

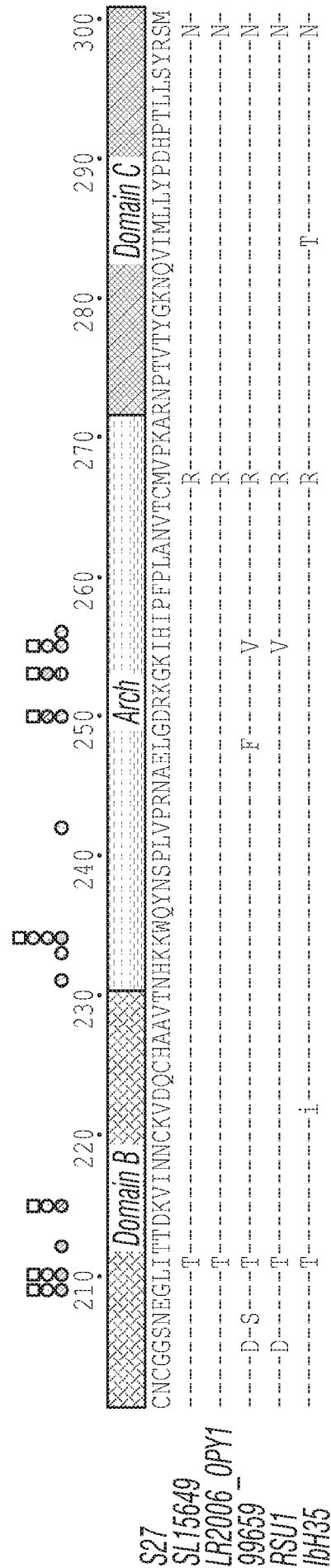
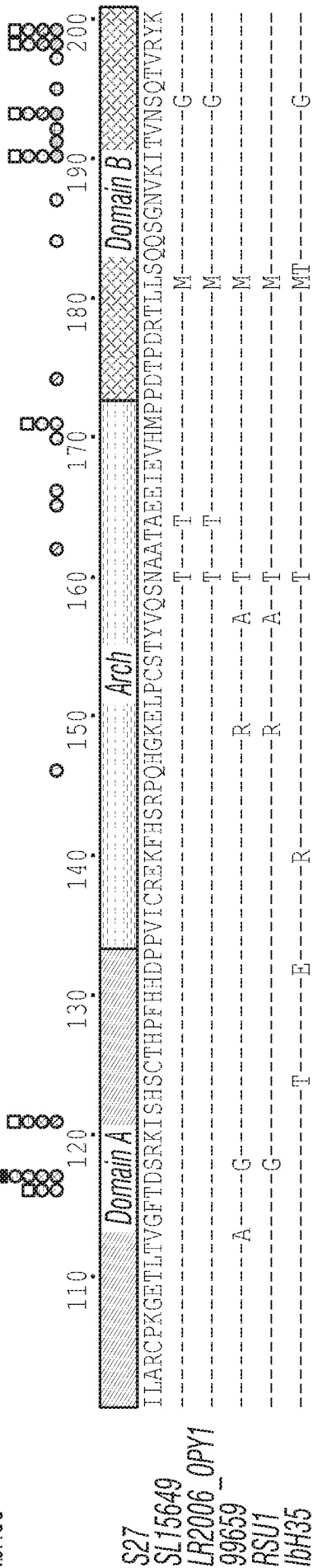
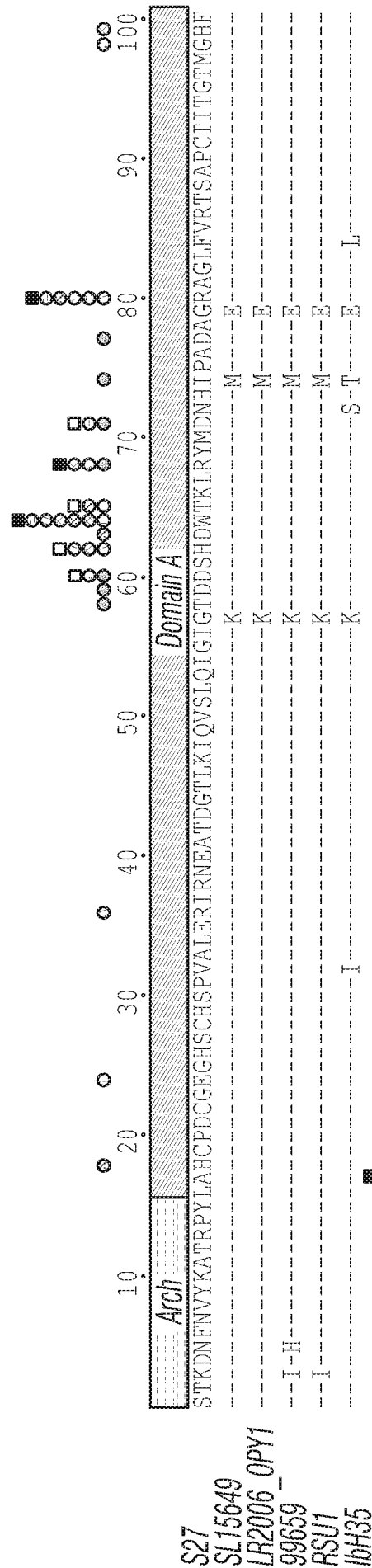


FIG. 1A

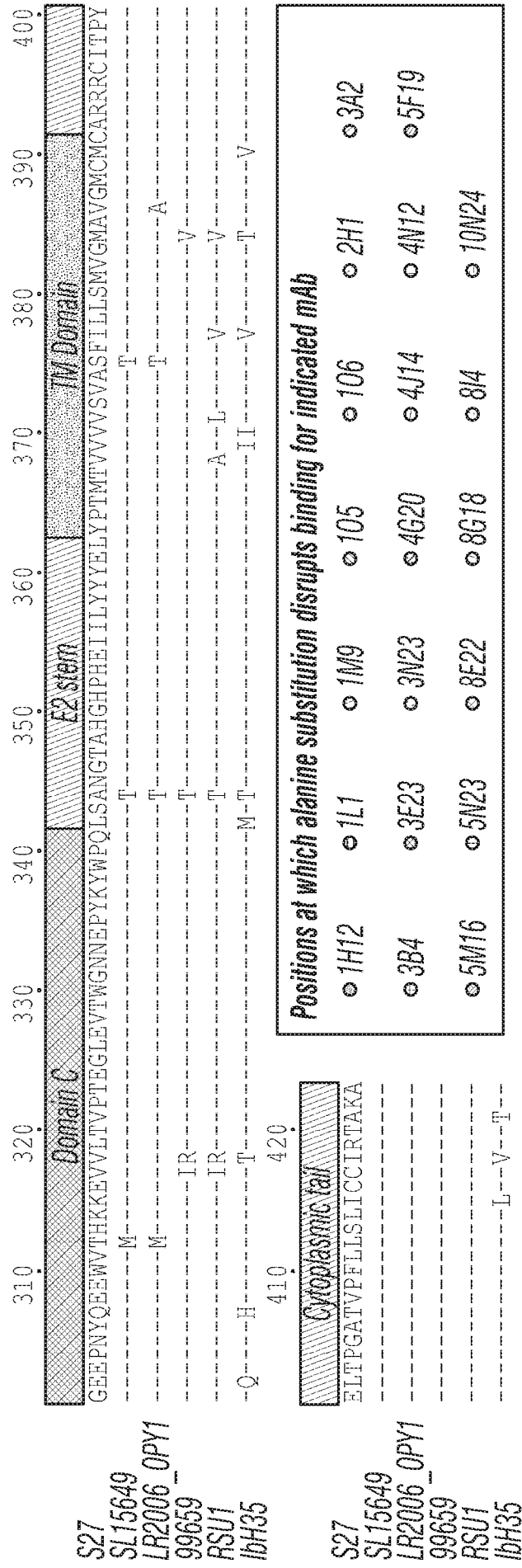


FIG. 1A
(Cont'd)

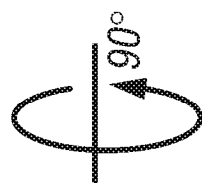
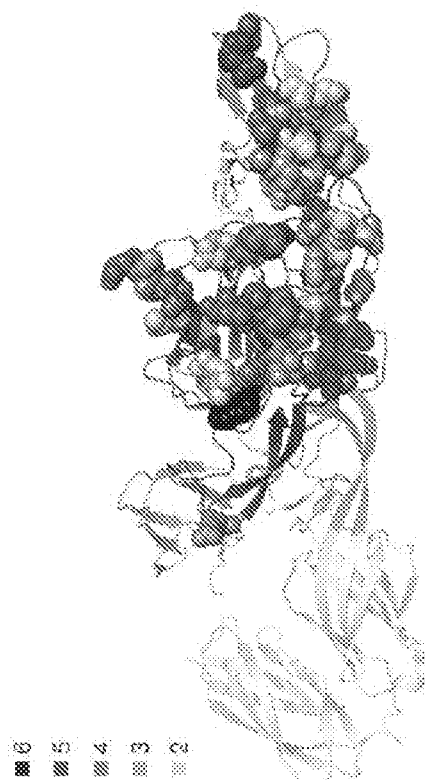


