

M2_protein

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VSV_Indiana	61	Y E K F P F T V K M T V R S N P F R T Y S D V A A V S H W H M Y I G M G K P F Y K I L A F L G S S N L K A T P A V L A D Q G Q P E
Morreton_virus	61	Y E K F Y S V K M T V R S N P F R T Y S D V A A V S H W H M Y I G M G K P F Y K I L A F L G S S N L K A T P A V L A D H G Q P E
Maraba_virus	61	Y E K F H S L K M T V R S N P F R T Y D V A A V S H W H M Y I G M G K P F Y K I L A F M G S T L L K A T P A V L A D Q G Q P E
Cocal_virus	61	H E K F H S V K L T V Q S N P F R T Y D V A A V S H W H M Y I G M G K P F Y K I L A F L A S H L R K A T P A V L A D Q G H P E
Alagoas_virus	61	Y E K F H S I K L T V Q S N P F R T C E D M I A V S H W H M Y I G L B G K P F Y K V L V L L G S S H L K A T P A V L A D Q G H P E
Carajas_virus	61	Y E K F K S V K I T L R T N P L R T Y D V C Q I L S K W D A M Y V G M G K P F Y K V L V L I G S S H L Q A T P A I L S D R G Q P E
VSV_New_Jersey	61	Y E K F R P M L K M T V R S N P F R S Y D V T A A V S Q W N S Y I G M V G K P F Y K I I A V I G S S H L Q A T P A V L A D L N Q P E
Chandipura_virus	64	T L K I Q K C V V N I N A I N P F R D F R I I S A M Q F W A D Y S G Y D G K P F Y R A I I L H T A R Q L K T S P I G I L D R G V P E
Piry_virus	64	T L K I Q K C V L Q V R S E S P F T S Y L D A V C N V W N Q Y N G F E G K P F Y R A V M V R A V Q A M K A N I M S L Q D G R S P E
Isfahan_virus	61	S L K I Q K C S L Q V R A E T P E T S D A R C I S L W T D Y Q V R A E G K K P F Y R L L M L I A T K K L R A A I M S L Q D G N R P E
consensus>50		.e k f .% .k m t v r s n .P f r .y .# .a v s .W # .Y i G m .G K r P F Y k i ls .\$.a t p a v l .D .g .P E

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The figure displays a multiple sequence alignment of various viruses, including VSV_Indiana, Morreton_virus, Maraba_virus, Cocal_virus, Alagoas_virus, Carajas_virus, VSV_New_Jersey, Chandipura_virus, Piry_virus, Isfahan_virus, and consensus>50. The alignment shows a highly conserved sequence of approximately 50 nucleotides highlighted in yellow across all sequences.

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VSV_Indiana	201	FREK _L MP _G LIVEKK _A S _G A _V W _I D _S I _H FK _S
Morreton_virus	201	FPEK _L LF _G LIVEKK _A TG _A W _I D _S I _S NFK _S
Maraba_virus	201	FREK _L LF _G LILEKK _A TG _N W _V I _D I _H FK _S
Cocal_virus	201	MKEK _L LF _G LILEKK _A TG _S W _V I _D I _S NFK _S
Alagoas_virus	201	LREN _L LM _G LIVERK _A TG _S W _V I _D I _S HFK _S
Carajas_virus	201	FLEH _L KR _G LVLSK _A PGGG _W ILD _D I _S AVCA _S
VSV_New_Jersey	201	IQCE _L LK _G LILSK _A ATGT _V W _I D _D I _L SPFK _S
Chandipura_virus	204	MIEG _A IM _G EIKKO _K KDNT _V W _I S _F .SH..
Piry_virus	204	MLSANT _L GLEVKK _S SDNN _V W _I S _F .SY..
Isfahan_virus	201	MTT _T QM _G EIKY _K NDNT _V W _I S _F .SY..
consensus>50		...e.a...fGLi...kk...g.wvld...s...