

ABCpred Prediction Server

INPUT INFORMATION

| | |
|--|------|
| Sequence name | |
| Length of the sequence | 625 |
| Number of 16mers from the input sequence | 610 |
| Threshold setting (Default value is 0.5) | 0.51 |

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 | VKELTGGKEPNKGVNP | 326 | 0.96 | |
| 2 | TSINLPYITVDADKNP | 251 | 0.95 | |
| 3 | EAHAEEDRKRREEADV | 494 | 0.91 | |
| 4 | APEISARILMKLKRDA | 88 | 0.90 | |
| 4 | RGIPQIEVTFDIDANG | 441 | 0.90 | |
| 5 | GEKEQRILVFDLGGGT | 160 | 0.88 | |
| 6 | EVRATSGDNHLGGDDW | 189 | 0.87 | |
| 7 | HMGSDWSIEIDGKKYT | 72 | 0.86 | |
| 7 | AHPGGEPPGAHPGSAD | 595 | 0.86 | |
| 7 | DRMIKDAEAHAEEDRK | 487 | 0.86 | |
| 7 | TKRSETFTTADDNQPS | 394 | 0.86 | |
| 7 | KGGVMTRLIERNTTIP | 378 | 0.86 | |

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|----|-------------------|-----|------|--|
| 7 | HVVLVGGSTRMPAVTD | 309 | 0.86 | |
| 7 | KGTSIDLTGDKMAMQ | 217 | 0.86 | |
| 7 | DAVITTPAYFNDAQRQ | 113 | 0.86 | |
| 8 | SGLSKEDIDRMKDAE | 479 | 0.83 | |
| 9 | KVPEDTLNKVDAVAE | 535 | 0.82 | |
| 10 | GGDDWDQRVVDWLVDK | 200 | 0.81 | |
| 10 | VVSVLEGGDPVVVANS | 15 | 0.81 | |
| 11 | EAEGGSKVPEDTLNKV | 529 | 0.80 | |
| 11 | FELTGIPPAPRGIPQI | 431 | 0.80 | |
| 11 | AVGIDLGTTNSVSVL | 4 | 0.80 | |
| 12 | DRTVRSVKRHMGS DWS | 63 | 0.79 | |
| 12 | GQAIYEAAQAASQATG | 578 | 0.79 | |
| 12 | IERNTTIPTKRSETFT | 386 | 0.79 | |
| 12 | FQRITQDLLDRTRKPF | 278 | 0.79 | |
| 12 | DKMAMQRLREAAEKAK | 227 | 0.79 | |
| 12 | AGQIAGLNVLRIVNEP | 133 | 0.79 | |
| 13 | GQESQALGQAIYEAAQ | 571 | 0.78 | |
| 13 | SLGIETKGGVMTRLIE | 372 | 0.78 | |
| 13 | GDPVVVANSEGSRTTP | 22 | 0.78 | |
| 13 | DAQRQATKDAGQIAGL | 124 | 0.78 | |
| 14 | DDVVDAEVVDDGREAK | 610 | 0.77 | |
| 14 | HVTAKDKGTGKENTIR | 459 | 0.77 | |
| 14 | TFDIDANGIVHVTAKD | 449 | 0.77 | |
| 15 | DGKKYTAPEISARILM | 82 | 0.76 | |
| 15 | AHPGSADDVVDAEVVD | 604 | 0.76 | |
| 15 | EVLVGQPAKNQAVTNV | 47 | 0.76 | |
| 15 | KRDAEAYLGEDITDAV | 100 | 0.76 | |
| 16 | QAASQATGAAHPGGEP | 586 | 0.75 | |
| 16 | GKEPNKGVNPDEVVAV | 332 | 0.75 | |
| 16 | SVSEIDHVVLVGGSTR | 303 | 0.75 | |
| 16 | EAAEKAKIELSSSQST | 236 | 0.75 | |
| 17 | GSDISAIKSAMEKLGQ | 557 | 0.74 | |
| 17 | SIVAFARNGEVLVGP | 38 | 0.74 | |
| 17 | VVAVGAALQAGVLKGE | 344 | 0.74 | |