FIG. 1B

FIG. 1C

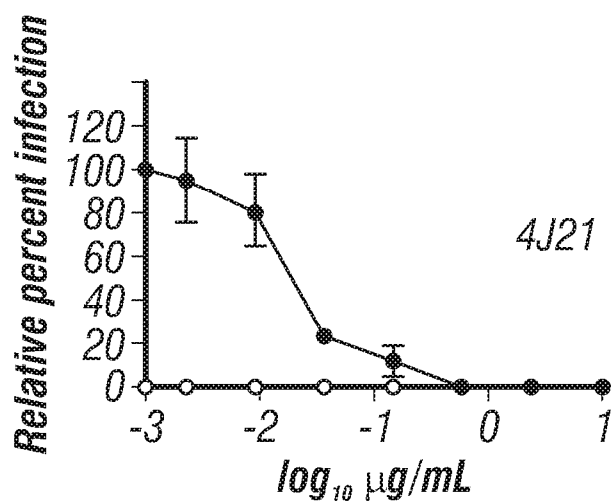
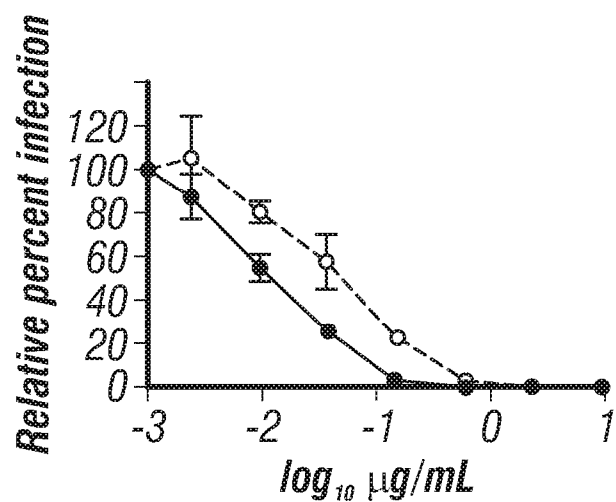
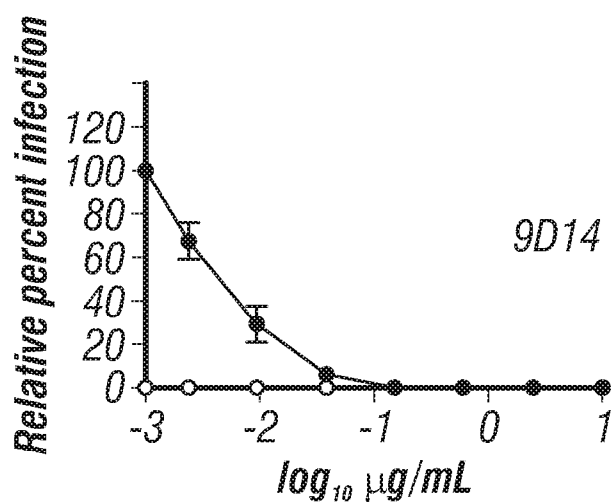
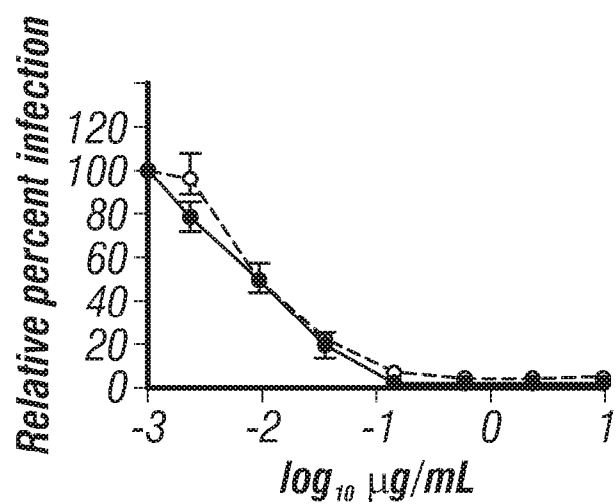
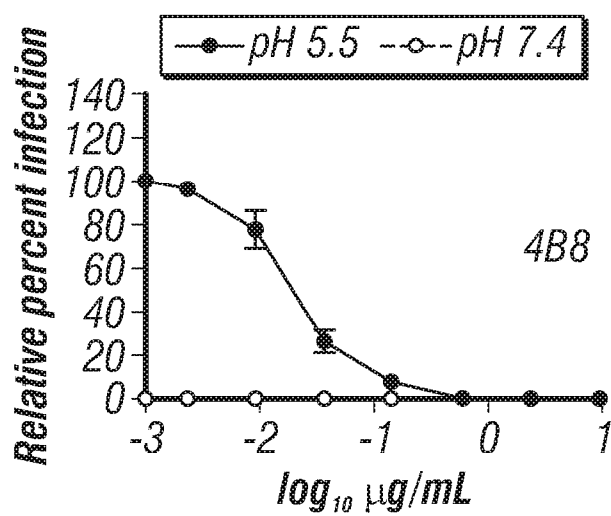
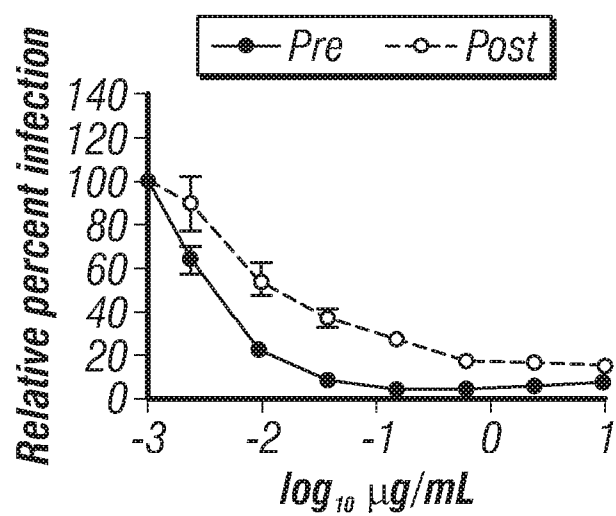
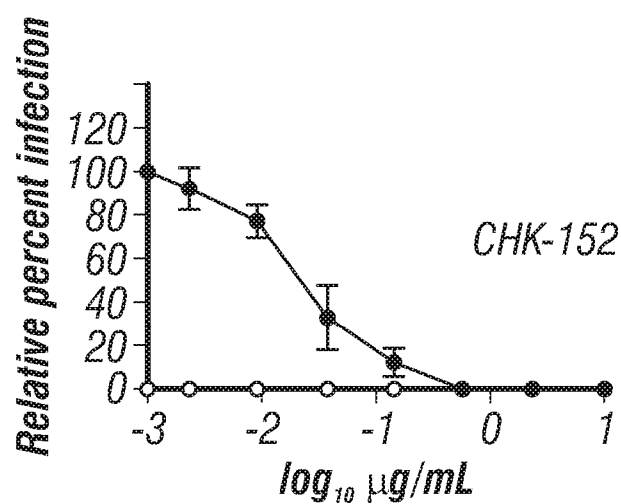
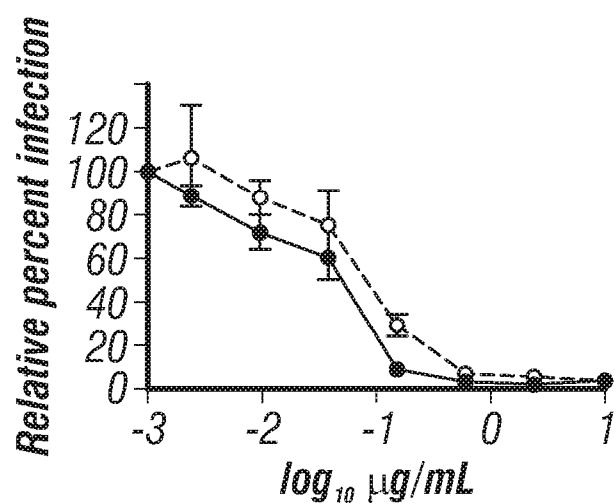
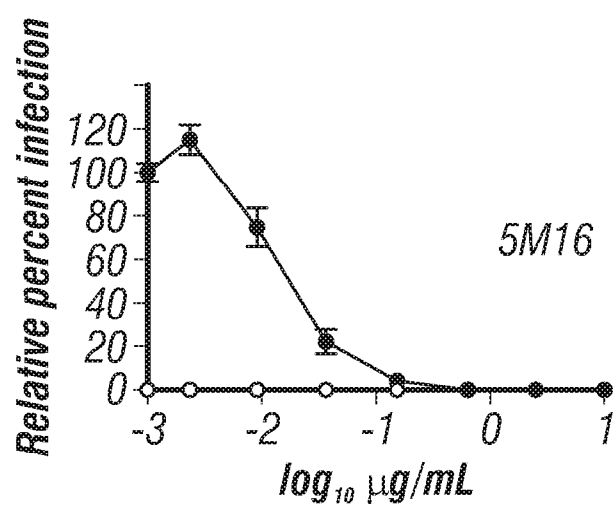
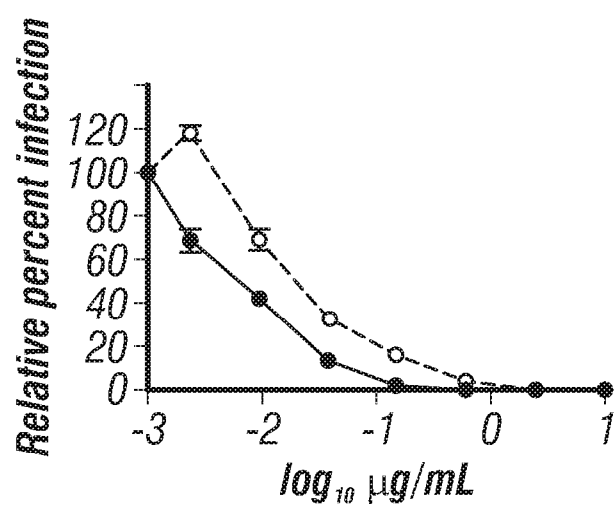
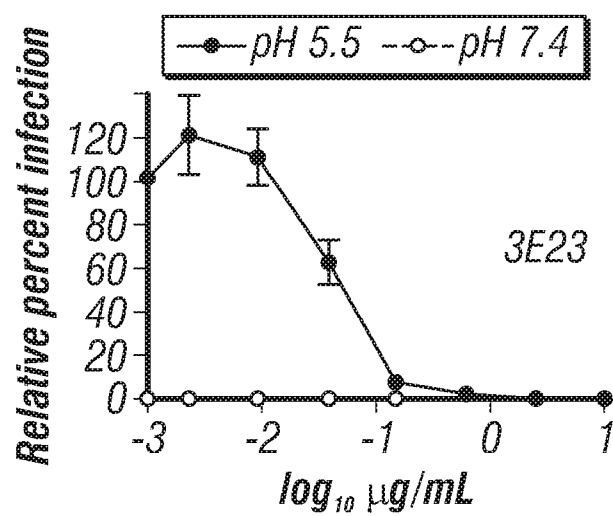
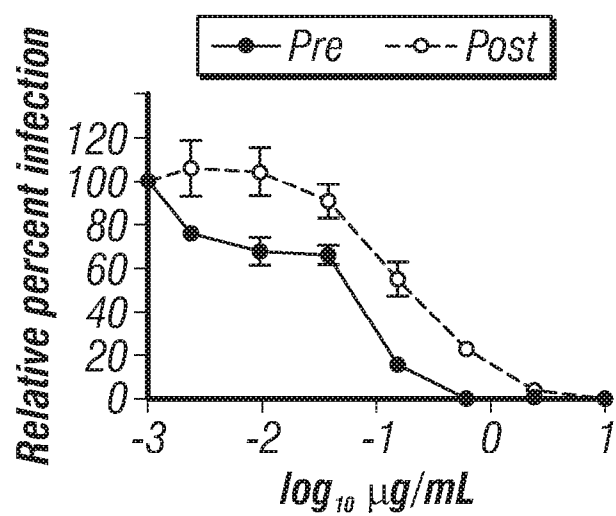


