T CELL PREDICTION

MHC 1

1) nucleoprotein

|  |  |  |  |
| --- | --- | --- | --- |
| peptide | score | length | +ve or -ve |
| QAFEAGVDF | 0.25655 | 9 | positive |
| LEEEYPPWL | 0.23927 | 9 | positive |
| YQVNNLEEI | 0.13315 | 9 | positive |
| RLHPLARTAK | 0.13098 | 10 | positive |
| RLEELLPAV | 0.12551 | 9 | positive |
| RFSGLLIVK | 0.0956 | 9 | positive |
| RLHPLARTA | 0.09173 | 9 | positive |
| RGVRLHPLAR | 0.08924 | 10 | positive |
| GVRLHPLAR | 0.0402 | 9 | positive |
| FLSFASLFL | 0.00551 | 9 | positive |

2) spike glycoprotein

|  |  |  |  |
| --- | --- | --- | --- |
| peptide | length | score | +ve or -ve |
| TTIGEWAFW | 9 | 0.48473 | positive |
| RQWIPAGIGV | 10 | 0.39714 | positive |
| RTRREAIVNA | 10 | 0.36082 | positive |
| GVTGVIIAV | 9 | 0.34736 | positive |
| DEGAAIGLAW | 10 | 0.26347 | positive |
| EGAAIGLAW | 9 | 0.22707 | positive |
| KVVNYEAGEW | 10 | 0.22472 | positive |
| GTNETEYLF | 9 | 0.2211 | positive |
| VVNYEAGEW | 9 | 0.21561 | positive |
| ITGGRRTRR | 9 | 0.20722 | positive |
| GPCAGDFAF | 9 | 0.19741 | positive |
| GIRGFPRCR | 9 | 0.16664 | positive |
| TELRTFSIL | 9 | 0.13462 | positive |
| QRTFSIPLGV | 10 | 0.0989 | positive |
| KAIDFLLQRW | 10 | 0.09076 | positive |
| ATQVEQHHRR | 10 | 0.07663 | positive |
| LESRFTPQF | 9 | 0.07188 | positive |
| NTTGKLIWK | 9 | 0.068 | positive |
| SGYYSTTIRY | 10 | 0.05088 | positive |
| GYYSTTIRY | 9 | 0.04923 | positive |
| ATQVEQHHR | 9 | 0.0386 | positive |
| SEELSFTVV | 9 | 0.02732 | positive |
| RTFSILNRK | 9 | 0.01547 | positive |
| EAIVNAQPK | 9 | 0.01103 | positive |
| FAFHKEGAF | 9 | 0.00626 | positive |
| RTFSIPLGV | 9 | 0.00113 | positive |

3) Polymerase complex protein

|  |  |  |  |
| --- | --- | --- | --- |
| peptide | length | score | +ve or -ve |
| SLEQRITSL | 9 | 0.02772 | positive |

MHC 2

1. NUCLEOPROTEIN

|  |  |  |  |
| --- | --- | --- | --- |
| PEPETIDES | +VE OR -VE | SCORE | METHOD |
| EISFQQTNAMVTLRK | POSITIVE | 0.16493705 | SVM |
| YAPFARLLNLSGVNN | POSITIVE | 0.12201505 | SVM |

2) SPIKE GLYCOPROTEIN

|  |  |  |  |
| --- | --- | --- | --- |
| PEPETIDES | +VE OR -VE | SCORE | METHOD |
| DFAFHKEGAFFLYDR | POSITIVE | 0.28204595 | SVM |
| SSGYYSTTIRYQATG | POSITIVE | 0.10820377 | SVM |
| VIILFQRTFSIPLGV | POSITIVE | 0.97913731 | SVM |
| ELSFTVVSNGAKNIS | POSITIVE | 0.21547824 | SVM |
| WVIILFQRTFSIPLG | POSITIVE | 0.90665226 | SVM |
| MASENSSAMVQVHSQ | POSITIVE | 0.098068143 | SVM |
| SENSSAMVQVHSQGR | POSITIVE | 0.13226809 | SVM |

3) POLYMERASE COMPLEX PROTEIN

|  |  |  |  |
| --- | --- | --- | --- |
| PEPTIDES | +VE OR -VE | SCORE | METHODS |
| VPIFQDAAPPVIHIR | POSITIVE | 0.38717591 | SVM |
| VVQQQTIASESLEQR | POSITIVE | 0.17115285 | SVM |
| EQRITSLENGLKPVY | POSITIVE | 0.40069625 | SVM |
| VPIFQDAAPPVIHIR | POSITIVE | 0.38717591 | SVM |
| LEQRITSLENGLKPV | POSITIVE | 0.44696074 | SVM |