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-sillico 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

1

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	LYSC_CHICK	P00698	129	2.3e-61	129	100.0	na

```
19 KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTP
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1  KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTP

   GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR 147
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
   GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR 129
```

2

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	XP_014705584	XP_014705584	148	2.3e-32	150	48.0	na

```
1 MRSLLILVL--CFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDG
  ::: ::. :  ::.  .   .:::..:::: .: . .: . ::::.:::: :..::::::.: : .: .:
1 MRSTLIISLLSCFFAVYE-AKVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANG

  STDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTD
  :.:::..:.:.:.:::.:.. .: : ::: :: :....:  ..:::..: : .:.:: :: ..::  :
  SSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKD

  VQAWIRGCR 147
  .. .. .:
  LSEYLASCN 148
```

3

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	LYSC1_HORSE	P11376	129	1.6e-30	130	49.2	na

```
19  KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRT
    :::..::::  .:  .  .:..  ::::.:::: :..:::::.: :  :..::.::..:.:..::.:..
1   KVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR

    PGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR 147
     .: : ::: :: ::. .:  ..:::..: : .::.:: :: ..::  :.. .. .:
    SSS-NACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLSEYLASCN 129
```

4

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	LALBA_BOVIN	P00711	123	1.4e-18	120	40.0	na

```
23  RCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRN
    .::.   .:   :  .: : :: .::..   :..:::   .:.: ::.::..::.. ::.: ..: : :
5   KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKDDQNPHSSN

    LCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAW 142
    .::: :. .:..:.: .. .:::. :  .: :.: .  :.   .. :
    ICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLAHKALCS-EKLDQW 119
```

5

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	TLP_ACTCC	P83958	201	1.8	60	31.7	23.77

```
56  FNTQATNRNTDGSTDYGI-LQINSRWWC-NDGRTPGSRNLCNIPCSALLSSDITA-SVN 112
    :.:      :.:.   ::    :    :  :.  :.::.    ::  ::...  ...   :  :
103 FNVAMEFSPTSGGCTRGIKCTANINEQCPNELRAPGG---CNNPCTVFKTDQYCCNSGN 159
```

6

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHI	147	4X9U_A	4X9U_A	189	2.3	53	26.4	17.49

```
94  CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146
4   CNGPCRDL--NDCDGQLICIKGKCNDDPQVGTHI-----CRGTTXSXQPGGC 49
```

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

```
56  FNTQATNRNTDGSTDYGI---LQINSRWWC-NDGRTPGSRNLCNIPCSALLSSDITA-SVNC 112
103 FNVAMEFSPTSGGCTRGIKCTADINGQ--CPNELRAPGG---CNNPCTVFKTDQYCCNSGNC 159
```

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

```
85 GRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMN 125
28 GCCSGVRSLNN---AARTTADRRAACNCLKNAAAGVSGLN 65
```

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

```
94  CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146
4   CNGPCRDL--NDCDGQLICIKGKCNDDPQVGTHI-----CRGTTPSPQPGGC 49
```

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

```
94  CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146
4   CNGPCRDL--NDCDGQLICIKGKCNDDPQVGTHI-----CRGTTPSPQPGGC 49
```

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

```
94  CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146
4   CNGPCRDL--NDCDGQLICIKGKCNDDPEVGTHI-----CRGTTPSPQPGGC 49
```

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

```
89 GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNA--WVAWRNRCKGTD 138
30 GIRNINNL---AKTTADRQTACNCLKQLSASVPGVNANNAAALPGKC-GVN 77
```

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

```
89 GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNA--WVAWRNRCKGTD 138
30 GIRNINNL---AKTTADRQTACNCLKQLSASVPGVNANNAAALPGKC-GVN 77
```

14

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	E7CLQ2_PRUAV	E7CLQ2	91	3.9	52	30.8	20.02

```
89 GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNA--WVAWRNRCKGTD 138
30 GIRNINNL---AKTTADRQTACNCLKQLSASVPGVNANNAAALPGKC-GVN 77
```

15

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	Q1M0Y6_PERAM	Q1M0Y6	331	4.5	29	41.4	15.01

```
73  ILQINSRWWCNDGRTPGSRNLCNIPCSAL 101
232 IKKINDRLGCTN-KVIGSRTLCVFDCDKL 259
```

16

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	E7BQV5_PERAM	E7BQV5	331	4.5	29	41.4	15.01

```
73  ILQINSRWWCNDGRTPGSRNLCNIPCSAL 101
232 IKKINDRLGCTN-KVIGSRTLCVFDCDKL 259
```

17

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	L7TUJ3_ACTER	L7TUJ3	190	5.1	52	26.9	17.48

```
94 CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG 145
5  CNGPCRDL--NDCDGQLICIKGKCNDDPQVGTHI-----CRGTTPSPQPGG 49
```