FIG. 2A

FIG. 2B

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

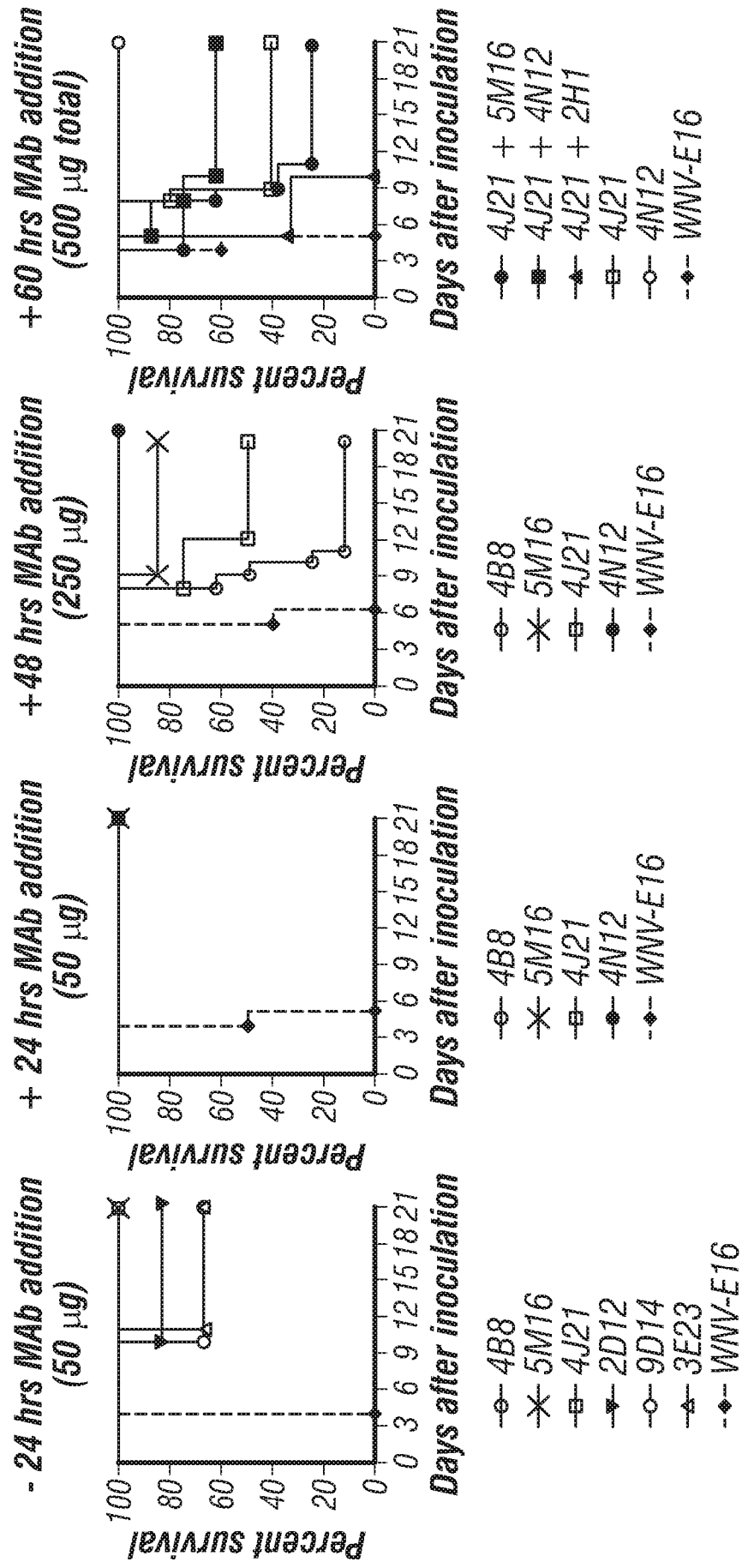


FIG. 3A

FIG. 3B

FIG. 3C

FIG. 3D

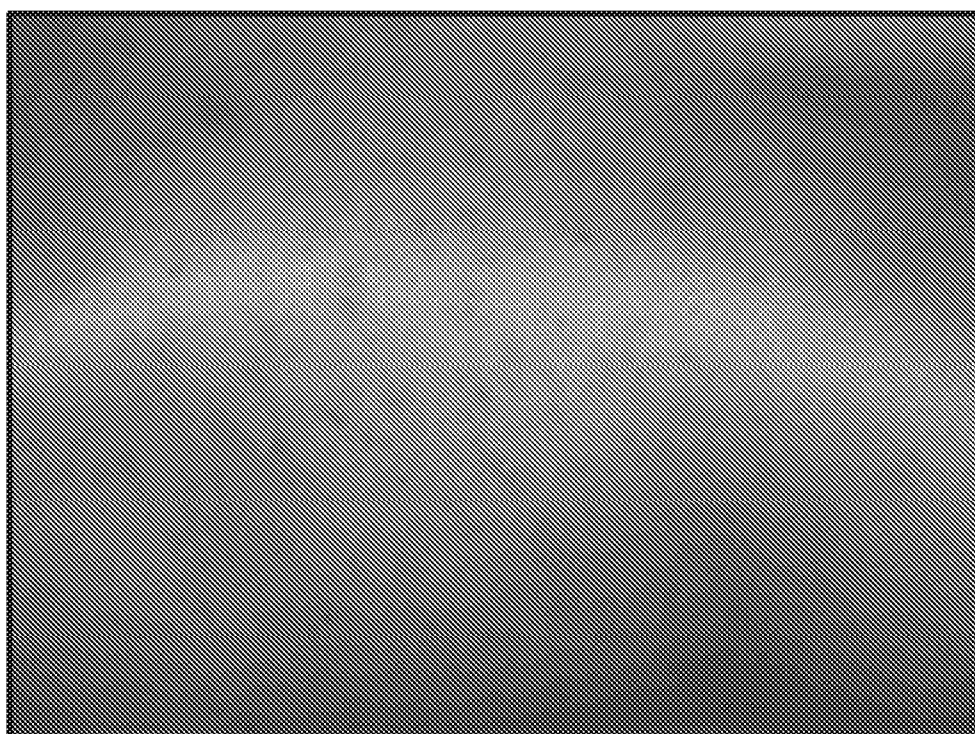


FIG. 4

Domain(s)
identified by
mutagenesis
studies

Competing antibody

mAb	5N23	CHK-84	CHK-141	5014	5M16	106	9D14	4B8	1H12	5F10	CHK-265	CHK-88	342	5F19
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
5014	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

DA, Arch

DA

DA

NR

DA

DA

NotR

NR

DA/DB Arch

DB

DB

DB

FIG. 5

Primary antibody

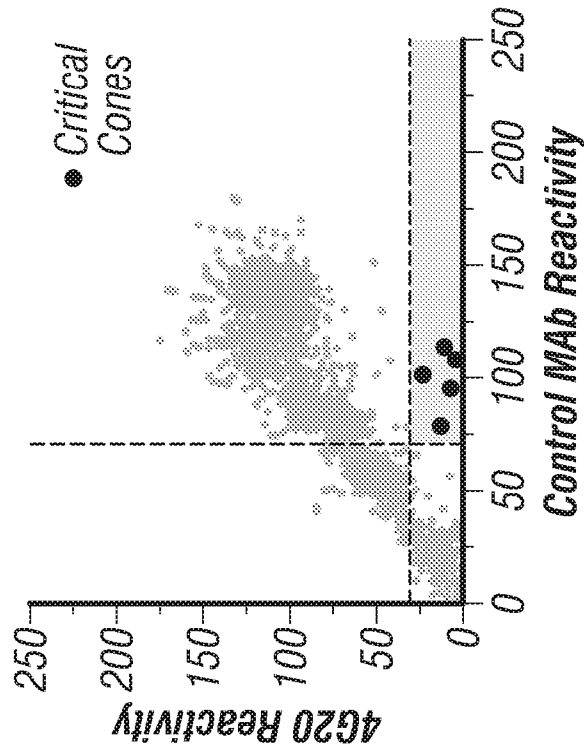


FIG. 6B

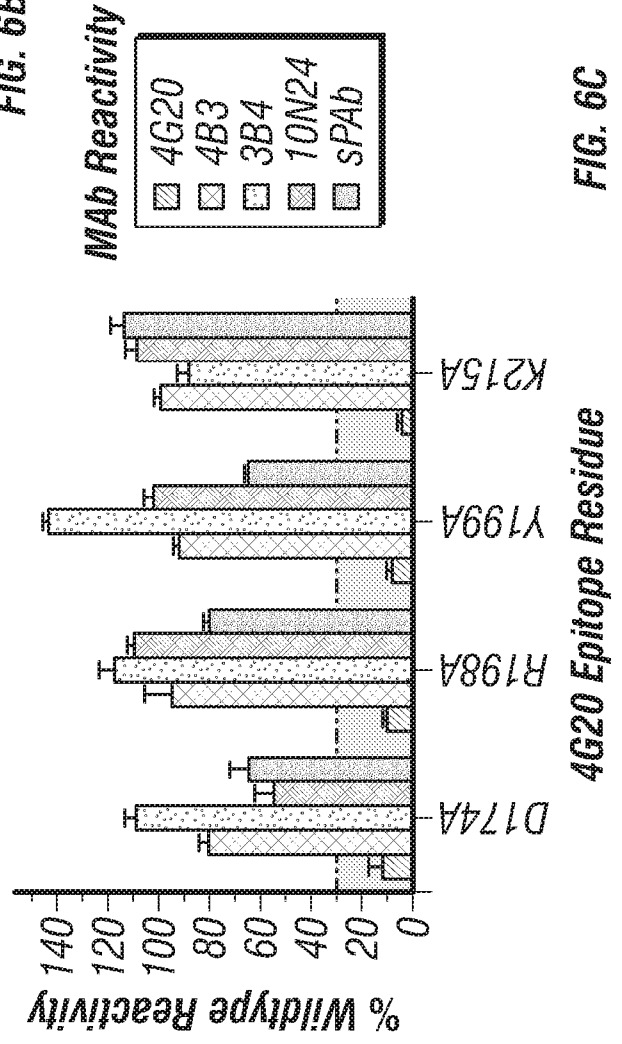


FIG. 6C

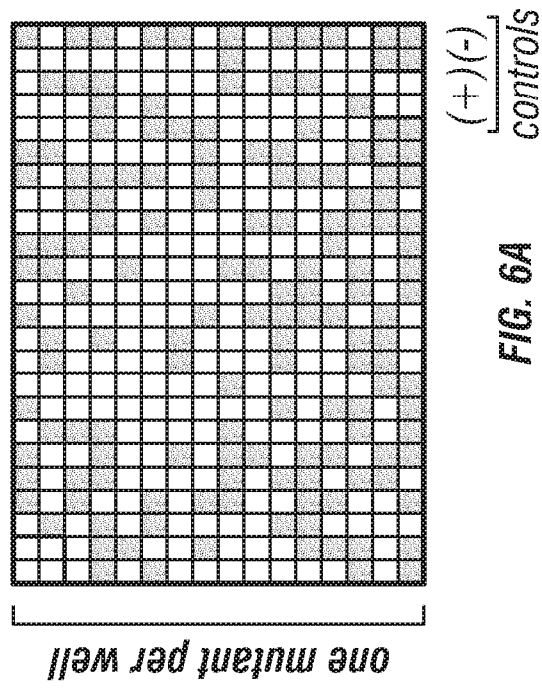


FIG. 6A

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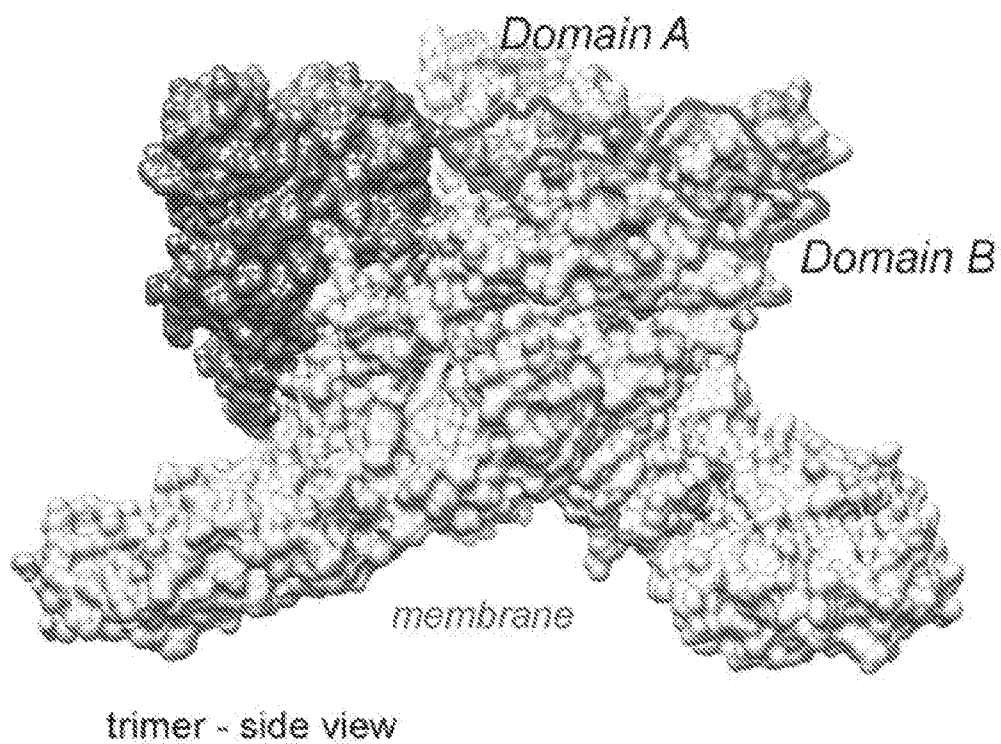


FIG. 6E

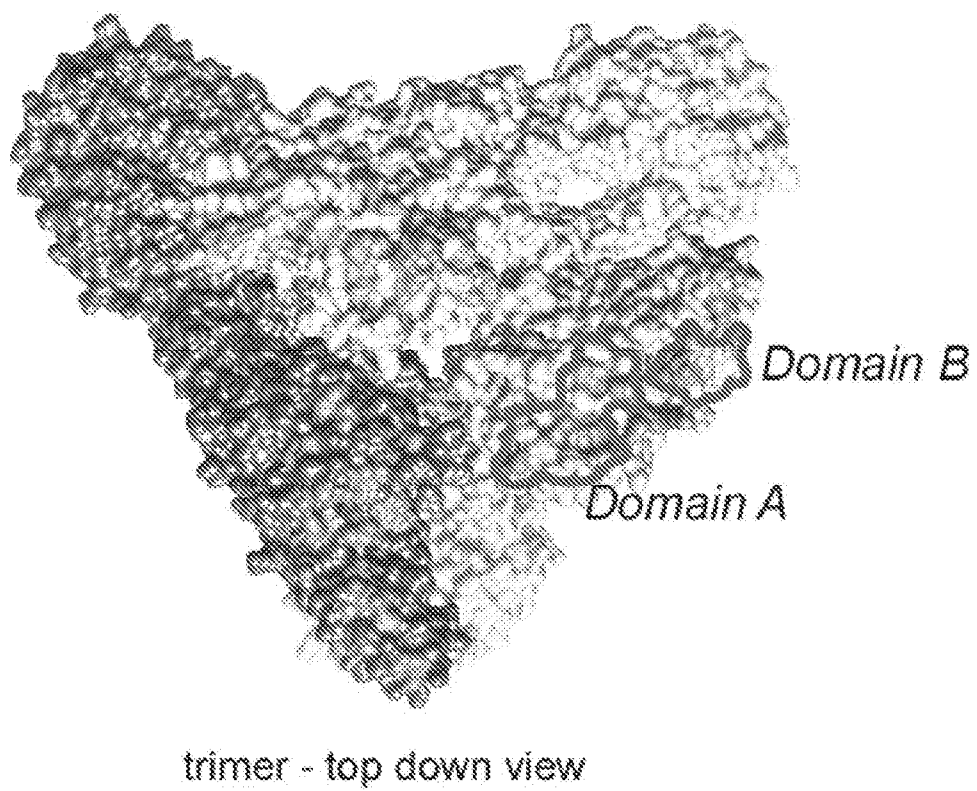


FIG. 6F

- Group 1
- Group 2
- Group 3
- Group 4
- Groups 1 and 2
- Groups 2 and 3
- Groups 1, 2, and 3
- Putative RBD

