

Jul-28-2021
WFSR
Report: test

2

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

gk

| | |
|---|--|
| 1 | MRSLLI LVL--CFLPLAALGKVFGRCELAAAMKRHGLDNYRGYS LGNWWCAAKFESNFNTQATN-RNTDG ::: :: MRSTLIISLLSCFFAVYE-AKVF SKCELAHKLKAQE MDGFGGYSLANWVCMAEYESNFNTRAFNGKNANG STDYGILQINSRWWCNDGRTPGSRNL CNIPCSALLSSDITASVNC AKKIVSDGNMGNAWVAWRNRCKGTD : SSDYGLFQLNNKWCKDNKR-SSSNAC NIMCSKLLDDNIDDD ISCAKRVVRDPKGMSAWKAWVKHCKDKD VQAWIRGC 147 ::: LSEYLASCN 148 |
|---|--|

3

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

19 KVFGRC ELAAAMKRHGLDNYRGYS LGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRT
 ::
 1 KVFSKCELAHKLKAQEMDGGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWCKDNKR
 PGRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCR 147
 ::
 SSS-NACNIMCSKLLDENIDDDISCAKRVRDPKGMSAWKAWVKHCKDKDLSEYLASCN 129

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 |

2³⁵ RCELA AAMKRHGLDNYRGYS LGNVCAAKFESNFNTQATNRNTDGSTDY GILQINSRWWCNDGRTPGSRN
 5 KCEVFRELK--DLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNN--STEYGLFQINNKIWCKDDQNP HSSN
 LCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAW 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 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 |
| <p>9/4 CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCND DPQVGTHI-----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 GRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMN 125</p> <p>28 GCCSGVRSLNN---AARTTADRRACNCLKNAAAGVSGLN 65</p> | | | | | | | | |

9

| ID | Length | Hit ID | Accession | Length | E-value | Overlap | Identity | Recalc |
|---|--------|--------------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147 | L7TY87_ACTDE | L7TY87 | 189 | 3.1 | 53 | 26.4 | 17.49 |
| <p>9/4 CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCND DPQVGTHI-----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 CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCND DPQVGTHI-----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 CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC 146</p> <p>4 CNGPCRDL--NDCDGQLICIKGKCND DPQVGTHI-----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 GSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNA--WVAWRNRCKGTD 138</p> <p>30 GIRNINNL---AKTTADRQTACNCLKQLSASVPGVNANNAALPGKC-GVN 77</p> | | | | | | | | |

13

| ID | Length | Hit ID | Accession | Length | E-value | Overlap | Identity | Recalc |
|---|--------|------------|------------------------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147 | NLTP_PRUAV | Q9M5X8 | 91 | 3.9 | 52 | 30.8 | 20.02 |
| <p>8/9 GSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNA--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 |
| 69 GSRNL CNIPCSALLSSDITASVNC AKKIVSDGNGMNA--WVAWRNRCKGTD 138 ::: 30 GIRNNL--- AKTTADROTAC NCLKOLSA SVPGVNANNAAL PGKC-GVN 77 | | | | | | | | |

15

[illegible]

16

[illegible]

17

| ID | Length | Hit ID | Accession | Length | E-value | Overlap | Identity | Recalc |
|-----------|--|--------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147 | L7TUJ3_ACTER | L7TUJ3 | 190 | 5.1 | 52 | 26.9 | 17.48 |
| 64 | CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG | 145 | | | | | | |
| 5 | CNGPCRDL--NDCDGOLICIKGKCND DPOVGTHI-----CRGTTPSPOPGG | 49 | | | | | | |

18

[illegible]

19

| ID | Length | Hit ID | Accession | Length | E-value | Overlap | Identity | Recalc |
|---|--------|--------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147 | L7TY92_ACTER | L7TY92 | 190 | 6.1 | 52 | 26.9 | 17.48 |
| 64 CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG | 145 | | | | | | | |
| 5 CNGPCRDL--NDCDGOLICIKGKCNDPDPEVGTHI-----CRGTTSPSPOPGG | 49 | | | | | | | |

20

[illegible]

21

| ID | Length | Hit ID | Accession | Length | E-value | Overlap | Identity | Recalc |
|-----------|---|-------------|-----------|--------|---------|---------|----------|--------|
| >LYSC_CHI | 147 | KIWEL_ACTCC | P85261 | 189 | 8.3 | 53 | 24.5 | 16.23 |
| 94 | CNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGC | 146 | | | | | | |
| 4 | CNGPCRDL--NDCDGOLICIEGKCND DPEVGTHI-----CRGTPSPQPGGC | 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 |

