

Protein	Position	Mean F_{st}	Enc residue	Hem residue	LGTV residue	Number of LGTV sequences	Highly specific	Absolutely specific
M	9	0.916	K _(87/22)	R _(78/13)	R	3		
	145	0.950	L _(98/0)	M _(98/2)	L	3		
E	76*	1.000	T _(100/0)	A _(100/0)	T	3		
	130	0.958	H _(88/16)	Y _(84/12)	Y	3		
	176	0.958	M _(78/22)	L _(78/22)	L	3		
	335	0.937	T _(77/22)	S _(78/22)	T	3		
	364	0.989	I _(100/1)	M _(99/0)	M	3		
	457	1.000	K _(100/0)	R _(100/0)	K	3		
NS1	148	0.926	R _(92/0)	K _(100/8)	R	3		
	161	0.976	V _(99/0)	M _(99/0)	I	3		
	262	0.937	S _(84/22)	A _(78/16)	A	3		
	274	0.950	I _(80/22)	L _(78/19)	V	3		
NS2a	52	0.943	R _(62/0)	T _(100/0)	S	3		
	155	0.926	L _(90/17)	Y _(78/0)	L	3		
NS2b	33	0.947	V _(89/8)	A _(92/0)	L	3		
	63	0.99	E _(99.4/0)	D _(100/0)	E	3		
NS3	314	0.958	K _(89/15)	R _(85/11)	R	3		
	404	0.947	D _(77/22)	E _(78/22)	K/R	1/2		
	584	0.958	R _(96/8)	K _(92/4)	R	3		
NS4a	56	0.916	M _(87/22)	V _(78/13)	F/L	1/2		
NS4b	54	0.916	I _(86/22)	M _(78/14)	M	3		
	208	0.947	L _(100/0)	V _(80/0)	L	3		
NS5	20	0.916	K _(68/24)	R _(76/32)	K	3		
	31	0.926	I _(90/18)	V _(82/10)	V	3		
	44	0.919	R _(96/7)	K _(93/3)	K	3		
	113	0.916	K _(84/7)	R _(93/16)	R	3		
	162	0.958	K _(75/22)	R _(78/25)	R	3		
	226	1.000	T _(100/0)	S _(100/0)	T	3		
	260	0.920	V _(82/22)	T _(78/14)	V	3		
	290	1.000	E _(99.6/0)	D _(100/0.4)	D	3		
	404	0.958	K _(78/22)	R _(78/22)	R	3		
	590	0.958	I _(80/22)	V _(78/20)	V	3		
	696	0.950	H _(78/22)	P _(78/22)	P	3		
	854	0.947	K _(96/0)	R _(100/4)	G	3		
	872	0.979	K _(96/4)	R _(96/4)	K/R	1/2		
	890	0.960	D _(99/0)	E _(100/0)	D	3		

Blue color – encephalitic form

Red color – hemorrhagic form

Green color – unique LGTV aa residues

* - absolutely specific positions are bolded