

## 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

[illegible]

3

[illegible]

**4**

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHI	147	LALBA_BOVIN	<a href="#">P00711</a>	123	1.4e-18	120	40.0	na
<a href="#">Q9RCELA</a>	AAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGGSTDYGILQINSRWWCNDGRTPGSRN							
5	KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKDDQNPHSSN							
	LCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAW 142							
	ICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLAHKALCS-EKLDQW 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-----CRGTTXSXQPGGC 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 GCCSGVRSLNN---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 GSRNLNIPCSALLSSDITASVNCAKKIVSDGNGMNA--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 GSRNLNIPCSALLSSDITASVNCAKKIVSDGNGMNA--WVAWRNRCKGTD 138</p> <p>30 GIRNINNL---AKTTADRQTACNCLKQLSASVPGVNANNAALPGKC-GVN 77</p>								

14

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHI	147	E7CLQ2_PRUAV	E7CLQ2	91	3.9	52	30.8	20.02
6k GSRNL	CNIPCSALLSSDITASVNCAKKIVSDGNGMNA--WVAWRNRCKGTD	138						
: : :	: : :	:	:	:	:	:	:	:
30 GIRNNL---	AKTTADRQTACNCLKQLSASVPGVNANNAALPGKC-GVN	77						

15

[illegible]

16

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHI 978 ILQINSRWWCNDGRTPGSRNLCNIPCSAL 101	147	E7BQV5_PERAM	E7BQV5	331	4.5	29	41.4	15.01
: : : : : : : : : : : : : : :								
232 IKKINDRLGCTN-KVIGSRTLGVFDCDKL 259								

17

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHI 9K4_CNIPG	147	L7TUJ3_ACTER	L7TUJ3	190	5.1	52	26.9	17.48
SALLSSDITASVNC AKKI VSDGN GMNAWVAWRNRCKGT DVQAWIRG	145							
5_CNGPCRDL--NDCDGQLICIKGCND DP QVGTHI-----CRGTT P SPQP GG	49							

18

[illegible]

19

[illegible]

20

[illegible]

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---LLSSDITASVNC AKKIVSDGNG 123
   :  :  :      :      :      :      :      :
2  NYCKIKRSGIHTLCKFGISTKPNCGKNVVK-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  
TASVNCACKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR L 147

Name	Accession ID	Description	Species	No exact words	Hit %
0					
KVFGRCELAAMKRGHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGS TDY GILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI					
TASVNCACKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR L 129					

52 ESNFNT 58  
.....  
34 ESNFNT 40

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

52 ESNFNT 58  
.....  
53 ESNFNT 59

### Sliding window results:

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

### Alignments containing 68 window(s):

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

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

```

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

```

YGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQA  
 ::  
 YGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQA

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

Name	Accession ID	Description	Species	No windows	Hit %
XP_014705584	XP_014705584	PREDICTED: lysozyme C, 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  MRSLILVL--CFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDG
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1  MRSTLIISLLSCFFAVYE-AKVFSKCELAHKLKAQEMDGGYSLANWVCMAYESNFNTRAFNGKNANG

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

```

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

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

```

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

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-AKVFSKCELAHKLKAQEMDGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYG

ILQINSRWWCNDGRTPGS 91
..  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
LFQLNNKWWCKDNKRSSS 92

```



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

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

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

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

```

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

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

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

```

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

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

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

```

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

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

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

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

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

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

```

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

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

```
21 FGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPG
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
22 FSKCELAHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSS

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

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

```
22 GRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGS
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
23 SKCELAHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SS

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

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

```
26 LAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLC
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
27 LAHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSS-NAC

NIPCSALLSSD 106
: : : : : : : :
NIMCSKLLDDN 106
```

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

```
27 AAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCN
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
28 AHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACN

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

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

```

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

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

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

```

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

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

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

```

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

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

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

```

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

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

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

```

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

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

```

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

```

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

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

```

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

```

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

KIVSDGNGMNA 126
.: : .:::
RVVRDPKGMSA 126

```

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

```

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

IVSDGNGMNAVAV 130
.: : .:::
VVRDPKGMSAWKAW 130

```

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

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

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

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

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

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

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

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

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

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

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

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

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 TNRNTDGSTDYGILQINSRWWCNDGRTPGSRLNCNIPCSALLSSDITASVNC AKKIVSDGNMGMAWVAWRNRCKGTDVQA 141  
... : ... : ... : ... : ... :  
63 NGKNANGSSDYGLFQLNNKWCKDNKRSSS-NACNIMCSKLLDDNI DD DISCAKRVVRDPKGMSAWKA WKHKDKDLSE 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 GKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVK
RCKGTDVQAWIRG 145
HCKDKDLSEYLAS 145

```

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

66 DGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146  
 :::::::::::::::::::: : :::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: :  
 68 NGSSDYGLFQLNNKWCKDNKRSS-NACNIMCSKLDDNIDDDISCAKRVVRDPKGMSAWKAVVKHCKDKDLSEYLASC 146

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

```

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

```

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

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

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

```

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

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

```

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

```

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

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

```

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

