2009 H1N1 Expression Clone Set, Recombinant in *Escherichia coli*

Catalog No. NR-19435

Table 1: 2009 H1N1 Expression Clones

Clone	Well Position	ORF Length	Description	Average Depth of Coverage	Class[1]
10043	A01	792	CDS(M1)_MP-NY1682	9.2	A
10020	A02	324	CDS(M2)_MP-NY1682	7.7	A
10030	A03	399	CDS(NS2)_NS-NY1669	7.3	BLM
10041	A04	399	CDS(NS2)_NS-NY1682	7.3	A
10609	A05	2307	CDS_PB1-NY1682	7.5	BLM
10562	A06	1623	CDS(-TM)_HA-NY1682	5.6	BLM
10579	A07	1374	CDS_NA_splice-NY1682	6.6	BSC
10565	A08	726	CDS(NS1)_NS-NY1669	4.1	A
10646	A09	2184	CDS_PA-NY1682	9.6	A
10564	A10	726	CDS(NS1)_NS-NY1669	-	V
10695	A11	2327	CDS_PB2-NY1682	7.9	BLM
10756	A12	2321	CDS_PB1-NY1682	7.5	BLM
10697	B01	1637	CDS(-TM)_HA-NY1682	8.0	CFC
10194	B02	1388	CDS_NA_splice-NY1669	8.1	BLM
10728	B03	1388	CDS_NA_splice-NY1682	7.0	BSC
10193	B04	806	CDS(M1)_MP-NY1669	7.0	A
10310	B05	338	CDS(M2)_MP-NY1669	3.7	A
10272	B06	707	CDS(NS1)_NS-NY1669	5.9	A
10700	B07	413	CDS(NS2)_NS-NY1682	5.3	A
10394	B08	1388	CDS_NA_splice-NY1669	7.9	A
10373	B09	806	CDS(M1)_MP-NY1669	5.8	A
10831	B10	2321	CDS_PB1-NY1682	6.9	BLM
10920	B11	2327	CDS_PB2-NY1682	8.0	CSPT
10820	B12	413	CDS(NS2)_NS-NY1682	5.3	A
10818	C01	1388	CDS_NA_splice-NY1682	6.9	BSC
10092	C02	740	CDS(NS1)_NS-NY1669	5.1	D
10090	C03	338	CDS(M2)_MP-NY1669	3.5	A
12035	C04	1544	CDS_NP-NY1669	3.6	BLM
12043	C05	1637	CDS(-TM)_HA-NY1669	4.9	CFC
12044	C06	1637	CDS(-TM)_HA-NY1669	3.7	CFC

[1] **A:** Full-length sequence validation, 2X or greater coverage, 100% sequence identity with the reference ORF.
B: Full-length sequence validation, sequence variation (less than 100% sequence identity with the reference ORF); remains valid.
BLM: B class clone with substitutions in CDS only at ≤ 0.2% mutation rate.
BSC: B class clone with substitutions in CDS only leading to silent mutations.
C: Full-length sequence validation, sequence variation (less than 100% sequence identity with the reference ORF); becomes invalid.
CFC: C class clone with frameshift mutations in CDS only.
CSPT: C class clone with substitution resulting in truncated protein (nonsense mutation).
D: Partial sequence validation, single contig with missing end-sequence (less than 90% sequence identity with the reference ORF).

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