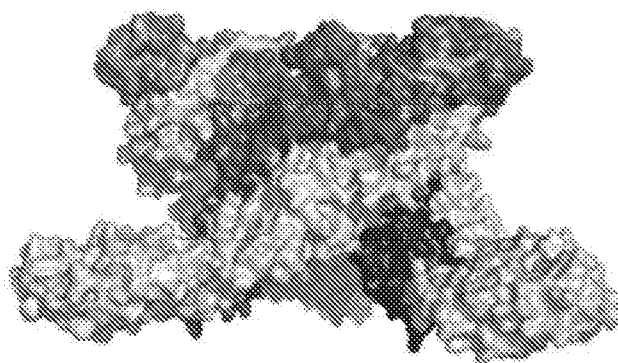
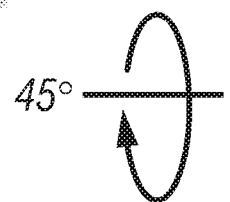
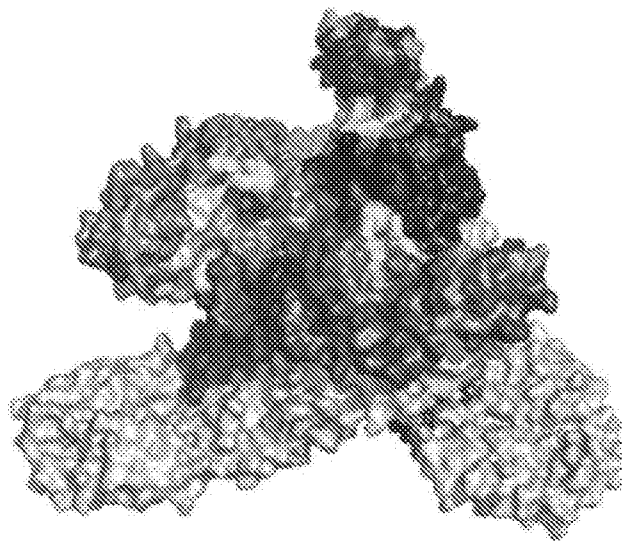
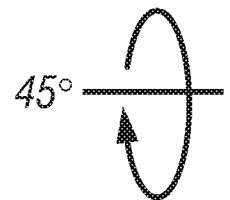
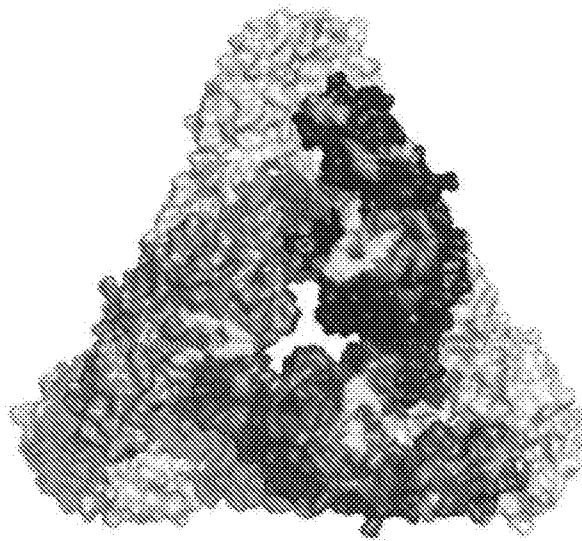


FIG. 7

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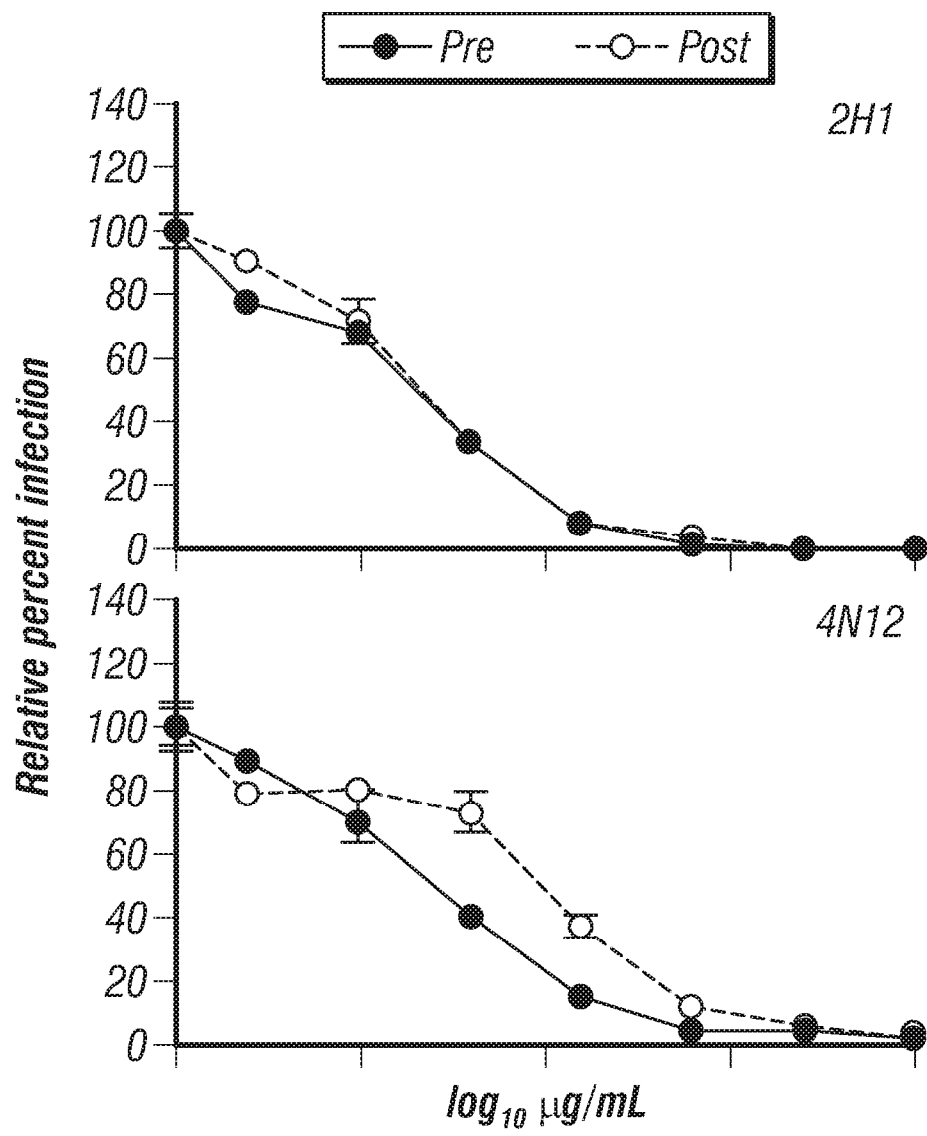
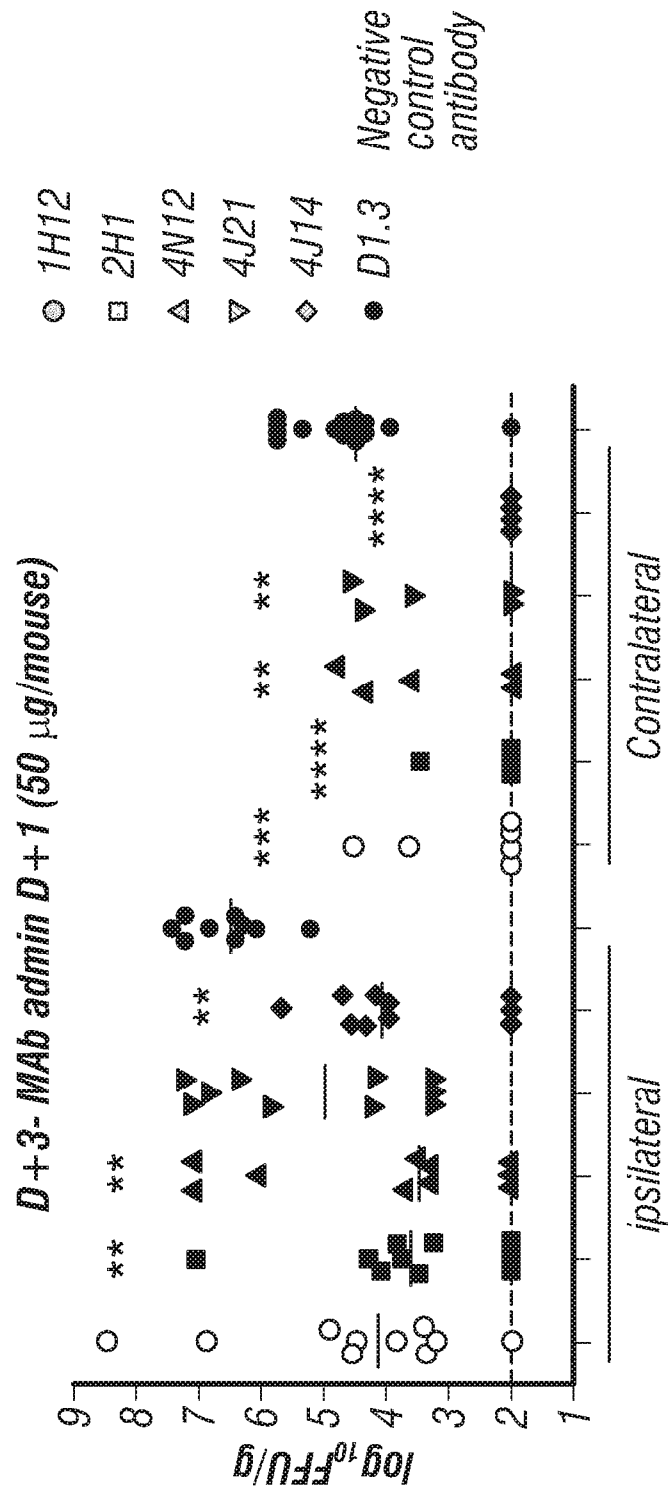


FIG. 8

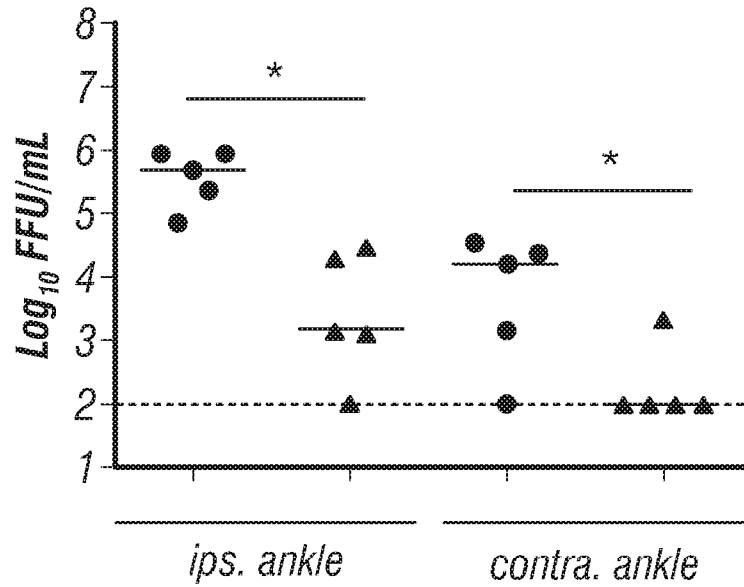


Kruskal-Wallis test for each tissue compared to D1.3

FIG. 9

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**MAbs: 50 μ g/mouse on D+3
(Analyze on D+5)**