```

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

   GRTPGSRNLN 96
   ..: : :
   NKRSSS-NACN 77

```

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

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

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

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

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

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

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

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

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

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

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

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 VCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACK
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
29 VCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKR

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

```

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

```

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

```

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

```

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

```

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

```

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

```

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

```

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

```

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

```

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

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

```

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

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

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

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

```

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

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

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

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

```

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

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

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

```

59 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	0.013	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
   :: ::
7  ESPFSQQ 13
```

2

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Glt-156 minimal epitope	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
   :: ::
9  ESPFSQQ 15
```



3

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Glt-156 minimal epitope in considered Deamidated form	15	0.017	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_CHIC K	147	LMW glutenin-glt-156 (p40-p59; E48 and E51)	20	0.029	7	57.1	71.4	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/12055577">https://pubmed.ncbi.nlm.nih.gov/12055577</a>								

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

5

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	alpha gliadin 123-132	10	0.031	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_CHIC K	147	LMW glutenin-glt-156 (p40-p59; E51)	20	0.031	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_CHIC K	147	gamma5-gliadin (p227-237; E232)	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

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	Wheat peptide W09	14	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  
:::  
5 FLP 7

11

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Wheat peptide W09	12	0.035	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	0.037	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_CHIC K	147	DQ2-gamma-II peptide	11	0.042	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

14

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	alpha-Glia AG11 (p78 -p95; E86)	17	0.043	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_CHIC K	147	alpha gliadin P11	15	0.045	3	100.0	100.0	ProPepper
<a href="https://www.iedb.org/epitope/139589">https://www.iedb.org/epitope/139589</a>								

11 FLP 13  
:::  
5 FLP 7

16

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	alpha-Glia AG11 (p78 -p95)	17	0.046	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_CHIC K	147	Wheat peptide W36	15	0.05	9	44.4	88.9	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/20650871">https://pubmed.ncbi.nlm.nih.gov/20650871</a>								

1 MRSLILVL 9  
:::  
5 IRSLVLRTL 13

18

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

53 ESNFNTQ 59  
: : : : :  
2 EQSFPQQ 8

19

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	alpha gliadin 78-95 AG11	17	0.054	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	gamma gliadin 1	9	0.054	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

21

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 IRSLVLRTL 13

22

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

23

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	W09	20	0.061	3	100.0	100.0	ProPepper
<a href="https://www.iedb.org/epitope/238729">https://www.iedb.org/epitope/238729</a>								

11 FLP 13  
:::  
10 FLP 12

24

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Wheat peptide W36	16	0.064	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 K	147	Glia-gamma30-gliadin (p222-236; E225 and E231)	15	0.065	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

26

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Wheat peptide W09	20	0.066	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

27

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Rye peptide R12	12	0.069	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_CHICK	147	Glt-156 minimal epitope in considered native form	15	0.072	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	W36s	16	0.077	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

30

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glia-gamma30-gliadin (p222-236; E225)	15	0.077	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

31

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

12 LPL 14  
.:.  
2 LPL 4

32

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W36	20	0.08	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

33

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Glia-gamma30-gliadin (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

34

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	R12E	12	0.081	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

35

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Wheat peptide W37	12	0.081	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

36

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	alpha2-gliadin 1448 (p231-p245)	15	0.082	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

37

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	DQ2-y -II y-Glia (p 222-p236; E229)	15	0.086	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

38

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	HMW glutenin-glt04 (p707-p742)	36	0.086	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 QGQRPQGWLQPGQGQGGYPTSPQQSGQGQ 31

39

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Sec-gammal in Deamidated form	14	0.088	7	42.9	71.4	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/14517794">https://pubmed.ncbi.nlm.nih.gov/14517794</a>								

53 ESNFNTQ 59  
 5 EQSFPEQ 11

40

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	LMW glutenin-glt-156 (p40-p59; E48)	20	0.089	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 QSPFSSQ 18

41

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	DQ2-y -II y-Glia (p222-p236)	15	0.09	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

42

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Glt-156 minimal epitope in considered native form	15	0.09	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 QSPFSSQ 14



43

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	LMW glutenin-glt-156 (p46-p54; E48 and E 51)	9	0.09	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

44

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Rye peptide R01, R09	20	0.096	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_CHIC K	147	alpha-gliadin 4037	17	0.097	9	44.4	66.7	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/21091908">https://pubmed.ncbi.nlm.nih.gov/21091908</a>								

71 YGILQINSR 79  
:::  
9 FGIFGTNYR 17

46