18

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	L7TRW9_ACTER	L7TRW9	189	6	52	26.9	17.48

```
94 CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG 145
4  CNGPCRDL--NDCDGQLICIKGKCNDDPEVGTHI-----CRGTTPSPQPGG 48
```

19

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	L7TY92_ACTER	L7TY92	190	6.1	52	26.9	17.48

```
94 CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG 145
5  CNGPCRDL--NDCDGQLICIKGKCNDDPEVGTHI-----CRGTTPSPQPGG 49
```

20

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	L7TV12_ACTDE	L7TV12	189	8.3	53	24.5	16.23

```
94 CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146
4  CNGPCRDL--NDCDGQLICIEGKCNDDPEVGTHI-----CRGTTPSPQPGGC 49
```

21

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity	Recalc
>LYSC_CHICK	147	KIWEL_ACTCC	P85261	189	8.3	53	24.5	16.23

```
94 CNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146
4  CNGPCRDL--NDCDGQLICIEGKCNDDPEVGTHI-----CRGTTPSPQPGGC 49
```

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

```
Qk
78 SRW-WCNDGRTPGSRNLCNIPCS 100
   ... ::  : ::    . :.  ..
19 SQWGWC--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

```
Qk
78 SRW-WCNDGRTPGSRNLCNIPCS 100
   ... ::  : ::    . :.  ..
19 SQWGWC--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

```
Qk
92 NLCNIPCSA----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
KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI
TASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL 147

:::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
:::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
0
KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI
TASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL 129
52 ESNFNT 58
   ::::::
34 ESNFNT 40
```

Name	Accession ID	Description	Species	No exact words	Hit %
XP_014705584	XP_014705584	PREDICTED: lysozyme C, milk isozyme	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 MRSLLILVLCFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTD
                  :::::::::::::::::::::::::::::::::::::::::::::::::::::
1 ------------------KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTD

  YGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQA
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
  YGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQA

  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-AKVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANG

  STDYGILQINSRWW 82
  :.:::..:.:..::
  SSDYGLFQLNNKWW 83
```

Alignments containing 1 window(s):
(3:83-4:84) 51.2% identity

```
3 SLLILVL-CFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTD
  .:.: .: ::. .   .:::..::::  .: . .:.. ::::.:::: :..::::::.: : .:..::.:
4 TLIISLLSCFFAVYE-AKVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSD

  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-AKVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYG

  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

   GRTPGSRNLCN 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 FSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSS

   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 SKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SS

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

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

```
26 LAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLC
   ::  .: . .:.. ::::.:::: :..::::::.: : .:..::.:::..:.:..:::.:..  .: : :
27 LAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-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 AHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACN

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

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

```
31 KRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCS
   : . .:.. ::::.:::: :..::::::.: : .:..::.:::..:.:..:::.:..  .: : ::: ::
32 KAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-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 AQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSK

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

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

```
36 DNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSS
   :.. ::::.:::: :..::::::.: : .:..::.:::..:.:..:::.:..  .: : ::: :: ::..
37 DGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-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 GFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDN

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

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

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

   VNCAKKIVSDG 121
   ..:::..: :
   ISCAKRVVRDP 121
```

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

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

   NCAKKIVSDGNGMN 125
   .:::..: : .::.
   SCAKRVVRDPKGMS 125
```

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

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

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

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

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

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

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

```
51 KFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSD
   ..::::::.: : .:..::.:::..:.:..:::.:..  .: : ::: :: ::...:  ...:::..: :
52 EYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDDNIDDDISCAKRVVRD

   GNGMNAWVAWR 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 FESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDG
   .::::::.: : .:..::.:::..:.:..:::.:..  .: : ::: :: ::...:  ...:::..: :
53 YESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDP

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

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

```
56 FNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMN
   :::.: : .:..::.:::..:.:..:::.:..  .: : ::: :: ::...:  ...:::..: : .::.
57 FNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDDNIDDDISCAKRVVRDPKGMS

   AWVAWRNRCKG 136
   :: :: ..::
   AWKAWVKHCKD 136
```

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

```
57 NTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNA
   ::.: : .:..::.:::..:.:..:::.:..  .: : ::: :: ::...:  ...:::..: : .::.:
58 NTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSA

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

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

```
60 ATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQ 140
    ...:..::.:::..:.:..:::.:..  .: : ::: :: ::...:  ...:::..: : .::.:: :: ..::  :..
62 FNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLS 140
```

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