- Control antibody
- ▲ CHO cell produced recombinant 4N12 antibody

FIG. 10

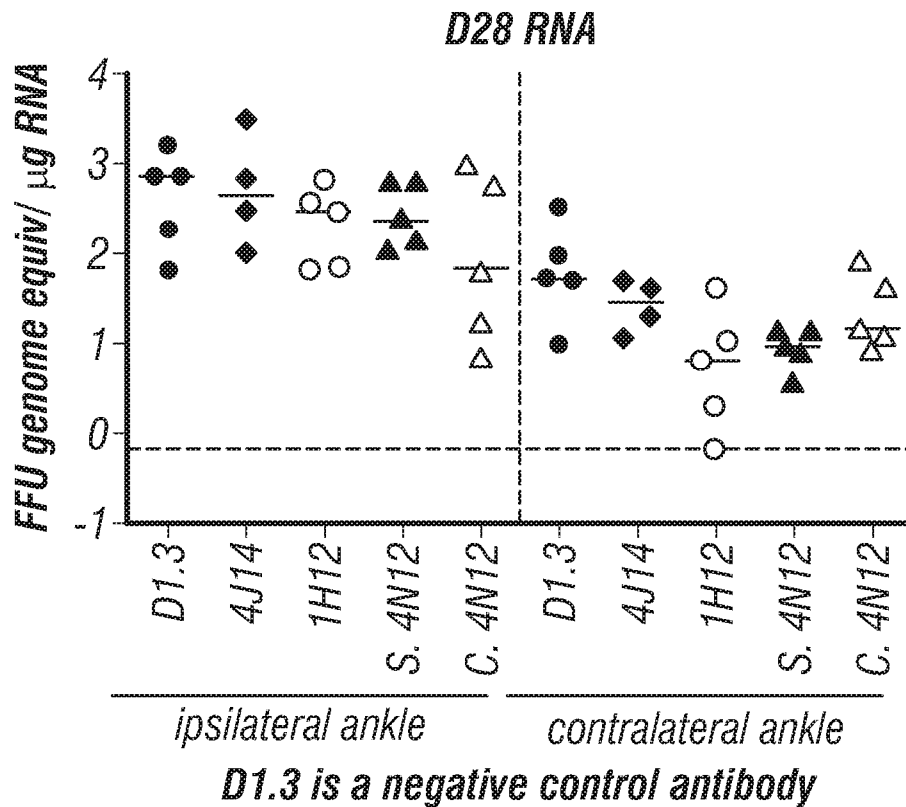


FIG. 11

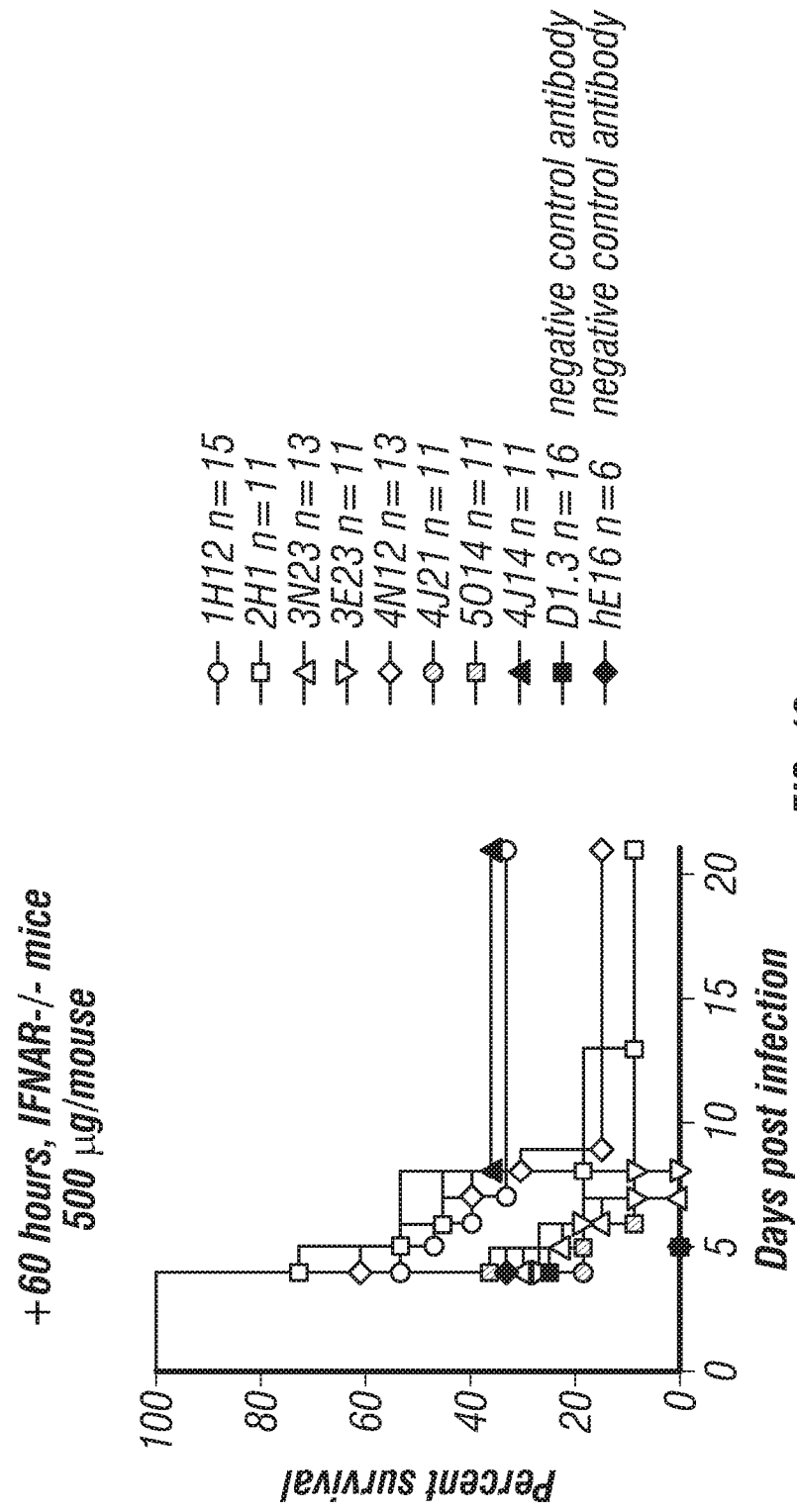


FIG. 12

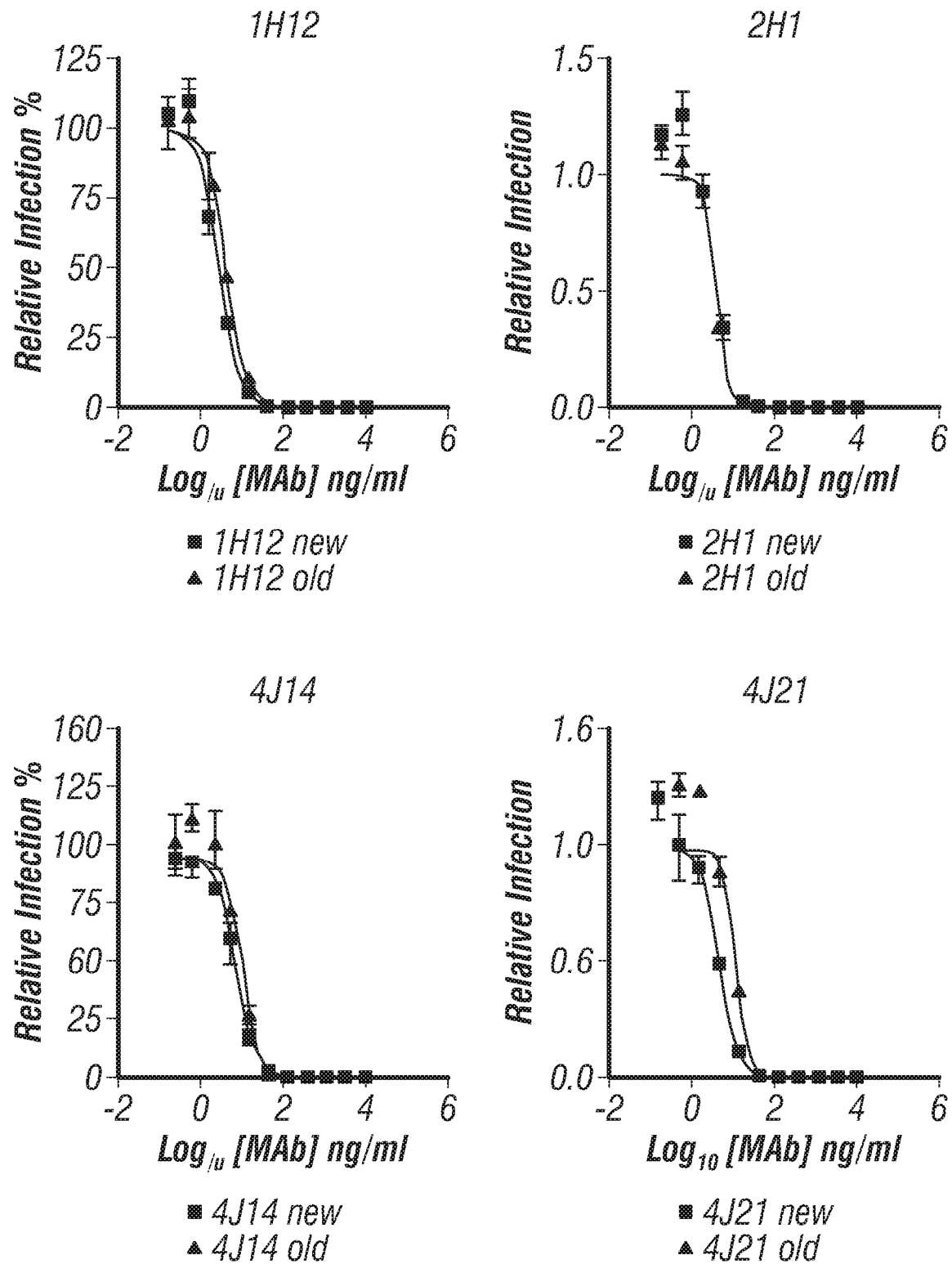


FIG. 13

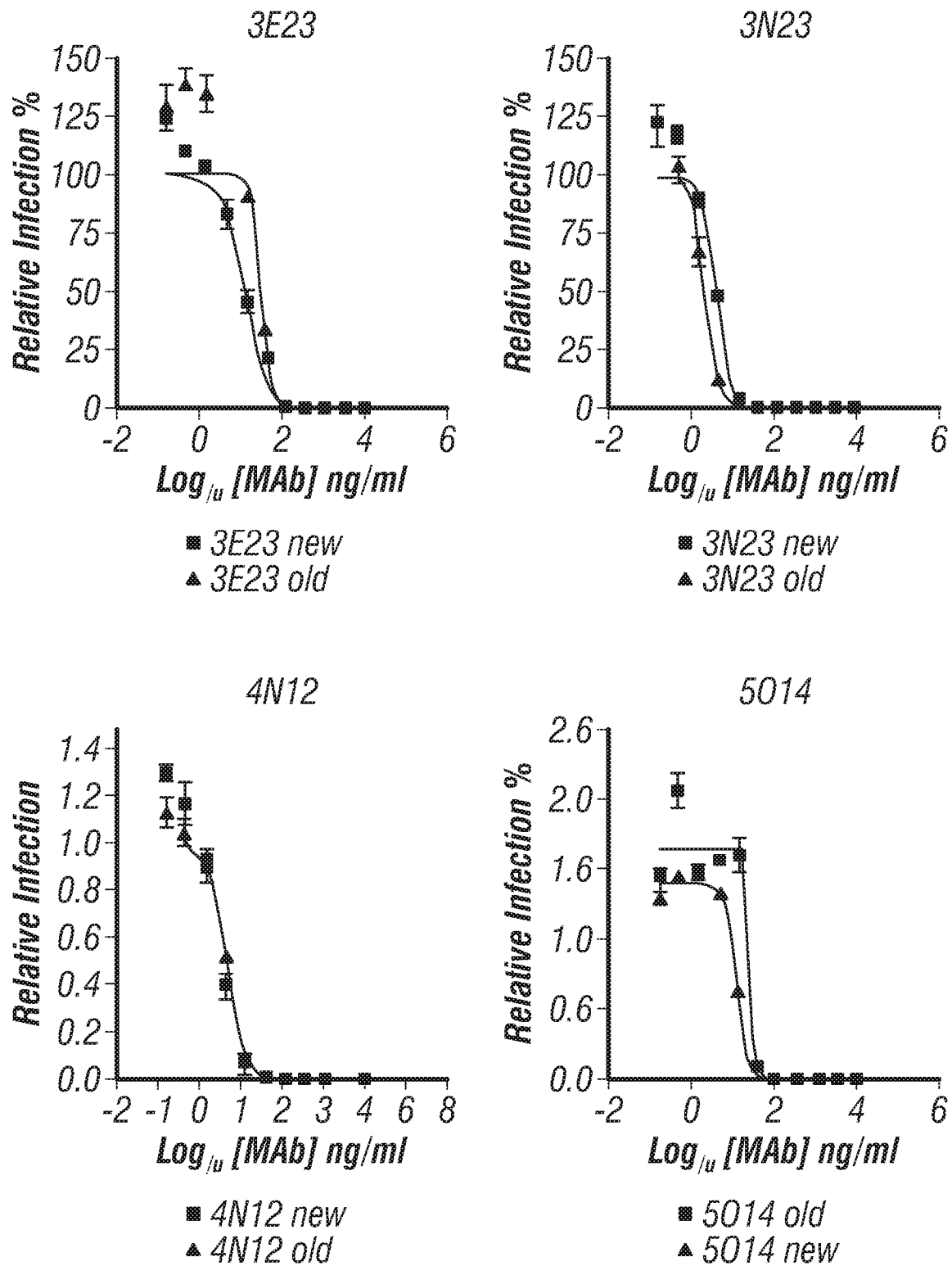


FIG. 13
(Cont'd)

<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	TACGAACACGTAACAGTGATCCCGAACACCGGTGGAGTACCGTATTAAGACTCTAGTCAAC
EE1_SL15649_GU189061.1	TACGAACACGTAACAGTGATCCCGAACACCGGTGGAGTACCGTATTAAGACTCTAGTCAAT
EE1_LR2006_KT449801.1	TACGAACACGTAACAGTGATCCCGAACACCGGTGGAGTACCGTATTAAGACTCTAGTCAAT
EE1_181/25_L37661.3	TACGAACACGTAACAGTGATCCCGAACACCGGTGGAGTACCGTATTAAGACTCTAGTCAAC
EE1_99659_KJ451624.1	TACGAACACGTAACAGTGATCCCGAACACCGGTGGAGTACCGTATTAAGACTCTAGTCAAC
EE1_IbH35_HM045786.1	TACGAACACGTAACAGTGATCCCGAACACCGGTGGAGTACCGTATTAAGACTCTTGTCAAC
	*****:*****
EE1_S27_NC004162.2	AGACCGGGCTACAGCCCCCATGGTACTGGAGATGGAGTACTGTCACTCACTTTGGAGCCA
EE1_SL15649_GU189061.1	AGACCTGGCTACAGCCCCCATGGTATTGGAGATGGAACACTACTGTCACTCACTTTGGAGCCA
EE1_LR2006_KT449801.1	AGACCTGGCTACAGCCCCCATGGTATTGGAGATGGAACACTACTGTCACTCACTTTGGAGCCA
EE1_181/25_L37661.3	AGACCGGGCTACAGCCCCCATGGTACTGGAGATGGAGCTTCTGTCACTCACTTTGGAGCCA
EE1_99659_KJ451624.1	AGACCGGGCTACAGCCCCCATGGTATTGGAGATGGAGCTTCTGTCTGTCACTTTGGAACCA
EE1_IbH35_HM045786.1	AGACCGGGTTACAGCCCCCATGGTATTGGAGATGGAGCTACAATCGGTCACTTTGGAACCA
	*****:*****
EE1_S27_NC004162.2	ACGCTATCGCTTGATTACATCACGTGCGGAATACAAAACCGTCAATCCCGTCTCCGTACGTG
EE1_SL15649_GU189061.1	ACACTATCGCTTGATTACATCACGTGCGGAGTACAAAACCGTCAATCCCGTCTCCGTACGTG
EE1_LR2006_KT449801.1	ACACTATCGCTTGATTACATCACGTGCGGAGTACAAAACCGTCAATCCCGTCTCCGTACGTG
EE1_181/25_L37661.3	ACGCTATCGCTTGATTACATCACGTGCGGAGTACAAAACCGTCAATCCCGTCTCCGTACGTG
EE1_99659_KJ451624.1	ACGCTATCGCTTGATTACATCACGTGCGGAGTACAAAACCGTCAATCCCGTCTCCGTACGTG
EE1_IbH35_HM045786.1	ACACTGTCACTTGACTACATCACGTGCGGAGTACAAAACGTCAATCCCGTCCCGTACGTG
	*****:*****
EE1_S27_NC004162.2	AAATGCTGCGGTACAGCAGAGTGC AAGGACAAAAACCTACCTGACTACAGCTGTAAGGTC
EE1_SL15649_GU189061.1	AAGTGCTGCGGTACAGCAGAGTGC AAGGACAAAAACCTACCTGACTACAGCTGTAAGGTC
EE1_LR2006_KT449801.1	AAGTGCTGCGGTACAGCAGAGTGC AAGGACAAAAACCTACCTGACTACAGCTGTAAGGTC
EE1_181/25_L37661.3	AAATGCTGCGGTACAGCAGAGTGC AAGGACAAAGAGCCTACCTGATTACAGCTGTAAGGTC
EE1_99659_KJ451624.1	AAATGCTGCGGTACAGCAGAGTGC AAGGACAAAGAGCCTACCTGATTACAGCTGTAAGGTC
EE1_IbH35_HM045786.1	AAGTGCTGTGTTACAGCAGAGTGC AAGGACAAAGAGCCTACCACTACAGCTGCAAGGTC
	*****:*****

Fig. 15 (Cont'd)

E1_S27_NC004162.2	TTCACCGGCTCTACCCATTATGTGGGGGGCCCTACTGCTTCTGCGACGCTGAAAAAC
E1_SL15649_GU189061.1	TTCACCGGCTCTACCCATTATGTGGGGGGGGCCCTACTGCTTCTGCGACGCTGAAAAAC
E1_LR2006_KT449801.1	TTCACCGGCTCTACCCATTATGTGGGGGGGGCCCTACTGCTTCTGCGACGCTGAAAAAC
E1_181/25_L37661.3	TTCACCGGCTCTACCCATTATGTGGGGGGGGCCCTACTGCTTCTGCGACGCTGAAAAAT
E1_99659_KJ451624.1	TTCACCGGCTCTACCCATTATGTGGGGGGGGCCCTACTGCTTCTGCGACGCTGAAAAAT
E1_IbH35_HM045786.1	TTTACTGGAGTCTACCCATTATGTGGGGGGGGCCCTACTGCTTCTGCGACGCTGAAAAAT
	** ** **.*.***** **.*.***** **.*.***** **.*.***** **.*.*****
E1_S27_NC004162.2	ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTGCAATCA
E1_SL15649_GU189061.1	ACGCAGTTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTGCAATCA
E1_LR2006_KT449801.1	ACGCAGTTGAGCGAAGCACACACGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTGCAATCA
E1_181/25_L37661.3	ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTGCAATCA
E1_99659_KJ451624.1	ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAACAGAAATTGCAATCA
E1_IbH35_HM045786.1	ACGCAATTGAGCGAGGCACATGTAGAGAAATCTGAATCTTGCAAAACAGAGTTGCAATCG
	*****.*.***** **.*.***** **.*.***** **.*.***** **.*.*****
E1_S27_NC004162.2	GCATACAGGGCTCATACCGCATCCGCATCAGCTAAGCTCCGCGTCCTTTACCAAGGAAAT
E1_SL15649_GU189061.1	GCATACAGGGCTCATACCGCATCTGCATCAGCTAAGCTCCGCGTCCTTTACCAAGGAAAT
E1_LR2006_KT449801.1	GCATACAGGGCTCATACCGCATCTGCATCAGCTAAGCTCCGCGTCCTTTACCAAGGAAAT
E1_181/25_L37661.3	GCATATAGGGCTCATACCGCATCCGCATCAGCTAAGCTCCGCGTCCTTTACCAAGGAAAT
E1_99659_KJ451624.1	GCATACAGGGCTCATACCGCATCCGCATCAGCTAAGCTCCGCGTCCTTTACCAAGGAAAT
E1_IbH35_HM045786.1	GCCTACAGAGCCCCACACCGCATCCGCGTCGGGAAAGCTCCGCGTCCTTTACCAAGGAAAC
	.*.*.*.*.*.*** **.*.***** **.*.***** **.*.***** **.*.*****
E1_S27_NC004162.2	AACATCACTGTAACTGCCTATGCAAAACGGCGACCATGCCGTACAGTTAAGGACGCCAAA

FIG. 15 (Cont'd)

[illegible]

Fig. 15 (Contd.)

E1_S27_NC004162.2	CTGCAGAGACCGGCTGCGGGTACGGTACACGTGCCATACTCTCAGGCACCATCTGGCTTT
E1_SL15649_GU189061.1	CTGCAGAGACCGGCTGCGGGTACGGTACACGTGCCATACTCTCAGGCACCATCTGGCTTT
E1_LR2006_KT449801.1	CTGCAGAGACCGGCTGCGGGTACGGTACACGTGCCATACTCTCAGGCACCATCTGGCTTT
E1_181/25_L37661.3	CTGCAGAGACCGTCCGCGGTACGGTGCACGTGCCGTACTCTCAGGCACCATCTGGCTTC
E1_99659_KJ451624.1	CTGCAGAGACCGTCCGCGGTACGGTGCACGTGCCGTACTCTCAGGCACCATCTGGCTTC
E1_IbH35_HM045786.1	CTACAGAGCCAGCAGCAGGACGGTACATGTACCATACTCTCAGGCACCATCTGGCTTC
	..***.***. * * . ** *****. **..***.*****.*****.*****.
E1_S27_NC004162.2	AAGTATTGGTTAAAGAACGAGGGGCGTCGCTACAGCACACAGCACCATTTGGCTGCCAA
E1_SL15649_GU189061.1	AAGTATTGGTTAAAGAACGCGGGGCGTCACTGCAGCACACAGCACCATTTGGCTGCCAA
E1_LR2006_KT449801.1	AAGTATTGGTTAAAGAACGCGGGGCGTCACTGCAGCACACAGCACCATTTGGCTGCCAA
E1_181/25_L37661.3	AAGTATTGGTTAAAGAACGAGGGGCGTCGCTGCAGCACACAGCACCATTTGGCTGTCAA
E1_99659_KJ451624.1	AAGTATTGGTTAAAGAACGAGGGGCGTCGCTGCAGCACACAGCACCATTTGGCTGTCAA
E1_IbH35_HM045786.1	AAGTATTGGCTGAAGGAACGAGGAGCATCGCTACAGCACACGGCACCGTTGCGTTGCCAG
	*****.***.*****.***.***.***.***.***.***.***.***.***.***.***.
E1_S27_NC004162.2	ATAGCAACAAACCCGGTAAGAGCGGATGAACCTGCGCCGTAGGGAACATGCCCATCTCCATC
E1_SL15649_GU189061.1	ATAGCAACAAACCCGGTAAGAGCGGTAACCTGCGCCGTAGGGAACATGCCCATCTCCATC
E1_LR2006_KT449801.1	ATAGCAACAAACCCGGTAAGAGCGGTAACCTGCGCCGTAGGGAACATGCCCATCTCCATC
E1_181/25_L37661.3	ATAGCAACAAACCCGGTAAGAGCGGATGAACCTGCGCCGTAGGGAACATGCCATCTCCATC
E1_99659_KJ451624.1	ATAGCAACAAACCCGGTAAGAGCGGATGAACCTGCGCCGTAGGGAACATGCCATCTCCATC
E1_IbH35_HM045786.1	ATTGCGACAAACCCCGGTAAGAGCTGTAAATTGCGCTGTGGGGAACATACCAATTTCATC
	..*.*****.*****.*****.***.***.***.***.***.***.***.***.
E1_S27_NC004162.2	GACATACCGGATGCGGCCCTTCACTAGGGTCGTCGACGCGCCCTCTTTAACGGACATGTCA
E1_SL15649_GU189061.1	GACATACCGGAAGCGGCCCTTCACTAGGGTCGTCGACGCGCCCTCTTTAACGGACATGTCA
E1_LR2006_KT449801.1	GACATACCGGAAGCGGCCCTTCACTAGGGTCGTCGACGCGCCCTCTTTAACGGACATGTCA
E1_181/25_L37661.3	GACATACCGGACGCGGCCCTTCACTAGGGTCGTCGACGCGCCCTCTTTAACGGACATGTCA
E1_99659_KJ451624.1	GACATACCGGACGCGGCCCTTACCCAGGGTCGTCGACGCGCCCTCTTTAACGGACATGTCA
E1_IbH35_HM045786.1	GACATACCGGATGCGGCCCTTCACTAGGGTTGTCGATGCACCCCTCTGTAAACGGACATGTCA
	*****.*****.*****.***.***.***.***.***.***.***.***.***.***.