| | | | | |
|----|-------------------|-----|------|--|
| 18 | ANSEGSRTTPSIVAF | 28 | 0.73 | |
| 19 | WLVDKFKGTSGIDLTK | 211 | 0.72 | |
| 19 | LVFDLGGGTFDVSLE | 167 | 0.72 | |
| 20 | RKRREEADVRNQAETL | 501 | 0.71 | |
| 20 | TVDADKNPLFLDEQLT | 259 | 0.71 | |
| 21 | SVQIQVYQGEREIAAH | 409 | 0.69 | |
| 22 | SAMEKLGQESQALGQA | 565 | 0.68 | |
| 23 | FTTADDNQPSVQIQVY | 400 | 0.67 | |
| 23 | GVNPDEVVAVGAAALQA | 338 | 0.67 | |
| 24 | LDEQLTRAEFQRITQD | 269 | 0.66 | |
| 25 | ETLVYQTEKQVKEQRE | 514 | 0.65 | |
| 25 | QAGVLKGEVKDVLLLD | 352 | 0.65 | |
| 26 | SLLEIGEGVVEVRATS | 179 | 0.64 | |
| 27 | YQGEREIAAHNKLLGS | 415 | 0.63 | |
| 27 | PTAAALAYGLDKGEKE | 148 | 0.63 | |
| 28 | MPAVTDLVKELTGGKE | 319 | 0.61 | |
| 29 | DRTRKPFQSVIADTGI | 287 | 0.59 | |
| 30 | GGTFDVSLEIGEGVV | 173 | 0.57 | |

OVERLAP DISPLAY

MARAVGIDLGTTNSVSVLEGGDPVVVANSEGSRTTPSIVAFARNGEVLVGQPAKNQAVTNVDRTVRSV
KRHMGS DWSIEIDGKKYTAPEISARILMKLKRDAEAYLGEDITDAVITTPAYFNDAQRQATKDAGQIAG
LNVLRIVNEPTAAALAYGLDKGEKEQRILVFDLGGGTFDVSLEIGEGVVEVRATSGDNHLGGDDWDQR
VVDWLVDKFKGTSGIDLTKDKMAMQRLREAAEKAKIELSSSQSTSINLPYITVDADKNPLFLDEQLTRA
EFQRITQDLLDRTRKPFQSVIADTGISVSEIDHVVLVGGSTRMPAVTDLVKELTGGKEPNKGVNPDEVV
AVGAALQAGVLKGEVKDVLLLDVTPSLGLIETKGGVMTRLIERNTTIPTKRSETFTTADDNQPSVQIQV
YQGEREIAAHNKLLGSFELTGIPAPRGIPQIEVTFDIDANGIVHVTAKDKGTGKENTIRIQEGSGLSK
EDIDRMIKDAEAHAEDRKRREEADVRNQAETLVYQTEKQVKEQREAEAGGSKVPEDTLNKVDAAVAEAK
AALGGSDISAIKSAMEKLGQESQALGQAIYEAAQAASQATGAAHPGGEPGGAHPGSADDVVDAEVVDDG
REAK⁶²⁵

GEKEQRILVFDLGGGT

EVRATSGDNHLGGDDW

HMGSDWSIEIDGKKYT

AHPGGEPPGGAHPGSAD

DRMIKDAEAHAEEEDRK

TKRSETFTTADDNQPS

KGGVMTRLIERNTTIP

HVVLVGGSTRMPAVTD

KGTSGLDLTKDKMAMQ

DAVITTPAYFNDAQRQ

EAEGGSKVPEDTLNKV

FELTGIPPAPRGIPQI

AVGIDLGTTNSVSVL

DRTVRSVKRHMGS DWS

GQAIYEAAQAASQATG

IERNTTIPTKRSETFT

FQRITQDLLDRTRKPF

DKMAMQRLREAAEKAK

AGQIAGLNVLIRIVNEP

GQESQALGQAIYEAAQ

SLGIETKGGVMTRLIE

GDPVVVANSEGSRTTP

DAQRQATKDAGQIAGL

DDVVDAEVVDDGREAK

HVTAKDKGTGKENTIR

TFDIDANGIVHVTAKD

DGKKYTAPPEISARILM

AHPGSADDVVDAEVVD

EVLVGQPAKNQAVTNV

KRDAEAYLGEDITDAV

QAASQATGAAHPGGEP

GKEPNKGVNPDEVVAV

SVSEIDHVVLVGGSTR

EAAEKAKIELSSSQST

GSDISAIKSAMEKLGQ

SIVAFARNGEVLVGQP

VVAVGAALQAGVLKGE

ANSEGSRTTPSIVAF

WLVDKFKGTSGIDLTK

LVFDLGGGTFDVSLLE

RKRREEADVNRQAETL

TVDADKNPLFLDEQLT

SVQIQVYQGEREIAAH

SAMEKLGQESQALGQA

FTTADDNQPSVQIQVY

GVNPDEVVAVGAALQA

LDEQLTRAEFQRITQD

ETLVYQTEKFVKEQRE

QAGVLKGEVKDVLLLLD

SLLEIGEGVVEVRATS

