

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	P00698	129	2.3e-61	129	100.0	na

1 KVFGRCELAAAMKRHGLDNRYGYS LGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTP
 GSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR 147
 GSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR 129

Jul-28-2021
WFSR
Report: test

2

[illegible]

3

[illegible]

4

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHI	147	LALBA_BOVIN	P00711	123	1.4e-18	120	40.0	na
Q9RCELA	AAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGGSTDYGILQINSRWWCNDGRTPGSRN							
5	KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKDDQNPSSN							
	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	4X9U_A	189	2.3	53	26.4	17.49
<p>9/4 CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCNDPQVGTHI-----CRGTTXSPQPGGC 49</p>								

7

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHI	147	TLP_ACTDE	P81370	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	P19656	93	2.5	41	34.1	17.48
<p>8/5 GRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMN 125</p> <p>28 GCCSGVRSNN---AARTTADRRACNCLKNAAAGVSGLN 65</p>								

9

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHI	147	L7TY87_ACTDE	L7TY87	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	P84527	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	L7TUI7	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	E7CLQ1	91	3.9	52	30.8	20.02
<p>8/9 GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNA--WVAWRNRCKGTD 138</p> <p>30 GIRNINNL---AKTTADRQTACNCLKQLSASVPGVNANNAALPGKC-GVN 77</p>								

13

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

14

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

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
9% ILQINSRWWCNDGRTPGSRNLCNIPCSAL 101								
232 IKKINDRLGCTN-KVIGSRTL CVFDCDKL 259								

17

[illegible]

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	P0DKH7	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	P86870	202	9.1	36	33.3	14.98

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

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

2 NYCKIKCRSGIHTLCKFGISTKPNCGKNVVK-GSG **36**

Exact word and sliding window results

Shown per ORF

Exact word results:

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

18

KVFGRCELAAMKRGHGLDNYRGYS LGNWVCAAKFESNFNTQATNRNTDGS TDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI
TASVNCACKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR L 147

.....

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

52 ESNFNT 58
.....
34 ESNFNT 40

Name	Accession ID	Description	Species	No exact words	Hit %
XP_014705584	XP_014705584	PREDICTED: lysozyme C, mi 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  MRSLLILVLCFLPLAALGKVFGRCELAAMKRGHLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTD
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1  -----KVFGRCELAAMKRGHLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTD

```

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-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
   .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
   GRTPGSRNLN 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 KKIVSDGNGMN 125
  :: :: :: :: ::
SCA KRVVRDPKGMS 125
  
```

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

```

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

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

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

```

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

60 ATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNMNAWVAWRNRCKGTDVQ 140
 :
 62 FNGKNANGSSDYGLFQLNNKWCKDNKR-SSSNACNIMCSKLDDNIDDDISCAKRVRDPKGMSAWKAWVKHCKDKDLS 140

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

61 TNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNMGMAWVAWRNRCKGTDVQA 141
... :
63 NGKNANGSSDYGLFQLNNKWCKDNKRSSS-NACNIMCSKLLDDNIDDISCAKRVRDPKGMSAWKA WKHKCDKDLSE 141

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

```

62 NRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRN
64 GKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVK
RCKGTDVQAWIRG 145
HCKDKDLSEYLAS 145

```

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

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

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

```

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

```

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

Alignments containing 14 window(s):

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

```

1  MRSLLILVLCFLPLAALGKVFGRCELAAMKRGHLDNRYGYS LGNVVCAAKFESNFNTQATN-RNTDGST
1  -----KVF SKCELA HKLKAQEMDGF GGYSLANVWVCM AEYESNFNTRAFNGKNANGSS
      DYGILQINSRWWCNDGRTPGSRNL  94
      :::::.....:
      DYGLFQLNNKWWCKDNKRSSSNAC 76

```

Alignments containing 1 window(s):

(15:95-1:76) 50.6% identity

```

15 AALGKVFGRCELAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCN
   :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
1 ---KVFSKCELAHKLKAQEEMDGFGGYSLANWWCMAEYESNFNTRAFNGKNANGSSDYGLFLNNKWCK
   ..:.:.:.:.
DGRPGRNL 95
DNKR-SSSNAC 76
```

