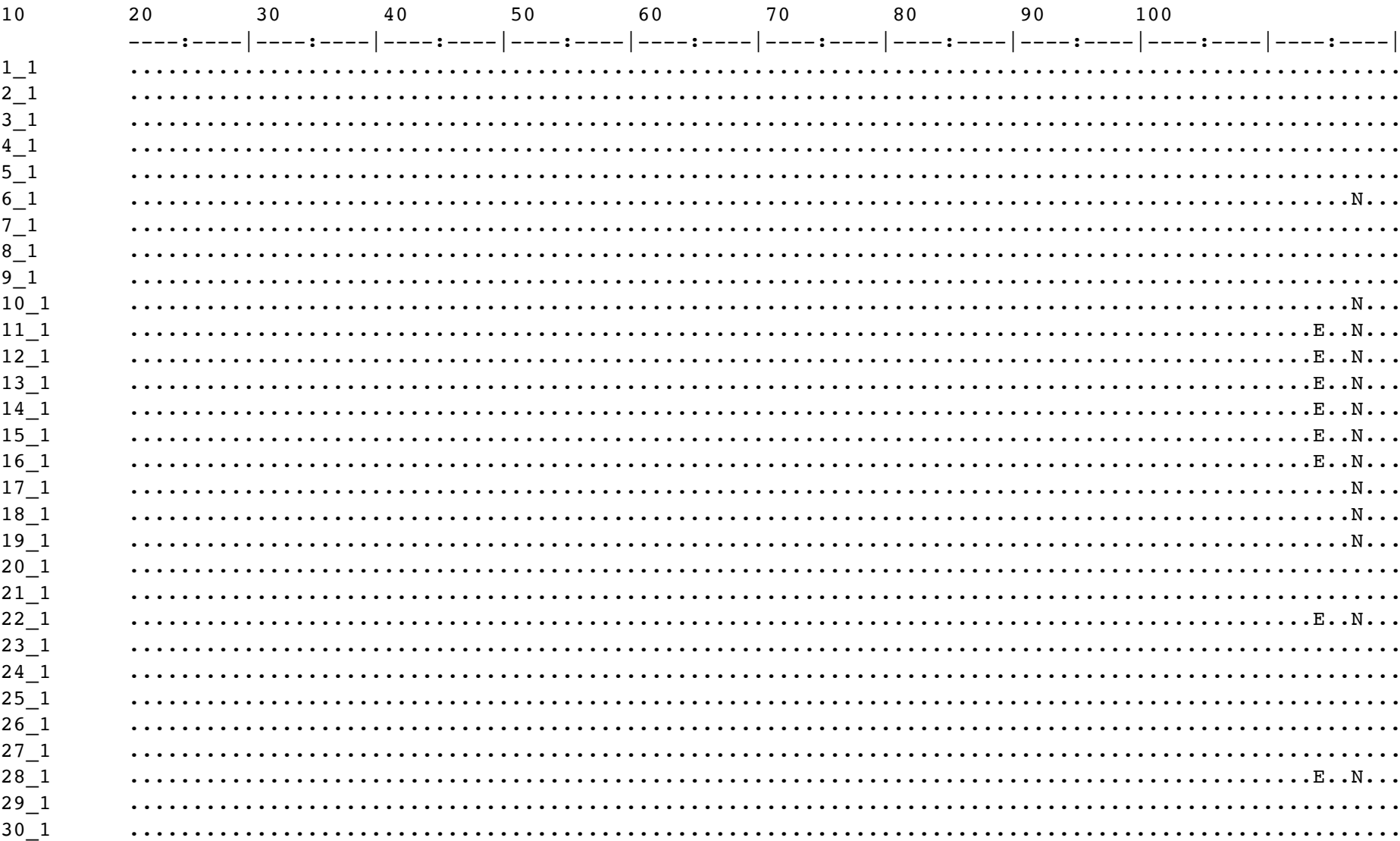


Supplementary Figure 1: Translate - aligned protein sequences BORD005031 (cyaA), Obtained from Locus Explorer - Bordetella MLST locus/sequence definitions (<https://pubmlst.org/bordetella/>)