```
61 TNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQA 141
   ...:..::.:::..:.:..:::.:..  .: : ::: :: ::...:  ...:::..: : .::.:: :: ..::  :..
63 NGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLSE 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 NRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRN
   ..:..::.:::..:.:..:::.:..  .: : ::: :: ::...:  ...:::..: : .::.:: :: .
64 GKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVK

   RCKGTDVQAWIRG 145
   .::  :.. .. .
   HCKDKDLSEYLAS 145
```

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

```
66 DGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146
   .::.:::..:.:..:::.:..  .: : ::: :: ::...:  ...:::..: : .::.:: :: ..::  :.. .. .:
68 NGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLSEYLASC 146
```

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

```
67 GSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGT
   ::.:::..:.:..:::.:..  .: : ::: :: ::...:  ...:::..: : .::.:: :: ..::
69 GSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDDNIDDDISCAKRVVRDPKGMSAWKAWVKHCKDK

   DVQAWIRGCRL 148
   :.. .. .: :
   DLSEYLASCNL 148
```

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

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

```
1 MRSLLILVLCFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGST
                    :::..::::  .: . .:.. ::::.:::: :..::::::.: : .:..::.
1 ------------------KVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSS

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

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

```
15 AALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCN
       :::..::::  .: . .:.. ::::.:::: :..::::::.: : .:..::.:::..:.:..:::.
1  ----KVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCK

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

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

```
16 ALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCND
      :::..::::  .: . .:.. ::::.:::: :..::::::.: : .:..::.:::..:.:..:::.:
1  ---KVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKD

   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  --KVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDN

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

Alignments containing 1 window(s):
(21:101-3:82) 53.1% identity

```
21 FGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPG
   :..::::  .: . .:.. ::::.:::: :..::::::.: : .:..::.:::..:.:..:::.:..  .
3  FSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSS

   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  SKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SS

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

Alignments containing 1 window(s):
(26:106-8:87) 51.9% identity

```
26 LAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLC
   ::  .: . .:.. ::::.:::: :..::::::.: : .:..::.:::..:.:..:::.:..  .: : :
8  LAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-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  AHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACN

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

Alignments containing 1 window(s):
(31:111-13:92) 50.6% identity

```
31 KRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCS
   : . .:.. ::::.:::: :..::::::.: : .:..::.:::..:.:..:::.:..  .: : ::: ::
13 KAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-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 AQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSK

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

Alignments containing 1 window(s):
(36:116-18:97) 53.1% identity

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

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

Alignments containing 4 window(s):
(37:117-19:98) 51.9% identity
(38:118-20:99) 53.1% identity
(39:119-21:100) 53.1% identity
(40:120-22:101) 54.3% identity

```
37 NYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSD
   .. :::.:::: :.:::::::: : .:.:::::::.:.:.::::.. .: : ::: :: :: . 
19 GFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDEN

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

Alignments containing 1 window(s):
(41:121-23:102) 53.1% identity

```
41 YSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITAS
   :.:.::: :.:::::::: : .:.:::::::.:.:.::::.. .: : ::: :: :: .:   .
23 YSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDD

   VNCAKKIVSDG 121
   ..:::.. :
   ISCAKRVVRDP 102
```

Alignments containing 4 window(s):
(42:122-24:103) 51.9% identity
(43:123-25:104) 51.9% identity
(44:124-26:105) 51.9% identity
(45:125-27:106) 51.9% identity

```
42 SLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASV
   :.:.::: :.:::::::: : .:.:::::::.:.:.::::..  .: : ::: :: :: .:   ..
24 SLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDI

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

Alignments containing 1 window(s):
(46:126-28:107) 51.9% identity

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

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

Alignments containing 4 window(s):
(47:127-29:108) 51.9% identity
(48:128-30:109) 50.6% identity
(49:129-31:110) 50.6% identity
(50:130-32:111) 51.9% identity

```
47 VCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKK
   :: :.:.:::::::: : .:.:.:::::.:.:.:::.:..  .: : ::: :: :: .:  ..:::::
29 VCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKR

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

Alignments containing 1 window(s):
(51:131-33:112) 50.6% identity

```
51 KFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSD
   .:::::::: : .:.:.:::::.:.:.:::.:..  .: : ::: :: :: .:  ..:::::: :
33 EYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDDISCAKRVVRD

   GNGMNAWVAWR 131
    .:::: ::
   PKGMSAWKAWV 112
```

Alignments containing 4 window(s):
(52:132-34:113) 50.6% identity
(53:133-35:114) 50.6% identity
(54:134-36:115) 50.6% identity
(55:135-37:116) 50.6% identity

```
52 FESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDG
   .:::::::: : .:.:.:::::.:.:.:::.:..  .: : ::: :: :: .:  ..:::::: :
34 YESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDP

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

Alignments containing 1 window(s):
(56:136-38:117) 49.4% identity