98 SRW-WCNDGRTPGSRNLCNIPCS 100
 ::::: :::
 19 SQWGC--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 SQWGC--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----LLSSDITASVNC AKKIVSDGNG 123
 2 NYCKIKCRSGIHTLCKFGISTKPN CGKNVVK-GSG 36

Exact word and sliding window results

Shown per ORF

Exact word results:

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

18
KVFGRCELAAMKRGHGLDNYRGYS LGNWVCAAKFESNFNTQATNRNTDGS TDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI
TASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG CRL 147

| Name | Accession ID | Description | Species | No exact words | Hit % |
|--|--------------|-------------|---------|----------------|-------|
| 0 | | | | | |
| KVFGRCELAAMKRGHGLDNYRGYS LGNWVCAAKFESNFNTQATNRNTDGS TDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDI | | | | | |
| TASVNC AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRG CRL 129 | | | | | |
| 52 ESNFNT 58 | | | | | |
| 52 ESNFNT 58 | | | | | |
| 34 ESNFNT 40 | | | | | |

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

52 ESNFNT 58
52 ESNFNT 58
53 ESNFNT 59

Sliding window results:

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

Alignments containing 68 window(s):

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

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

```

1  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  MRSLILVL--CFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDG
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
1  MRSTLIISLLSCFFAVYE-AKVFSKCELAHKLKAQEMDGGGYSLANWVCMAEYESNFNTRAFNGKNANG

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

```

Alignments containing 1 window(s):

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

```

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

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-AKVFSKCELAHKLKAQEMDGGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYG

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
   RNLNIPCSALLSS 105
   : : : : : : : :
   SNACNIMCSKLLDD 105
```

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

```
26 LAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLC
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
27 LAHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSS-NAC
   NIPCSALLSSD 106
   : : : : : : : :
   NIMCSKLLDDN 106
```

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

```
27 AAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCN
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
28 AHKLKAQEMDGFGGYSLANWVCMAYEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACN
   IPCSALLSSDITAS 110
   : : : : : : : :
   IMCSKLLDDNIDDD 110
```

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

```

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

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

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

```

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

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

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

```

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

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

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

```

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

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

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

```

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

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

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

```

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

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

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

```

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

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

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

```

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

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

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

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

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

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

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

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

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

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

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

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

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

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


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

Alignments containing 14 window(s):

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

```

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

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

```

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

```

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

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

```

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

```

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

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

```

Alignments containing 4 window(s):

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

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

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

Alignments containing 1 window(s):

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

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

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

Alignments containing 4 window(s):

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

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

RNLNIPCSALLSS 105
: : : : : : :
SNACNIMCSKLLDE 86
```

Alignments containing 1 window(s):

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

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

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


Alignments containing 4 window(s):

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

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

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

Alignments containing 1 window(s):

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

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

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

Alignments containing 4 window(s):

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

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

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

Alignments containing 1 window(s):

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

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

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

Alignments containing 4 window(s):

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

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

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

Alignments containing 1 window(s):

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

```
41 YSLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITAS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
23 YSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSS-NACNIMCSKLLDENIDDD

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

Alignments containing 4 window(s):

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

```
42 SLGNWVCAAKFESNFNTQATN-RNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
24 SLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDI

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

Alignments containing 1 window(s):

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

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

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

Alignments containing 4 window(s):

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

```
47 VCAAKFESNFNTQATN-RNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACK
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
29 VDMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKR

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

Alignments containing 1 window(s):

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

```
51 KFESNFNTQATN-RNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSD
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
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-RNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDG
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
34 YESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVVRDP

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

Alignments containing 1 window(s):

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

```
56 FNTQATN-RNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDGNGMN
   ::::::::::::::: : ::::::::::::::: : ::::::::::::::: : ::::::::::::::: :
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-SSSNACNIMCSKLLDENIDDDISCAKRVRDPKGMSA

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

Alignments containing 1 window(s):

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

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

Alignments containing 1 window(s):

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

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

Alignments containing 4 window(s):

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

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

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

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

```
62 NRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRN
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
45 GKNANGSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVRDPKGMSAWKAWVK

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

Alignments containing 1 window(s):

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

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

Alignments containing 2 window(s):

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

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