31_1E..N...
32_1E..N...
33_1N...
34_1E..N...
35_1N...
36_1E..N...
37_1
38_1
39_1
40_1N...
41_1E..N...
42_1
43_1
44_1
45_1
46_1
47_1
Consensus	MQQSHQAGYANAADRESGIPAAVLDGIKAVAKEKNATLMFRLVNPBSTSLIAEGVATKGLGVHAKSSDWGLQAGYIPVNPNL SKLF GRAPEVIARADNDV
	110 120 130 140 150 160 170 180 190 200
	----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:----
1_1
2_1
3_1
4_1
5_1
6_1D.....
7_1

[PubMLST Database home](#) [Contents](#)

8_1
9_1
10_1
11_1
12_1
13_1
14_1
15_1
16_1
17_1
18_1
19_1
20_1
21_1
22_1
23_1
24_1
25_1
26_1
27_1
28_1
29_1
30_1
31_1
32_1
33_1
34_1
35_1D.....
36_1
37_1
38_1
39_1
40_1D.....
41_1

42_1
43_1
44_1
45_1
46_1
47_1
Consensus	NSSLAHGHTAVDLTLSKERLDYLRQAGLVTGMADGVVASNHAGYEQFEFRVKETSDGRYAVQYRRKGGDDFEAVKVIGNAAGIPLTADIDMFAIMPHLSN
	210 220 230 240 250 260 270 280 290 300
	----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:----
1_1
2_1
3_1
4_1
5_1
6_1E.....
7_1
8_1
9_1
10_1P.....Q.....
11_1E.....G.....
12_1E.....G.....
13_1E.....
14_1E.....G.....
15_1E.....
16_1E.....G.....
17_1P.....
18_1P.....Q.....
19_1P.....Q.....
20_1
21_1
22_1E.....G.....
23_1
24_1
25_1

26_1
27_1
28_1E.....G.....
29_1
30_1
31_1E.....G.....
32_1E.....
33_1E.....

https://pubmlst.org/bigbdb?db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 2 sur 13

Locus Explorer - Bordetella MLST locus/sequence definitions 05/07/2017 12(36

34_1E.....
35_1E.....
36_1E.....G.....
37_1M.....
38_1
39_1
40_1E.....
41_1E.....
42_1
43_1
44_1
45_1V.....
46_1
47_1

Consensus FRDSARSSVTSGDSVTDYLARTTAAASEATGGLDRERIDLLWKIARAGARSavgTEARRQFRYDGMNIGVITDFELEVARNALNRRRAHAVGAQDVVQHGT

310 320 330 340 350 360 370 380 390 400

----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|

1_1F.....
2_1G.....
3_1G.....
4_1F.....
5_1G.....

6_1T.....
7_1F.....
8_1F.....
9_1F.....
10_1T.....
11_1T.....S.....
12_1T.....S.....
13_1T.....I.....
14_1T.....S.....
15_1T.....
16_1T.....S.....
17_1G.....
18_1T.....
19_1T.....
20_1G.....
21_1G.....
22_1T.....S.....
23_1
24_1
25_1G.....
26_1
27_1G.....
28_1T.....S.....
29_1
30_1G.....
31_1T.....S.....
32_1T.....
33_1T.....
34_1T.....
35_1T.....
36_1T.....S.....
37_1G.....
38_1
39_1G.....

```

40_1      .....T.....
41_1      .....I.....
42_1      .....F.....
43_1      .....F.....
44_1      .....F.....
45_1      .....
46_1      .....G.....
47_1      .....F.....
Consensus EQNNPFPEADEKIFVVSATGESQMLTRGQLKEYIGQQRGEGYVFYENRAYGVAGKSLFDDGLGAAPGVPSGRSKSSPDVLETVPASPLRRPSLGAVERO
          410      420      430      440      450      460      470      480      490      500
-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|
1_1      .....
2_1      .....
3_1      .....
4_1      .....
5_1      .....
6_1      .....V.....P.....L.....S.K.V.....
7_1      .....
8_1      .....