Alignments containing 1 window(s):

(16:96-1:77) 51.9% identity

```

16 ALGKVFGRCELA AAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCND
   :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
1 ---KVFSKCELAHKLKAQE MDGGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWCKD

GRTPGSRNLCN 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  AHKLKAQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACN

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

Alignments containing 1 window(s):

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

```
31 KRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCS
   : . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
13 KAQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-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 AQEMDGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSK

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

Alignments containing 1 window(s):

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

```
36 DNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSS
   . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
18 DGFGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-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

ITASVNC AKKIVSD 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-SSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSA

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

Alignments containing 1 window(s):

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

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

Alignments containing 1 window(s):

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

```
61 TNRTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNMNAWVAWRNRCKGTDVQA 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 NRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNMNAWVAWRN
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
45 GKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVK

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

Alignments containing 1 window(s):

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

```
66 DGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNMNAWVAWRNRCKGTDVQAWIRGC 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 GSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNMNAWVAWRNRCKGT
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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/celiacbrowse.shtml>) were combined and duplicates were removed.

Last database update: 02/14/2021

FASTA.

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

Identity search to known celiac epitopes.

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

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

Top 100 epitope match results

Based on E-Value

1

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Glt-156 minimal epitope in considered Deamidated form	15	0.012	7	57.1	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

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 in considered Deamidated form	15	0.016	7	57.1	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

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

3

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope	15	0.018	7	57.1	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

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

4

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p40-p59; E48 and E51)	20	0.026	7	57.1	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

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

5

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

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

6

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha gliadin 123-132	10	0.029	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/51376								

96 IPC 98
:: :: ::
3 IPC 5

7

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin(p123-p132)	10	0.032	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12594302								
https://pubmed.ncbi.nlm.nih.gov/18395083								

96 IPC 98
:: :: ::
3 IPC 5

8

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	gamma5-gliadin (p227 -237; E232)	11	0.032	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15972656								

72 GILQ 75
:::
1 GIIQ 4

9

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Wheat peptide W09	14	0.034	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

11 FLP 13
:::
5 FLP 7

10

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	alpha gliadin P11	15	0.035	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/139589								

11 FLP 13
:::
5 FLP 7

11

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Wheat peptide W09	12	0.035	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

11 FLP 13
:::
4 FLP 6

12

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	gamma5-gliadin (p227 -p237) ; gamma-II ep itope	11	0.035	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15972656								

72 GILQ 75
:::
1 GIIQ 4

13

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-Glia AG11 (p78 -p95; E86)	17	0.041	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/19299713								

11 FLP 13
:::
6 FLP 8

14

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-Glia AG11 (p78 -p95)	17	0.042	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/19299713								

11 FLP 13
:::
6 FLP 8

15