```
67 GSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGT
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
50 GSSDYGLFQLNNKWWCKDNKR-SSSNACNIMCSKLLDENIDDDISCAKRVRDPKGMSAWKAWVKHCKDK

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

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

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

```

9  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 | 15 | 0.017 | 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_CHIC K | 147 | Glt-156 minimal epitope in considered Deamidated form | 15 | 0.019 | 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_CHIC K | 147 | LMW glutenin-glt-156 (p40-p59; E48 and E51) | 20 | 0.022 | 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_CHIC K | 147 | LMW glutenin-glt-156 (p40-p59; E51) | 20 | 0.027 | 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_CHIC K | 147 | gamma5-gliadin (p227-237; E232) | 11 | 0.03 | 4 | 75.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/15972656 | | | | | | | | |

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

7

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | alpha-gliadin(p123-p132) | 10 | 0.033 | 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 | alpha gliadin 123-132 | 10 | 0.035 | 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 K | 147 | Wheat peptide W09 | 14 | 0.035 | 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 | 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

11

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

12

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|----------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK K | 147 | DQ2-gamma-II peptide | 11 | 0.039 | 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_CHIC K | 147 | Wheat peptide W09 | 14 | 0.039 | 3 | 100.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

11 FLP 13
:::
5 FLP 7

14

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | alpha-Glia AG11 (p78 -p95) | 17 | 0.04 | 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_CHIC K | 147 | alpha gliadin 78-95 AG11 | 17 | 0.046 | 3 | 100.0 | 100.0 | ProPepper |
| https://www.iedb.org/epitope/109723 | | | | | | | | |

11 FLP 13
:::
6 FLP 8

16

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | alpha-Glia AG11 (p78 -p95; E86) | 17 | 0.046 | 3 | 100.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/19299713 | | | | | | | | |

11 FLP 13
:::
6 FLP 8

17

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHIC K | 147 | alpha gliadin P11 | 15 | 0.049 | 3 | 100.0 | 100.0 | ProPepper |
| https://www.iedb.org/epitope/139589 | | | | | | | | |

11 FLP 13
:::
5 FLP 7

18

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|---------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK K | 147 | gamma gliadin | 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 K | 147 | Wheat peptide W09 | 20 | 0.054 | 3 | 100.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

11 FLP 13
: : :
10 FLP 12

20

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK K | 147 | gamma gliadin 1 | 9 | 0.056 | 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

21

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK K | 147 | Wheat peptide W36 | 15 | 0.058 | 9 | 44.4 | 88.9 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

1 MRSLILVL 9
: : : : :
5 IRSLVLRTL 13

22

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK K | 147 | W09 | 20 | 0.06 | 3 | 100.0 | 100.0 | ProPepper |
| https://www.iedb.org/epitope/238729 | | | | | | | | |

11 FLP 13
: : :
10 FLP 12

23

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | Wheat peptide W36 | 15 | 0.062 | 9 | 44.4 | 88.9 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

1 MRSLLILVL 9
.: : : : :
5 IRSVLRLTL 13

24

| 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

25

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | Rye peptide R12 | 12 | 0.065 | 3 | 100.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

12 LPL 14
.: :
10 LPL 12

26

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | Rye peptide R12 | 12 | 0.069 | 3 | 100.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

12 LPL 14
.: :
10 LPL 12

27

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK | 147 | W36s | 16 | 0.071 | 9 | 44.4 | 88.9 | ProPepper |
| https://www.iedb.org/epitope/238963 | | | | | | | | |

1 MRSLLILVL 9
.: : : : :
5 IRSVLRLTL 13

28

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | Glia-gamma30-gliadin (p222-236; E225 and E231) | 15 | 0.072 | 4 | 75.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/12055577 | | | | | | | | |

72 GILQ 75
:::
5 GIIQ 8

29

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | Wheat peptide W37 | 12 | 0.073 | 8 | 37.5 | 62.5 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

119 DGNGMNAW 126
:::
3 DPSGQVQW 10