```

https://pubmlst.org/bigdb?db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 3 sur 13

Locus Explorer - Bordetella MLST locus/sequence definitions 05/07/2017 12:36

```

9_1      .....
10_1     .....K...T.....
11_1     .....L.....M.D.....V.....P.....L.....K.V.....G.....
12_1     .....L.....D.....V.....V.....P.....L.....K.V.....G.....
13_1     .....V.....P.....L.....S.K.V.....
14_1     .....L.....D.....V.....V.....P.....L.....K.V.A.....G.....
15_1     .....G.....V.....P.....L.....S.K.V.....A.....
16_1     .....L.....M.D.....V.....P.....L.....K.V.....G.....
17_1     .....
18_1     .....K...T.....
19_1     .....K...T.....

```

20_1
21_1
22_1L.....M.D.....V.....V....P.....L....S.K.V.....
23_1
24_1K...T.....
25_1
26_1
27_1
28_1L.....D.....V.....V....P.....L....K.V.....G.....
29_1
30_1
31_1L.....M.D.....V.....P.....L....K.V.....G.....
32_1G.....V.....P.....L....S.K.V.....A.....
33_1V.....P.....L....S.K.V.....
34_1G.....V.....P.....L....S.K.V.....G.....
35_1V.....P.....L....S.K.V.....
36_1L.....D.....V.....V....P.....L....K.V.....G.....
37_1H.....
38_1
39_1
40_1V.....P.....L....S.K.V.....
41_1V.....P.....L....S.K.V.....
42_1G.....
43_1
44_1
45_1
46_1
47_1
Consensus	DSGYDSL ⁵¹⁰ DGVGSR ⁵²⁰ SFSLGEVSDMAA ⁵³⁰ VEAAELEMTRQVLHAGARQDDAEPGVSGASAHWGQ ⁵⁴⁰ RALQGAQAVAAAQRLV ⁵⁵⁰ HAIALMTQFGRAGSTNTPQEAA ⁵⁶⁰ SL ⁵⁷⁰ -----:----- -----:----- -----:----- -----:----- -----:----- -----:----- -----:----- -----:----- -----:----- 1_1..... 2_1..... 3_1.....V.....

4_1V.....
5_1V.....
6_1
7_1
8_1
9_1
10_1L.....
11_1
12_1
13_1
14_1
15_1
16_1
17_1
18_1L.....
19_1L.....
20_1
21_1
22_1
23_1
24_1L.....
25_1
26_1
27_1
28_1
29_1
30_1
31_1
32_1
33_1
34_1

https://pubmlst.org/bigsdb?db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 4 sur 13

35_1
36_1
37_1S.....
38_1
39_1V.....
40_1
41_1
42_1
43_1
44_1
45_1
46_1
47_1
Consensus	SAAVFGLGEASSAVAETVSGFFRGSSRWAGGFGVAGGAMALGGGIAAAVGAGMSLTDDAPAGQKAAAGAEIALQLTG GTVELASSIALALAAARGVTSGL
	610 620 630 640 650 660 670 680 690 700
	----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:----
1_1
2_1
3_1
4_1
5_1
6_1
7_1
8_1
9_1
10_1S.....
11_1
12_1
13_1
14_1
15_1
16_1A.....
17_1
18_1S.....

