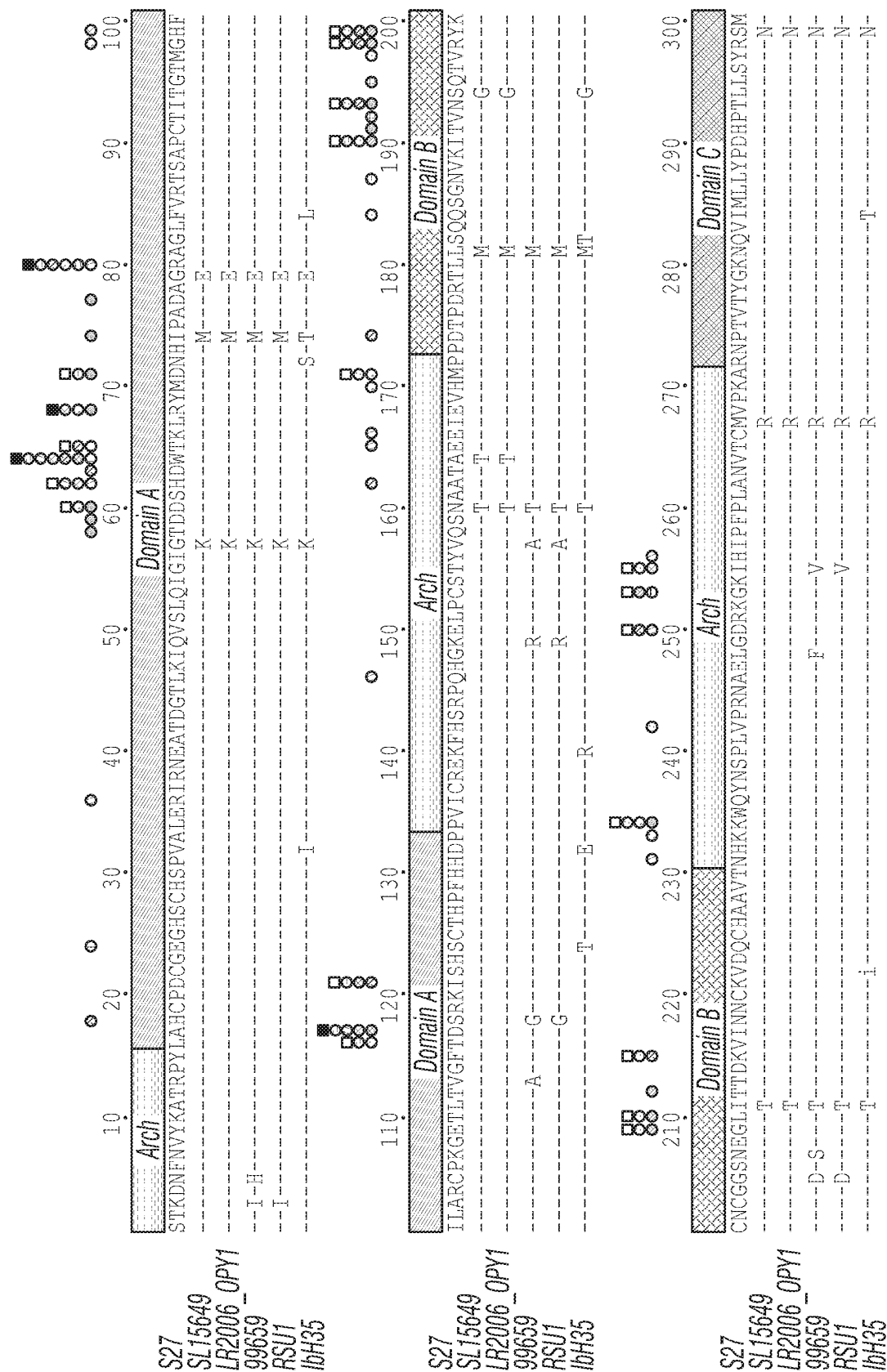




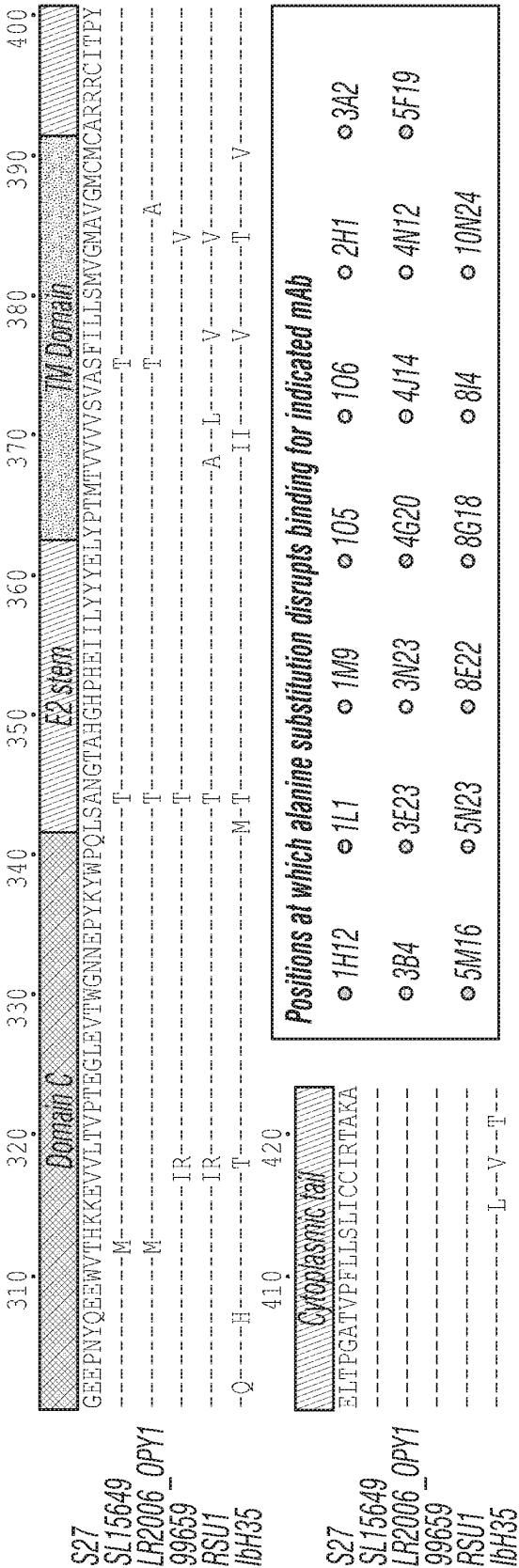


FIG. 1A
(Cont'd)

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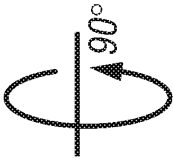
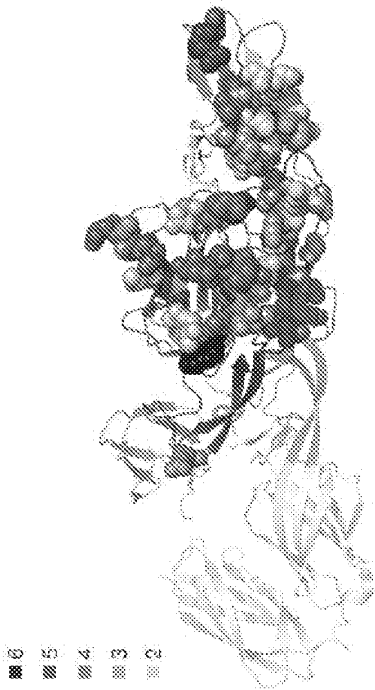


FIG. 1C

FIG. 1B

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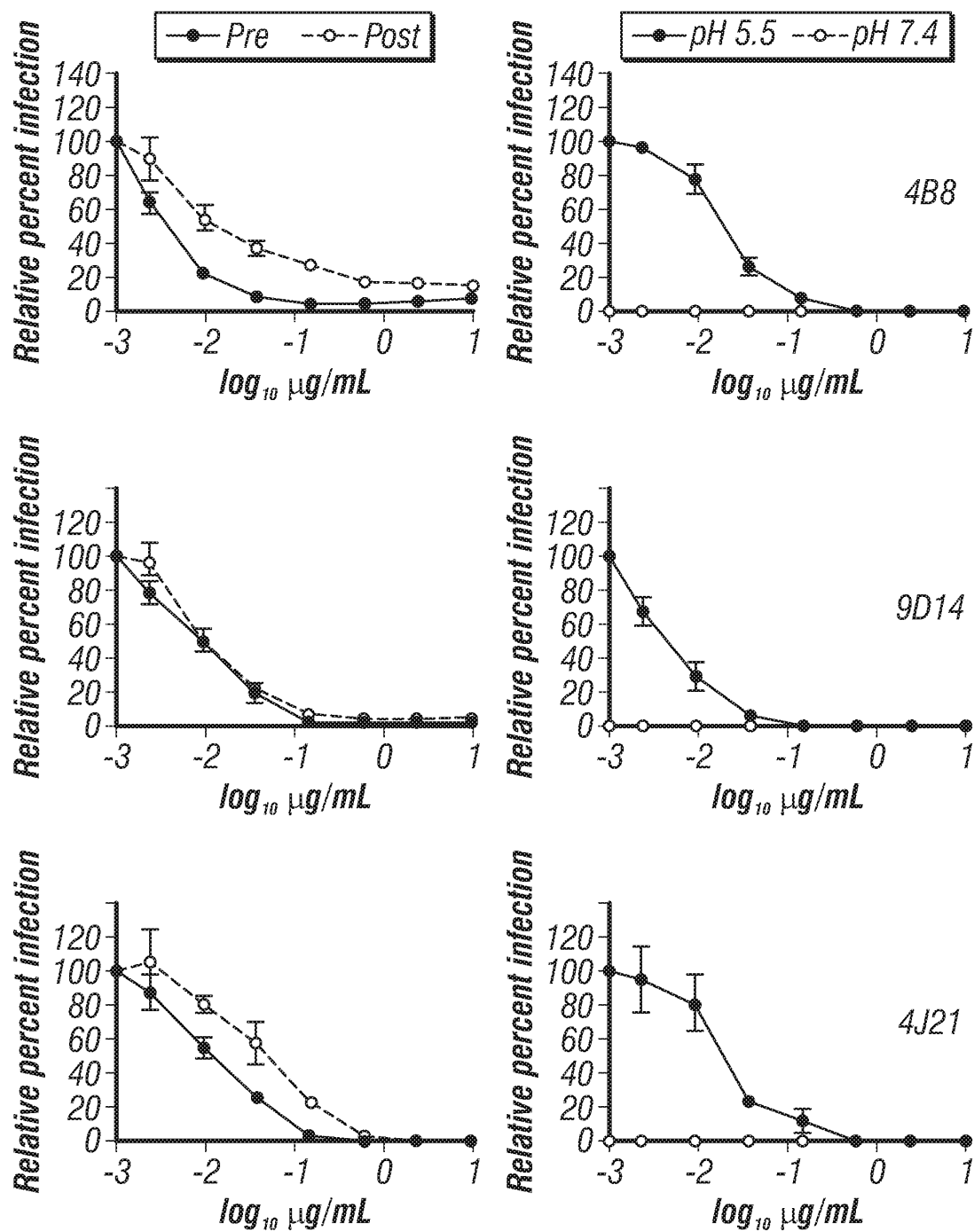
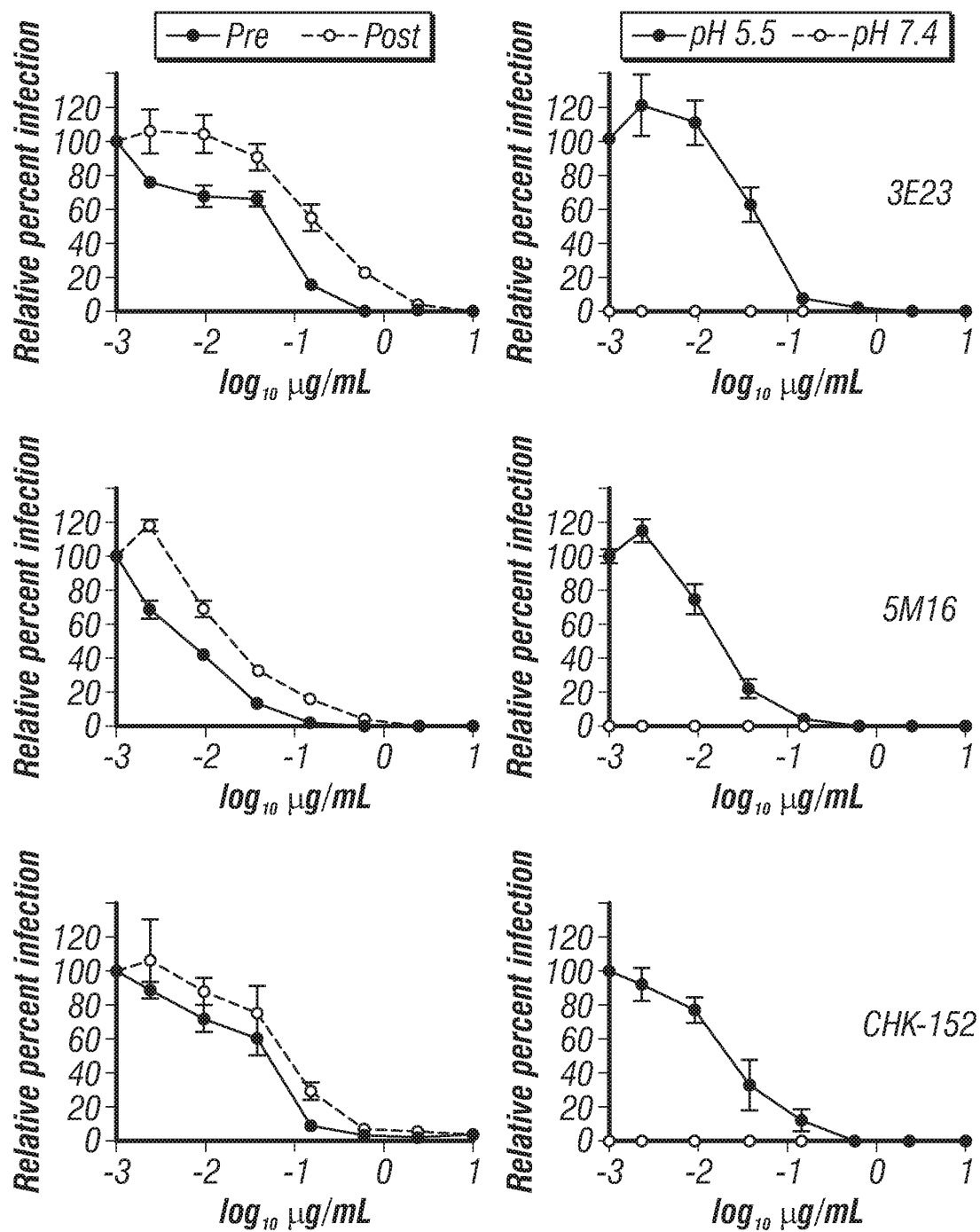


