# ABCpred Prediction Server

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INPUT INFORMATION

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| Sequence name | |
| Length of the sequence | 260 |
| Number of 16mers from the input sequence | 245 |
| Threshold setting (Default value is 0.5) | 0.51 |

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## TABULAR RESULT

## Predicted B-cell epitope

### The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network.<br>Higher score of the peptide means the higher probability to be as epitope.<br>All the peptides shown here are above the threshold value chosen.

| Rank | Sequence | Start position | Score | |
|---|---|---|---|---|
| 1 | AKAESDKMLADARANA | 121 | 0.92 | |
| 2 | TRLIEENSDLRQRINE | 40 | 0.91 | |
| 3 | EQLRTFEREYRTRLKT | 210 | 0.89 | |
| 3 | ATVAEARQRADAMLAD | 149 | 0.89 | |
| 3 | QILGEARHTADATVAE | 138 | 0.89 | |
| 4 | TQAIPAYEPEPGKPAP | 73 | 0.88 | |
| 5 | ELDQELAAGGGAGVTP | 55 | 0.85 | |
| 5 | AQLRQAQEKADALQAD | 171 | 0.85 | |
| 6 | HNVAFSKPPIGKRGYN | 9 | 0.84 | |
| 6 | AAGGGAGVTPQATQAI | 61 | 0.84 | |
| 6 | RVLSLAQDTADRLTNT | 105 | 0.84 | |

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|---|---|---|---|---|
| 7 | EPGKPAPAAVSAGMNE | 82 | 0.81 | |
| 8 | AVSAGMNEEQALKAAR | 90 | 0.79 | |
| 8 | GKRGYNEDEVDAFLDL | 19 | 0.79 | |
| 8 | MPLTPADVHNVAFSKP | 1 | 0.79 | |
| 9 | QRGSAAPVDSNADAGG | 236 | 0.78 | |
| 10 | DSNADAGGFDQFNRGK | 244 | 0.77 | |
| 11 | DAERKHSEIMGTINQQ | 186 | 0.73 | |
| 11 | AMLADAQSRSEAQLRQ | 160 | 0.73 | |
| 12 | MGTINQQRAVLEGRLE | 195 | 0.72 | |
| 13 | QRAVLEGRLEQLRTFE | 201 | 0.65 | |
| 14 | EDEVDAFLDLVENELT | 25 | 0.64 | |
| 15 | EREYRTRLKTYLESQL | 216 | 0.63 | |
| 16 | EQALKAARVLSLAQDT | 98 | 0.61 | |
| 17 | SDLRQRINELDQELAA | 47 | 0.59 | |

# OVERLAP DISPLAY

MPLTPADVHNVAFSKPPIGKRGYNEDEVDAFLDLVENELTRLIEENSDLRQRINELDQELAAGGGAGVTPQATQAIPAYEPEP
GKPAPAAVSAGMNEEQALKAARVLSLAQDTADRLTNTAKAESDKMLADARANAEQILGEARHTADATVAEARQRADAMLADAQ
SRSEAQLRQAQEKADALQADAERKHSEIMGTINQQRAVLEGRLEQLRTFEREYRTRLKTYLESQLEELGQRGSAAPVDSNADA
GGFDQFNRGKN$^{260}$

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AKAESDKMLADARANA-------------------------------------------------------------------
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TRLIEENSDLRQRINE-------------------------------------------------------------------
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EQLRTFEREYRTRLKT-----------------------------------
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ATVAEARQRADAMLAD-------------------------------------------------------------------
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QILGEARHTADATVAE-------------------------------------------------------------------
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TQAIPAYEPEPGKPAP-------------------------------------------------------------------
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ELDQELAAGGGAGVTP-------------------------------------------------------------------
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AQLRQAQEKADALQAD-------------------------------------------------------------------
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HNVAFSKPPIGKRGYN-------------------------------------------------------------------
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AAGGGAGVTPQATQAI-------------------------------------------------------------------
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RVLSLAQDTADRLTNT-------------------------------------------------------------------
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EPGKPAPAAVSAGMNE-------------------------------------------------------------------
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AVSAGMNEEQALKAAR-------------------------------------------------------------------
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GKRGYNEDEVDAFLDL-------------------------------------------------------------------
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MPLTPADVHNVAFSKP-------------------------------------------------------------------
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QRGSAAPVDSNADAGG---------
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DSNADAGGFDQFNRGK-
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DAERKHSEIMGTINQQ-----------------------------------------------------------
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AMLADAQSRSEAQLRQ-------------------------------------------------------------------
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MGTINQQRAVLEGRLE--------------------------------------------------
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QRAVLEGRLEQLRTFE--------------------------------------------
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EDEVDAFLDLVENELT-------------------------------------------------------------------
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EREYRTRLKTYLESQL-----------------------------
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