Accession	Sequence
19_1S.....
20_1
21_1
22_1
23_1
24_1S.....
25_1
26_1
27_1
28_1
29_1T.....
30_1
31_1A.....
32_1
33_1
34_1
35_1
36_1A.....
37_1
38_1
39_1
40_1
41_1
42_1
43_1
44_1
45_1T.....
46_1
47_1
Consensus	QVAGASAGAAAGALAAALSPMEIYGLVQQSHYADQLDKLAQESSAYGYEGDALLAQLYRDKTAAEGAVAGVSAVLSTVGAAVSIAAAASVVGAPVAVVTS
	710 720 730 740 750 760 770 780 790 800
	----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:----
1_1
2_1A

3_1A
4_1
5_1A
6_1
7_1
8_1
9_1

https://pubmlst.org/bigbdb?db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 5 sur 13

Locus Explorer - Bordetella MLST locus/sequence definitions 05/07/2017 12/36

10_1A
11_1
12_1
13_1
14_1
15_1
16_1
17_1A
18_1S.....
19_1S.....
20_1A
21_1A
22_1
23_1A
24_1S.....
25_1A
26_1A
27_1A
28_1
29_1A
30_1A
31_1
32_1

33_1
34_1
35_1
36_1
37_1A
38_1A
39_1A
40_1
41_1
42_1
43_1
44_1
45_1A
46_1A
47_1
Consensus	LLTGALNGILRGVQQPIIEKLANDYARKIDELGGPQAYFEKNLQARHEQLANS DGLRKMLADLQAGWNASSVIGVQTTEISKSALELAAITGNADNLKSV
	810 820 830 840 850 860 870 880 890 900
	----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:----
1_1
2_1I.....
3_1I.....
4_1
5_1I.....
6_1
7_1
8_1
9_1M.....
10_1I.....
11_1
12_1
13_1
14_1
15_1
16_1

17_1I.....
18_1I.....
19_1I.....
20_1I.....
21_1I.....
22_1
23_1I.....
24_1I.....
25_1I.....
26_1I.....
27_1I.....
28_1
29_1I.....
30_1I.....
31_1
32_1
33_1
34_1
35_1

https://pubmlst.org/bigsdbs?db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 6 sur 13

Locus Explorer - Bordetella MLST locus/sequence definitions 05/07/2017 12:36

36_1
37_1I.....
38_1I.....
39_1I.....
40_1
41_1
42_1
43_1
44_1
45_1I.....
46_1I.....

```

47_1 .....
Consensus DVFVDRFVQGERVAGQPVVLDVAAGGIDIASRKGERPALTFITPLAAPGEEQRRRTKTGKSEFTTFVEIVGKQDRWRIRDGAADTTIDLAKVVSQQLVDAN
          910      920      930      940      950      960      970      980      990      1000
-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|
1_1 .....
2_1 .....E.....K.....
3_1 .....E.....K.....
4_1 .....
5_1 .....E.....K.....
6_1 .....
7_1 .....
8_1 .....
9_1 .....
10_1 .....I.....E.....K.....
11_1 .....
12_1 .....
13_1 .....S.....
14_1 .....
15_1 .....S.....
16_1 .....
17_1 .....E.....I.....E.....K.....
18_1 .....I.....E.....K.....
19_1 .....I.....E.....K.....
20_1 .....E.....K.....
21_1 .....E.....K.....
22_1 .....S.....
23_1 .....E.....K.....
24_1 .....I.....E.....K.....
25_1 .....E.....K.....
26_1 .....E.....K.....
27_1 .....E.....K.....
28_1 .....
29_1 .....E.....K.....
30_1 .....E.....K.....

```

```

31_1 .....
32_1 .....S.....
33_1 .....S.....
34_1 .....
35_1 .....
36_1 .....
37_1 .....K.....
38_1 .....E.....K.....
39_1 .....E.....K.....
40_1 .....
41_1 .....S.....
42_1 .....
43_1 .....
44_1 .....
45_1 .....E.....K.....
46_1 .....E.....K.....
47_1 .....
Consensus GVLKHSIKLDVIGGDGDDVVLANASRIHYDGGAGTNTVSYAALGRQDSITVSADGERFNVRKQLNNANVYREGVATQTTAYGKRTENVQYRHVELARVGQ
          1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|
1_1  V.....Q.....
2_1  .....A.....H..V.....
3_1  .....A.....H..V.....
4_1  .....Q.....
5_1  .....A.....H..V.....
6_1  .....Q.....
7_1  .....Q.....
8_1  .....Q.....
9_1  .....Q.....
10_1 .....A.....A..H.....