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Glia-gamma30-gliadin (p222-p236)	15	0.097	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

47

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	1448	15	0.099	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

48

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	gamma gliadin 222-23 6 DQ2-gamma-II	15	0.1	4	75.0	100.0	ProPepper
<a href="https://www.iedb.org/epitope/109223">https://www.iedb.org/epitope/109223</a>								

72 GILQ 75  
:::  
3 GIIQ 6

49

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

12 LPL 14  
:::  
3 LPL 5

50

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

51

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	LMW glutenin-glt-156 (p45-p54; E48, E49 and E51) minimal epi tope	10	0.1	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

52

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

53

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

54

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gliadin-gamma30 (222-236)	15	0.11	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

55

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha gliadin 251-270	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

56

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin CAB769 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	147	CAUTION 100% match to Archaea protein lower to others and to gamma5 (p63-p71; E63, E68 and E71)	9	0.11	7	42.9	57.1	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/15972656">https://pubmed.ncbi.nlm.nih.gov/15972656</a>								

53 ESNFNTQ 59  
 . . . . .  
 1 EQPFPEQ 7

58

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Wheat peptide W37	20	0.11	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

59

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

53 ESNFNTQ 59  
: : : : :  
12 QSPFSQQ 18

60

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	LMW glutenin-glt-156 (p45-p54; E48 and E 51) 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

61

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	LMW glutenin-glt-156 (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 K	147	Sec-gammal in Deamid ated form	14	0.11	7	42.9	71.4	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/14517794">https://pubmed.ncbi.nlm.nih.gov/14517794</a>								

53 ESNFNTQ 59  
: : : : :  
5 EQSFPQQ 11

63

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

65

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

66

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

67

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

68

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	glt04 (p723-p735; E7 24)	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

69

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

12 LPL 14  
.: :.  
16 LPL 18

70

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	DQ2.5-glut-L2	9	0.12	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

71

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	DQ2.2-glut-L-1 conta ining 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

72

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	R21E	12	0.13	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

73

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope in considered Deamidated form	15	0.13	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

74

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p45-p54; E51) minimal epitope	10	0.13	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

75

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Naturally occurring glutenins (p722-p736) (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

76

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

12 LPL 14  
:::  
12 LPL 14

77

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

122 GMNAWVAW 129  
:::  
3 GPSGQVEW 10

78

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

79

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

97 PCSALL 102  
:::  
10 PCKNFL 15

80

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	alpha-gliadin (proli ne-rich domain)	16	0.14	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

81

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	gamma-gliadin 1383 (p141-p160)	20	0.14	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

82

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK 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_CHIC K	147	DQ8-glut-H1	9	0.14	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

84

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	gamma5 (p62-p74; E63 , E68 and E71)	13	0.15	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

85

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Deamidated Glt-156 m inimal 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

86

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 PTSPLQS 13

87

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC 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 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 DGNGMNAW 126  
: : : : :  
5 DPSGQVQW 12

89

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

85 GRTPGS 90  
: : : : :  
2 GYYPTS 7

90

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

91

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

92

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	gamma-gliadin M23 M3 6999 (221-240) homologous to DQ2-gamma-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 PLAALGKVF 22  
: : : : :  
3 PLFQLAQGLG 12

93

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	0.17	6	50.0	100.0	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/12198706">https://pubmed.ncbi.nlm.nih.gov/12198706</a>								
<a href="https://pubmed.ncbi.nlm.nih.gov/16878175">https://pubmed.ncbi.nlm.nih.gov/16878175</a>								

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

94

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

13 PL 14  
.:  
8 PL 9

95

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

96

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	glt04 (p723-p734)	12	0.17	6	50.0	50.0	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/10917890">https://pubmed.ncbi.nlm.nih.gov/10917890</a>								

85 GRTPGS 90  
.:  
3 GYYPTS 8

97

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

98

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	G4-9A gliadin (p62-p 75; E65 and A70)	14	0.18	5	60.0	60.0	AllergenOnline
<a href="https://pubmed.ncbi.nlm.nih.gov/12524402">https://pubmed.ncbi.nlm.nih.gov/12524402</a>								

12 LPLAA 16  
:::  
5 LPYPA 9

99

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Glutenin-Glt-17 (p50 -p58; E53 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

100

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

56 FNTQ 59  
:::  
2 FSVQ 5



Jul-28-2021  
WFSR  
Report: test

## Toxin Results

### Toxin database.

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

Last database update: 01/28/2021

### FASTA.

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

### Identity search to known toxins.

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

### Top 100 full-FASTA search results

Based on E-Value

1

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHI	147	TX219_APOSC	<a href="#">P49272</a>	76	0.036	82	26.8
<pre> 878 RNTDGSSTDYGILQINSRWWCNDGRTPG----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 DGRTEGSRNLCNIPCSALLSSDITASVNC 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	MAALEYKHGMRNYPHTVSHCDNQRFRSCL-MNVKDR TADLVGMTYFTVLKIS 95						

5

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

6

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHI	147	CRVP2_DISTY	Q2XXQ5	219	3.3	103	25.2
98 YRGY	SLGNWVCAAKF--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-DCQCCRDNAYCSCYNFFGIKSGCK--CS-VGNSGTGYSV-CLKKL--ECPNRRRAWTSWKKEC 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	PA2A1_TROCA	Q45Z30	124	7.5	54	31.5

82 CNDGRTPGSRNLCNIPCSALLSS-DITASVNC AKKIVSDGNGMNAW-VAWRNRC 133  
 77 CNDGELTCKDN--NDECKAFICNCDRTAAICFARTPYNDAN----WNIDTKTRC 124

13

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

14

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHI	147	CRVP_OPHHA	Q7ZT98	221	8.3	103	24.3

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



15

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

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