```
56 FNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMN
   :::.: : .:.:.:::::.:.:.:::.:..  .: : ::: :: :: .:  ..:::::: : .:::
38 FNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDDISCAKRVVRDPKGMS

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

Alignments containing 3 window(s):
(57:137-39:118) 48.1% identity
(58:138-40:119) 48.1% identity
(59:139-41:120) 46.9% identity

```
57 NTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNA
   ::.: : .:..::.:::..:.:..:::.:..  .: : ::: :: ::. .:  ...:::..: : .::.:
39 NTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSA

   WVAWRNRCKGTDV 139
   : :: ..::  :.
   WKAWVKHCKDKDL 120
```

Alignments containing 1 window(s):
(60:140-43:121) 45.0% identity

```
60 ATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQ 140
    ...:..::.:::..:.:..:::.:..  .: : ::: :: ::. .:  ...:::..: : .::.:: :: ..::  :..
43 FNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLS 121
```

Alignments containing 1 window(s):
(61:141-44:122) 45.0% identity

```
61 TNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQA 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 NRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRN
   ..:..::.:::..:.:..:::.:..  .: : ::: :: ::. .:  ...:::..: : .::.:: :: .
45 GKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVK

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

Alignments containing 1 window(s):
(66:146-49:127) 45.0% identity

```
66 DGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 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 GSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGT
   ::.:::..:.:..:::.:..  .: : ::: :: ::. .:  ...:::..: : .::.:: :: ..::
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--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKDDQNP 67
```

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

```
11 FLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGS 91
    :          .::.   .:   : .: : :: .:::..   :...:::  .:.: ::.::..:::.. ::.: ..: :
2  QLT---------KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKDDQNPHS 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--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIW

   CNDGRTPGSRNL 94
   :.: ..: : :.
   CKDDQNPHSSNI 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--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKD

   GRTPGSRNLCNI 97
    ..: : :.:::
   DQNPHSSNICNI 75
```

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

```
18 GKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIP 98
    ..  .::.   .:   : .: : :: .:::..   :...:::  .:.: ::.::..:::.. ::.: ..: : :.:::
1  EQLT-KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNND-STEYGLFQINNKIWCKDDQNPHSSNICNIS 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-STEYGLFQINNKIWCKDDQNPHSSNICN

   IPCSALLSSDITASVNCAKKIVSDGN 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-STEYGLFQINNKIWCKDDQNPHSSNICNISCDKFLDDDLTDDIMC

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

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

```
59 QATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVA
   ::  .:.: ::.::..:::.. ::.: ..: : :.::: :. .:..:.: .. :.:::. :  :.: :.:
39 QAIVQNND-STEYGLFQINNKIWCKDDQNPHSSNICNISCDKFLDDDLTDDIMCVKKIL-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-STEYGLFQINNKIWCKDDQNPHSSNICNISCDKFLDDDLTDDIMCVKKIL-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-STEYGLFQINNKIWCKDDQNPHSSNICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLAHKA

   RCKGTDVQAWIR 144
    :.   .. :.
   LCS-EKLDQWLC 120
```

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

```
65 TDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG 145
   .. ::.::..:::.. ::.: ..: : :.::: :. .:..:.: .. :.:::. :  :.: :.: .  :.   .. :.
44 NNDSTEYGLFQINNKIWCKDDQNPHSSNICNISCDKFLDDDLTDDIMCVKKIL-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 NDSTEYGLFQINNKIWCKDDQNPHSSNICNISCDKFLDDDLTDDIMCVKKIL-DKVGINYWLAHKALCS-

   TDVQAWIRGCRL 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-sillico 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 occurence 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_CHICK	147	Glt-156 minimal epitope in considered Deamidated form	15	0.013	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_CHICK	147	Glt-156 minimal epitope	15	0.015	7	57.1	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

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

3

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

```
53 ESNFNTQ 59
   :: :. :
8  ESPFSQQ 14
```

4

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p40-p59; E51)	20	0.024	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; E48 and 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(p123-p132)	10	0.031	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
```

7

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma5-gliadin (p227-237; E232)	11	0.031	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15972656								

```
72 GILQ 75
   :::.
1  GIIQ 4
```

8

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha gliadin 123-132	10	0.033	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/51376								

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

9

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W09	14	0.033	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	147	gamma5-gliadin (p227–p237) ; gamma-II epitope	11	0.037	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15972656								

```
72 GILQ 75
   ::::
1  GIIQ 4
```

11

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W09	12	0.039	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	147	DQ2-gamma-II peptide	11	0.041	4	75.0	100.0	ProPepper
https://www.iedb.org/epitope/20305								

```
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 gliadin P11	15	0.042	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/139589								

