# ABCpred Prediction Server

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INPUT INFORMATION

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|---|---|
| Sequence name | |
| Length of the sequence | 410 |
| Number of 16mers from the input sequence | 395 |
| 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.**
**Higher score of the peptide means the higher probability to be as epitope.**
**All the peptides shown here are above the threshold value chosen.**

| Rank | Sequence | Start position | Score | |
|---|---|---|---|---|
| 1 | VNAGGGMVVADAALTP | 342 | 0.93 | |
| 2 | GGTAGHVEPAMAVADA | 43 | 0.88 | |
| 3 | GGRGATAPRPADAASP | 10 | 0.86 | |
| 4 | VPMPRKPGGDLARLPS | 95 | 0.85 | |
| 5 | LELITAVPMPRKPGGD | 89 | 0.84 | |
| 5 | AVSGAAADLAAAGVCV | 247 | 0.84 | |
| 6 | ARDVLDDVDADVVVGF | 119 | 0.82 | |
| 7 | LPAIYVPLPIGNGEQR | 320 | 0.81 | |
| 7 | RRRAQGDPPYVAVPYL | 275 | 0.81 | |
| 7 | SGLRRAEVVGVPVRAS | 191 | 0.81 | |
| 8 | MVVADAALTPELVARQ | 348 | 0.80 | |

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| 8 | EQRLNALPVVNAGGGM | 333 | 0.80 | |
| 8 | PVVIHEANARAGLANR | 160 | 0.80 | |
| 8 | SRVWRAVREARDVLDD | 110 | 0.80 | |
| 9 | TPELVARQVAGLLTDP | 356 | 0.79 | |
| 9 | NRVGAHTADRVLSAVP | 174 | 0.79 | |
| 9 | AARGLPLPPRRRRRIP | 145 | 0.79 | |
| 10 | PRPADAASPSCGSSPS | 17 | 0.78 | |
| 10 | PRRRRRIPVVIHEANA | 153 | 0.78 | |
| 11 | ALVALDPRVRITALGT | 58 | 0.75 | |
| 11 | PLPIGNGEQRLNALPV | 326 | 0.75 | |
| 11 | LSAVPDSGLRRAEVVG | 185 | 0.75 | |
| 12 | VLRAEARAHFGFPDDA | 214 | 0.74 | |
| 13 | RVRITALGTLRGLETR | 65 | 0.73 | |
| 13 | VGHRDAAGQVARAALA | 384 | 0.73 | |
| 14 | AGLLTDPARLAAMTAA | 365 | 0.72 | |
| 14 | SVSVVLAGGGTAGHVE | 35 | 0.72 | |
| 14 | PQNVLELRRRAQGDPP | 268 | 0.72 | |
| 14 | GGYVALPAYLAARGLP | 135 | 0.72 | |
| 15 | AMTAAAARVGHRDAAG | 376 | 0.71 | |
| 15 | CRAGAMTVAEVSAVGL | 305 | 0.71 | |
| 15 | GGSQGAVSLNRAVSGA | 236 | 0.71 | |
| 16 | TRLVPQRGYHLELITA | 79 | 0.70 | |
| 16 | RASIAALDRAVLRAEA | 204 | 0.70 | |
| 17 | DRMELAYAAADLVICR | 291 | 0.69 | |
| 17 | GGDLARLPSRVWRAVR | 102 | 0.69 | |
| 18 | GQVARAALAVATGAGA | 391 | 0.68 | |
| 19 | RAHFGFPDDARVLLVF | 220 | 0.67 | |
| 20 | PSCGSSPSADSVSVVL | 25 | 0.66 | |
| 21 | CVLHAHGPQNVLELRR | 261 | 0.65 | |
| 22 | TVAEVSAVGLPAIYVP | 311 | 0.63 | |
| 22 | ADLAAAGVCVLHAHGP | 253 | 0.63 | |
| 23 | PYVAVPYLDRMELAYA | 283 | 0.62 | |
| 24 | EVVGVPVRASIAALDR | 197 | 0.59 | |

# OVERLAP DISPLAY

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VKDTVSQPAGGRGATAPRPADAASPSCGSSPSADSVSVVLAGGGTAGHVEPAMAVADALVALDPRVRITALGTLRGLETRLVP
QRGYHLELITAVPMPRKPGGDLARLPSRVWRAVREARDVLDDVDADVVVGFGGYVALPAYLAARGLPLPPRRRRRIPVVIHEA
NARAGLANRVGAHTADRVLSAVPDSGLRRAEVVGVPVRASIAALDRAVLRAEARAHFGFPDDARVLLVFGGSQGAVSLNRAVS
GAAADLAAAGVCVLHAHGPQNVLELRRRAQGDPPYVAVPYLDRMELAYAAADLVICRAGAMTVAEVSAVGLPAIYVPLPIGNG
EQRLNALPVVNAGGGMVVADAALTPELVARQVAGLLTDPARLAAMTAAAARVGHRDAAGQVARAALAVATGAGARTTT[410]
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---------VNAGGGMVVADAALTP-------------------------------------------------------
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GGTAGHVEPAMAVADA--------------------------------------------------------------------
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GGRGATAPRPADAASP---------------------------------------------------------------------
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VPMPRKPGGDLARLPS---------------------------------------------------------------------
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LELITAVPMPRKPGGD---------------------------------------------------------------------
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-------------------------------------------------------------------------------
AVSGAAADLAAAGVCV----------------------------------------------------------------------
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ARDVLDDVDADVVVGF----------------------------------------------------------------------
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-----------------------------------------------------------------------
LPAIYVPLPIGNGEQR----------------------------------------------------------------------
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CVLHAHGPQNVLELRR-------------------------------------------------------------
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TVAEVSAVGLPAIYVP-------------------------------------------------------------
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ADLAAAGVCVLHAHGP-------------------------------------------------------------
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PYVAVPYLDRMELAYA-------------------------------------------------------------
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EVVGVPVRASIAALDR-------------------------------------------------------------
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