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W09	14	0.042	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

11 FLP 13
:::
5 FLP 7

16

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha gliadin 78-95 AG11	17	0.043	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/109723								

11 FLP 13
:::
6 FLP 8

17

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma gliadin	9	0.044	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/32728397								
https://pubmed.ncbi.nlm.nih.gov/22726570								

53 ESNFNTQ 59
:::
2 EQSFPQQ 8

18

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

53 ESNFNTQ 59
: : : : :
2 EQSFPQQ 8

19

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ2-gamma-II peptide	11	0.053	4	75.0	100.0	ProPepper
https://www.iedb.org/epitope/20305								

72 GILQ 75
: : : : :
1 GIQ 4

20

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W09	20	0.056	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

11 FLP 13
: : :
10 FLP 12

21

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W36	16	0.057	9	44.4	88.9	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

1 MRSLILVL 9
: : : : :
5 IRSVLRLTL 13

22

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W36	15	0.057	9	44.4	88.9	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

1 MRSLILVL 9
: : : : :
5 IRSVLRLTL 13

23

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W36	15	0.057	9	44.4	88.9	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

1 MRSLLILVL 9
.:...:
5 IRSLLVLR TL 13

24

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

12 LPL 14
.:..
10 LPL 12

25

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope in considered native form	15	0.065	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

53 ESNFNTQ 59
.:...:
7 QSPFSQQ 13

26

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	W09	20	0.066	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/238729								

11 FLP 13
.:..
10 FLP 12

27

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R12	12	0.07	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

12 LPL 14
.:..
10 LPL 12

28

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Wheat peptide W37	12	0.074	8	37.5	62.5	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

119 DGNGMNAW 126
: : : : :
3 DPSGQVQW 10

29

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	W36s	16	0.079	9	44.4	88.9	ProPepper
https://www.iedb.org/epitope/238963								

1 MRSLILVL 9
: : : : :
5 IRSLVLR TL 13

30

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Glia-gamma30-gliadin (p222-236; E225 and E231)	15	0.079	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

72 GILQ 75
: : : : :
5 GIIQ 8

31

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Glia-gamma30-gliadin (p222-236; E225)	15	0.081	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

72 GILQ 75
: : : : :
5 GIIQ 8

32

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Rye peptide R09	12	0.081	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

12 LPL 14
: : : : :
2 LPL 4

33

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin 4037	17	0.084	9	44.4	66.7	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/21091908								

71 YGILQINSR 79
:::
9 FGIFGTNYR 17

34

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glia-gamma30-gliadin (p222-236; E231)	15	0.084	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

72 GILQ 75
:::
5 GLIQ 8

35

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R01, R09	20	0.084	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

12 LPL 14
:::
3 LPL 5

36

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p46-p54; E48 and E51)	9	0.086	4	75.0	75.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/16091925								
https://pubmed.ncbi.nlm.nih.gov/12055577								
https://pubmed.ncbi.nlm.nih.gov/32728397								

53 ESNF 56
:::
6 ESPF 9

37

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	R12E	12	0.088	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/238932								

12 LPL 14
:::
10 LPL 12

38

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope in considered native form	15	0.088	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

53 ESNFNTQ 59
: : : : :
8 QSPFSQQ 14

39

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W36	20	0.09	9	44.4	88.9	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

1 MRSLILVL 9
: : : : :
9 IRSVLRLTL 17

40

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha2-gliadin 1448 (p231-p245)	15	0.091	14	28.6	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/16878175								

55 NFNTQATNRNTDGS 68
: : : : :
2 SFQPSQQNPQAQGS 15

41

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ2-y -II y-Glia (p222-p236; E229)	15	0.091	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/19299713								

72 GILQ 75
: : : : :
3 GIIQ 6

42

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Sec-gammal in Deamidated form	14	0.091	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/14517794								

53 ESNFNTQ 59
: : : : :
5 EQSFPEQ 11

43

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	R01	20	0.093	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/238942								

12 LPL 14
:::
3 LPL 5

44

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glia-gamma30-gliadin (p222-p236)	15	0.093	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

72 GILQ 75
:::
5 GIIQ 8

45

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	HMW glutenin-glt04 (p707-p742)	36	0.095	29	13.8	62.1	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/10540324								