FIG. 2A

FIG. 2B

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FIG. 2A
(Cont'd)FIG. 2B
(Cont'd)

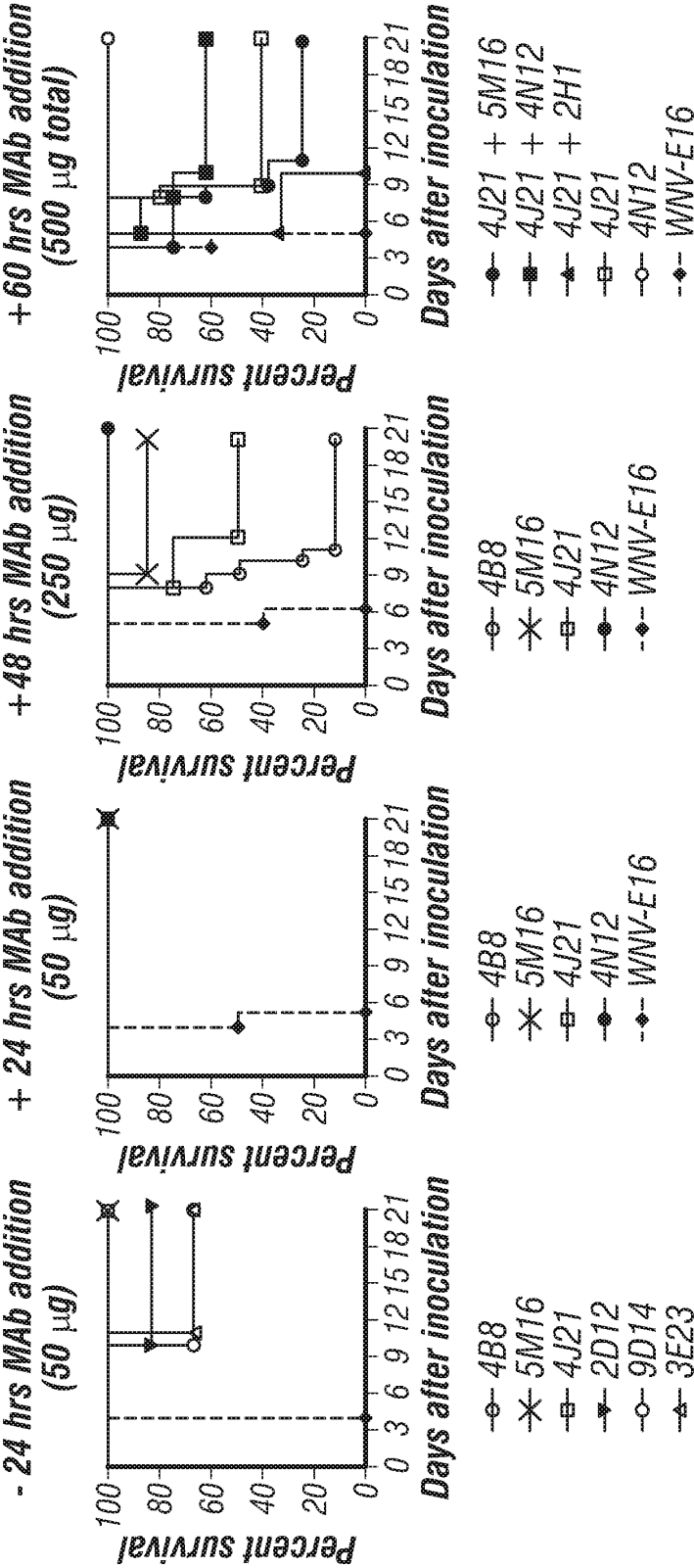


FIG. 3A

FIG. 3B

FIG. 3C

FIG. 3D

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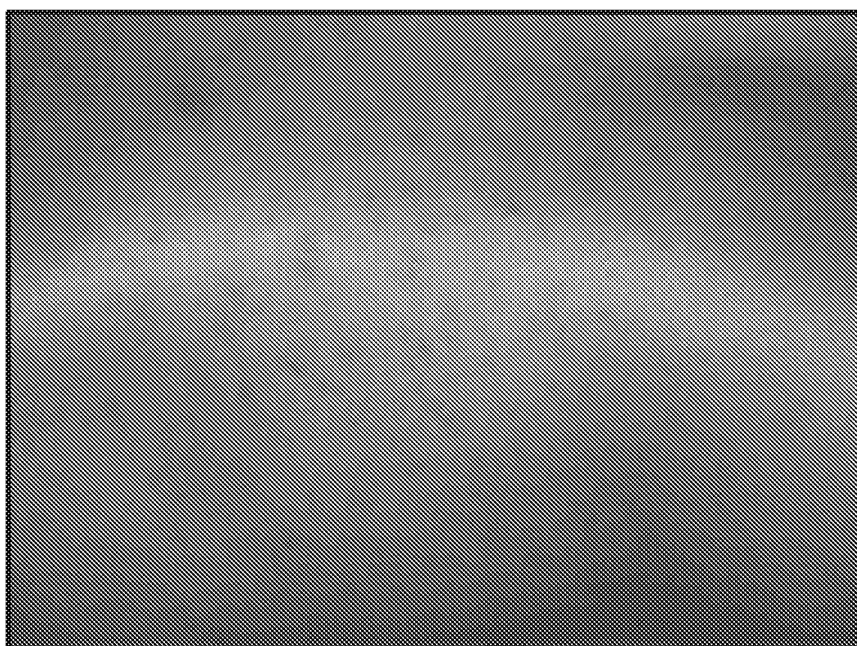
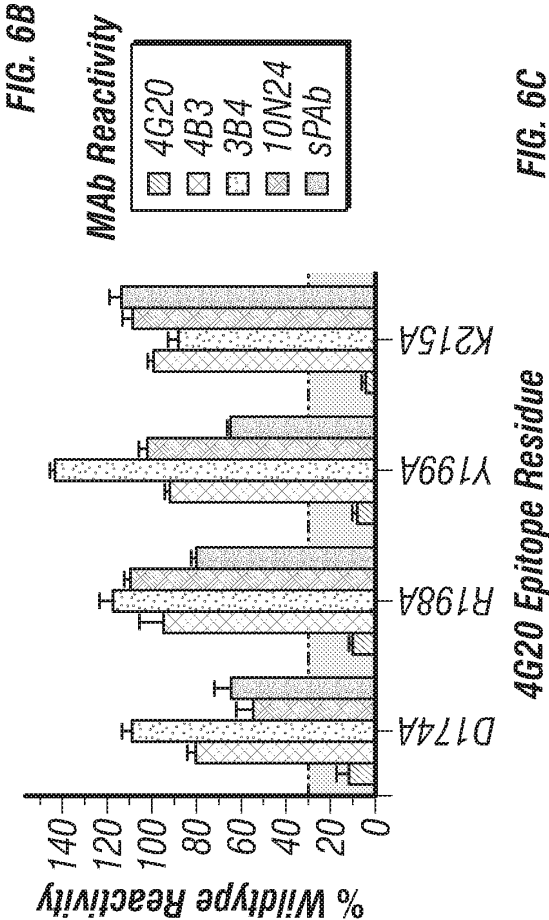
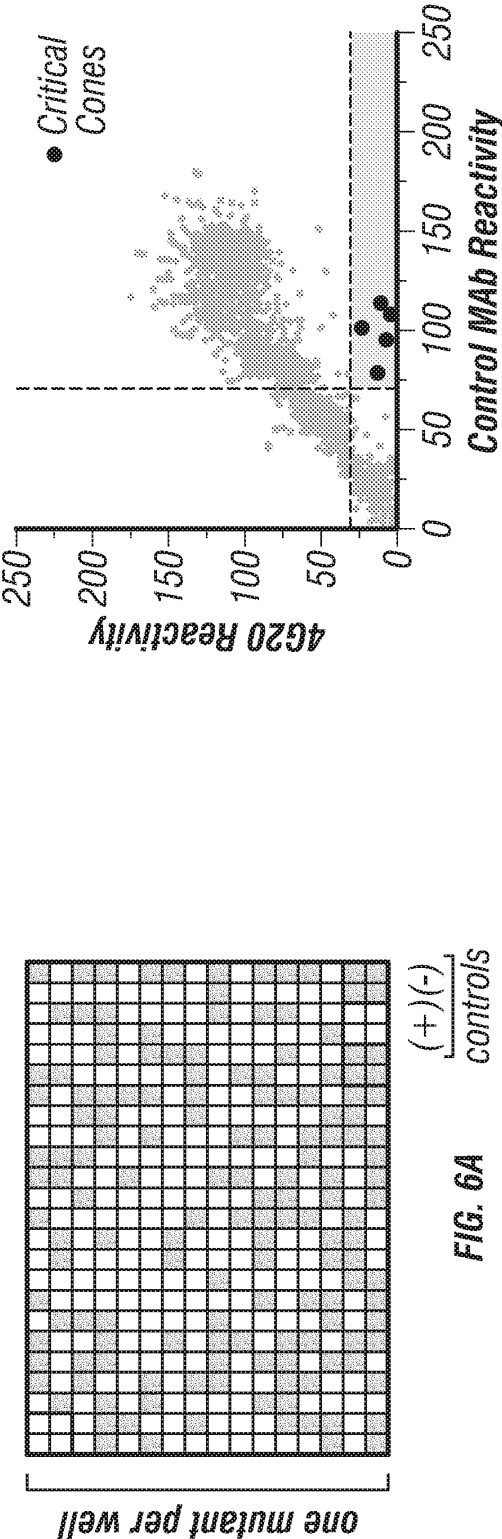