30

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | Wheat peptide W36 | 16 | 0.074 | 9 | 44.4 | 88.9 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

1 MRSLILVL 9
:::
5 IRSVLRLTL 13

31

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | DQ2-y -II y-Glia (p 222-p236; E229) | 15 | 0.075 | 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_CHIC K | 147 | R12E | 12 | 0.076 | 3 | 100.0 | 100.0 | ProPepper |
| https://www.iedb.org/epitope/238932 | | | | | | | | |

12 LPL 14
:::
10 LPL 12

33

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

72 GILQ 75
:::
5 GIIQ 8

34

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|---|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | Glt-156 minimal epitope in considered native form | 15 | 0.081 | 7 | 42.9 | 71.4 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/15714306 | | | | | | | | |

53 ESNFNTQ 59
:::
8 QSPFSQQ 14

35

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-----------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | Rye peptide R09 | 12 | 0.083 | 3 | 100.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

12 LPL 14
:::
2 LPL 4

36

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | Wheat peptide W36 | 20 | 0.084 | 9 | 44.4 | 88.9 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

1 MRSLILVL 9
:::
9 IRSLVLRTL 17

37

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK | 147 | R01 | 20 | 0.085 | 3 | 100.0 | 100.0 | ProPepper |
| https://www.iedb.org/epitope/238942 | | | | | | | | |

12 LPL 14
:::
3 LPL 5

38

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|----------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK K | 147 | Rye peptide R01, R09 | 20 | 0.085 | 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 K | 147 | alpha-gliadin 4037 | 17 | 0.087 | 9 | 44.4 | 66.7 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/21091908 | | | | | | | | |

71 YGILQINSR 79
:::
9 FGIFGTNYR 17

40

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK K | 147 | Glia-gamma30-gliadin (p222-p236) | 15 | 0.09 | 4 | 75.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/12055577 | | | | | | | | |

72 GILQ 75
:::
5 GIIQ 8

41

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

42

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

43

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | HMW glutenin-glt04 (p707-p742) | 36 | 0.091 | 29 | 13.8 | 62.1 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/10540324 | | | | | | | | |

39 RGYS LGNWVCAAKFESNFNTQATNRNTDGS 67
 :::::
 3 QGQRPGQWLQPGQGQGYPTSPQQSGQGQ 31

44

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | LMW glutenin-glt-156 (p45-p54; E48, E49 and E51) minimal epitope | 10 | 0.092 | 4 | 75.0 | 75.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/15714306 | | | | | | | | |

53 ESNF 56
 :::
 7 ESPF 10

45

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|---------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | Glia-gamma30-gliadin (p222-236; E231) | 15 | 0.094 | 4 | 75.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/12055577 | | | | | | | | |

72 GILQ 75
 :::
 5 GI IQ 8

46

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | DQ2-y -II y-Glia (p222-p236) | 15 | 0.096 | 4 | 75.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/19299713 | | | | | | | | |

72 GILQ 75
 :::
 3 GI IQ 6

47

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | Sec-gammal 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

48

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK | 147 | gamma gliadin 222-23 6 DQ2-gamma-II | 15 | 0.097 | 4 | 75.0 | 100.0 | ProPepper |
| https://www.iedb.org/epitope/109223 | | | | | | | | |

72 GILQ 75
:::
3 GIQ 6

49

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

53 ESNFNTQ 59
:::
5 EQSFPEQ 11

50

| 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

51

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | LMW glutenin-glt-156 (p40-p59; E48) | 20 | 0.1 | 7 | 42.9 | 71.4 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/12055577 | | | | | | | | |

53 ESNFNTQ 59
:::
12 QSPFSQQ 18

52

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

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 | DQ2.2-glut-L-1 containing peptide | 20 | 0.11 | 7 | 42.9 | 71.4 | ProPepper |
| https://www.iedb.org/epitope/167143 | | | | | | | | |

53 ESNFNTQ 59
:::
12 QSPFSQQ 18

56

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | alpha-gliadin CAB769 61 (p251-p270) | 20 | 0.11 | 9 | 44.4 | 66.7 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/17629515 | | | | | | | | |

71 YGILQINSR 79
:::
12 FGIFGTNYR 20

57

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | Wheat peptide W37 | 20 | 0.11 | 8 | 37.5 | 62.5 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

119 DNGMNAW 126
:::
8 DPSGQVQW 15

58

