

Article

Canine morbillivirus from Colombian lineage exhibits *in silico* and *in vitro* potential to infect human cells

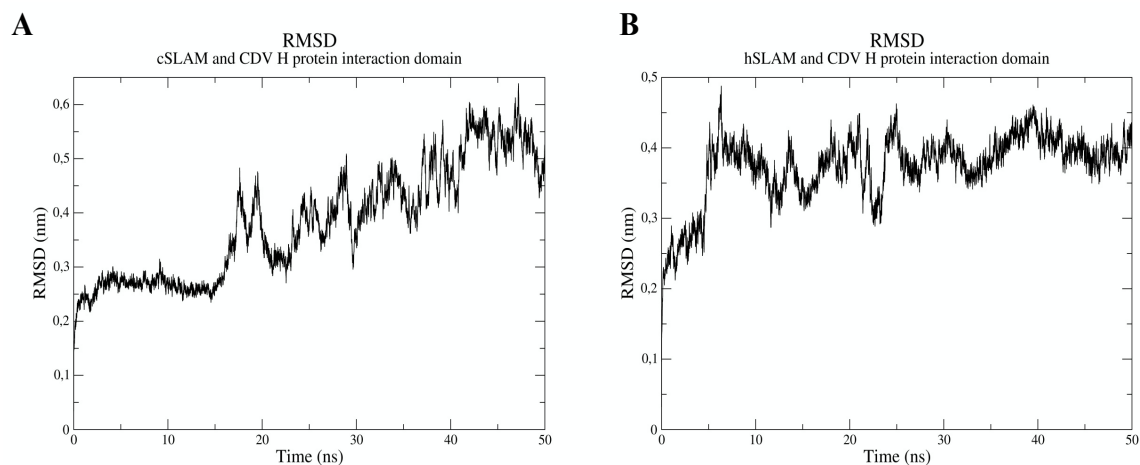
A

MeV	SRVEHAVVYYVYSPSRFSYFYPFR
REF	SRNDHAIVYYVYDPFRTIFYTYPFR
14COL	SRNDHAIVYYVYDPIRTISYTYPFR
CYN07-dV	SRGDHAIVYYVYDPFRTISYTYPFR
	** : ** : ***** . * * : : * *****

B

MeV	EHAVVYYVYSPSRFSYFYPFRLPI
14COL	DHAIVYYVYDPIRTISYTYPFRLTT
REF	DHAIVYYVYDPFRTIFYTYPFRLTT
CYN07-dV	DHAIVYYVYDPFRTISYTYPFRLTT
	: ** : ***** . * * : : * *****

Supplementary Figure S1. Interaction domain of either MeV or CDV-H protein. A) Hemagglutinin interaction peptide with SLAM cellular receptor, **B)** Hemagglutinin interaction peptide with Nectin-4 cellular receptor. Alignment was carried out with Clustal Omega form EMBL-EBI (<https://www.ebi.ac.uk/Tools/msa/clustalo/>).



Supplementary Figure S2. Molecular dynamic simulations RMSD through the evaluated time. A) RMSD plot of complex of cSLAM and the CDV-H-South-3 interaction peptide. B) RMSD plot of complex of hSLAM and the CDV-H-South-3 interaction peptide.

Table S1. Identity percentage of modelled proteins and employed templates with PDB number.

Proteins to model	Template obtained (#PDB)	Percentage of identity
CDV-H-South-3	MeV-H protein (2RKC)	34.9 %
CDV Onderstepoort (vaccine strain)	MeV-H protein (2RKC)	34.6 %
cSLAM receptor	hSLAM (3ALX)	57.2 %
cNectin-4 receptor	hNectin-4 (4GJT)	93.1 %