FIG. 4

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Primary antibody	Competing antibody												Domain(s) identified by mutagenesis studies		
	mAb	5N23	CHK-84	CHK-141	5D14	5M16	106	9D14	4B8	1H12	5F10	CHK-265		CHK-88	342
5N23		0	-1	-3	82	92	111	79	96	-2	103	98	96	108	96
CHK-84		5	2	4	5	-2	48	103	102	-4	100	92	90	99	81
CHK-141		5	5	-1	-9	38	65	97	101	30	96	86	85	92	80
5D14		77	47	49	-1	27	15	44	33	1	89	85	89	15	91
5M16		93	21	34	-10	5	-3	20	18	-2	96	84	87	64	88
106		89	68	79	-20	-12	-7	34	3	-4	82	85	110	86	87
9D14		98	105	98	26	25	30	23	27	24	118	105	116	114	94
4B8		92	88	94	-1	6	4	4	6	4	96	92	91	112	103
1H12		31	38	54	5	26	19	48	36	-10	52	52	49	56	91
5F10		92	94	101	86	95	97	84	90	45	-3	-3	5	93	99
CHK-265		100	94	100	77	90	79	80	88	45	2	2	10	101	96
CHK-88		97	85	101	77	91	108	89	91	38	3	3	8	53	97
342		92	95	94	37	72	89	71	92	44	88	95	44	3	103

FIG. 5



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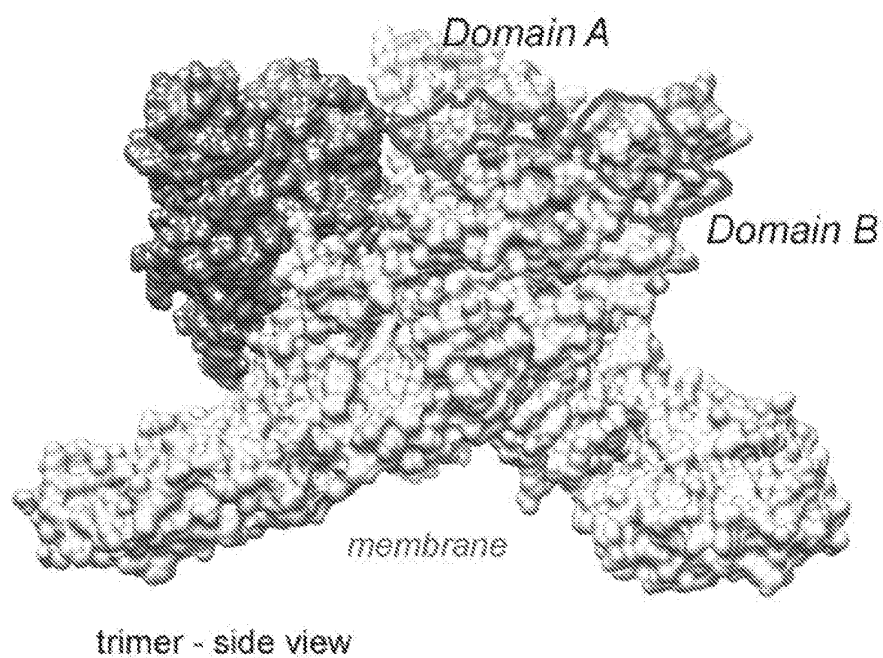


FIG. 6E

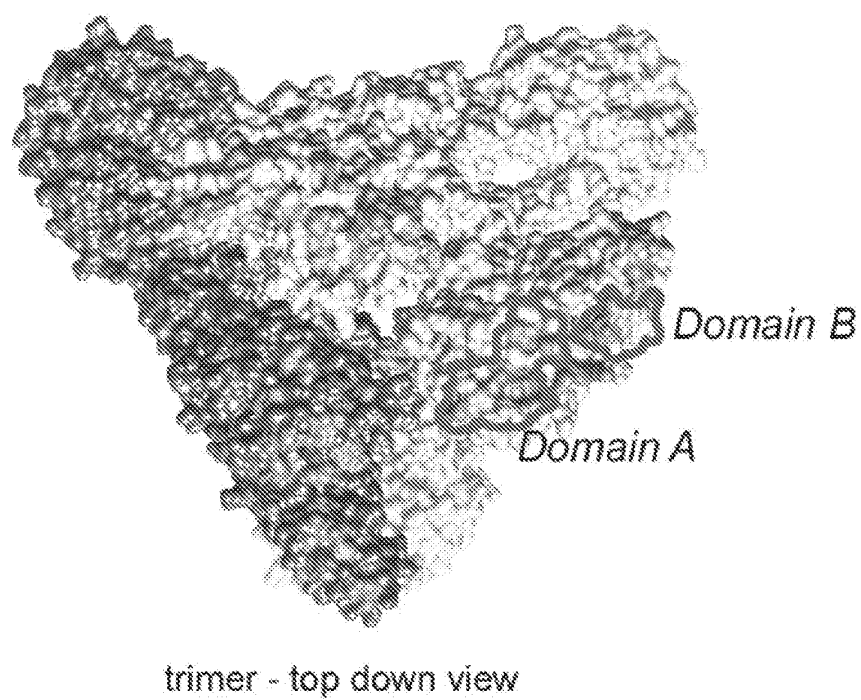


FIG. 6F

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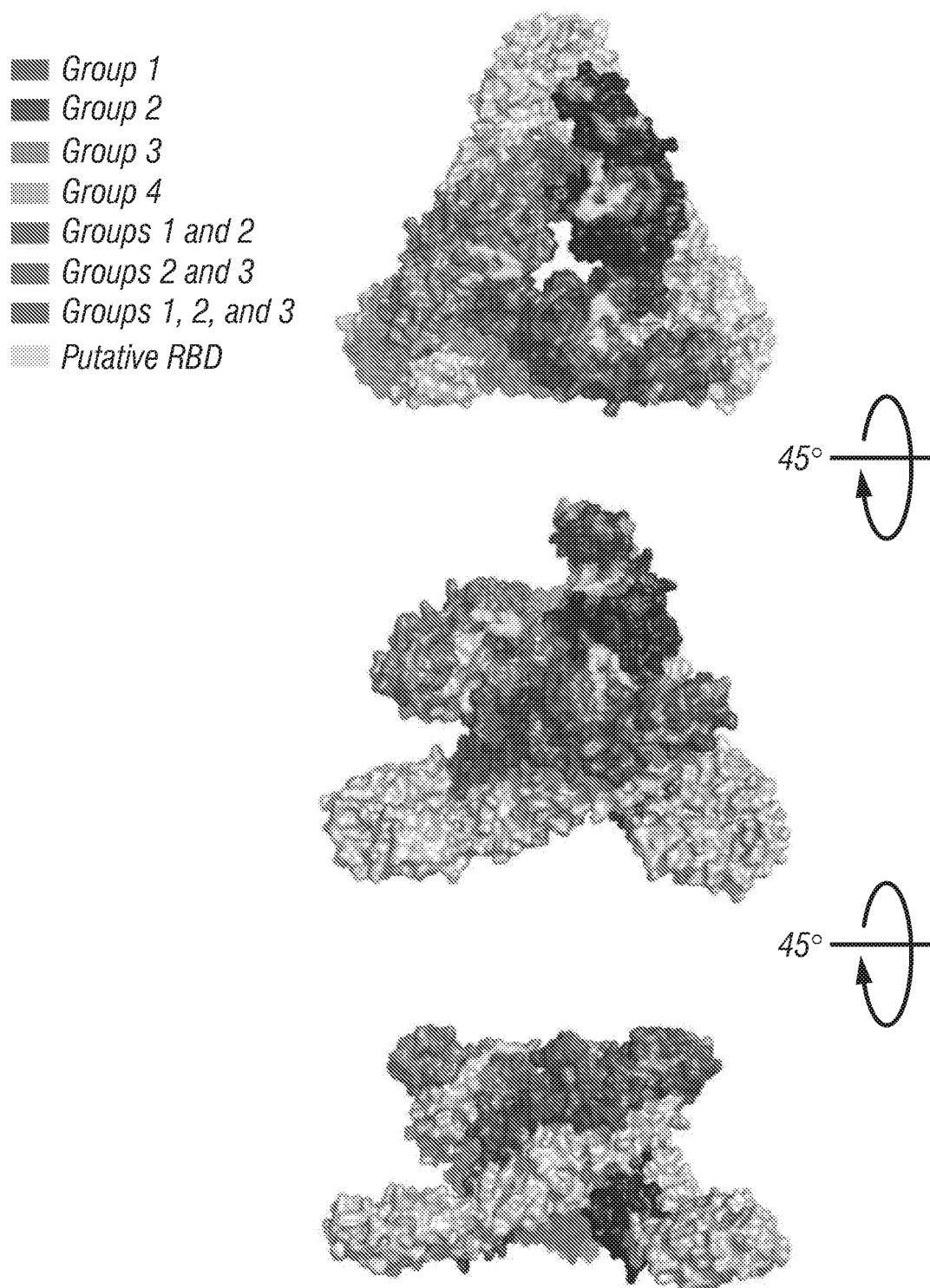


FIG. 7
SUBSTITUTE SHEET (RULE 26)

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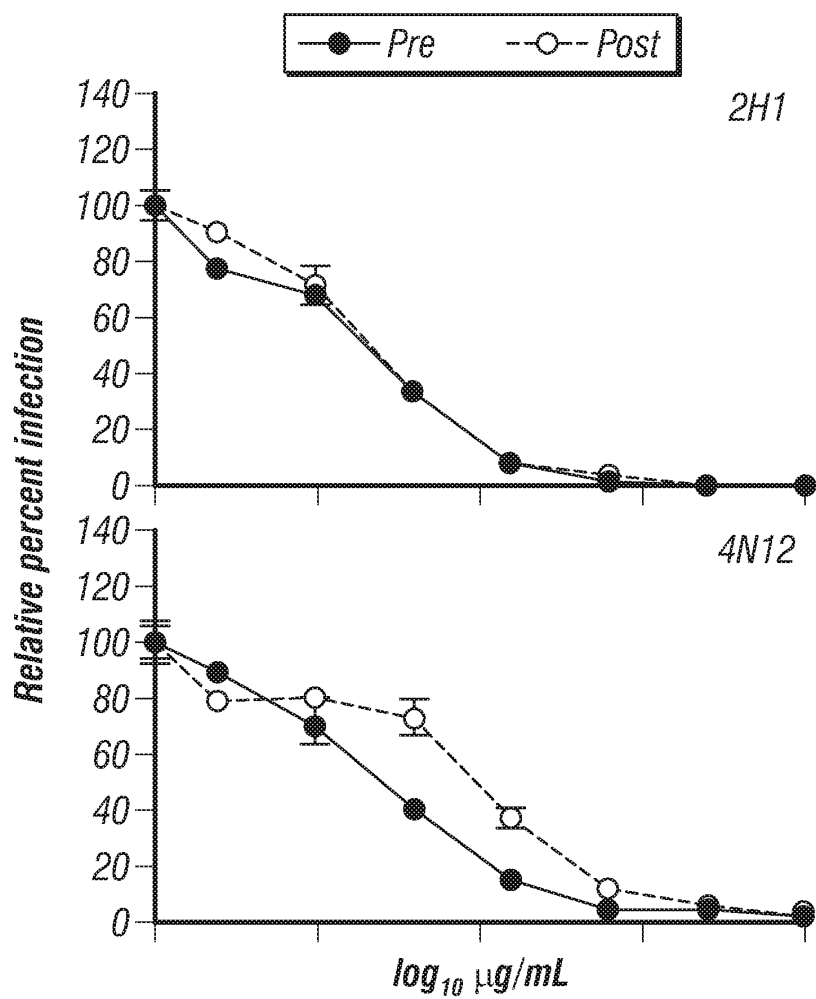


