# ABCpred Prediction Server

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INPUT INFORMATION

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|---|---|
| Sequence name | |
| Length of the sequence | 525 |
| Number of 16mers from the input sequence | 510 |
| 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 | PVSSEDAMTADWTRVP | 474 | 0.90 | |
| 1 | AGVQYHPEVMHTPHGQ | 174 | 0.90 | |
| 1 | GGIVAHTGTREYGRTE | 104 | 0.90 | |
| 2 | PADIDVPETPARPVLV | 4 | 0.89 | |
| 3 | TGTREYGRTELKVLGG | 110 | 0.88 | |
| 4 | AMTADWTRVPYEVLER | 480 | 0.87 | |
| 5 | SIEEIRARQPVALVLS | 49 | 0.86 | |
| 5 | SGTANIKSHHNVGGLP | 349 | 0.86 | |
| 5 | DAVTAAPDGFDVVASS | 143 | 0.86 | |
| 6 | LVTVDAAETFLEALSG | 283 | 0.85 | |
| 7 | EELTAAGLDNQIWQCP | 432 | 0.84 | |

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|---|---|---|---|---|
| 7 | VGRELGLPEEIVARQP | 386 | 0.84 |  |
| 8 | GRTYGHPIVLRPVSSE | 463 | 0.83 |  |
| 8 | EEIVARQPFPGPGLGI | 394 | 0.83 |  |
| 8 | QPVWMSHGDAVTAAPD | 135 | 0.83 |  |
| 9 | SVYADGAPKLDPALLD | 69 | 0.82 |  |
| 9 | VGVQGDGRTYGHPIVL | 457 | 0.82 |  |
| 9 | AATGANLVTVDAAETF | 277 | 0.82 |  |
| 9 | HGLLRAGERAQVQRDF | 260 | 0.82 |  |
| 10 | QRAIGDRLTCVFVDHG | 246 | 0.81 |  |
| 10 | FAGLGAQWTPANIANA | 199 | 0.81 |  |
| 11 | EVLERISTRITNEVAE | 491 | 0.80 |  |
| 11 | DSAVAAALVQRAIGDR | 237 | 0.80 |  |
| 12 | NQIWQCPVVLLADVRS | 441 | 0.79 |  |
| 12 | AFEAFDRRLAGVQYHP | 165 | 0.79 |  |
| 13 | EFLVQGTLYPDVVESG | 331 | 0.78 |  |
| 14 | LSGVSAPEGKRKIIGR | 296 | 0.77 |  |
| 15 | STRITNEVAEVNRVVL | 497 | 0.76 |  |
| 15 | GIRIVGEVTAKRLDTL | 408 | 0.76 |  |
| 15 | YPDVVESGGGSGTANI | 339 | 0.76 |  |
| 15 | YAQLIARRVREARVFS | 26 | 0.76 |  |
| 16 | DVVASSAGAPVAAFEA | 153 | 0.75 |  |
| 17 | VIPHTASIEEIRARQP | 43 | 0.74 |  |
| 18 | VNRVVLDITSKPPATI | 507 | 0.73 |  |
| 18 | HNVGGLPDDLKFTLVE | 358 | 0.73 |  |
| 19 | AKRLDTLRHADSIVRE | 417 | 0.72 |  |
| 20 | PVVLLADVRSVGVQGD | 447 | 0.71 |  |
| 20 | GERAQVQRDFVAATGA | 266 | 0.71 |  |
| 20 | DGHAICGLSGGVDSAV | 225 | 0.71 |  |
| 21 | VRTQIGDGHAICGLSG | 219 | 0.70 |  |
| 22 | QAMAQALGGIVAHTGT | 97 | 0.69 |  |
| 22 | IGRQFIRAFEGAVRDV | 309 | 0.69 |  |
| 23 | VPVLGICYGFQAMAQA | 87 | 0.68 |  |
| 24 | ARQPVALVLSGGPASV | 55 | 0.65 |  |
| 24 | KVLGGKLHSDLPEVQP | 121 | 0.65 |  |

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|---|---|---|---|---|
| 25 | FEGAVRDVLDGKTAEF | 317 | 0.64 |  |
| 26 | SRFLHDFAGLGAQWTP | 193 | 0.62 |  |
| 27 | RRVREARVFSEVIPHT | 32 | 0.60 |  |
| 28 | PARPVLVVDFGAQYAQ | 13 | 0.58 |  |
| 29 | GLSGGVDSAVAAALVQ | 231 | 0.57 |  |
| 30 | KFTLVEPLRLLFKDEV | 368 | 0.56 |  |
| 31 | DVLDGKTAEFLVQGTL | 323 | 0.53 |  |
| 32 | TPANIANALIEQVRTQ | 207 | 0.51 |  |

# OVERLAP DISPLAY

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VVQPADIDVPETPARPVLVVDFGAQYAQLIARRVREARVFSEVIPHTASIEEIRARQPVALVLSGGPASVYADGAPKLDPALL
DLGVPVLGICYGFQAMAQALGGIVAHTGTREYGRTELKVLGGKLHSDLPEVQPVWMSHGDAVTAAPDGFDVVASSAGAPVAAF
EAFDRRLAGVQYHPEVMHTPHGQQVLSRFLHDFAGLGAQWTPANIANALIEQVRTQIGDGHAICGLSGGVDSAVAAALVQRAI
GDRLTCVFVDHGLLRAGERAQVQRDFVAATGANLVTVDAAETFLEALSGVSAPEGKRKIIGRQFIRAFEGAVRDVLDGKTAEF
LVQGTLYPDVVESGGGSGTANIKSHHNVGGLPDDLKFTLVEPLRLLFKDEVRAVGRELGLPEEIVARQPFPGPGLGIRIVGEV
TAKRLDTLRHADSIVREELTAAGLDNQIWQCPVVLLADVRSVGVQGDGRTYGHPIVLRPVSSEDAMTADWTRVPYEVLERIST
RITNEVAEVNRVVLDITSKPPATIEWE525
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