

Outil de classification des virus influenza * et de comparaison au vaccin régional VIPAR2026

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SITE DE PRODUCTION: H1N1panTest

DATE DE L'ANALYSE: 2026-09-18

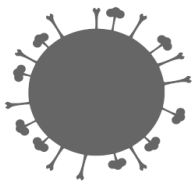
SÉQUENCE:

>H1N1_pdm_Test
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CAGTGTAGAATATGTATTTAA

RÉSULTAT:

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

* 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