FIG. 8

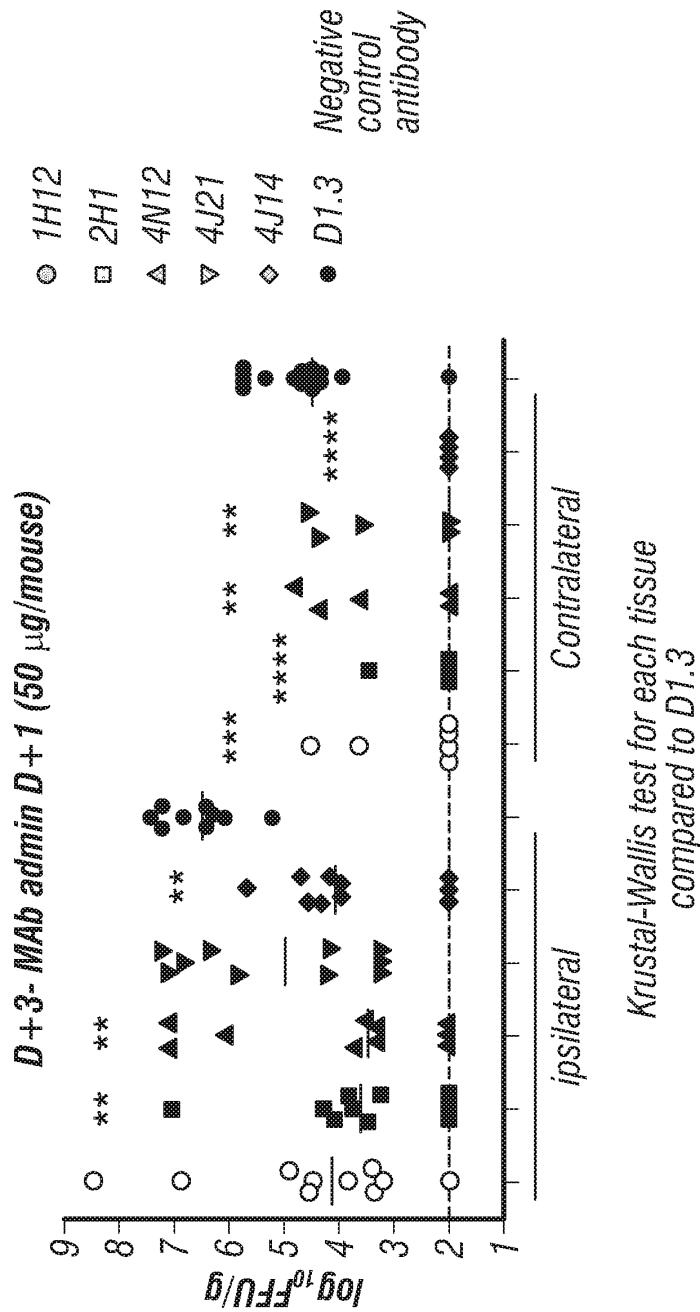


FIG. 9

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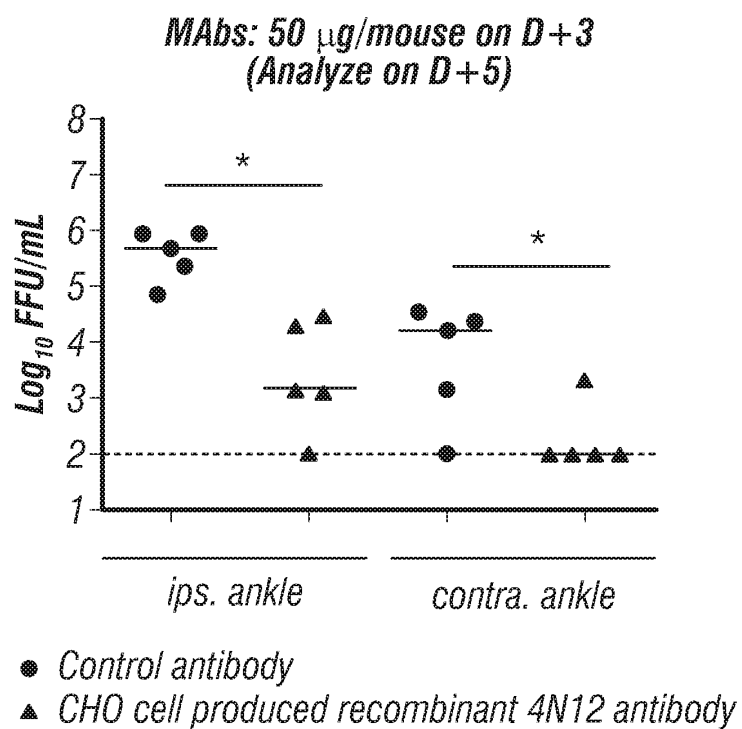


FIG. 10

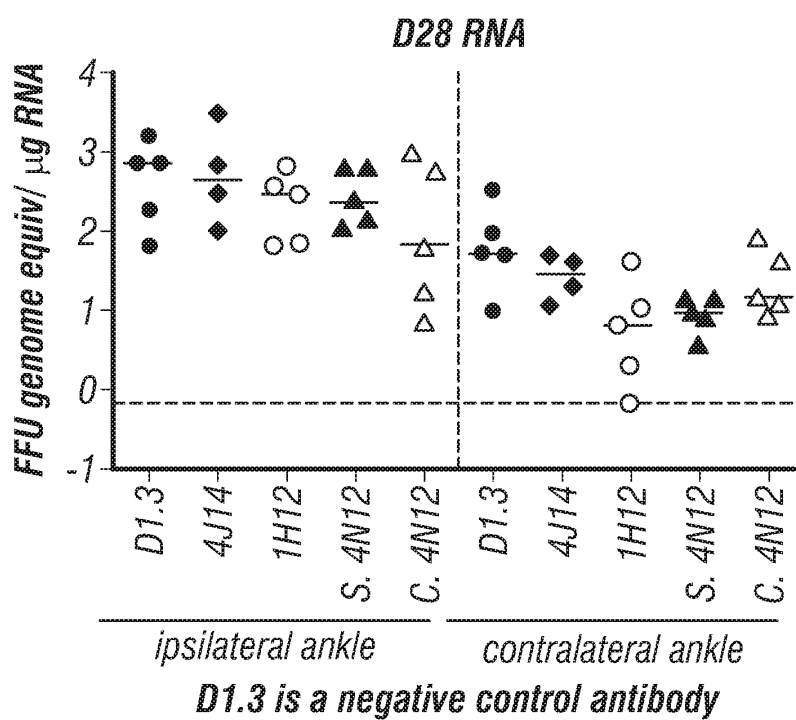


FIG. 11

SUBSTITUTE SHEET (RULE 26)

