

DOM	Y	T	F	T	A	N	A	D	T	L	C	I	G	Y	H	A	N	S	T	D	T	V	D	T	V	L	E	K	N	V	T	V	T	H	S	V	N	L	E	D	K	H	N	G	K	I	C	59	
DOM	I	L	C	L	V	F	A	Q	K	I	P	G	N	D	S	T	A	T	L	C	L	G	H	H	A	V	P	N	G	T	V	K	T	I	T	D	N	R	L	E	V	T	N	A	T	L	V	59	
EPI1818121 (H1N1)	Y	T	F	T	A	N	A	D	T	L	C	I	G	Y	H	A	N	S	T	D	T	V	D	T	V	L	E	K	N	V	T	V	T	H	S	V	N	L	E	D	K	H	N	G	K	I	C	59	
EPI1818137 (H3N2)	I	L	C	L	V	F	A	Q	K	I	P	G	N	D	S	T	A	T	L	C	L	G	H	H	A	V	P	N	G	T	V	K	T	I	T	D	D	R	L	E	V	T	N	A	T	L	V	59	
EPI2026200 (H7N9)	L	I	A	I	P	T	N	A	D	K	I	C	L	G	H	A	V	S	N	G	T	K	V	N	T	L	T	E	R	E	V	E	V	N	A	T	E	V	R	T	N	I	P	R	I	59			
EPI2161544 (H9N2)	L	L	A	A	T	V	S	N	A	D	K	I	C	I	G	Y	Q	S	S	N	S	T	D	T	V	D	T	L	T	E	N	V	P	V	T	H	A	K	E	L	H	T	E	H	N	G	M	L	59

DOM		K	L	R	G	V	A	P	L	H	L	G	K	C	N	I	A	G	W	I	L	G	N	P	E	C	S	L	S	T	A	R	S	W	S	I	V	E	T	S	N	S	D	N	G	T	C	P		109	
DOM		Q	N	S	S	I	G	E	I	C	D	S	P	H	O	V	L	D	G	G	N	C	T	I	D	A	L	L	G	D	P	P	C	D	G	F	N	K	E	W	D	L	F	V	E	R	S	A		109	
EPI1818121	(H1N1)	K	L	R	G	V	A	P	L	H	L	G	K	C	N	I	A	G	W	I	L	G	N	P	E	C	S	L	S	T	A	R	S	W	S	I	V	E	T	S	N	S	D	N	G	T	C	P		109	
EPI1818137	(H3N2)	Q	N	S	S	I	G	E	I	C	D	S	P	H	O	V	L	D	G	G	N	C	T	I	D	A	L	L	G	D	P	P	C	D	G	F	N	K	K	W	D	L	F	V	E	R	S	A		109	
EPI2026200	(H7N9)	C	S	K	G	K	R	T	V	D	L	G	K	C	G	L	I	G	T	I	G	P	P	C	D	Q	F	L	E	F	S	A	D	L	I	E	R	R	E	G	S	D	V	C	P	G	K		109		
EPI2161544	(H9N2)	C	A	T	G	L	G	P	L	V	L	D	T	C	T	I	E	G	L	I	Y	G	N	P	S	C	D	L	S	L	E	G	R	E	W	S	I	V	E	R	S	S	A	V	H	G	L	C	Y		109

DOM	DOM	GDFINYE	ELRQ	LS	VS	SF	ERFE	IFPK	TSS	W	P	HD	SD	KG	VT	A	CP	H	AG	A	K	159																									
EPI1818121	(H1N1)	NS	NC	YP	EL	DP	VG	Y	AS	LR	SL	VS	AS	G	LF	E	KN	S	F	N	WT	GT	VG	KN	GT	SS	AC	IR	GS	159																	
EPI1818137	(H3N2)	GDFINYE	ELRQ <th>LS</th> <th>VS</th> <th>SF</th> <th>ERFE</th> <th>IFPK</th> <th>TSS</th> <th>W</th> <th>P</th> <th>HD</th> <th>SD</th> <th>KG</th> <th>VT</th> <th>A</th> <th>CP</th> <th>H</th> <th>AG</th> <th>A</th> <th>K</th> <th>159</th>	LS	VS	SF	ERFE	IFPK	TSS	W	P	HD	SD	KG	VT	A	CP	H	AG	A	K	159																									
EPI2026200	(H7N9)	YV	NC	YP	EL	DP	VG	Y	AS	LR	SL	VS	AS	G	LF	E	KN	S	F	N	WT	GT	VG	KN	GT	SS	AC	IR	GS	159																	
EPI2026200	(H7N9)	FS	N	EE	AL	R	Q	I	L	R	S	GG	I	D	E	A	M	G	F	T	Y	IN	G	R	T	NG	S	S	F	Y	A	M	K	159													
EPI2161544	(H9N2)	PG	N	VE	DL	E	EL	R	S	L	F	S	S	A	R	S	Y	Q	R	I	Q	F	P	D	T	I	W	N	V	S	Y	D	G	T	S	T	A	C	S	S	S	F	Y	K	S	M	159