39 RGYSLGNWVCAAKFESNFNTQATNRNTDGS 67
:::
3 QGQRPQWLQPGQGQGYPTSPQQSGQGQ 31

46

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ2-y -II y-Glia (p222-p236)	15	0.099	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/19299713								

72 GILQ 75
:::
3 GIIQ 6

47

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Sec-gammal in Deamidated form	14	0.099	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/14517794								

53 ESNFNTQ 59
:::
5 EQSFPEQ 11

48

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

1 MRSLILVL 9
.: :.
9 IRSVLRTL 17

49

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p40-p59)	20	0.1	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

53 ESNFNTQ 59
.: :.
12 QSPFSQQ 18

50

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 epi tope	10	0.1	4	75.0	75.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

53 ESNF 56
.: :.
7 ESPF 10

51

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
https://pubmed.ncbi.nlm.nih.gov/16091925								
https://pubmed.ncbi.nlm.nih.gov/12055577								
https://pubmed.ncbi.nlm.nih.gov/32728397								

53 ESNF 56
.: :.
6 ESPF 9

52

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
https://www.iedb.org/epitope/70564								

72 GILQ 75
.: :.
5 GIIQ 8

53

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
https://www.iedb.org/epitope/72058								

71 YGILQINSR 79

 12 FGIFGTNYR 20

54

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin CAB76961 (p251-p270)	20	0.11	9	44.4	66.7	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/17629515								

71 YGILQINSR 79

 12 FGIFGTNYR 20

55

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
https://pubmed.ncbi.nlm.nih.gov/15972656								

53 ESNFNTQ 59

 1 EQPFPEQ 7

56

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p40-p59; E48)	20	0.11	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

53 ESNFNTQ 59

 12 QSPFSQQ 18

57

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
https://pubmed.ncbi.nlm.nih.gov/12055577								
https://pubmed.ncbi.nlm.nih.gov/15714306								

53 ESNF 56

 7 ESPF 10

58

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Rye peptide R12	20	0.11	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

12 LPL 14
:::
16 LPL 18

59

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

53 ESNFNTQ 59
:::
5 EQSFPQQ 11

60

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

53 ESNFNTQ 59
:::
5 EQSFPQQ 11

61

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

53 ESNF 56
:::
6 ESPF 9

62

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	gamma gliadin 222-236 DQ2-gamma-II	15	0.12	4	75.0	100.0	ProPepper
https://www.iedb.org/epitope/109223								

72 GILQ 75
:::
3 GIHQ 6

63

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	1448	15	0.12	14	28.6	71.4	ProPepper
https://www.iedb.org/epitope/22327								

55 NFNTQATNRNTDGS 68

 2 SFQPSQQNPQAQGS 15

64

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
https://www.iedb.org/epitope/167143								

53 ESNFNTQ 59

 12 QSPFSQQ 18

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
https://www.iedb.org/epitope/52130								

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
https://pubmed.ncbi.nlm.nih.gov/8315377								

12 LPLAALGKVFGR 23

 2 VPLVQQQQLGQ 13

67

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

97 PCSALL 102

 10 PCKNFL 15

68

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope (p41-p55)	15	0.12	5	60.0	80.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

53 ESNFN 57
:::
11 ESPFS 15

69

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
https://pubmed.ncbi.nlm.nih.gov/15714306								

53 ESNF 56
:::
7 ESPF 10

70

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	glt04 (p723-p735; E724)	13	0.12	7	42.9	57.1	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/22342873								
https://pubmed.ncbi.nlm.nih.gov/10540324								

84 DGRTPGS 90
:::
2 EGYPTS 8

71

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
https://pubmed.ncbi.nlm.nih.gov/20650871								

12 LPL 14
:::
12 LPL 14

72

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

53 ESNFNTQ 59
:::
2 EQPFPEQ 8

73

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Wheat peptide W37	20	0.13	8	37.5	62.5	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

119 DGNGMNAW 126
: : : : :
8 DPSGQVQW 15

74

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Glt-156 minimal epitope in considered Deamidated form	15	0.13	5	60.0	80.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

53 ESNFN 57
: : : : :
10 ESPFS 14

75

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	R12	20	0.14	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/238384								

12 LPL 14
: : :
16 LPL 18

76

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Wheat peptide W05	20	0.14	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

53 ESNFNTQ 59
: : : : :
11 EQPFSQQ 17

77

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

53 ESNF 56
: : :
7 ESPF 10

78

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Naturally occurring glutenins (p722-p736) (homolog of glt04)	15	0.14	7	57.1	57.1	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/10540324								

97 PCSALLS 103
: : :
7 PTSPQLS 13

79

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Rye peptide R21	12	0.14	8	37.5	62.5	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