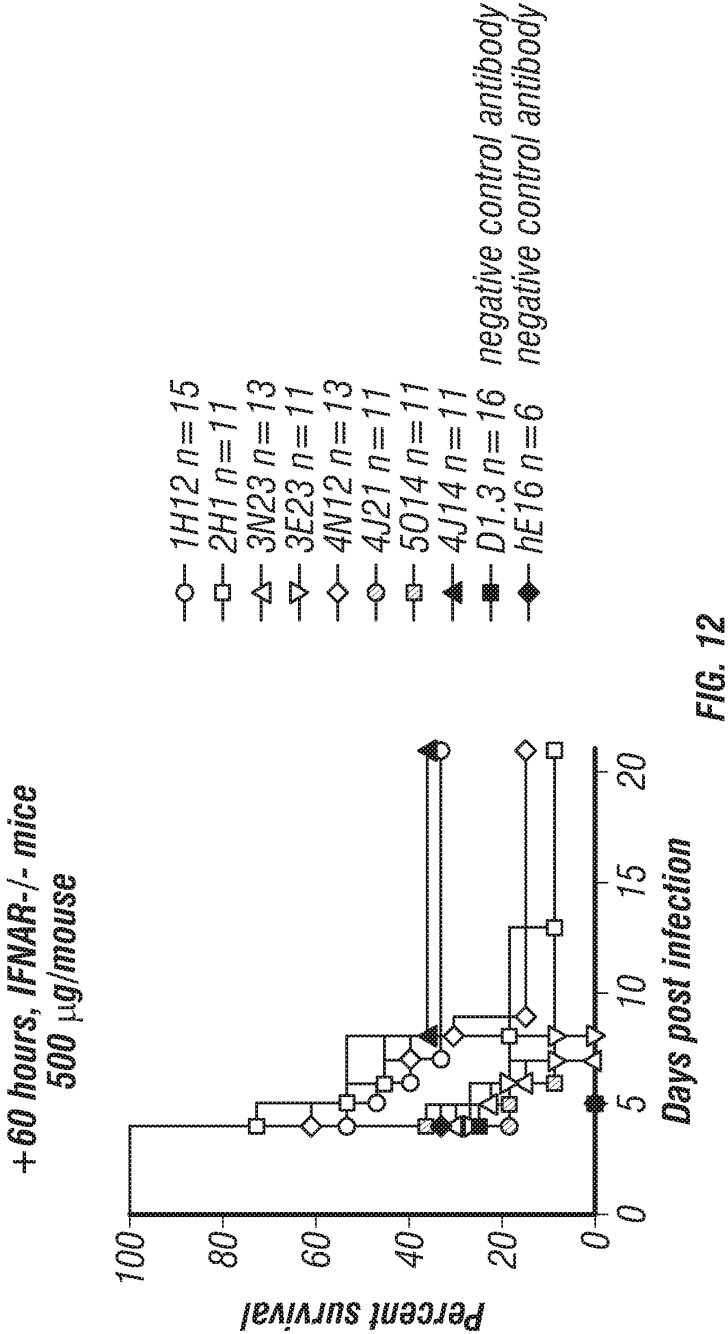


FIG. 12

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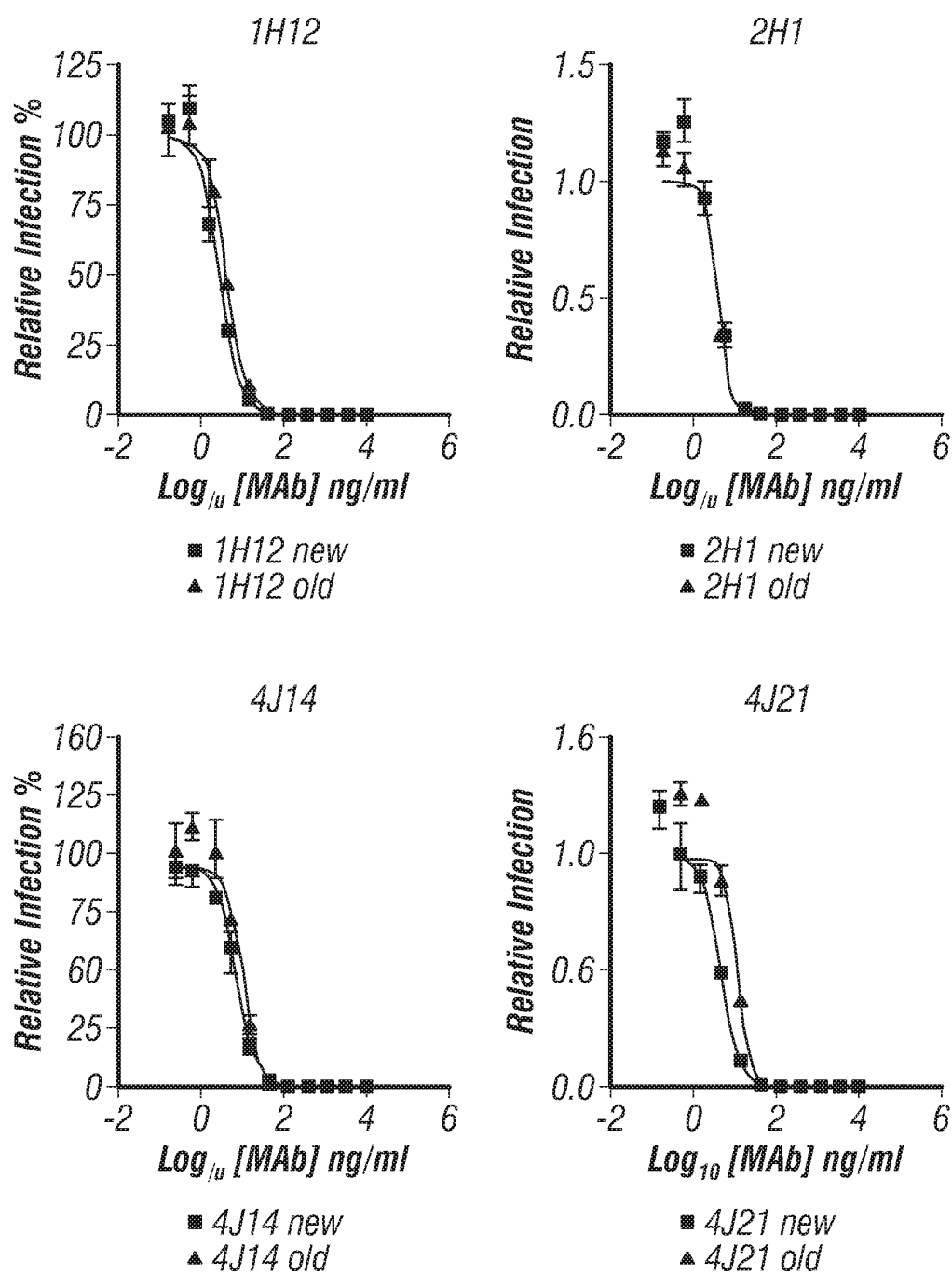


FIG. 13

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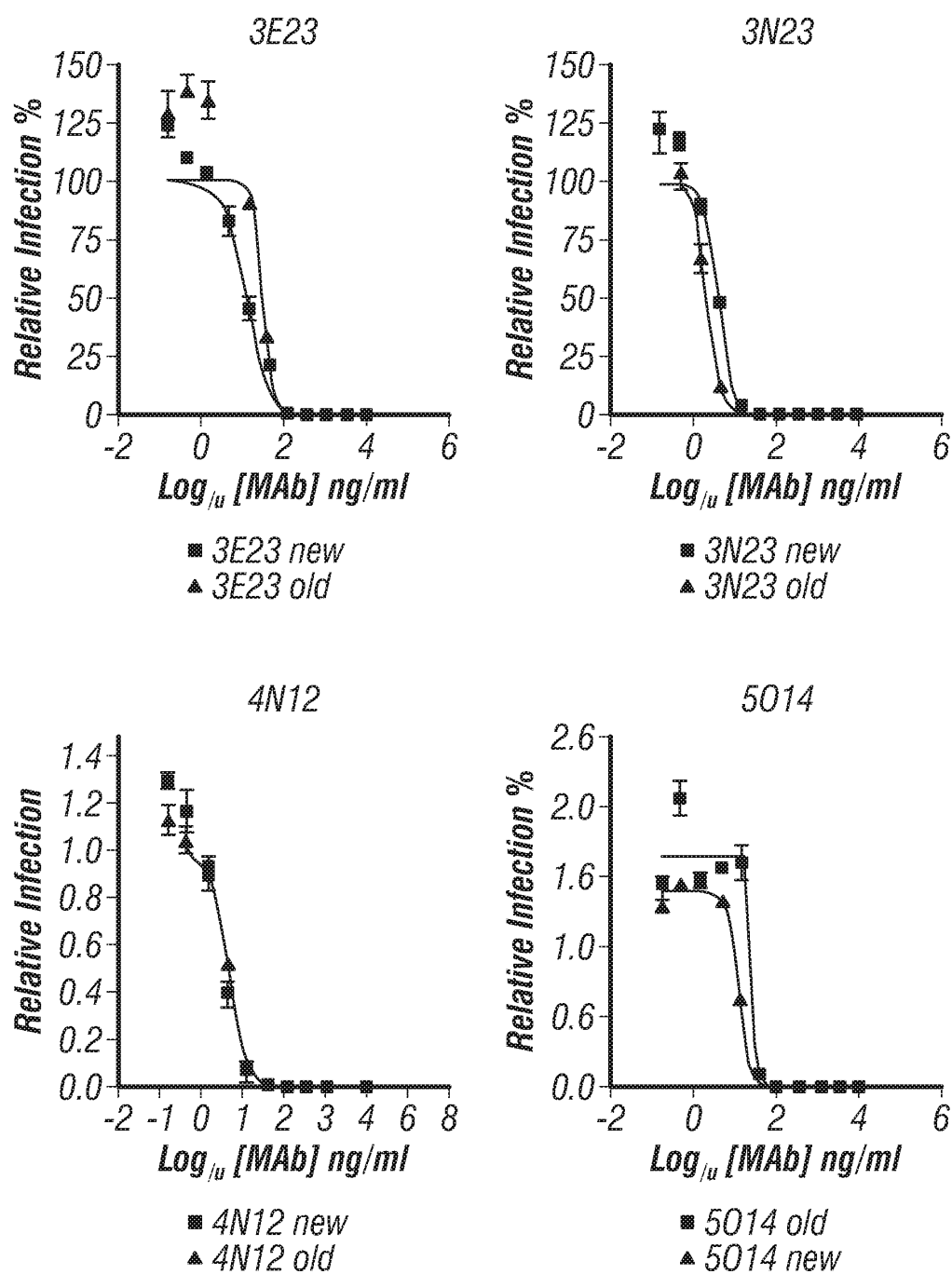


FIG. 13
(Cont'd)

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<i>Clone</i>	<i>Hybridoma- produced mAb (‘old’)</i>	<i>Recombinant CHO cell- produced mAb (‘new’)</i>
1H12	4.2	2.7
2H1	4	3.8
(3E)23	34	13.8
3N23	2.1	4.5
4J14	8.6	5.7
4J21	11.4	4.8
4N12	4.8	5
5M16	5.9	1,094
5(O)14	14.3	34.8

FIG. 14*Chikungunya virus E1/E2 alignment:*

ECSA Genotypes: LR2006
 S27
 SL15649

Asian Genotypes: 181/25
 99659

West African Genotype: IbH35

Aligned sequences are shown as Protein_Strain_Genbank accession number

FIG. 15

EE1_S27_NC004162.2	TACGAACACGTAACAGTATCCCGAACACGGTGGAGTACCGTATAAGACTCTAGTCAAC
EE1_SL15649_GU189061.1	TACGAACACGTAACAGTATCCCGAACACGGTGGAGTACCGTATAAGACTCTAGTCAAT
EE1_LR2006_KT449801.1	TACGAACACGTAACAGTATCCCGAACACGGTGGAGTACCGTATAAGACTCTAGTCAAT
EE1_181/25_L37661.3	TACGAACACGTAACAGTATCCCGAACACGGTGGAGTACCGTATAAGACTCTAGTCAAC
EE1_99659_KJ451624.1	TACGAACACGTAACAGTATCCCGAACACGGTGGAGTACCGTATAAGACTCTAGTCAAC
EE1_IbH35_HM045786.1	TACGAACACGTAACAGTATCCCGAACACGGTGGAGTACCGTATAAGACTCTTTGTCAAC

EE1_S27_NC004162.2	AGACCGGGCTACAGCCCCATGGTACTGTGAGATGGAGCTACTGTAGTCACCTTTGGAGCCCA
EE1_SL15649_GU189061.1	AGACCTGGCTACAGCCCCATGGTATTGGAGATGGAATACTGTAGTCACCTTTGGAGCCCA
EE1_LR2006_KT449801.1	AGACCTGGCTACAGCCCCATGGTATTGGAGATGGAATACTGTAGTCACCTTTGGAGCCCA
EE1_181/25_L37661.3	AGACCGGGCTACAGCCCCATGGTACTGTGAGATGGAGCTTCTGTAGTCACCTTTGGAGCCCA
EE1_99659_KJ451624.1	AGACCGGGCTACAGCCCCATGGTATTGGAGATGGAGCTTCTGTCTGTACACCTTTGGAACCCA
EE1_IbH35_HM045786.1	AGACCGGGTTACAGCCCCATGGTATTGGAGATGGAGCTACAAATCGGTACACCTTTGGAACCCA

EE1_S27_NC004162.2	ACGTATCGCTTGATTACATCACGTGCGAATACAAAAACCGTCATCCCGTCTCCGTACGTG
EE1_SL15649_GU189061.1	ACACTATCGCTTGATTACATCACGTGCGAGTACAAAAACCGTCATCCCGTCTCCGTACGTG
EE1_LR2006_KT449801.1	ACACTATCGCTTGATTACATCACGTGCGAGTACAAAAACCGTCATCCCGTCTCCGTACGTG
EE1_181/25_L37661.3	ACGTATCGCTTGATTACATCACGTGCGAGTATAAAAAACCGTCATCCCGTCTCCGTACGTG
EE1_99659_KJ451624.1	ACGTATCGCTTGATTACATCACGTGCGAGTATAAAAAACCGTTATCCCGTCTCCGTACGTG
EE1_IbH35_HM045786.1	ACACTGTCACTTGACTACATCACGTGCGAGTACAAAACTGTATCCCGTCCCGTACGTG

EE1_S27_NC004162.2	AAATGCTGCGGTACACGACAGAGTGCAAGGACAAAAACCTACCTGACTACAGCTGTAAGGTC
EE1_SL15649_GU189061.1	AAATGCTGCGGTACACGACAGAGTGCAAGGACAAAAACCTACCTGACTACAGCTGTAAGGTC
EE1_LR2006_KT449801.1	AAATGCTGCGGTACACGACAGAGTGCAAGGACAAAAACCTACCTGACTACAGCTGTAAGGTC
EE1_181/25_L37661.3	AAATGCTGCGGTACACGACAGAGTGCAAGGACAAAGAGCCCTACCTGATTACAGCTGTAAGGTC
EE1_99659_KJ451624.1	AAATGCTGCGGTACACGACAGAGTGTAAGGACAAAGAGCCCTACCTGATTACAGCTGTAAGGTC
EE1_IbH35_HM045786.1	AAATGCTGCGGTACACGACAGAGTGCAAGGACAAAGAGCCCTACCTGACTACAGCTGCAAGGTC

FIG. 15 (Cont'd)