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

53 ESNFNTQ 59
 : : : : :
 12 QSPFSQQ 18

59

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | LMW glutenin-glt-156 (p45-p54; E49 and E 49) minimal epitope | 10 | 0.11 | 4 | 75.0 | 75.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/15714306 | | | | | | | | |

53 ESNF 56
 : : :
 7 ESPF 10

60

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | LMW glutenin-glt-156 (p46-p54; E51) | 9 | 0.11 | 4 | 75.0 | 75.0 | AllergenOnline |
| 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

61

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

53 ESNFNTQ 59
 : : : : :
 5 EQSFPQQ 11

62

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

72 GILQ 75
 : : : :
 5 GI IQ 8

63

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-----------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK | 147 | alpha gliadin 251-270 | 20 | 0.12 | 9 | 44.4 | 66.7 | ProPepper |
| https://www.iedb.org/epitope/72058 | | | | | | | | |

71 YGILQINSR 79

 12 FGIFGTNYR 20

64

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | gamma5 (p62-p72; E68, E63 and E71) | 11 | 0.12 | 7 | 42.9 | 57.1 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/15972656 | | | | | | | | |

53 ESNFNTQ 59

 2 EQPFPEQ 8

65

| 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

66

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

53 ESNFN 57

 10 ESPFS 14

67

| 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

68

| 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

69

| 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

70

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK | 147 | W37s | 16 | 0.13 | 8 | 37.5 | 62.5 | ProPepper |
| https://www.iedb.org/epitope/238519 | | | | | | | | |

119 DNGMNAW 126
.:.:
5 DPSGQVQW 12

71

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-----------------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK | 147 | DQ2.2-glut-L-1 containing peptide | 20 | 0.13 | 7 | 42.9 | 71.4 | ProPepper |
| https://www.iedb.org/epitope/52130 | | | | | | | | |

53 ESNFNTQ 59
.:.:
12 QSPFSQQ 18

72

| 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 | 0.13 | 7 | 42.9 | 57.1 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/15972656 | | | | | | | | |

53 ESNFNTQ 59
.:.:
1 EQPFPEQ 7

73

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK K | 147 | gamma-gliadin 1383 (p141-p160) | 20 | 0.13 | 6 | 50.0 | 83.3 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/16878175 | | | | | | | | |

97 PCSALL 102
:::
10 PCKNFL 15

74

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

12 LPL 14
:::
12 LPL 14

76

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

12 LPL 14
:::
16 LPL 18

77

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-----------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK K | 147 | alpha-gliadin p19 (p21-p40) | 20 | 0.14 | 12 | 25.0 | 66.7 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/8315377 | | | | | | | | |

12 LPLAALGKVFGR 23
:::
2 VPLVQQQQLGQ 13

78

| 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 EQPFSSQ 17

79

| 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

80

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

97 PCSALL 102
 : : : : :
 10 PCKNFL 15

81

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

122 GMNAWVAW 129
 : : : : :
 3 GPSGQVEW 10

82

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

48 CAAKFES 54
 : : : : :
 1 CPQPFPS 7

83

| 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 | 0.15 | 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_CHIC K | 147 | Glutenin-Glt-17 (p50 -p58; E52, E53 and E 55) | 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_CHIC K | 147 | Naturally occurring glutenins (p722-p736) (homolog of glt04) | 15 | 0.15 | 7 | 57.1 | 57.1 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/10540324 | | | | | | | | |

97 PCSALLS 103
:: ::
7 PTSPQLS 13

86

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------|--------|---------|---------|----------|------------|----------|
| >LYSC_CHIC K | 147 | DQ8-glut-H1 | 9 | 0.15 | 6 | 50.0 | 50.0 | Sollid |
| https://pubmed.ncbi.nlm.nih.gov/10540324 | | | | | | | | |

85 GRTPGS 90
:: ::
2 GYYPTS 7

87

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

85 GRTPGS 90
:: ::
2 GYYPTS 7

88

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|----------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK | 147 | DQ8-glut-H1, DQ8.5-glut-H1 | 9 | 0.16 | 6 | 50.0 | 50.0 | ProPepper |
| https://www.iedb.org/epitope/161144 | | | | | | | | |

85 GRTPGS 90
: : :
2 GYYPTS 7

89

| 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

90

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------------|--------|---------|---------|----------|------------|-----------|