```
11 FLP 13
   :::
5  FLP 7
```

15

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

```
11 FLP 13
   :::
6  FLP 8
```

16

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma gliadin	9	0.042	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
```

17

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
```

18

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W09	14	0.043	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
11 FLP 13
   :::
5  FLP 7
```

19

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma gliadin 1	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
```

20

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W36	15	0.045	9	44.4	88.9	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
1 MRSLLILVL 9
  :::.. .:
5 IRSLVLRTL 13
```

21

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	W09	20	0.055	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/238729								

```
11 FLP 13
   :::
10 FLP 12
```

22

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

```
1 MRSLLILVL 9
  :::.. .:
5 IRSLVLRTL 13
```

23

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R12	12	0.056	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
12 LPL 14
   :::
10 LPL 12
```

24

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W09	20	0.058	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
11 FLP 13
   :::
10 FLP 12
```

25

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W36	16	0.06	9	44.4	88.9	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
1 MRSLLILVL 9
  :::::.. .:
5 IRSLVLRTL 13
```

26

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glia-gamma30-gliadin (p222–236; E225 and E231)	15	0.065	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

```
72 GILQ 75
   ::::
5  GIIQ 8
```

27

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

```
53 ESNFNTQ 59
   : : : :
7  QSPFSQQ 13
```

28

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ2-y -II y-Glia (p 222-p236; E229)	15	0.075	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/19299713								

```
72 GILQ 75
   ::::
3  GIIQ 6
```

29

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R12	12	0.076	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
12 LPL 14
   :::
10 LPL 12
```

30

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	W36s	16	0.078	9	44.4	88.9	ProPepper
https://www.iedb.org/epitope/238963								

```
1 MRSLLILVL 9
  :::.:. .:
5 IRSLVLRTL 13
```

31

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ2-y -II y-Glia (p 222-p236)	15	0.079	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/19299713								

```
72 GILQ 75
   ::::
3  GIIQ 6
```

32

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R09	12	0.079	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	Wheat peptide W37	12	0.08	8	37.5	62.5	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
119 DGNGMNAW 126
    : :::: :
3   DPSGQVQW 10
```

34

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p45-p54; E48, E49 and E51) minimal epitope	10	0.08	4	75.0	75.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

```
53 ESNF 56
   :: :
7  ESPF 10
```

35

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

36

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope in considered native form	15	0.083	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

```
53 ESNFNTQ 59
   :: :: :
8  QSPFSQQ 14
```

37

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glia-gamma30-gliadin (p222–236; E231)	15	0.087	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

```
72 GILQ 75
   :::.
5  GIIQ 8
```

38

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R01, R09	20	0.087	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
12 LPL 14
   :::
3  LPL 5
```

39

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p46-p54; E48 and E51)	9	0.088	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
```

40

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha2-gliadin 1448 (p231-p245)	15	0.09	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	R01	20	0.091	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/238942								

```
12 LPL 14
   :::
3  LPL 5
```

42

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Wheat peptide W36	20	0.091	9	44.4	88.9	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
1 MRSLLILVL 9
  :::::. .:
9 IRSLVLRTL 17
```

43

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glia-gamma30-gliadin (p222-p236)	15	0.094	4	75.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

```
72 GILQ 75
   ::::
5  GIIQ 8
```

44

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	HMW glutenin-glt04 (p707-p742)	36	0.094	29	13.8	62.1	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/10540324								

```
39 RGYSLGNWVCAAKFESNFNTQATNRNTDGS 67
   :  :::: .. ::::: : :::: : :
3  QGQRPGQWLQPGQGQQGYYPTSPQQSGQGQ 31
```

45

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	R12E	12	0.095	3	100.0	100.0	ProPepper
https://www.iedb.org/epitope/238932								

```
12 LPL 14
   :::
10 LPL 12
```

46

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Sec-gamma1 in Deamidated form	14	0.095	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/14517794								

```
53 ESNFNTQ 59
   :::: :
5  EQSFPEQ 11
```

47

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin 4037	17	0.096	9	44.4	66.7	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/21091908								

```
71 YGILQINSR 79
   :::: : :
9  FGIFGTNYR 17
```

48

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Sec-gamma1 in Deamidated form	14	0.096	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/14517794								

```
53 ESNFNTQ 59
   :.:.: :
5  EQSFPEQ 11
```

49

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	W36	20	0.097	9	44.4	88.9	ProPepper
https://www.iedb.org/epitope/238943								

```
1 MRSLLILVL 9
  :::.:. :
9 IRSLVLRTL 17
```

50

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p40-p59; E48)	20	0.099	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12055577								

```
53 ESNFNTQ 59
   :: :. :
12 QSPFSQQ 18
```

