

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

DEMANDEUR: ChristianKlopfenstein

SITE DE PRODUCTION: Test

DATE DE L'ANALYSE: 2026-09-15

SÉQUENCE:

>TestEssai

ATGAAGACTATCATTGCTTTGAGCCACATTCTATGTCTGATTTTCGCTCAAAAACCTTCTGGTAATGACAACAACATGGCAACGCTGTGCCTTGACACCATGCA
GTGCCAAACGGAACGATAGTGAAAACAATCACGAATGACCAAAATTGAAGTTACTAATGCTACTGAGCTGGTTCAGAGTTTCTCTACAGGTGAAATATGCAACAGT
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AGGTGCAACATTTGCATTTGA

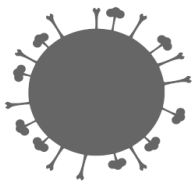
RÉSULTAT:

type HA	Clade (Nomenclature nord américaine)	% Homologie avec séquence vaccinale Nucleotides Acides aminés(HA1)	
H3	2010_human-like	94.47	86.06

Lien de récupération:

http://51.222.25.122/results/ChristianKlopfenstein_Test_1789493474.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

A

vaccin KSNVAQDASSKRSSNSRNM
* |||* ||||| ||||| |||||
NSNVTQDASSKRSSNSRNM
Distance = 0.11

B

vaccin TGTHLNFKALEATDKDISLAQA
||| ||||| ||||| ||||| |||||*
TGTHLNFKALEATDKDISLAQT
Distance = 0.05

C

vaccin QNFSTEINSPGKNSAFVRIACRYVKQN
|* ||||| ||||| ||||| ||||| |||||
QSFSTEINSPGKNSAFVRIACRYVKQN
Distance = 0.04

D

vaccin DVPTNTNNEQFDKLIVRIKRNTVIPNIGSIPSRIKGILNST
* ||||| ||||| ||||| |||||* ||||| ||||| |||||* |||||
NVPTNTNNEQFDKLIVRIKRSVIPNIGSIPSRIKRGTLNST
Distance = 0.12

E

vaccin QLGNIQGQNNKLFVSKHRIRSS
||* ||||| ||||| ||||| |||||
QLENIQGQNNKLFVSKHRIRSS
Distance = 0.05

Distance d'épitope = 1.42

Acides aminés putatifs

vaccin NTHNFKS
||| |||||
NTHNFKS