

Outil de classification des virus influenza * et de comparaison au vaccin régional VIPAR2026VX

DEMANDEUR: ChristianKlopfenstein

SITE DE PRODUCTION: H1N1panTest

DATE DE L'ANALYSE: 2026-09-18

SÉQUENCE:

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>H1N1_pdm_Test
ATGAAGGCAATACTAGTAGTTATGCTGTATACATTTACAACCGCAAATGCAGACACATTATGTATAGGTTATCATGCGAACCAATTCAACAGACACTGTGGACACA
GTACTAGAAAAAGAAATGTAACAGTAACACACTCTGTCAATCTTCTAGAAGACAAGCATAACGGAAGAACTATGCAAACCTAAGAGGGGTAGCCCCATTGCATTTGGGT
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CCAAAGATCAACCAACCTACATTAATGATAAAGGGAAAGAAGTCCTCGTGCTGTGGGGCATTACCATCCACCCACTATTACTGACCAAGAACGCTCTATCAG
AATGCAGATGCATATGTTTTGTGGGGACATCAAGATACAGCAAGAAGTTCAAGCCGGAATAGCAGCAAGACCCAAAGTGAGGGATCAAGCAGGGGAGAATGAAC
TATTACTGGACACTAGTGGAACCGGGAGACAAAATAACATTCGAAGCAACTGGTAACCTAGTGCCACCGAGGTATGCATTACAATGAAAAAAGGAGCTGGATCT
GGTATTATCATTTTCAGATACACCAAGTCCACGATTGCAATGCAACTTGTGAGACACCCGAGGGTGCTATAAACACCAGCCTCCCATTTCAAATGTACATCCGATC
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AGGATTTACCAGATTTTGGCAATCTATTCAACTGTTGCCAGTTTATTGGTACTGGTAGTCTCCCTGGGGCAATCAGCTTCTGGATGTGCTCTAATGGGTCTCTA
CAGTGTAGAATATGTATTTAA
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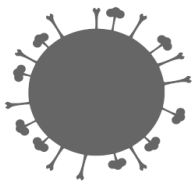
RÉSULTAT:

type HA	Clade (Nomenclature nord américaine)	% Homologie avec séquence vaccinale Nucleotides Acides aminés(HA1)	
H1	pdm	96.12	94.5

Lien de récupération:

http://51.222.25.122/results/ChristianKlopfenstein_H1N1panTest_1789708359.fasta_output

* Chang, J., Anderson, T.K., Zeller, M.A., Gauger, P.C., Vincent, A.L. (2019). octoFLU: Automated classification to evolutionary origin of influenza A virus gene sequences detected in U.S. swine. Microbiology Resource Announcements 8:e00673-19.



Analyse des épitopes

Sa

vaccin PNKKGN^{*}SPKINQT
 |||||*|||||||
 PNKKGTSPKINQT
 Distance = 0.08

Sb

vaccin TIAQQSYQNA
 ||*||**|||
 TITQERYQNA
 Distance = 0.3

Ca1

vaccin INDKGTSRYEPG
 |||||
 INDKGTSRYEPG
 Distance = 0.0

Ca2

vaccin SHAGAKSR
 |||||*||
 SHAGARSR
 Distance = 0.12

Cb

vaccin LSTARS
 |||||
 LSTARS
 Distance = 0.0

Distance d'épitope = 2.01