51

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin CAB76961 (p251-p270)	20	0.1	9	44.4	66.7	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/17629515								

```
71 YGILQINSR 79
   :::. : :
12 FGIFGTNYR 20
```

52

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Sec-gamma1 in Deamidated form	14	0.1	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/14517794								

```
53 ESNFNTQ 59
   :.:.: :
5  EQSFPQQ 11
```

53

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Sec-gamma1 in Deamidated form	14	0.1	7	42.9	71.4	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/14517794								

```
53 ESNFNTQ 59
   :.:.: :
5  EQSFPQQ 11
```

54

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	1448	15	0.11	14	28.6	71.4	ProPepper
https://www.iedb.org/epitope/22327								

```
55 NFNTQATNRNTDGS 68
   :.. .  : .:.::
2  SFQPSQQNPQAQGS 15
```

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

```
71 YGILQINSR 79
   :::. : :
12 FGIFGTNYR 20
```

56

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin p19 (p21-p40)	20	0.11	12	25.0	66.7	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/8315377								

```
12 LPLAALGKVFGR 23
   :.:. . .:.:
2  VPLVQQQQFLGQ 13
```

57

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

```
53 ESNFNTQ 59
   :: :.:
12 QSPFSQQ 18
```

58

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

```
53 ESNF 56
   :: :
6  ESPF 9
```

59

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma gliadin 222-23 6 DQ2-gamma-II	15	0.12	4	75.0	100.0	ProPepper
https://www.iedb.org/epitope/109223								

```
72 GILQ 75
   ::.:
3  GIIQ 6
```

60

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
```

61

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
```

62

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma gliadin peptid 1383	20	0.12	6	50.0	83.3	ProPepper
https://www.iedb.org/epitope/52318								

```
97 PCSALL 102
   :: .. :
10 PCKNFL 15
```

63

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gliadin-gamma30 (222-236)	15	0.12	4	75.0	100.0	ProPepper
https://www.iedb.org/epitope/70564								

```
72 GILQ 75
   ::::
5  GIIQ 8
```

64

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	CAUTION 100% match to Archaea protein lower to others and to gamma5 (p63-p71; E63, E68 and E71)	9	0.12	7	42.9	57.1	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15972656								

```
53 ESNFNTQ 59
   :: : : :
1  EQPFPEQ 7
```

65

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

```
119 DGNGMNAW 126
    : :::  :
8   DPSGQVQW 15
```

66

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
```

67

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
```

68

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glt-156 minimal epitope in considered De amidated form	15	0.12	5	60.0	80.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15714306								

```
53 ESNFN 57
   :: : :
10 ESPFS 14
```

69

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

71

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	LMW glutenin-glt-156 (p46-p54; E51)	9	0.12	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
```

72

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  EGYYPTS 8
```

73

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R12	20	0.12	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
12 LPL 14
   :::
16 LPL 18
```

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

```
53 ESNF 56
   :: :
7  ESPF 10
```

75

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	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_CHICK	147	W37s	16	0.14	8	37.5	62.5	ProPepper
https://www.iedb.org/epitope/238519								

```
119 DGNGMNAW 126
    : :: :
5   DPSGQVQW 12
```

77

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	R21E	12	0.14	8	37.5	62.5	ProPepper
https://www.iedb.org/epitope/238962								

```
122 GMNAWVAW 129
    : .. : :
3   GPSGQVEW 10
```

78

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma5 (p62-p72; E68, E63 and E71)	11	0.14	7	42.9	57.1	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15972656								

```
53 ESNFNTQ 59
   :.:.:.:
2  EQPFPEQ 8
```

79

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

80

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Rye peptide R12	16	0.14	3	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/20650871								

```
12 LPL 14
   :::
12 LPL 14
```

81

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

```
122 GMNAWVAW 129
    :.:.:.:
3   GPSGQVEW 10
```

82

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma5 (p62-p74; E63, E68 and E71)	13	0.15	7	42.9	57.1	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/15972656								

```
53 ESNFNTQ 59
   :.:.:.:
2  EQPFPEQ 8
```

83

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma-gliadin M23 M36999 (221-240) homologous to DQ2-gamma-II	20	0.15	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
```

84

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
```

85

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	G4-9A gliadin (p62-p75; E65 and A70)	14	0.16	5	60.0	60.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12524402								

```
12 LPLAA 16
   ::.:
5  LPYPA 9
```

86

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	alpha-gliadin (proline-rich domain)	16	0.16	7	42.9	42.9	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/1720424								