```

https://pubmlst.org/bigsdb?db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 7 sur 13

11_1Q.....
12_1Q.....
13_1Q.....
14_1Q.....
15_1Q.....
16_1Q.....
17_1A.....H...V.....
18_1A.....A...H.....
19_1A.....A...H.....
20_1A.....H...V.....
21_1A.....H...V.....
22_1Q.....
23_1A.....H...V.....
24_1A.....A...H.....
25_1A.....H...V.....
26_1A.....H...V.....
27_1A.....H...V.....
28_1Q.....
29_1A.....H...V.....
30_1A.....H...V.....
31_1Q.....L.....
32_1Q.....
33_1Q.....
34_1Q.....
35_1Q.....
36_1Q.....
37_1A.....H...V.....N.....
38_1A.....H...V.....
39_1A.....H...V.....
40_1Q.....
41_1Q.....
42_1Q.....
43_1G.....Q.....
44_1Q.....

```

45_1      .....A.....H..V.....
46_1      .....A.....H..V.....
47_1      .....Q.....
Consensus LVEVDTL1110EHVQHI1120IIGGAGNDSITGNAHDN1130FLAGGSGDDRLDGGAGND1140TLVGGE1150GxNTVIGGAGDD1160VFLQDLGV1170WSNQLDGGAGV1180DTVKYN1190VHQPS1200EERLE
          1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
          ----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|----:----|
1_1        .....Q.....
2_1        .....S..S.....D.....H.....
3_1        .....S..S.....D.....H.....
4_1        .....Q.....
5_1        .....TS..S.....D.....H.....
6_1        .....
7_1        .....Q.....
8_1        .....Q.....
9_1        .....Q.....
10_1       .....N.....L.....S..S.....D.....
11_1       .....V.....
12_1       .....V.....
13_1       .....Q.....
14_1       .....V.....
15_1       .....Q.....
16_1       .....V.....W.....
17_1       ...E.....S..S.....D.....H.....
18_1       .....N.....L.....S..S.....D.....
19_1       .....L.....S..S.....D.....H.....
20_1       .....S..S.....D.....H.....D.....
21_1       ...E.....S..S.....D.....H.....
22_1       .....V.....
23_1       ...E.....S..S.....D.....H.....
24_1       .....N.....L.....S..S.....D.....
25_1       .....S..S.....D.....H.....
26_1       ...E.....S..S.....D.....H.....
27_1       ...E.....S..S.....D.....H.....
28_1       .....V.....

```

```

29_1      ...E.....S..S.....D.....H.....
30_1      ...E.....S..S.....D.....H.....
31_1      .....Q.....
32_1      .....
33_1      .....
34_1      .....V.....
35_1      .....
36_1      .....V.....

```

https://pubmlst.org/bigsdbs/db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 8 sur 13

Locus Explorer - Bordetella MLST locus/sequence definitions 05/07/2017 12:36

```

37_1      .....S..S.....D.....H.....
38_1      .....S..S.....D.....H.....
39_1      ...E.....S..S.....D.....H.....
40_1      .....
41_1      .....Q.....
42_1      .....Q.....
43_1      .....Q.....
44_1      .....Q.....
45_1      ...E.....S..S.....D.....H.....
46_1      ...E.....S..S.....D.....H.....
47_1      .....Q.....

```

Consensus RMGDTGIHADLQKGTVEKWPALNLFSDHVKNIENLHGSRLNDRIAGDDRDNELWGHGNDTIRGRGGDDILRGGLGLDTLYGEDGNDIFLQDDETVSDD

```

          1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|

```

```

1_1      .....
2_1      .....A.K.....EG....ARR.M....S..S.....
3_1      .....A.K.....EG....ARR.MG...S..S.....
4_1      .....
5_1      .....A.K.....EG....ARR.MG...S..S.....
6_1      .....
7_1      .....
8_1      .....

