Table 5. F protein linear epitopes of the VII.2 NDV and the vaccine strains. Analogous epitopes with similar locations in the F protein sequences were shown in a row with an epitope number. Experimentally determined antibody epitopes in previous studies were shown in bold. Cells were left blanked when no epitopes were predicted at the specified epitope number. Values in parenthesis are identity percentage of each vaccinal epitope compared to its analogous epitope of the VII.2 NDV.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No.** | **ND viruses** | | | | | | | | | |
| **VII.2** | **B1** | **F** | **I-2** | **LaSota** | **PHY.LMV.42** | **R2B** | **Ulster** | **V4** | **VG/GA** |
| 1 | 93TPLGDSIRKIQGSVATTGGRRQKR116 | 93TPLGDSIRRIQESVTTSGGGRQGRL117 (46%) | 93TPLGDSIRRIQESVTTSGGGRQ114 (50%) | 93TPLGDSIRRIQESVTTSGGRKQGR116 (50%) | 93TPLGDSIRRIQESVTTSGGGRQGR116 (50%) | 93TPLGDSIRRIQESVTTSGGGKQGR116 (42%) | 93TPLGDSIRRIQESVTTSGGRRQKR116 (67%) | 93TPLGDSIRRIQESVTTSGGGKQGRL117 (42%) | 93TPLGDSIRRIQESVTTSGGGKQGRL117 (42%) | 93TPLGDSIRRIQESVTTSGGGKQGRL117 (42%) |
| 2 | 251TKLGV255 | 251TKLGI255 (60%) | 251TKLGV255 (100%) | 251TKLGV255 (100%) | 251TKLGV255 (100%) | - | 251TKLGV255 (100%) | 251TKLGV255 (100%) | 251TKLGV255 (100%) | 251TKLGV255 (100%) |
| 3 | 274ILYDSQTQ281 | 274ILYDSQTQL282 (88%) | 274ILYDSQTQ281 (100%) | 274ILYDSQTQ281 (100%) | 274ILYDSQTQ281 (100%) | 274ILYDSQTQ281 (100%) | 274IFYDSQTQ281 (75%) | 274ILYDSQTQ281 (100%) | 274ILYDSQTQ281 (100%) | 274ILYDSQTQ281 (100%) |
| 4 | 290PSVGNLNNM298 | 290PSVGNLNN297 (89%) | 290PSVGNLNNM298 (100%) | 290PSVGNLNNM298 (100%) | 290PSVGNLNNM298 (100%) | 290PSVGNLNN297 (89%) | 290PSVGNLNNM298 (100%) | 290PSVGNLNNM298 (100%) | 290PSVGNLNNM298 (100%) | 290PSVGNLNNM298 (100%) |
| 5 | 306LSVSTTKGFASA317 | 306LSVSTTRGFASA317 (83%) | 306LSVSTTRGFAS316 (75%) | 306LSVSTTKGFAS316 (92%) | 306LSVSTTRGFAS316 (75%) | 306LSVSTTKGFAS316 (92%) | 306LSVSTTKGFA315 (83%) | 306LSVSTTKGFAS316 (92%) | 306LSVSTTKGFASA317 (100%) | 306LSVSTTKGFAS316 (92%) |
| 6 | 348TRIVTFPMSP357 | 348TRIVTFPMSP357 (100%) | - | 348TRIVTFPMSP357 (100%) | - | 348TRIVTFPMSPG358 (90%) | - | - | - | 348TRIVTFPMSP357 (100%) |
| 7 | 364SGNTSACMYSKTEG**A**LTTPY383 | 360YSCLSGNTSACMYSKTEG**A**LTTPY383 (80%) | 364SGNTSACMYSKTEG**A**LTTPY383 (100%) | 364SGNTSACMYSKTEG**A**LTTPY383 (100%) | 364SGNTS368 (90%) | 364SGNTSA369 (90%) | 364SGNTSACMYSKTEG**A**LTTPY383 (100%) | 353FPMSPGIYSCLSGNTSACMYSKTEG**A**LTTPY383 (45%) | 364SGNTSACMYSKTEG**A**LTTPY383 (100%) | 364SGNTSACMYSKTEG**A**LTTPY383 (100%) |
| 8 | 390VIANCKITTCRCADPPGIISQNYGEAVSLIDRHSCNVLSLDGITLKLSGEF440 | 390VIANCKMTTCRCVNPPGIISQNYGEAVSLIDKQSCNVLSLGGITLRLSGEF440 (73%) | 390VIANCKMTTCRCVNPPGIISQNYGEAVSLIDKQSCNVLSLDGITLRLSGEFDA442 (61%) | 390VIANCKMTTCRCADPPGIISQNYGEAVSLIDRQSCNILSLDGITLRLSGEFDA442 (82%) | 390VIANCKMTTCRCVNPPGIISQNYGEAVSLIDKQSCNVLSLGGITLRLSGEFDV442 (69%) | 390VIANCKMTTCRCADPPGIISQNYGEAVSLIDRQSCNVLSLDGITLRLSGEFDATYQKNISIQD452 (65%) | 390VVANCQMTTCRCADPPGIISQNYGEAVSLIDKHSCNVVSLDGITLRLSGEFDAT443 (71%) | 390VIANCKMTTCRSADPPGIISQNYGEAVSLIDRQSCNVLSLDGITLRLSGEFDA442 (80%) | 390VIANCKMTTCRCADPPGIISQNYGEAVSLIDRQSCNILSLDGITLRLSGEF440 (84%) | 390VIANCKMTTCRCADPPGIISQNYGEAVSLIDRQSCNILSLDGITLRLSGEFD441 (82%) |
| 9 | 448ISILDSQ454 | - | 447NISIQDSQ454 (57%) | 450IQDSQ454 (43%) | 448ISIQDSQ454 (71%) | - | - | - | - | - |