```
48 CAAKFES 54
   :  : :
1  CPQPFPS 7
```

87

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	gamma-gliadin 1391 (p231-p250) ; gamma-gliadin M24 M36999 (231-250) identical to DQ2-gamma-II	20	0.16	6	50.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/12198706								
https://pubmed.ncbi.nlm.nih.gov/16878175								

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

88

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Glutenin-Glt-17 (p50-p58; E52 and E53)	9	0.16	2	100.0	100.0	AllergenOnline
https://pubmed.ncbi.nlm.nih.gov/16091925								

```
13 PL 14
   ::
8  PL 9
```

89

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	Deamidated Glt-156 minimal 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
```

90

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

```
97 PCSALLS 103
   : :  ::
7  PTSPQLS 13
```

91

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

```
85 GRTPGSRNLCNIP 97
   :. :  .    ::
1  GQQPFPQPEQPIP 13
```

92

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

```
85 GRTPGS 90
   : : :
2  GYYPTS 7
```

93

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ8.5-glut-H1	9	0.16	6	50.0	50.0	Sollid
https://pubmed.ncbi.nlm.nih.gov/22013116								

```
85 GRTPGS 90
   : : :
2  GYYPTS 7
```

94

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	DQ8-glut-H1, DQ8.5-glut-H1	9	0.17	6	50.0	50.0	ProPepper
https://www.iedb.org/epitope/161144								

```
85 GRTPGS 90
   : : :
2  GYYPTS 7
```

95

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

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

96

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
```

97

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

```
13 PL 14
   ::
8  PL 9
```

98

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
```

99

ID	Length	Hit ID	Length	E-value	Overlap	Identity	Similarity	Database
>LYSC_CHICK	147	HMW glutenin (p724-p734)	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	147	Homolog of oat avenin-derived T cell-stimulatory 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
```

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_CHI6K	147	TX219_APOSC	P49272	76	0.036	82	26.8

```
63  RNTDGSTDYGILQINSRWWCNDGRTPG----SRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVA
    .:  ..  . :... .  ::   .:::    ::. :   :.:  :...: : .:...  :: .:.
4   QNLGSDIPHDIIKLPNGQWC---KTPGALCSSRSEC---CKAKHSDSVTYSSGCSRQW-SDQQGL-----

    WRNRCKGTDVQA 140
    . :.:.  .:..
    FINQCRTCNVES 73
```

2

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHI6K	147	SCX12_CENNO	P63019	67	0.7	46	34.8

```
84  DGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAW 129
    ::  : . : :.. ::.:  .. : .  : ::  :: .   ::. .
2   DGY-PLASNGCKFGCSGLGENNPTCNHVCEKKAGSDYGYCYAWTCY 46
```

3

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHI6K	147	SX15F_RHOJU	E7CLP4	65	0.97	59	33.9

```
88  PGSRNLCNIPCSALLSSDITASVNC-AKKIVSDGNGMNAWVAWRNRCKGT----DVQAW 141
    : .:: :.:.:.    .:   .:.: ::   :::  .    .:   :  :    :...:
5   PMGRNGCKIPCAI---NDNICKVECQAKWKQSDGYCY----SWGLSCYCTNLLEDAEVW 56
```

4

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHICK	147	PA2A2_HELSU	P80003	142	1	54	29.6

```
26 LAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTD--GSTDYGILQIN 77
   .::    .:.:. ::: .....   :   .:.: .   .. .:..:  : :  .  .:.:.
43 MAALEYKHGMRNYRPHTVSHCDCDNQFRSCL-MNVKDRTADLVGMTYFTVLKIS 95
```

5

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHICK	147	CRVP2_DISTY	Q2XXQ5	219	3.3	103	25.2

```
38  YRGYSLGNWVCAAKF--ESNFNTQATNRNTDGSTDYGILQI--NSRWWCNDGRTPGSRNLCNIPCSALLS
    :..: .:    ::.:..   :..:   .  .   ...  :.     .:   :.:   .  . .:.:. :::
122 YKSYRVG---CAASYCPSSSYNYFYVCQYCPAGNFAGLTATPYKSGPTCGDCPSACDNGLCTNPCS---R

    SDITASVNCAKKIVSDGNGMNAWVAWRNRCKGT 136
     :.   .:: :.:.:..:  .. ..   :. :  .:
    EDVF--MNC-KSLVAQSNCQDDYI--RKNCPAT 213
```

6

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHICK	147	CRVP1_DISTY	Q2XXQ6	219	3.3	103	25.2

```
38  YRGYSLGNWVCAAKF--ESNFNTQATNRNTDGSTDYGILQI--NSRWWCNDGRTPGSRNLCNIPCSALLS
    :..: .:    ::.:..   :..:   .  .   ...  :.     .:   :.:   .  . .:.:. :::
122 YKSYRVG---CAASYCPPSSYNYFYVCQYCPAGNFAGLTATPYKSGPTCGDCPSACDNGLCTNPCS---R

