.16	4	50.0	100.0	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/17629515">https://pubmed.ncbi.nlm.nih.gov/17629515</a>								

93 LCNI 96  
.:.:  
2 MCNV 5

88

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	gamma-gliadin M23 M3 6999 (221-240) homol ogous to DQ2-gamma-I I	20	0.16	10	40.0	70.0	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/12198706">https://pubmed.ncbi.nlm.nih.gov/12198706</a>								
<a href="https://pubmed.ncbi.nlm.nih.gov/16878175">https://pubmed.ncbi.nlm.nih.gov/16878175</a>								

13 PLAALGKVFVG 22  
.:.:  
3 PLFQLAQGLG 12

89

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

97 PCSALLS 103  
.:.:  
7 PTSPLQS 13

90

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

85 GRTPGS 90  
.:.:  
2 GYYPTS 7

91

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	DQ8.5-glut-H1	9	0.16	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

92

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin (proline-rich domain)	16	0.17	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

93

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

13 PL 14  
: : :  
8 PL 9

94

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glutenin-Glt-17 (p50-p58; E52 and E55)	9	0.17	2	100.0	100.0	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/16091925">https://pubmed.ncbi.nlm.nih.gov/16091925</a>								

13 PL 14  
: : :  
8 PL 9

95

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

13 PL 14  
: : :  
8 PL 9

96

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	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 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 K	147	Barley peptide B03	16	0.18	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 GQQPFPPQPEQPI 13

99

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

56 FNTQ 59  
: : : : :  
2 FSVQ 5

100

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	G4-9A gliadin (p62-p75; E65 and A70)	14	0.19	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



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	P84093	80	4.7	77	27.3

67 NTQATNRNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRC 133  
 2 NCIELNND CDGSKD-DCQCCRD NAYCSCYNFFGIKSGCK--CS-VGNSGTGYSV-CLKKL--ECPNRRAWTSWKKEC 71

10

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHI	147	PA2A3_TROCA	Q45Z28	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	P49269	76	6.4	81	22.2

63 RNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIP---CSALLSSDITASVNC AKKIVSDGNGMNAWVAW  
 4 QNLGSGIPHDRIKLPNGQWC---KTPG--DLCSSSSECCAKHSNSVTYASFCSREW-SGQQGL-----F  
 RNRCKGTDVQA 140  
 INQCRTCNVE 73

12

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHI	147	PA2A2_TROCA	Q45Z29	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	Q45Z30	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_OPHHA	Q7ZT98	221	8.3	103	24.3

68 YRGYSLGNWV--CAAKFESNFNT--QATNRNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLS  
 122 YKTYRIGCAVNYCPSSEYSYFYVCQYCPSGNMRGST---ATPYKSGPTCGDCPSACDNGLC TNPCT--LY  
 SDITASVNC AKKIVSDGNGMNAWVAWRNCKGT 136  
 NEYT---NC-DSL VKQSSCQDEWI--KSKCPAS 213



15

[illegible]

16

[illegible]