```

9_1
10_1A.K.....S.....
11_1
12_1S.....D.....
13_1
14_1S.....D.....
15_1
16_1S.....
17_1A.K.....S.....
18_1A.K.....S.....
19_1A.K.....S.....
20_1Q.....T.L..A.E.....EG.....ARR.M.....S..S.....
21_1A.K.....S.....
22_1
23_1A.K.....S.....
24_1A.K.....S.....
25_1A.K.....EG.....ARR.M.....S..S.....
26_1A.K.....S.....
27_1A.K.....S.....
28_1
29_1A.K.....S.....
30_1A.K.....S.....
31_1
32_1
33_1
34_1
35_1
36_1
37_1T.L..A.E.....EG.....ARR.M.....S..S.....
38_1A.K.....S.....
39_1A.K.....S.....
40_1
41_1
42_1

```

43_1      .....
44_1      .....K.....
45_1      .....A.K.....S.....
46_1      .....A.K.....S.....
47_1      .....
Consensus IDGGAGLDTVDYSAMIHGPRIVAPHEYGFGIEADLSREWVRKASALGVDYYDNVRNVENVIGTSMKDVLIQDAQANTLMGQGGDDTVRGGDGDLLFGGD
           1310       1320       1330       1340       1350       1360       1370       1380       1390       1400
-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|-----:-----|
1_1       .....Q.....
2_1       .....P.....A.....A.....V.T.....
3_1       .....P.....A.....A.....V.T.....
4_1       .....Q.....
5_1       .....P.....A.....A.....V.T.....
6_1       .....Q.....
7_1       .....Q.....
8_1       .....Q.....
9_1       .....Q.....
10_1      .....P.....A.....A.....V.T.....
11_1      .....Q.....

```

https://pubmlst.org/bigsdb?db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 9 sur 13

Locus Explorer - Bordetella MLST locus/sequence definitions 05/07/2017 12/36

```

12_1      .....Q.....T.....
13_1      .....Q.....
14_1      .....Q.....T.....
15_1      .....Q.....T.....
16_1      .....Q.....A.....
17_1      .....P.....A.....A.....V.T.....
18_1      .....P.....A.....A.....V.T.....
19_1      .....P.....A.....A.....V.T.....
20_1      .....P.....A.....A.....V.T.....
21_1      .....P.....A.....A.....V.T.....
22_1      .....Q.....

```

23_1P.....A.....A.....V.T.....
24_1P.....A.....A.....V.T.....
25_1P.....A.....A.....V.T.....
26_1P.....A.....A.....V.T.....
27_1P.....A.....A.....V.T.....
28_1Q.....
29_1P.....A.....A.....V.T.....
30_1P.....A.....A.....V.T.....
31_1Q.....Q.....T.....
32_1Q.....
33_1Q.....A.....T.....
34_1Q.....T.....
35_1Q.....
36_1Q.....
37_1P.....A.....A.....V.T.....
38_1P.....A.....A.....V.T.....
39_1P.....A.....A.....V.T.....
40_1Q.....
41_1P.....
42_1Q.....
43_1Q.....
44_1Q.....
45_1P.....A.....A.....V.T.....
46_1P.....A.....A.....V.T.....
47_1Q.....
Consensus	GNDMLYGDAGNDTLYGGLGDDTLEGGAGNDWFGQTxAREHDVLRGGDGVDTVDYSQTGAHAGIAAGRIGLGILADLGAGRVDKLGEGSSAYDTVSGIEN
	1410 1420 1430 1440 1450 1460 1470 1480 1490 1500
	----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:----
1_1
2_1N.....
3_1E.....N.....
4_1
5_1E.....N.....
6_1

7_1	
8_1	
9_1	
10_1	N
11_1	
12_1	
13_1	
14_1	
15_1	
16_1	N
17_1E.....	N
18_1	N
19_1E.....	N
20_1E.....	N
21_1E.....	N
22_1	
23_1E.....	N
24_1	N
25_1	N
26_1E.....	N
27_1E.....	N
28_1	
29_1E.....	N
30_1E.....	N
31_1	
32_1	
33_1	
34_1	
35_1	
36_1	
37_1E.....	N

https://pubmlst.org/bigsdb?db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 10 sur 13