    SDITASVNCAKKIVSDGNGMNAWVAWRNRCKGT 136
     :.   .:: :.:.:..:  .. ..   :. :  .:
    EDVF--MNC-KSLVAQSNCQDDYI--RKNCPAT 213
```

7

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHICK	147	SX17F_RHOJU	E7CLP5	65	4.2	55	29.1

```
88 PGSRNLCNIPCSALLSSDITASVNC-AKKIVSDGNGMNAWVAWRNRCKGTDVQAW 141
   : .:: :.:::.    .:   ...: ::   :::  ..  ..          :...:
5  PMGRNGCKIPCAI---NDNICKTECQAKWKQSDGYCYSPGMSCYCTNLPEDAEVW 56
```

8

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHICK	147	TX216_APOSC	P49270	76	4.4	81	22.2

```
63 RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIP---CSALLSSDITASVNCAKKIVSDGNGMNAWVAW
   .:  ..  .  ... .   ::   .:.:  .:.      :.:  :....: .   :...      .:..:
4  QNLGSGIPHDKIKLPNGQWC---KTPG--DLCSSSSECCKAKHSNSVTYASFCSRQW----SGQQALFI-

   RNRCKGTDVQA 140
    :.:.   .:..
   -NQCRTCNVES 73
```

9

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHICK	147	TOPC5_PHONI	P84093	80	4.7	77	27.3

```
57  NTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRC 133
2   NCIELNNDCDGSKD-DCQCCRDNAYCSCYNFFGIKSGCK--CS-VGNSGTGYSV-CLKKL--ECPNRRAWTSWKKEC 71
```

10

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHICK	147	PA2A3_TROCA	Q45Z28	124	6.2	54	31.5

```
82 CNDGRTPGSRNLCNIPCSALLSS-DITASVNCAKKIVSDGNGMNAW-VAWRNRC 133
77 CNDGELTCKDN--NDECKAFICNCDRTAAICFARTPYNDAN----WNINTKTRC 124
```

11

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHICK	147	TX214_APOSC	P49269	76	6.4	81	22.2

```
63 RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIP---CSALLSSDITASVNCAKKIVSDGNGMNAWVAW
4  QNLGSGIPHDRIKLPNGQWC---KTPG--DLCSSSSECCKAKHSNSVTYASFCSREW-SGQQGL-----F

   RNRCKGTDVQA 140
   INQCRTCNVES 73
```

12

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

```
82 CNDGRTPGSRNLCNIPCSALLSS-DITASVNCAKKIVSDGNGMNAW-VAWRNRC 133
77 CNDGELTCKDN--NDECKAFICNCDRTAAICFARTPYNDAN----WNIDTKTRC 124
```

13

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

```
82 CNDGRTPGSRNLCNIPCSALLSS-DITASVNCAKKIVSDGNGMNAW-VAWRNRC 133
77 CNDGELTCKDN--NDECKAFICNCDRTAAICFARAPYNDAN----WNIDTKTRC 124
```

14

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHICK	147	CRVP_PHIOL	Q09GJ9	221	8.3	103	23.3

```
38  YRGYSLG--NWVCAAKFESNFNT--QATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLS
122 YKSYRIGCAAYYCPSSLYNYFYVCQYCPAGNFAGRT---ATPYNSGPTCGDCPSACDNGLCTNPCSE--K

    SDITASVNCAKKIVSDGNGMNAWVAWRNRCKGT 136
    NEFT---NC-NELVQQSSCQDDWI--KSNCAAT 213
```

15

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

```
38  YRGYSLGNWV--CAAKFESNFNT--QATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLS
    :. : .:  :  : ..  : : .     . :  :.:       .:   :.:  .  . .:.. :..  :
122 YKTYRIGCAVNYCPSSEYSYFYVCQYCPSGNMRGST---ATPYKSGPTCGDCPSACDNGLCTNPCT--LY

    SDITASVNCAKKIVSDGNGMNAWVAWRNRCKGT 136
    .. :   :.  ..:.... .. :.  ...: ..
    NEYT---NC-DSLVKQSSCQDEWI--KSKCPAS 213
```

16

ID	Length	Hit ID	Accession	Length	E-value	Overlap	Identity
>LYSC_CHICK	147	VM3B1_BOTJA	Q0NZY0	166	9.5	57	29.8

```
82 CNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSD-----GNGMNAWVAWRNRC 133
   :. :: ::.   :. ::    .  .: . .::  .  :     : : .  .: :..:
19 CDCGR-PGK---CQNPCCNATTCKLTPGSQCADGLCCDQCRFKGAGTECRAA-RSEC 70
```