FIG. 15 (Contd)

E1_S27_NC004162.2	TGCGAGGTACCGCTGCACCCATTCCCTCAGACTTTGGGGCGTCGCCATTATTAAATAT
E1_SL15649_GU189061.1	TGCGAGGTACTAGCCTGCACCCATTCCCTCAGACTTTGGGGCGTCGCCATTATTAAATAT
E1_LR2006_KF449801.1	TGCGAGGTACCGCTGCACCCATTCCCTCAGACTTTGGGGCGTCGCCATTATTAAATAT
E1_181/25_L37661.3	TGTGAGGTACCGCTGCACCCACTCCCTCAGACTTTGGGGCGTAGCCATCATTTAAATAT
E1_99659_KJ451624.1	TGTGAGGTATCAGCCTGCACCCATTCCCTCAGACTTTGGGGCGTAGCCATCATTTAAATAT
E1_IbH35_HM045786.1	TGCGAAGTACCGCTGCACCTCCTCCGACTTTGGGGCGTCGCCATCATCAAAATAT
	** **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.*
E1_S27_NC004162.2	GCAGTCAGCAAGAAAGGCAAGTGTGCGGTGCATTTCGATGACCAACGCCGTCACATATCCGG
E1_SL15649_GU189061.1	GCAGCCAGCAAGAAAGGCAAGTGTGCGGTGCATTTCGATGACTAACGCCGTCACATATTCGG
E1_LR2006_KF449801.1	GCAGCCAGCAAGAAAGGCAAGTGTGCGGTGCATTTCGATGACTAACGCCGTCACATATTCGG
E1_181/25_L37661.3	GCAGCCAGCAAGAAAGGCAAGTGTGCGGTGCATTTCGATGACTAACGCCGTCACATATTCGG
E1_99659_KJ451624.1	GCAGCCAGTAAGAAAGGCAAGTGTGCGGTGCATTTCGATGACTAACGCCGTCACATATTCGG
E1_IbH35_HM045786.1	ACAGCTAGCAAGAAAGGTAATGTGCAGTACATTTCGATGACCAACGCCGTTACCATTCGA
	.*** **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.*
E1_S27_NC004162.2	GAAGCTGAGATAGAAGTTGAAGGGAATTCTCAGCTGCAAAATCTCTTTCGACGGCCTTG
E1_SL15649_GU189061.1	GAAGCTGAGATAGAAGTTGAAGGGAATTCTCAGCTGCAAAATCTCTTTCGACGGCCTTA
E1_LR2006_KF449801.1	GAAGCTGAGATAGAAGTTGAAGGGAATTCTCAGCTGCAAAATCTCTTTCGACGGCCTTA
E1_181/25_L37661.3	GAAGCTGAAATAGAAGTAGAAGGGAACCTCTCAGTTGCAAAATCTCTTTCGACGGCCTA
E1_99659_KJ451624.1	GAAGCTGAAATAGAAGTAGAAGGGAACCTCTCAGTTGCAAAATCTCTTTCGACGGCCTA
E1_IbH35_HM045786.1	GAAGCCGACGTAGAAGTAGAGGGGAATTCCCAGCTGCAAAATATCCTTCTCAACAGCCTTG
	***** **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.*
E1_S27_NC004162.2	GCCAGCGCCGAATTCCGCGTACAAGTCTGTCTACACAAGTACACTGTGCAGCCGAGTGC
E1_SL15649_GU189061.1	GCCAGCGCCGAATTCCGCGTACAAGTCTGTCTACACAAGTACACTGTGCAGCTGAGTGC
E1_LR2006_KF449801.1	GCCAGCGCCGAATTCCGCGTACAAGTCTGTCTACACAAGTACACTGTGCAGCCGAGTGC
E1_181/25_L37661.3	GCCAGCGCCGAATTCCGCGTACAAGTCTGTCTACACAAGTACACTGTGCAGCCGAGTGC
E1_99659_KJ451624.1	GCCAGCGCCGAATTCCGCGTACAAGTCTGTCTACACAAGTACACTGTGCAGCCGAGTGC
E1_IbH35_HM045786.1	GCAAGCGCCGAGTTTCGCGTGCAAGTGTCTCCACACAAGTACACTGCGCAGCCGATGC
	**.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.*

FIG. 15 (Cont'd)

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E1_S27_NC004162.2
E1_SL15649_GU189061.1
E1_LR2006_KF449801.1
E1_181/25_L37661.3
E1_99659_KJ451624.1
E1_IbH35_HM045786.1

CACCTCCGAAGGACCACATAGTCAACTACCCGGCGTCACATACCACCTCGGGGTCCAG
CACCCCGAAGGACCACATAGTCAACTACCCGGCGTCACATACCACCTCGGGGTCCAG
CACCCCGAAGGACCACATAGTCAACTACCCGGCGTCACATACCACCTCGGGGTCCAG
CATCCACCGAAAGACCATAATAGTCAATTACCCGGCGTCACACACCCCTCGGGGTCCAA
CATCCACCGAAAGACCATAATAGTCAATTACCCGGCGTCACACACCCCTCGGGGTCCAA
CACCTCCAAAGGACCACATAGTCAATTACCCAGCATCACACACCCCTTGGGGTCCAG
** ** ** . ** . ** . ** . ** . ** . ** . ** . ** . ** . ** .
GACATTTCCGCTACGGCGATGTCAATGGGTGCAGAAGATCACGGGAGGTGTGGGACTGGTT
GACATCTCCGCTACGGCGATGTCAATGGGTGCAGAAGATCACGGGAGGTGTGGGACTGGTT
GACATCTCCGCTACGGCGATGTCAATGGGTGCAGAAGATCACGGGAGGTGTGGGACTGGTT
GACATTTCCGTTACGGCGATGTCAATGGGTGCAGAAGATCACGGGAGGTGTGGGACTGGTT
GACATTTCCGCTACGGCGATGTCAATGGGTGCAGAAGATCACGGGAGGTGTGGGACTGGTT
GATATATCCACAACGGCAATGTCTTGGGTGCAGAAGATTACGGGAGGAGTAGGATTAATT
** ** ** . ; ** ** . ** ** . ** ** . ** ** . ** ** . ** ** . **
GTCGCTGTTGCAGCACTGATTCTAATCGTGTGCTATGCCGTGTCGTTTCAGCAGGCAC
GTTGCTGTTGCCGCACTGATTCTAATCGTGTGCTATGCCGTGTCGTTTCAGCAGGCAC
GTTGCTGTTGCCGCACTGATTCTAATCGTGTGCTATGCCGTGTCGTTTCAGCAGGCAC
GTCGCTGTTGCAGCACTGATCCTAATCGTGTGCTATGCCGTGTCGTTTCAGCAGGCAC
GTCGCTGTTGCAGCACTGATCCTAATCGTGTGCTATGCCGTGTCGTTTCAGCAGGCAC
GTTGCTGTTGCTGCCCTTAATTTAATTGTGTGCTATGCCGTGTCGTTTCAGCAGGCAC
** ** ** . ** . ** . ** . ** . ** . ** . ** . ** . ** . **

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FIG. 15 (Cont'd)

CLUSTAL O(1.2.1) multiple sequence alignment

E1_IbH35_HM045786.1	YEHVTVIPNTVGVPYKTLVNRPGYSPMVLEMELQSVTLEPTLSLDYITCEYKTVIPSPYV
E1_S27_NC004162.2	YEHVTVIPNTVGVPYKTLVNRPGYSPMVLEMELLSVTLEPTLSLDYITCEYKTVIPSPYV
E1_SL15649_GUI89061.1	YEHVTVIPNTVGVPYKTLVNRPGYSPMVLEMELLSVTLEPTLSLDYITCEYKTVIPSPYV
E1_LR2006_KT449801.1	YEHVTVIPNTVGVPYKTLVNRPGYSPMVLEMELLSVTLEPTLSLDYITCEYKTVIPSPYV
E1_99659_KJ451624.1	YEHVTVIPNTVGVPYKTLVNRPGYSPMVLEMELLSVTLEPTLSLDYITCEYKTVIPSPYV
E1_181/25_L37661.3	YEHVTVIPNTVGVPYKTLVNRPGYSPMVLEMELLSVTLEPTLSLDYITCEYKTVIPSPYV
E1_IbH35_HM045786.1	KCCGTAECKDKSLPDYSCKVFTGVYPFMWGGAYCFCDAAENTQLSEAHVEKSESCKTEFAS
E1_S27_NC004162.2	KCCGTAECKDKNLPDYSCKVFTGVYPFMWGGAYCFCDAAENTQLSEAHVEKSESCKTEFAS
E1_SL15649_GUI89061.1	KCCGTAECKDKNLPDYSCKVFTGVYPFMWGGAYCFCDAAENTQLSEAHVEKSESCKTEFAS
E1_LR2006_KT449801.1	KCCGTAECKDKNLPDYSCKVFTGVYPFMWGGAYCFCDAAENTQLSEAHVEKSESCKTEFAS
E1_99659_KJ451624.1	KCCGTAECKDKSLPDYSCKVFTGVYPFMWGGAYCFCDTENTQLSEAHVEKSESCKTEFAS
E1_181/25_L37661.3	KCCGTAECKDKSLPDYSCKVFTGVYPFMWGGAYCFCDTENTQLSEAHVEKSESCKTEFAS
E1_IbH35_HM045786.1	AYRAHTASAKLRVLYQGNNITVAAYANGDHAVTVKDAKFVVGPMSSAWTPFDNKiVVY
E1_S27_NC004162.2	AYRAHTASAKLRVLYQGNNITVTAYANGDHAVTVKDAKFIVGPMSSAWTPFDNKiVVY
E1_SL15649_GUI89061.1	AYRAHTASAKLRVLYQGNNITVTAYANGDHAVTVKDAKFIVGPMSSAWTPFDNKiVVY
E1_LR2006_KT449801.1	AYRAHTASAKLRVLYQGNNITVTAYANGDHAVTVKDAKFIVGPMSSAWTPFDNKiVVY
E1_99659_KJ451624.1	AYRAHTASAKLRVLYQGNNITVAAYANGDHAVTVKDAKFIVGPMSSAWTPFDNKiVVY
E1_181/25_L37661.3	AYRAHTASAKLRVLYQGNNITVSAAYANGDHAVTVKDAKFIVGPMSSAWTPFDNKiVVY
E1_IbH35_HM045786.1	KGDVYNMDYPPFGAGRPGQFGDIQSRTPESKDVYANTQLVLQRPAAAGTVHVPYSQAPSGF
E1_S27_NC004162.2	KGDVYNMDYPPFGAGRPGQFGDIQSRTPESKDVYANTQLVLQRPAAAGTVHVPYSQAPSGF
E1_SL15649_GUI89061.1	KGDVYNMDYPPFGAGRPGQFGDIQSRTPESKDVYANTQLVLQRPAAAGTVHVPYSQAPSGF
E1_LR2006_KT449801.1	KGDVYNMDYPPFGAGRPGQFGDIQSRTPESKDVYANTQLVLQRPAAAGTVHVPYSQAPSGF
E1_99659_KJ451624.1	KGDVYNMDYPPFGAGRPGQFGDIQSRTPESEDVYANTQLVLQRPAAAGTVHVPYSQAPSGF
E1_181/25_L37661.3	KGDVYNMDYPPFGAGRPGQFGDIQSRTPESEDVYANTQLVLQRPAAAGTVHVPYSQAPSGF