122 GMNAWVAW 129
: : : :
3 GPSGQVEW 10

80

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	W37s	16	0.15	8	37.5	62.5	ProPepper
https://www.iedb.org/epitope/238519								

119 DGNGMNAW 126
: : : :
5 DPSGQVQW 12

81

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	gamma gliadin peptid 1383	20	0.15	6	50.0	83.3	ProPepper
https://www.iedb.org/epitope/52318								

97 PCSALL 102
: : : :
10 PCKNFL 15

82

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	R21E	12	0.15	8	37.5	62.5	ProPepper
https://www.iedb.org/epitope/238962								

122 GMNAWVAW 129
: : : :
3 GPSGQVEW 10

83

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin CAB76960 (p253-p272)	20	0.15	4	50.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/17629515								

93 LCNI 96
.:.
2 MCNV 5

84

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

48 CAAKFES 54
.:.
1 CPQPFPS 7

85

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glutenin-Glt-17 (p50-p58; E52, E53 and E55)	9	0.15	2	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/16091925								

13 PL 14
.:.
8 PL 9

86

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ8.5-glut-H1	9	0.15	6	50.0	50.0	Sollid
https://pubmed.ncbi.nlm.nih.gov/22013116								

85 GRTPGS 90
.:.
2 GYYPTS 7

87

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

53 ESNFNTQ 59
.:.
2 EQPFPEQ 8

88

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Deamidated Glt-156 m inimal epitope (p40- p59)	15	0.16	4	75.0	75.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

53 ESNF 56
:::
12 ESPF 15

89

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	Barley peptide B03	16	0.16	13	30.8	46.2	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

85 GRTPGSRNLCNIP 97
:::
1 GQQPFPQPEQPI 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
https://pubmed.ncbi.nlm.nih.gov/10540324								

85 GRTPGS 90
:::
2 GYYPTS 7

91

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	0.17	10	40.0	70.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12198706								
https://pubmed.ncbi.nlm.nih.gov/16878175								

13 PLAALGKVFG 22
:::
3 PLFQLAQGLG 12

92

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHIC K	147	gamma-gliadin 1391 (p231-p250) ; gamma-g liadin M24 M36999 (2 31-250) identical to DQ2-gamma-II	20	0.17	6	50.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12198706								
https://pubmed.ncbi.nlm.nih.gov/16878175								

1 MRSLLI 6
:::
15 IRSLLV 20

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
https://pubmed.ncbi.nlm.nih.gov/16091925								

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
https://pubmed.ncbi.nlm.nih.gov/16091925								

13 PL 14
:::
8 PL 9

95

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Naturally occurring glutenins (p722-p736) (homolog of glt04)	15	0.17	7	57.1	57.1	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/10540324								

97 PCSALLS 103
:::
7 PTSPLQS 13

96

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ8-glut-H1, DQ8.5-glut-H1	9	0.18	6	50.0	50.0	ProPepper
https://www.iedb.org/epitope/161144								

85 GRTPGS 90
:::
2 GYYPTS 7

97

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma5 (p62-p74; E63 and E68)	13	0.18	7	42.9	57.1	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15972656								

53 ESNFNTQ 59
:::
2 EQPFPEQ 8

98

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Glutenin-Glt-17 (p50 -p58; E53 and E55)	9	0.18	2	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/16091925								

13 PL 14
:::
8 PL 9

99

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	HMW glutenin (p724-p 734)	11	0.18	6	50.0	50.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/16091925								
https://pubmed.ncbi.nlm.nih.gov/10540324								
https://pubmed.ncbi.nlm.nih.gov/22013116								

85 GRTPGS 90
:::
2 GYYPTS 7

100

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK K	147	Homolog of oat aveni n-derived T cell-sti mulatory peptide in Deamidated form	15	0.18	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

73 ILQ 75
:::
12 ILQ 14



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	P49272	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	P63019	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	E7CLP4	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	MAALEYKHGMRNYPHTVSHCDNQRSC L-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 NTQATNRNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDGNGMNAWVAWRNRC 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-DITASVNCACKIVSDGNGMNAW-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---CSALLSSDITASVNCACKIVSDGNGMNAWVAW
 4 QNLGSGIPHDRIKLPNGQWC---KTPG--DLCSSSSECCAKHSNSVTYASFCSREW-SGQQGL-----F
 RNRCKGTDVQA 140
 INQCRTCNVE 73

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ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHI	147	PA2A2_TROCA	Q45Z29	124	7.5	54	31.5

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

13

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHI	147	PA2A1_TROCA	Q45Z30	124	7.5	54	31.5

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

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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 YKTYRIGCAVNYCPSEYSYFYVCQYCPSGNMRGST---ATPYKSGPTCGDCPSACDNGLCNTPCT--LY
 SDITASVNCACKIVSDGNGMNAWVAWRNCKGT 136
 NEYT---NC-DSLVKQSSCQDEWI--KSKCPAS 213

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

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