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E1_S27_NC004162.2
 E1_SL15649_GU189061.1
 E1_LR2006_KT449801.1
 E1_181/25_L37661.3
 E1_99659_KJ451624.1
 E1_IbH35_HM045786.1
 TTCACGGCGTCTACCCATTATATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAC
 TTCACGGCGTCTACCCATTATATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAC
 TTCACGGCGTCTACCCATTATATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAC
 TTCACGGCGTCTACCCATTATATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAC
 TTCACGGCGTCTACCCATTATATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAC
 TTCACGGCGTCTACCCATTATATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAC
 TTCACGGCGTCTACCCATTATATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAC
 TTTACTGGAGTCTACCCATTATATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAC
 ** ** *.***** ** ** *.***** ** ** *.***** ** ** *.*****
 ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTTGCATCA
 ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTTGCATCA
 ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTTGCATCA
 ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTTGCATCA
 ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTTGCATCA
 ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTTGCATCA
 ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTTGCATCG
 *****.***** ** *.***** ** *.*****.*****.*****.
 GCATACAGGGCTCATACCGCATCCGCATCAGCTAAGCTCCGGCTCCTTTACCAAGGAAAT
 GCATACAGGGCTCATACCGCATCTGCATCAGCTAAGCTCCGGCTCCTTTACCAAGGAAAT
 GCATACAGGGCTCATACCGCATCTGCATCAGCTAAGCTCCGGCTCCTTTACCAAGGAAAT
 GCATATAGGGCTCATACCGCATCCGCATCAGCTAAGCTCCGGCTCCTTTACCAAGGAAAT
 GCATACAGGGCTCATACCGCATCCGCATCAGCTAAGCTCCGGCTCCTTTACCAAGGAAAT
 GCCTACAGAGCCCAACCGCATCCGGCTCGGCGAAGCTCCGGCTCCTTTACCAAGGAAAC
 .* ** *.***** ** *.***** ** *.***** ** *.*****
 AACATCACTGTAAGTGCCTATGCAAAACGGCGACCATGCCGTCACAGTTAAGGACGCCAAA
 E1_S27_NC004162.2

FIG. 15 (Cont'd)

SUBSTITUTE SHEET (RULE 26)

E1 SL15649 GU189061.1	AAATCACTGTAAC	TGCCCTATGCAAA	CGCGACCATGCCG	TACACAGTTAAAG	CACGCCCAAA
E1_LR2006_KT449801.1	AAATCACTGTAAC	TGCCCTATGCAAA	CGCGACCATGCCG	TACACAGTTAAAG	CACGCCCAAA
E1_181/25_L37661.3	AAATGTTACTGTAT	CGCTTATGCAAA	CGCGATCATGCCG	TACACAGTTAAAG	CACGCTAAA
E1_99659_KJ451624.1	AAATATCACTGTGG	CTGCTTATGCAAA	CGCGACCATGCCG	TACACAGTTAAAG	CACGCTAAA
E1_1bH35_HM045786.1	AAACATTACTGTAG	TCGCTACGCTAAC	GGCGACCATGCCG	TACACAGTTAAAG	CACGCCCAAG
	**	*	*****	**	**
	**	*	*****	**	**
	**	*	*****	**	**
E1 S27 NC004162.2	TTTCATTGTGGG	CCAAATGTCTTCA	GCCTGGACACCTTT	TGACAAACAAAAT	CGTGGTGTAC
E1_SL15649 GU189061.1	TTTCATTGTGGG	CCAAATGTCTTCA	GCCTGGACACCTTT	TGACAAACAAAAT	CGTGGTGTAC
E1_LR2006_KT449801.1	TTTCATTGTGGG	CCAAATGTCTTCA	GCCTGGACACCTTT	TGACAAACAAAAT	CGTGGTGTAC
E1_181/25_L37661.3	TTTCATTGTGGG	CCAAATGTCTTCA	GCCTGGACACCTTT	TGACAAACAAAAT	CGTGGTGTAC
E1_99659_KJ451624.1	TTTCATAGTGGG	CCAAATGTCTTCA	GCCTGGACACCTTT	TGACAAACAAAAT	CGTGGTGTAC
E1_1bH35_HM045786.1	TTTGTCGTGGG	ACCAATGTCTCCT	CCGCTGGACACCTTT	TGACAAACAAAAT	CGTGGTGTAC
	**	*	*****	**	**
	**	*	*****	**	**
	**	*	*****	**	**
E1 S27 NC004162.2	AAAGGTGACGTTT	ACAACATGGACTAC	CCCGCCCTTTGG	CGCAGGAAGACC	AGGACAAATTT
E1_SL15649 GU189061.1	AAAGGTGACGTTT	ACAACATGGACTAC	CCCGCCCTTTGG	CGCAGGAAGACC	AGGACAAATTT
E1_LR2006_KT449801.1	AAAGGTGACGTTT	ACAACATGGACTAC	CCCGCCCTTTGG	CGCAGGAAGACC	AGGACAAATTT
E1_181/25_L37661.3	AAAGGCGACGTT	ACAACATGGACTAC	CCCGCCCTTTGG	CGCAGGAAGACC	AGGACAAATTT
E1_99659_KJ451624.1	AAAGGCGACGTT	ACAACATGGACTAC	CCCGCCCTTTGG	CGCAGGAAGACC	AGGACAAATTT
E1_1bH35_HM045786.1	AAAGGCGACGTT	ACAACATGGACTAC	CCCGCCCTTTGG	CGCAGGAAGACC	AGGACAAATTT
	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
E1 S27 NC004162.2	GGCGATATCCAAA	GTCCGACGCCTG	AGAGCAAAAGACG	TCTATGCTAACACA	CAACTGGTA
E1_SL15649 GU189061.1	GGCGATATCCAAA	GTCCGACGCCTG	AGAGCAAAAGACG	TCTATGCTAACACA	CAACTGGTA
E1_LR2006_KT449801.1	GGCGATATCCAAA	GTCCGACGCCTG	AGAGCAAAAGACG	TCTATGCTAACACA	CAACTGGTA
E1_181/25_L37661.3	GGCGACATCCAAA	GTCCGACGCCTG	AGAGCGAAAGACG	TCTATGCTAACACA	CAACTGGTA
E1_99659_KJ451624.1	GGCGACATCCAAA	GTCCGACGCCTG	AGAGCGAAAGACG	TCTATGCTAACACA	CAACTGGTA
E1_1bH35_HM045786.1	GGTGACATTCAAA	GTCTACACCCG	GAAGTAAAGACG	TTTATGCCAACACT	CAGTTGGTA
	**	**	*****	**	**
	**	**	*****	**	**
	**	**	*****	**	**

FIG. 15 (Cont'd)

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E1 S27 NC004162.2
 E1 SL15649 GU189061.1
 E1 LR2006 KT449801.1
 E1 181/25 L37661.3
 E1 99659 KJ451624.1
 E1 IbH35_HM045786.1
 TGGAGGTACCAGCCTGCACCCATTCTCAGACTTTGGGGCGTCGCCATTATTAAATAT
 TGGAGGTACTAGCCTGCACCCATTCTCAGACTTTGGGGCGTCGCCATTATTAAATAT
 TGGAGGTACCAGCCTGCACCCATTCTCAGACTTTGGGGCGTCGCCATTATTAAATAT
 TGTGAGGTACCAGCCTGCACCCACTCTCAGACTTTGGGGCGTAGCCATCATTAATAT
 TGTGAGGTATCAGCCTGCACCCATTCTCAGACTTTGGGGCGTAGCCATCATTAATAT
 TGCGAAGTACCAGCCTGCACCTCACTCCTCCGACTTTGGGGCGTCGCCATCATCAATAT
 ** ** .*** ** ** ** ** ** .*** ** ** ** ** .*** ** ** **
 GCAGTCAGCAAGAAAGGCAAGTGTGCGGTGCATTGATGACCAACGCCGTCACTATCCGG
 GCAGCCAGCAAGAAAGGCAAGTGTGCGGTGCATTGATGACTAACGCCGTCACTATCCGG
 GCAGCCAGCAAGAAAGGCAAGTGTGCGGTGCATTGATGACTAACGCCGTCACTATCCGG
 GCAGCCAGCAAGAAAGGCAAGTGTGCGGTGCATTGATGACTAACGCCGTCACTATCCGG
 GCAGCCAGTAAGAAAGGCAAGTGTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG
 ACAGCTAGCAAGAAAGGTAATGTGTCAGTACATTGATGACCAACGCCGTACCATTCGA
 .*** ** ** ** ** .*** ** ** ** .*** ** ** **
 GAAGCTGAGATAGAAGTTGAAGGGAATTCTCAGCTGCAAAATCTCTTTCTCGACGGCCTTG
 GAAGCTGAGATAGAAGTTGAAGGGAATTCTCAGCTGCAAAATCTCTTTCTCGACGGCCTTA
 GAAGCTGAGATAGAAGTTGAAGGGAATTCTCAGCTGCAAAATCTCTTTCTCGACGGCCTTA
 GAAGCTGAAATAGAAGTAGAAGGGAACCTCAGTTGCAAAATCTCTTTTTCGACGGCCCTA
 GAAGCTGAAATAGAAGTAGAAGGGAACCTCAGTTGCAAAATCTCTTTTTCGACGGCCCTA
 GAAGCCGACGTAGAAGTAGAGGGGAATTCCCAGCTGCAAAATATCCTTCTCAACAGCCTTG
 **** ** .*** ** .*** ** .*** ** .*** ** .*** ** .
 GCCAGCGCCGAATTCCCGGTACAAAGTCTGTCTACACAAGTACACTGTGCGAGCCGAGTGC
 GCCAGCGCCGAATTCCCGGTACAAAGTCTGTCTACACAAGTACACTGTGCGAGCTGAGTGC
 GCCAGCGCCGAATTCCCGGTACAAAGTCTGTCTACACAAGTACACTGTGCGAGCCGAGTGC
 GCCAGCGCCGAATTCCCGGTACAAAGTCTGTCTACACAAGTACACTGTGCGAGCCGAGTGC
 GCCAGCGCCGAATTCCCGGTACAAAGTCTGTCTACACAAGTACACTGTGCGAGCCGAGTGC
 GCAAGCGCCGAGTTTCGGGTGCAAGTGTGCTCCACACAAGTACACTGCGCAGCCGCAATGC
 ** .*** ** .*** ** .*** ** .*** ** .*** ** .*** ** .*** ** .

FIG. 15 (Cont'd)

SUBSTITUTE SHEET (RULE 26)

E1_S27_NC004162.2	CACCTCCGAAGACCACATAGTCAACTACCGCGGTACATACCACTCGGGGTCCAG
E1_SL15649_GU189061.1	CACCCCCGAAGACCACATAGTCAACTACCGCGGTACATACCACTCGGGGTCCAG
E1_LR2006_KT449801.1	CACCCCCGAAGACCACATAGTCAACTACCGCGGTACATACCACTCGGGGTCCAG
E1_181/25_L37661.3	CATCCACCAGAACCATATAGTCAATTACCGCGGTACACACCACTCGGGGTCCAA
E1_99659_KJ451624.1	CATCCACCAGAACCATATAGTCAATTACCGCGGTACACACCACTCGGGGTCCAA
E1_IbH35_HM045786.1	CACCTCCAAAGACCACATAGTCAATTACCCAGCATCACACCACTTGGGGTCCAG
	** ** *.**.*.*** ** ** ** **.*** ** ** ** * ** ** ** *
E1_S27_NC004162.2	GACATTTCCGCTACGGCGATGTCAATGGGTGCAGAAAGATCACGGGAGGTGTGGACTGGTT
E1_SL15649_GU189061.1	GACATCTCCGCTACGGCGATGTCAATGGGTGCAGAAAGATCACGGGAGGTGTGGACTGGTT
E1_LR2006_KT449801.1	GACATCTCCGCTACGGCGATGTCAATGGGTGCAGAAAGATCACGGGAGGTGTGGACTGGTT
E1_181/25_L37661.3	GACATTTCCGTTACGGCGATGTCAATGGGTGCAGAAAGATCACGGGAGGTGTGGACTGGTT
E1_99659_KJ451624.1	GACATTTCCGCTACGGCGATGTCAATGGGTGCAGAAAGATCACGGGAGGTGTGGACTGGTT
E1_IbH35_HM045786.1	GATATATCCACAACGGCAATGTCTTGGGTGCAGAAAGATTACGGGAGGAGTAGGATTAATT
	** ** *.**.*.*** ** ** ** * ** ** ** * ** ** ** *
E1_S27_NC004162.2	GTCGCTGTTGCAGCACTGATTCTAATCGTGGTGTATCGCGTGTCTGTTAGCAGGCAC
E1_SL15649_GU189061.1	GTTGCTGTTGCCGCACTGATTCTAATCGTGGTGTATCGCGTGTCTGTTAGCAGGCAC
E1_LR2006_KT449801.1	GTTGCTGTTGCCGCACTGATTCTAATCGTGGTGTATCGCGTGTCTGTTAGCAGGCAC
E1_181/25_L37661.3	GTCGCTGTTGCAGCACTGATCCTAATCGTGGTGTATCGCGTGTCTGTTAGCAGGCAC
E1_99659_KJ451624.1	GTCGCTGTTGCAGCACTGATCCTAATCGTGGTGTATCGCGTGTCTGTTAGCAGGCAC
E1_IbH35_HM045786.1	GTTGCTGTTGCTGCCCTTAATTTTAATTGTGGTGTATCGCGTGTCTGTTAGCAGGCAC
	** ** ** ** ** ** * ** * ** * ** * ** * ** * ** * ** *