DOM	DOM	Sequence	Position
EPI1818121 (H1N1)		SSSFSSRLNWL TSLNLT YPALNV MPNKEQFDKLY IWGVVHHPTD DKNQIS	209
EPI1818137 (H3N2)		SSSFSSRLNWL TSLNLT YPALNV MPNKEQFDKLY IWGVVHHPTD DKNQIS	209
EPI2026200 (H7N9)		SSSFSSRLNWL TSLNLT YPALNV MPNKEQFDKLY IWGVVHHPTD DKNQIS	209
EPI2161544 (H9N2)		SSSFSSRLNWL TSLNLT YPALNV MPNKEQFDKLY IWGVVHHPTD DKNQIS	209

DOM	Q	N	A	D	A	V	V	F	V	G	T	S	R	Y	S	K	K	F	P	E	I	A	T	R	P	K	V	R	D	Q	E	G	R	M	N	Y	Y	W	T	L	V	E	P	G	D	K	I	T	F	259	
DOM	L	F	A	Q	S	S	G	R	I	T	V	S	T	K	R	S	Q	Q	A	V	I	P	N	I	G	S	R	P	R	I	D	I	P	S	R	I	S	I	Y	W	T	V	K	P	G	D	I	L	259		
EPI1818121 (H1N1)	Q	N	A	D	A	V	V	F	V	G	T	S	R	Y	S	K	K	F	P	E	I	A	T	R	P	K	V	R	D	Q	E	G	R	M	N	Y	Y	W	T	L	V	E	P	G	D	K	I	T	F	259	
EPI1818137 (H3N2)	L	Y	A	R	S	S	G	R	I	V	S	T	K	R	S	Q	Q	A	V	I	P	N	I	G	S	R	P	R	I	D	I	P	S	R	I	S	I	Y	W	T	V	K	P	G	D	I	L	259			
EPI2026200 (H7N9)	L	V	T	V	S	S	E	N	N	Y	Q	S	F	V	P	S	I	G	P	A	R	P	Q	N	I	G	S	R	I	D	I	P	H	W	L	M	L	N	P	N	D	T	V	T	S	F	S	G	N	L	259
EPI2161544 (H9N2)	T	S	V	A	T	E	E	I	N	R	I	K	F	P	L	I	G	P	R	P	L	V	I	G	L	M	G	R	I	N	Y	Y	S	V	L	K	P	N	Q	T	R	I	K	S	D	G	N	L	259		

DOM	EATGNLVVPRYAFT	MERDA	GSGI	I	ISDTPVHDCNTTCQTPEGAINTSLPF	309
DOM	LINSTGNLIAPRGYFK	IRSGKSS	MRSDAPIGRC	KSEC	ITPNGSI PN DKP	309
EPI1818121 (H1N1)	EATGNLVAPRYAFT	MERDA	GSGI	I	ISDTPVHDCNTTCQTPEGAINTSLPF	309
EPI1818137 (H3N2)	LINSTGNLIAPRGYFK	IRSGKSS	MRSDAPIGRC	KSEC	ITPNGSI PN DKP	309
EPI2026200 (H7N9)	FIAPDRASFLRGKSG	IRSGGVQDANCEGDCVHSGGTI	ISNLPFQNI	DSR		309
EPI2161544 (H9N2)	IAPWYGHILSGESHGR	LKTDLRKNGCTVQCQTE	GGGLN	ITLTPFQNVSKY		309

DOM QNVHPITIGKCPKYVKS **TKLR** LATGLRNVPSIQSRGL **FGAI** 350
DOM FQNVNRIITYGACPRYVKQSTLKLATGMRNVPEKQTR **GIFGA** 350
EPI1818121 (H1N1) QNVHPITIGKCPKYVKS **TKLR** LATGLRNVPSIQSRGL **FGAI** 350
EPI1818137 (H3N2) FQNVNRIITYGACPRYKQSTLKLATGMRNVPEKQTR **GIFGA** 350
EPI2026200 (H7N9) AVGKCPRYVQKRSLLLATGMKNVPEIPKGRGLFGAIA **GFIE** 350
EPI2161544 (H9N2) AFGNCSRYVIGVKSLLKAVGL **LRNV** PSRSSRGLFGAIA **GFIE** 350

- ☐ non-conserved
- ☒ $\geq 50\%$ conserved
- ☐ all match