38_1E.....N.....
39_1E.....N.....
40_1G.....
41_1
42_1
43_1
44_1
45_1E.....N.....
46_1E.....N.....
47_1
Consensus	VVGTELADRITGDAQANVLRGAGGADVLAGGEGDDVLLGGDGDDQLSGDAGRDRLYGEAGDDWFFQDAANAGNLLDGGDGRDTVDFSGPGRGLDAGAKGV
	1510152015301540155015601570158015901600
	----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:----
1_1N.....
2_1V.....A.....
3_1V.....A.....
4_1N.....
5_1V.....A.....
6_1
7_1N.....
8_1N.....
9_1N.....
10_1V.....A.....
11_1
12_1N.....
13_1
14_1N.....
15_1
16_1
17_1V.....A.....
18_1V.....A.....
19_1V.....A.....
20_1V.....A.....
21_1V.....A.....

22_1	
23_1V.....	A.....
24_1V.....	A.....
25_1V.....	A.....
26_1V.....T.....	A.....
27_1V.....	A.....
28_1	
29_1V.....	A.....
30_1V.....	A.....
31_1	
32_1	
33_1N.....	
34_1	
35_1	
36_1	
37_1V.....	A.....
38_1V.....	A.....
39_1V.....T.....	A.....
40_1L.....	
41_1	
42_1N.....	
43_1N.....	
44_1N.....	
45_1V.....	A.....
46_1V.....	A.....
47_1N.....	
Consensus	FLSLGKGFASLMDEPETS NVLRHIENAVGSARDDVLIGDAGANVLNGLAGNDVLSGGAGDDVLLGDEGSDLLSGDAGNDDLFGGQGGDDTYLFGVGYGHDT	
	1610 1620 1630 1640 1650 1660 1670 1680 1690 1700	
	----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:---- ----:----	
1_1I.....Q.....	
2_1I.....	
3_1I.....	
4_1I.....Q.....	
5_1I.....	

6_1I.....Q.....
7_1I.....Q.....
8_1I.....Q.....
9_1I.....Q.....
10_1T.....
11_1
12_1

https://pubmlst.org/bigbdb?db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 11 sur 13

Locus Explorer - Bordetella MLST locus/sequence definitions 05/07/2017 12:36

13_1
14_1
15_1
16_1
17_1I.....
18_1T.....
19_1I.....
20_1I.....
21_1I.....
22_1
23_1I.....
24_1T.....
25_1I.....
26_1I.....
27_1I.....
28_1
29_1I.....
30_1I.....
31_1R.....
32_1
33_1
34_1
35_1

36_1I.....P.....
37_1I.....P.....
38_1I.....
39_1I.....
40_1
41_1
42_1I.....Q.....
43_1I.....Q.....
44_1I.....Q.....
45_1I.....
46_1I.....
47_1I.....Q.....
Consensus	IYESGGGHD TIRINAGADQLW FARQGNDLEIRILGTDDALTVHDWYRDADHRVEAIHAANQAVDPAGIEKLVEAMAQYPDPGAAAAAPPAARVPDTLMQS
	----:-
1_1
2_1
3_1
4_1
5_1
6_1
7_1
8_1
9_1
10_1
11_1
12_1
13_1
14_1
15_1
16_1
17_1
18_1
19_1
20_1

21_1
22_1
23_1
24_1
25_1
26_1
27_1
28_1
29_1
30_1
31_1
32_1
33_1
34_1
35_1
36_1
37_1
38_1

https://pubmlst.org/bigsdb?db=pubmlst_bordetella_seqdef&page=alleleQuery&locus=BORD005031&submit=1 Page 12 sur 13

Locus Explorer - Bordetella MLST locus/sequence definitions 05/07/2017 12:36

39_1
40_1
41_1
42_1
43_1
44_1
45_1
46_1
47_1

Consensus LAVNWR

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