| >LYSC_CHICK | 147 | LMW glutenin 17 (53-60) | 8 | 0.17 | 4 | 50.0 | 75.0 | ProPepper |
| https://www.iedb.org/epitope/47569 | | | | | | | | |

56 FNTQ 59
: : :
2 FSQQ 5

91

| 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 | 0.17 | 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

92

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | Deamidated Glt-156 minimal epitope (p40-p59) | 15 | 0.17 | 4 | 75.0 | 75.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/15714306 | | | | | | | | |

53 ESNF 56
: : :
12 ESPF 15

93

| 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

94

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | G4-9A gliadin (p62-p75; E65 and A70) | 14 | 0.18 | 5 | 60.0 | 60.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/12524402 | | | | | | | | |

12 LPLAA 16
:::
5 LPYPA 9

95

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|------------------------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | alpha-gliadin CAB76960 (p253-p272) | 20 | 0.18 | 4 | 50.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/17629515 | | | | | | | | |

93 LCNI 96
:::
2 MCNV 5

96

| 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

97

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHICK | 147 | Wheat peptide W16 | 16 | 0.18 | 4 | 50.0 | 75.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

85 GRTP 88
:::
1 GQQP 4

98

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|-------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | Wheat peptide W11 | 15 | 0.18 | 7 | 42.9 | 71.4 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

53 ESNFNTQ 59
:::
8 EQTFPHQ 14

99

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | Glutenin-Glt-17 (p50 -p58; E52 and E55) | 9 | 0.18 | 2 | 100.0 | 100.0 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/16091925 | | | | | | | | |

13 PL 14
:::
8 PL 9

100

| ID | Length | Hit ID | Length | E-value | Overlap | Identity | Similarity | Database |
|---|--------|--------------------|--------|---------|---------|----------|------------|----------------|
| >LYSC_CHIC K | 147 | Barley peptide B03 | 16 | 0.18 | 13 | 30.8 | 46.2 | AllergenOnline |
| https://pubmed.ncbi.nlm.nih.gov/20650871 | | | | | | | | |

85 GRTPGSRNLCNIP 97
:::
1 GQQPFPQPEQPIIP 13



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 RNTDGS TDY GILQINSRWWCNDGRTPG----SRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVA ::::: 4 QNLGSDIPHDIIKLPNGQWC---KTPGALCSSRSEC---CKAKHSDSVTYSSGCSRQW-SDQQGL----- ::::: WRNRCKGTDVQA 140 ::::: FINQCRTC NVES 73 </pre> | | | | | | | |

2

| ID | Length | Hit ID | Accession | Length | E-value | Overlap | Identity |
|---|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI | 147 | SCX12_CENNO | P63019 | 67 | 0.7 | 46 | 34.8 |
| <pre> 874 DGRTE GSRNLCNIPCSALLSSDITASVNC AKKIVSDGNGMNAWVAW 129 ::::: 2 DGY-PLASNGCKFGCSGLGENNPTCNHVCEKKAGSDYGYCYAWTCY 46 </pre> | | | | | | | |

3

| ID | Length | Hit ID | Accession | Length | E-value | Overlap | Identity |
|--|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI | 147 | SX15F_RHOJU | 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 | KRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTD--GSTDYGILQIN 77 | | | | | | |
| 43 | MAALEYKHGMRNYPHTVSHCDNQRSCS-LMNVKDRADLVGMTYFTVLKIS 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--ESNFNTQATNRNTDGDSTDYGILQI--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--ESNFNTQATNRNTDGDSTDYGILQI--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---NDNICKTECQAKWKQSDGYCYSPGMSYCTNLPEDAENV 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 | STDYGILQINSRWWCNDGRTPGSRNLCNIP---CSALLSSDITASVNC AKKIVSDGNGMNAWVAW | | | | | | |
| 4 | QNLGSGIPHDKIKLPNGQWC---KTPG--DLCSSSSECCAKHSNSVTYASFCRQW---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

12

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

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

13

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

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

14

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

68 YRGYSLGNWV--CAAKFESNFNT--QATNRNTDGGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLS
 122 YKTYRIGCAVNYCPSSEYSYFYVCQYCPSGNMRGST---ATPYKSGPTCGDCPSACDNGLCNTPCT--LY
 SDITASVNCACKIVSDGNGMNAWVAWRNCKGT 136
 NEYT---NC-DSLVKQSSCQDEWI--KSKCPAS 213

15

[illegible]

16

| ID | Length | Hit ID | Accession | Length | E-value | Overlap | Identity |
|------------------------------------|--------|-------------|------------------------|--------|---------|---------|----------|
| >LYSC_CHI82 | 147 | VM3B1_BOTJA | Q0NZY0 | 166 | 9.5 | 57 | 29.8 |
| CNDGRTPGSRNLCNIPCSALLSSDITASVNC | | | | | | | |
| AKKIVSD---- | | | | | | | |
| GNMNAVVAWRNRC | 133 | | | | | | |
| 19 CDCGR-PGK--- | | | | | | | |
| CQNPCCNATTC | | | | | | | |
| KLTGPSQCADGLCCDQCRFKGAGTECRAA-RSEC | 70 | | | | | | |