FIG. 15 (Cont'd)

CLUSTAL O(1.2.1) multiple sequence alignment

AGTATTAAGGACAACTTCAATGCTATATAAGCCATAAGACCGTACCTAGCTCACTGTCCTCCC	181/25	L37661.3
AGTACTAAGGACAAATTTAAATGCTATATAAGCTACAAGACCATATCTAGCTCATTTGTCCT	1bH35	HM045786.1
AGCACCAAGGACAACTTCAATGCTATATAAGCCACAAGACCATACTTAGCTCACTGTCCTCC	LR2006	KT449801.1
AGCACCAAGGACAACTTCAATGCTATATAAGCCACAAGACCATACTTAGCTCACTGTCCTCC	SL15649	GU189061.1
AGCACCAAGGACAACTTCAATGCTATATAAGCCACAAGACCATACTTAGCTCACTGTCCTCC	S27	NC004162.2
AGTATTAAGGACCACTTCAATGCTATATAAGCCACAAGACCGTACCTAGCTCACTGTCCTCC	99659	KJ451624.1

EE2_181/25_L37661.3	GA	CTGTGGAGAA	GGGCACTC	GTGCCATAGT	CCCGTAGCGCTAGAA	CGCATCAGAAACGAA
EE2_IbH35_HM045786.1	GA	CTGCGGAGAA	GGGCATTTC	GTGCCACAGCCCTAT	CGCATTGGAGCGCATCAGAAATGAA	
EE2_LR2006_KT449801.1	GA	CTGTGGAGAA	GGGCACTC	GTGCCATAGT	CCCGTAGCACTAGAACGCATCAGAAATGAA	
EE2_SL15649_GU189061.1	GA	CTGTGGAGAA	GGGCACTC	GTGCCATAGT	CCCGTAGCACTAGAACGCATCAGAAATGAA	
EE2_S27_NC004162.2	GA	CTGTGGAGAA	GGGCACTC	GTGCCATAGT	CCCGTAGCACTAGAACGCATCAGAAATGAA	
EE2_99659_KJ451624.1	GA	CTGTGGAGAA	GGGCACTC	GTGCCATAGT	CCCGTAGCGCTAGAACGCATCAGAAACGAA	
	****	*****	*****	*****	*****	*****

EE2_181/25_L37661.3	GGACAGACGGGACGCTGAAAATCCAGGTTTCCTTGCAAATCGGAATAAAGACGGATGAT
EE2_IbH35_HM045786.1	GCAACGGACGGAACGCTGAAAATCCAGGTCCTTTGCAGATCGGGATAAAGACAGATGAC
EE2_LR2006_KT449801.1	GGACAGACGGGACGCTGAAAATCCAGGTCCTCTTGCAAATCGGAATAAAGACGGATGAC
EE2_SL15649_GU189061.1	GGACAGACGGGACGCTGAAAATCCAGGTCCTCTTGCAAATCGGAATAAAGACGGACGAC
EE2_S27_NC004162.2	GGACAGACGGGACGCTGAAAATCCAGGTCCTCTTGCAAATCGGAATAAGGACGGATGAT
EE2_99659_KJ451624.1	GGACAGACGGGACGCTGAAAATCCAGGTTTCCTTGCAAATCGGAATAAAGACGGATGAT

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

FIG. 15 (Cont'd)

Exhibit 15 (Contd)

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E2_181/25_L37661.3	CTGGTCCCGGTAATGCTGAACTCGGGGACCGAAAGGAAAGTTACATTCCTTCCT
E2_IbH35_HM045786.1	TTAGTCCCGGTAACGCTGAACTCGGGGACCGTAAAGGAAAGATTACATCCCATTCCTCA
E2_LR2006_KT449801.1	CTGGTCCCGGTAATGCTGAACTTGGGGACCGAAAGGAAATTCACATCCCGTTTCCG
E2_SL15649_GU189061.1	CTGGTCCCGGTAATGCTGAACTTGGGGACCGAAAGGAAATTCACATCCCGTTTCCG
E2_S27_NC004162.2	CTGGTCCCGGTAACGCTGAACTCGGGGACCGAAAGGAAATTCACATCCCGTTTCCG
E2_99659_KJ451624.1	CTGGTCCCGGTAATGCTGAACTCGGGGACCGGAAAGGAAAGTTACATTCCTTCCT
	*.***** *
E2_181/25_L37661.3	CTGGCAAATGTGACATGCAGGGTGCCCTAAGGCAAGGAACCCACCGTGACGTACGGAAAA
E2_IbH35_HM045786.1	TTGGCAAACGTGACTTGCAGAGTGCCAAAAGCAAGAAACCCACAGTAACGTACGGAAAA
E2_LR2006_KT449801.1	CTGGCAAATGTAAACATGCAGGGTGCCCTAAGCAAGGAACCCACCGTGACGTACGGGAAA
E2_SL15649_GU189061.1	CTGGCAAATGTAAACATGCAGGGTGCCCTAAGCAAGGAACCCACCGTGACGTACGGGAAA
E2_S27_NC004162.2	CTGGCAAATGTAAACATGCATGGTGCCCTAAGCAAGGAACCCACCGTGACGTACGGGAAA
E2_99659_KJ451624.1	CTGGCAAATGTGACATGCAGGGTGCCCTAAGCAAGGAACCCACCGTGACGTACGGAAAA
	***** ** *
E2_181/25_L37661.3	AACCAAGTCATCATGCTGCTGTATCCTGACCAACCCAAACGCTCCTGTCTACCGGAATATG
E2_IbH35_HM045786.1	AACCAAGTCACCATGCTGCTGTATCCTGACCATCCGACACTCTTGTCTTATCGTAACATG
E2_LR2006_KT449801.1	AACCAAGTCATCATGCTACTGTATCCTGACCAACCCAAACACTCCTGTCTACCGGAATATG
E2_SL15649_GU189061.1	AACCAAGTCATCATGCTACTGTATCCTGACCAACCCAAACACTCCTGTCTACCGGAATATG
E2_S27_NC004162.2	AACCAAGTCATCATGCTACTGTATCCTGACCAACCCAAACACTCCTGTCTACCGGAGTATG
E2_99659_KJ451624.1	AACCAAGTCATCATGTTGCTGTATCCTGACCAACCCAAACGCTCCTGTCTACAGGAATATG
	***** *
E2_181/25_L37661.3	GGAGAAACCAAACTATCAAGAAAGAGTGGGTGACGCATAGAAGGAGATCAGGTTAAAC
E2_IbH35_HM045786.1	GGACAGGAACCAAAATTACCACGAGGAGTGGGTGACACACAAGAAGGAGTTACCTTGACC
E2_LR2006_KT449801.1	GGAGAAACCAAACTATCAAGAAAGAGTGGGTGATGCATAGAAGGAGTCTGCTAAAC
E2_SL15649_GU189061.1	GGAGAAACCAAACTATCAAGAAAGAGTGGGTGATGCATAGAAGGAGTCTGCTAAAC
E2_S27_NC004162.2	GGAGAAACCAAACTATCAAGAAAGAGTGGGTGACGCACAAGAAGGAGTCTGCTAAAC
E2_99659_KJ451624.1	GGAGAAACCAAACTATCAAGAAAGAGTGGGTGACGCATAGAAGGAGATCAGGTTAAAC
	*** *

FIG. 15 (Cont'd)

E2_181/25_L37661.3	GTCCCGACTGAAGGGCTCGAGGTCACGTGGGGCAACAACGAGCCGTACAAGTATTGGCCG
E2_IbH35_HM045786.1	GTGCTACTGAGGGTCTCGAGGTCACTTGGGGCAACAACGAAACCATACAAGTACTGGCCG
E2_LR2006_KT449801.1	GTGCCGACTGAAGGGCTCGAGGTCACGTGGGGCAACAACGAGCCGTATAAGTATTGGCCG
E2_SL15649_GU189061.1	GTCCCGACTGAAGGGCTCGAGGTCACGTGGGGCAACAACGAGCCGTATAAGTATTGGCCG
E2_S27_NC004162.2	GTCCCGACTGAAGGGCTCGAGGTTACGTGGGGCAACAACGAGCCGTATAAGTATTGGCCG
E2_99659_KJ451624.1	GTCCCGACTGAGGGGCTCGAGGTCACGTGGGGTAACAATGAGCCGTACAAGTATTGGCCG
	*****.*** ** ***** ** ***** **.* ** ***** *****
E2_181/25_L37661.3	CAGTTATCCACAACGGTACAGCCCCACGGCCACCCCGCATGAGATAATTTTGTATTATTAT
E2_IbH35_HM045786.1	CAGATGTCTACGAACGGTACTGCTCATGTGTCAACCCACATGAGATAATCTTGTACTATTAT
E2_LR2006_KT449801.1	CAGTTATCTACAACGGTACAGCCCCATGGCCACCCCGCATGAGATAATCTTGTATTATTAT
E2_SL15649_GU189061.1	CAGTTATCTACAACGGTACAGCCCCATGGCCACCCCGCATGAGATAATCTTGTATTATTAT
E2_S27_NC004162.2	CAGTTATCTGCAACGGTACAGCCCCACGGCCACCCCGCATGAGATAATCTTGTACTATTAT
E2_99659_KJ451624.1	CAGTTATCCACAACGGTACAGCCCCACGGCCACCCCGCATGAGATAATCTTGTATTATTAT
	;*..***.*****;*.*** ** *****.***** ***** *****
E2_181/25_L37661.3	GAGCTGTACCCCTACTATGACTGTGGTAGTTGTGTCAGTGGCCCTCGTTTCGTACTCCTGTGCG
E2_IbH35_HM045786.1	GAGCTGTACCCCTACTATGACTGTAAATCATTTGTGTCGGTGGCCCTCGTTTCGTCTTCTGTGCG
E2_LR2006_KT449801.1	GAGCTGTACCCCTACTATGACTGTAGTAGTTGTGTCAGTGGCCACGTTTCATACCTCCTGTGCG
E2_SL15649_GU189061.1	GAGCTGTACCCCTACTATGACTGTAGTAGTTGTGTCAGTGGCCACGTTTCATACCTCCTGTGCG
E2_S27_NC004162.2	GAGCTGTACCCCTACTATGACTGTAGTAGTTGTGTCAGTGGCCCTCGTTTCATACCTCCTGTGCG
E2_99659_KJ451624.1	GAGCTGTACCCCTACTATGACTGCGGTAGTTTGTGTCAGTGGCCCTCGTTTCATACCTCCTGTGCG
	*****.***** *****.*** ** *****.*****;*****.*.*** *****
E2_181/25_L37661.3	ATGCTGGGGTGTGGCAGTGGGGATGTGCATGTGTGCACGACGACGAGATGCATTACACCGTAC
E2_IbH35_HM045786.1	ATGCTGGGCACAGCAGTGGGGATGTGTGTGTGCGCACGGCGCAGATGCATTACACCATAT
E2_LR2006_KT449801.1	ATGCTGGGTATGGCAGCGGGGATGTGCATGTGTGCACGACGACGAGATGCATCACACCGTAT
E2_SL15649_GU189061.1	ATGCTGGGTATGGCAGTGGGGATGTGCATGTGTGCACGACGACGAGATGCATCACACCGTAT
E2_S27_NC004162.2	ATGCTGGGTATGGCAGTGGGGATGTGCATGTGTGCACGACGACGAGATGCATCACACCATAC
E2_99659_KJ451624.1	ATGCTGGGTGTGGCAGTGGGGATGTGCATGTGTGCACGACGACGAGATGCATTACACCGTAC
	*****.***.***** *****.***** *****.***** *****.***

FIG. 15 (Cont'd)

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
GCTAAAGCG
ACCAAGCGG
GCTAAAGCG
GCTAAAGCG
GCTAAAGCG
GCTAAAGCG

FIG. 15 (Cont'd)

CLUSTAL O(1.2.1) multiple sequence alignment

[illegible]

FIG. 15 (Cont'd)

