

December 2019

November 2020

May 2021

Continued evolution, complex  
selection dynamics, transition to  
endemic?

Coord	Gene/site	Recent	Type	Periods	Freq	Codon	AA	Predicted	HRank	AScore
28687	<a href="#">N/139</a>	+	Alternating	14	0.0022	TTG→TTT	<a href="#">L→F</a>	0	0.002	4.645
23398	<a href="#">S/613</a>	+	Alternating	13	0.0039	CAG→CAT	<a href="#">Q→H</a>	0	0	4.615
<input type="checkbox"/> 28687	<a href="#">N/139</a>	+	Alternating	14	0.0018	TTG→TTC	<a href="#">L→F</a>	0	0.006	4.613
17685	<a href="#">helicase/484</a>	+	Alternating	8	0.0002	GTT→TTT	<a href="#">V→F</a>	0	0.006	4.32
28678	<a href="#">N/136</a>	+	Alternating	8	0.0008	GAG→GAT	<a href="#">E→D</a>	0	0.006	4.319
26175	<a href="#">ORF3a/262</a>	+	Alternating	7	0.0006	CCA→TCA	<a href="#">P→S</a>	0	0.004	4.293
18969	<a href="#">exonuclease...</a>	+	Alternating	8	0.0004	AAG→AAT	<a href="#">K→N</a>	0	0.01	4.289
11740	<a href="#">nsp6/257</a>	+	Alternating	8	0.0002	CAG→CAT	<a href="#">Q→H</a>	0	0.011	4.277
25632	<a href="#">ORF3a/81</a>	+	Alternating	8	0.0002	TGC→TTC	<a href="#">C→F</a>	0	0.012	4.269
28678	<a href="#">N/136</a>	+	Alternating	8	0.0001	GAG→CAG	<a href="#">E→Q</a>	0	0.013	4.255
29299	<a href="#">N/343</a>	+	Alternating	7	0.0003	GAT→CAT	<a href="#">D→H</a>	0	0.008	4.253
26175	<a href="#">ORF3a/262</a>	+	Alternating	7	0.0003	CCA→CTA	<a href="#">P→L</a>	0	0.009	4.244
29347	<a href="#">N/359</a>	+	Alternating	6	0.0008	GCA→TCA	<a href="#">A→S</a>	0	0.005	4.24
29299	<a href="#">N/343</a>	+	Alternating	7	0.0001	GAT→TAT	<a href="#">D→Y</a>	0	0.01	4.235
24871	<a href="#">S/1104</a>	+	Alternating	5	0.0041	GTA→TTA	<a href="#">V→L</a>	0	0	4.235

- Better prediction of near-term evolutionary trajectories
- Prioritization of low frequency sites and site combinations for testing
- Detection of intra-host adaptation
- Analysis of selective forces associated with vaccine “breakthrough” infections
- Development of additional meta-signatures for “delta-like” and emergent lineages.
- Inter-operation with phenotypic annotation services and databases.
- Better prediction of phenotype from genotype.