FIG. 15 (Cont'd)

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E1_IbH35_HM045786.1	KYWLKERGASLQHTAPFGCQIATNPVRVAVNCAVGNIPISIDIPDAAAFTRVVDAPSVTDMS
E1__S27_NC004162.2	KYWLKERGASLQHTAPFGCQIATNPVRAMNCAVGNMPISIDIPDAAAFTRVVDAPSLTDMS
E1__SL15649_GUI89061.1	KYWLKERGASLQHTAPFGCQIATNPVRVAVNCAVGNMPISIDIPDAAAFTRVVDAPSLTDMS
E1_LR2006_KT449801.1	KYWLKERGASLQHTAPFGCQIATNPVRVAVNCAVGNMPISIDIPDAAAFTRVVDAPSLTDMS
E1__99659_KJ451624.1	KYWLKERGASLQHTAPFGCQIATNPVRAMNCAVGNMPISIDIPDAAAFTRVVDAPSLTDMS
E1__181/25_L37661.3	KYWLKERGASLQHTAPFGCQIATNPVRAMNCAVGNMPISIDIPDAAAFTRVVDAPSLTDMS
E1_IbH35_HM045786.1	*** **
E1__S27_NC004162.2	CEVPACTHSSDEGGVAI IKYTASKKGKCAVHSMTNNAVTIREADVEEGNSQLQISFSTAL
E1__SL15649_GUI89061.1	CEVPACTHSSDEGGVAI IKYAVSKKGKCAVHSMTNNAVTI REAEIEVEGNSQLQISFSTAL
E1_LR2006_KT449801.1	CEVLACTHSSDEGGVAI IKYAAASKKGKCAVHSMTNNAVTI REAEIEVEGNSQLQISFSTAL
E1__99659_KJ451624.1	CEVPACTHSSDEGGVAI IKYAAASKKGKCAVHSMTNNAVTI REAEIEVEGNSQLQISFSTAL
E1__181/25_L37661.3	CEVSACTHSSDEGGVAI IKYAAASKKGKCAVHSMTNNAVTI REAEIEVEGNSQLQISFSTAL
E1_IbH35_HM045786.1	CEVPACTHSSDEGGVAI IKYAAASKKGKCAVHSMTNNAVTI REAEIEVEGNSQLQISFSTAL
E1__S27_NC004162.2	*** **
E1__SL15649_GUI89061.1	ASAEFRVQVCSTQVHCAAACHPPKPDHIVNYPASHTTTLGVQDISTSATMSWVQKITGGVGLI
E1_LR2006_KT449801.1	ASAEFRVQVCSTQVHCAAACHPPKPDHIVNYPASHTTTLGVQDISTSATMSWVQKITGGVGLV
E1__99659_KJ451624.1	ASAEFRVQVCSTQVHCAAACHPPKPDHIVNYPASHTTTLGVQDISTSATMSWVQKITGGVGLV
E1__181/25_L37661.3	ASAEFRVQVCSTQVHCAAACHPPKPDHIVNYPASHTTTLGVQDISTSATMSWVQKITGGVGLV
E1_IbH35_HM045786.1	ASAEFRVQVCSTQVHCAAACHPPKPDHIVNYPASHTTTLGVQDISTSATMSWVQKITGGVGLV
E1__S27_NC004162.2	*** **
E1__SL15649_GUI89061.1	VAVAALILIVVLCVSFSRH
E1_LR2006_KT449801.1	VAVAALILIVVLCVSFSRH
E1__99659_KJ451624.1	VAVAALILIVVLCVSFSRH
E1__181/25_L37661.3	VAVAALILIVVLCVSFSRH

FIG. 15 (Cont'd)

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CLUSTAL O(1.2.1) multiple sequence alignment

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E2_181/25_L37661.3      AGTATTAAAGGACAACTTCAATGTTCTATAAAGCCATAAGACCCTACCTAGCTCACTGTGCCC
E2_ibH35_HM045786.1     AGTACTAAGGACAAATTTTAATGTTCTATAAAGCTACAAGACCATACTAGCTCATTTGTCCT
E2_LR2006_KT449801.1    AGCACCAAGGACAACTTCAATGTTCTATAAAGCCACAAGACCATACTAGCTCACTGTGCCC
E2_SL15649_GU189061.1   AGCACCAAGGACAACTTCAATGTTCTATAAAGCCACAAGACCATACTAGCTCACTGTGCCC
E2_S27_NC004162.2      AGCACCAAGGACAACTTCAATGTTCTATAAAGCCACAAGACCATACTAGCTCACTGTGCCC
E2_99659_KJ451624.1    AGTATTAAAGGACCACTTCAATGTTCTATAAAGCCACAAGACCCTACCTAGCTCACTGTGCCC
** * *****,* ** *****,* *****,* *****,* *****,* *****,* *****,*
** * *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

E2_181/25_L37661.3      GACTGTGGAGAGGGCACTCGTGCCATAGTCCCGTAGCGCTAGAACGCATCAGAAAACGAA
E2_ibH35_HM045786.1     GACTGCGGAGAGGGCACTCGTGCCACAGCCCTATCGCATTTGGAGCGCATCAGAAAATGAA
E2_LR2006_KT449801.1    GACTGTGGAGAGGGCACTCGTGCCATAGTCCCGTAGCACTAGAACGCATCAGAAAATGAA
E2_SL15649_GU189061.1   GACTGTGGAGAGGGCACTCGTGCCATAGTCCCGTAGCACTAGAACGCATCAGAAAATGAA
E2_S27_NC004162.2      GACTGTGGAGAGGGCACTCGTGCCATAGTCCCGTAGCACTAGAACGCATCAGAAAATGAA
E2_99659_KJ451624.1    GACTGTGGAGAGGGCACTCGTGCCATAGTCCCGTAGCGTAGAACGCATCAGAAAACGAA
**** * *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*
**** * *****,* *****,* *****,* *****,* *****,* *****,* *****,* *****,*

E2_181/25_L37661.3      GCGACAGACGGGACGCTGAAAAATCCAGGTTTCTTGCATAATCGGAATAAAGACGGATGAT
E2_ibH35_HM045786.1     GCAACGGACGGAAACGCTGAAAAATCCAGGTTCTCTTTGCAGATCGGGATAAAGACAGATGAC
E2_LR2006_KT449801.1    GCGACAGACGGGACGCTGAAAAATCCAGGTTCTCTTTGCATAATCGGAATAAAGACGGATGAC
E2_SL15649_GU189061.1   GCGACAGACGGGACGCTGAAAAATCCAGGTTCTCTTTGCATAATCGGAATAAAGACGGACGAC
E2_S27_NC004162.2      GCGACAGACGGGACGCTGAAAAATCCAGGTTCTCTTTGCATAATCGGAATAAGGACGGATGAT
E2_99659_KJ451624.1    GCGACAGACGGGACGTTGAAAAATCCAGGTTTCTTTGCATAATCGGAATAAAGACGGATGAT
**..*****,* **** * *****,* *****,* *****,* *****,* *****,* *****,*
**..*****,* **** * *****,* *****,* *****,* *****,* *****,* *****,*

E2_181/25_L37661.3      AGCCATGATTGGACCAAGCTGCGTTACATGGACAATCATATGCCAGCAGACGCAGAGAGG
E2_ibH35_HM045786.1     AGCCACGATTGGACCAAGCTGCGTTATATGGATAGCCATACGCCAGCGGACGCGGAGCGGA
E2_LR2006_KT449801.1    AGCCACGATTGGACCAAGCTGCGTTATATGGACAACCATATGCCAGCAGACGCAGAGAGG
E2_SL15649_GU189061.1   AGCCACGATTGGACCAAGCTGCGTTATATGGACAACCATATGCCAGCAGACGCAGAGAGG
E2_S27_NC004162.2      AGCCATGATTGGACCAAGCTGCGTTACATGGACAATCACAATACCAGCAGACGCAGAGAGG
E2_99659_KJ451624.1    AGCCATGATTGGACCAAGCTGCGTTATATGGACAATCACAATGCCAGCAGACGCAGAGCGG
**** * *****,* *****,* *****,* **** * *****,* *****,* *****,* *****,*
**** * *****,* *****,* *****,* **** * *****,* *****,* *****,* *****,*

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FIG. 15 (Cont'd)

FIG. 15 (Cont'd)

FIG. 15 (Cont'd)

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E2_181/25_L37661.3
 E2_ibH35_HM045786.1
 E2_LR2006_KT449801.1
 E2_SL15649_GU189061.1
 E2_S27_NC004162.2
 E2_99659_KJ451624.1
 CTGGTCCCGGTAATGCTGAACCTCGGGACCGGAAAGGAAAAAGTTACATTCCTGTTTCCT
 TTAGTCCCGGTAACGCTGAACCTCGGGACCGGTAAGGAAAAAGTTACATTCCTGTTTCCT
 CTGGTCCCGGTAATGCTGAACCTCGGGACCGGAAAGGAAAAAGTTACATTCCTGTTTCCT
 CTGGTCCCGGTAATGCTGAACCTCGGGACCGGAAAGGAAAAAGTTACATTCCTGTTTCCT
 CTGGTCCCGGTAACGCTGAACCTCGGGACCGGAAAGGAAAAAGTTACATTCCTGTTTCCT
 CTGGTCCCGGTAATGCTGAATTCGGGACCGGAAAGGAAAAAGTTACATTCCTGTTTCCT
 *.*****
 E2_181/25_L37661.3
 E2_ibH35_HM045786.1
 E2_LR2006_KT449801.1
 E2_SL15649_GU189061.1
 E2_S27_NC004162.2
 E2_99659_KJ451624.1
 CTGGCAAAATGTGACATGCAGGGTGCCCTAAGGCAAGGAAACCCACCGTGACGTACGGAAAA
 TTGGCAAAACGTGACTTGCAGAGTGCCAAAAGCAAGAAACCCACAGTAACGTACGGAAAA
 CTGGCAAAATGTAACATGCAGGGTGCCCTAAGCAAGGAAACCCACCGTGACGTACGGAAAA
 CTGGCAAAATGTAACATGCAGGGTGCCCTAAGCAAGGAAACCCACCGTGACGTACGGAAAA
 CTGGCAAAATGTAACATGCATGGTGCCCTAAGCAAGGAAACCCACCGTGACGTACGGAAAA
 CTGGCAAAATGTGACATGCAGGGTGCCCTAAGCAAGGAAACCCACCGTGACGTACGGAAAA
 *.*****
 E2_181/25_L37661.3
 E2_ibH35_HM045786.1
 E2_LR2006_KT449801.1
 E2_SL15649_GU189061.1
 E2_S27_NC004162.2
 E2_99659_KJ451624.1
 AACCAGTCATCATGTGCTGTATCCTTGACCAACCCACCGTCTCTTACCGGAATATG
 AACCAGTCACCATGCTGTATCCTTGACCATCCGACACTCTTGTCTTATCGTAACATG
 AACCAGTCATCATGTACTGTATCCTTGACCAACCCACACTCTTGTCTTACCGGAATATG
 AACCAGTCATCATGTACTGTATCCTTGACCAACCCACACTCTTGTCTTACCGGAATATG
 AACCAGTCATCATGTACTGTATCCTTGACCAACCCACACTCTTGTCTTACCGGAATATG
 AACCAGTCATCATGTACTGTATCCTTGACCAACCCACACTCTTGTCTTACCGGAATATG
 AACCAGTCATCATGTACTGTATCCTTGACCAACCCACACTCTTGTCTTACCGGAATATG
 *.*****
 E2_181/25_L37661.3
 E2_ibH35_HM045786.1
 E2_LR2006_KT449801.1
 E2_SL15649_GU189061.1
 E2_S27_NC004162.2
 E2_99659_KJ451624.1
 GGAGAAGAACCAAACTATCAAGAAGAGTGGGTGACGCATAAGAAGGAGATCAGGTTAACC
 GGACAGGAACCAAAATTACCACGAGGAGTGGGTGACACACAAGAAGGAGGTTACCTTGACC
 GGAGAAGAACCAAACTATCAAGAAGAGTGGGTGATGCATAAGAAGGAGTCTGCTAACC
 GGAGAAGAACCAAACTATCAAGAAGAGTGGGTGATGCATAAGAAGGAGTCTGCTAACC
 GGAGAAGAACCAAACTATCAAGAAGAGTGGGTGACGCACAAGAAGGAGTCTGCTAACC
 GGAGAAGAACCAAACTATCAAGAAGAGTGGGTGACGCATAAGAAGGAGATCAGGTTAACC
 *.*****

FIG. 15 (Cont'd)

E2_181/25_L37661.3	GTCCGACTGAAGGGCTCGAGGTCACGTGGGGCAACAACGAGCCGTACAAGTATTGGCCG
E2_ibH35_HM045786.1	GTCCCTACTGAGGGTCTCGAGGTCACATTGGGGCAACAACGAGCCGTACAAGTATTGGCCG
E2_LR2006_KT449801.1	GTCCGACTGAAGGGCTCGAGGTCACGTGGGGCAACAACGAGCCGTATAAGTATTGGCCG
E2_SL15649_GU189061.1	GTCCGACTGAAGGGCTCGAGGTCACGTGGGGCAACAACGAGCCGTATAAGTATTGGCCG
E2_S27_NC004162.2	GTCCGACTGAAGGGCTCGAGGTCACGTGGGGCAACAACGAGCCGTATAAGTATTGGCCG
E2_99659_KJ451624.1	GTCCGACTGAAGGGCTCGAGGTCACGTGGGGTAACAATGAGCCGTACAAGTATTGGCCG ***** . ** ** ***** ** ***** ** ** . ** ***** *****
E2_181/25_L37661.3	CAGTTATCCACAACGGGTACAGCCCAACGGCCACCCGCGCATGAGATAATTTGTATTATTAT
E2_ibH35_HM045786.1	CAGATGTCTACGAACGGTACTGCTCATGTGTCACCCACATGAGATAATCTTGACTATTAT
E2_LR2006_KT449801.1	CAGTTATCFACAAACGGTACAGCCCATGGCCACCCGCGCATGAGATAATCTTGATTATTAT
E2_SL15649_GU189061.1	CAGTTATCFACAAACGGTACAGCCCATGGCCACCCGCGCATGAGATAATCTTGATTATTAT
E2_S27_NC004162.2	CAGTTATCFACAAACGGTACAGCCCATGGCCACCCGCGCATGAGATAATCTTGATTATTAT
E2_99659_KJ451624.1	CAGTTATCCACAACGGTACAGCCCAACGGCCACCCGCGCATGAGATAATCTTGATTATTAT ***;*. ** . ** *****;*. ** ** ** *****. ***** ***** ***** ***** ***** . ** ** ***** . ** ** *****; ***** . ** *****
E2_181/25_L37661.3	GAGCTGTACCCCTACTATGACTGTGGTAGTTGTGTGTCAGTGGCCTCGTTCGTAATCCTGTCTG
E2_ibH35_HM045786.1	GAGCTGTACCCCTACTATGACTGTAAATCATTTGTGTCGGTGGCCTCGTTCGTTCTGTCTG
E2_LR2006_KT449801.1	GAGCTGTACCCCTACTATGACTGTAGTAGTTGTGTGTCAGTGGCCACGTTTCATACTCCTGTCTG
E2_SL15649_GU189061.1	GAGCTGTACCCCTACTATGACTGTAGTAGTTGTGTGTCAGTGGCCACGTTTCATACTCCTGTCTG
E2_S27_NC004162.2	GAGCTGTACCCCTACTATGACTGTAGTAGTTGTGTGTCAGTGGCCTCGTTCATACTCCTGTCTG
E2_99659_KJ451624.1	GAGCTGTACCCCTACTATGACTGTAGTAGTTGTGTGTCAGTGGCCTCGTTCATACTCCTGTCTG ***** ***** . ** ** ***** . ** ** *****; ***** . ** *****
E2_181/25_L37661.3	ATGGTGGGTGTGGCAGTGGGGATGTGCATGTGTGCACGACGAGATGCATTACACCGTAC
E2_ibH35_HM045786.1	ATGGTGGGCACAGCAGTGGGGATGTGTGTGCGCACGGCGCAGATGCATTACACCATAT
E2_LR2006_KT449801.1	ATGGTGGGTATGGCAGCGGGGATGTGCATGTGTGCACGACGAGATGCATCACACCGTAT
E2_SL15649_GU189061.1	ATGGTGGGTATGGCAGTGGGGATGTGCATGTGTGCACGACGAGATGCATCACACCGTAT
E2_S27_NC004162.2	ATGGTGGGTATGGCAGTGGGGATGTGCATGTGTGCACGACGAGATGCATCACACCATAC
E2_99659_KJ451624.1	ATGGTGGGTGTGGCAGTGGGGATGTGCATGTGTGCACGACGAGATGCATTACACCGTAC ***** . ** ** ***** . ** ** *****; ***** ***** *****

FIG. 15 (Cont'd)

E2_181/25_L37661.3	GAACTGACACACGAGGAGCTACCGTCCCTTTCCCTGCTTAGCCCTAAATATGCTGCATTAGAACA
E2_IbH35_HM045786.1	GAAATTAACACACGAGGAGCCACCGTTCCCTTTCTGCTCAGCCTGCTATGTTGCGTCAGAACG
E2_LR2006_KT449801.1	GAACTGACACACGAGGAGCTACCGTCCCTTTCCCTGCTTAGCCCTAAATATGCTGCATCAGAACA
E2_SL15649_GU189061.1	GAACTGACACACGAGGAGCTACCGTCCCTTTCCCTGCTTAGCCCTAAATATGCTGCATCAGAACA
E2_S27_NC004162.2	GAACTGACACACGAGGAGCTACCGTCCCTTTCCCTGCTTAGCCCTAAATATGCTGCATCAGAACA
E2_99659_KJ451624.1	GAACTGACACACGAGGAGCTACCGTCCCTTTCCCTGCTTAGCCCTAAATATGCTGCATTAGAACA
	*** * .***** ** ** ** **
E2_181/25_L37661.3	GCTAAAGCG
E2_IbH35_HM045786.1	ACCAAGGCG
E2_LR2006_KT449801.1	GCTAAAGCG
E2_SL15649_GU189061.1	GCTAAAGCG
E2_S27_NC004162.2	GCTAAAGCG
E2_99659_KJ451624.1	GCTAAAGCG
	. * ** .***

FIG. 15 (Cont'd)

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CLUSTAL O(1.2.1) multiple sequence alignment

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E2_IbH35_HM045786.1      STKDNFNVYKATRPYLAHCPDCGEGHSCHSPIALERIRNEATDGTGTLKIQVSLQIGIKTDD
E2_99659_KJ451624.1      SIKDHFNVYKATRPYLAHCPDCGEGHSCHSCHSPVALERIRNEATDGTGTLKIQVSLQIGIKTDD
E2_181/25_L37661.3      SIKDHFNVYKATRPYLAHCPDCGEGHSCHSCHSPVALERIRNEATDGTGTLKIQVSLQIGIKTDD
E2_S27_NC004162.2      STKDNFNVYKATRPYLAHCPDCGEGHSCHSCHSPVALERIRNEATDGTGTLKIQVSLQIGIKTDD
E2_SL15649_GU189061.1  STKDNFNVYKATRPYLAHCPDCGEGHSCHSCHSPVALERIRNEATDGTGTLKIQVSLQIGIKTDD
E2_LR2006_KT449801.1   STKDNFNVYKATRPYLAHCPDCGEGHSCHSCHSPVALERIRNEATDGTGTLKIQVSLQIGIKTDD
* * * * *
SHDWTKLRYMDSHTPADAERAGLLVRTSAPCTITGTMGHFILARCPKGETLTVGFTDSRK
SHDWTKLRYMDNHNMPADAERAGLFLVRTSAPCTITGTMGHFILARCPKGETLTVGFTDGRK
SHDWTKLRYMDNHNMPADAERAGLFLVRTSAPCTITGTMGHFILARCPKGETLTVGFTDGRK
SHDWTKLRYMDNHNIPADAGRAGLFLVRTSAPCTITGTMGHFILARCPKGETLTVGFTDSRK
SHDWTKLRYMDNHNMPADAERAGLFLVRTSAPCTITGTMGHFILARCPKGETLTVGFTDSRK
SHDWTKLRYMDNHNMPADAERAGLFLVRTSAPCTITGTMGHFILARCPKGETLTVGFTDSRK
* * * * *
ISHSCTHPFHHEPPVIGREKFFHSRPPQHGHKELPCSTYVQSTAATAEEIEVHMPPDTPDRTL
ISHSCTHPFHHDPPVIGREKFFHSRPPQHGHRELPCSTYVQSTAATAEEIEVHMPPDTPDRTL
ISHSCTHPFHHDPPVIGREKFFHSRPPQHGHRELPCSTYVQSTAATAEEIEVHMPPDTPDRTL
ISHSCTHPFHHDPPVIGREKFFHSRPPQHGHRELPCSTYVQSTAATAEEIEVHMPPDTPDRTL
ISHSCTHPFHHDPPVIGREKFFHSRPPQHGHRELPCSTYVQSTAATAEEIEVHMPPDTPDRTL
ISHSCTHPFHHDPPVIGREKFFHSRPPQHGHRELPCSTYVQSTAATAEEIEVHMPPDTPDRTL
* * * * *
MTQQSGNVKITVNGQTVRYKNCNCGGSEGLTTTDKVINNCKIDQCHAAVTNHHKKWQYNSE
MSQQSGNVKITVNSQTVRYKNCNCGGSEGLTTTDKVINNCKVDQCHAAVTNHHKKWQYNSE
MSQQSGNVKITVNSQTVRYKNCNCGGSEGLTTTDKVINNCKVDQCHAAVTNHHKKWQYNSE
LSQQSGNVKITVNSQTVRYKNCNCGGSEGLTTTDKVINNCKVDQCHAAVTNHHKKWQYNSE
MSQQSGNVKITVNGQTVRYKNCNCGGSEGLTTTDKVINNCKVDQCHAAVTNHHKKWQYNSE
MSQQSGNVKITVNGQTVRYKNCNCGGSEGLTTTDKVINNCKVDQCHAAVTNHHKKWQYNSE
* * * * *

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FIG. 15 (Cont'd)

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[illegible]

FIG. 15 (Cont'd)

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