

Range 1: 1 to 760 Graphics

Next Match Previous Match

T127

CTTTGGAGATCTCTTACACACACATAT
 |||||
 CTTTGGAGATCTCTTACACACATAT

Score	Expect	Method	Identities	Positives	Gaps
1584 bits(4102) 0.0	Compositional matrix adjust.	760/760(100%)	760/760(100%)	0/760(0%)	
Query 1	NKTLKIVFGVATSAVLALLVWCIVLRPSRVHSEGGTTRALTLEDILNGITFTYKTFPPH	60			
Seqct 1	NKTLKIVFGVATSAVLALLVWCIVLRPSRVHSEGGTTRALTLEDILNGITFTYKTFPPH	60			
Query 61	WISGQYHLHSTQIDIDIVYHIEGESYTIISLNATHKSNVHSGVLSPOQFAVLESQYK	120			
Seqct 61	WISGQYHLHSTQIDIDIVYHIEGESYTIISLNATHKSNVHSGVLSPOQFAVLESQYK	120			
Query 121	LWRYSYATYHYHILWGEFIRHNLPRPIQYLQUSPVGSKLAVYQMIYKQRPEDPP	180			
Seqct 121	LWRYSYATYHYHILWGEFIRHNLPRPIQYLQUSPVGSKLAVYQMIYKQRPEDPP	180			
Query 181	FQITYMREMKIFNGIPDNYEEMLATKHALMASPBGKFLAYAEFNDTEIPVIAYSYYG	240			
Seqct 181	FQITYMREMKIFNGIPDNYEEMLATKHALMASPBGKFLAYAEFNDTEIPVIAYSYYG	240			
Query 241	DEQYRTIINIPYKAGAKIPWRIIFIIDITYPQQTGPREVPVPANIASDYVFSMLTWT	300			
Seqct 241	DEQYRTIINIPYKAGAKIPWRIIFIIDITYPQQTGPREVPVPANIASDYVFSMLTWT	300			
Query 301	DERVCLQMLKRIQNSVLSICDFREGQNTQDCPKAQEHIESRTGAGGFFVSTPVSFYD	360			
Seqct 301	DERVCLQMLKRIQNSVLSICDFREGQNTQDCPKAQEHIESRTGAGGFFVSTPVSFYD	360			
Query 361	AISVYKIFSDQGYKHIVTKDTVENAIIQITSGKWEATNIFRVTQOSLFYSSNEFEDYPG	420			
Seqct 361	AISVYKIFSDQGYKHIVTKDTVENAIIQITSGKWEATNIFRVTQOSLFYSSNEFEDYPG	420			
Query 421	RNNIYRISIGSSPPSKCITCHLKERQCYTASFQYKAYVALICYGPGLPSTLHGGH	480			
Seqct 421	RNNIYRISIGSSPPSKCITCHLKERQCYTASFQYKAYVALICYGPGLPSTLHGGH	480			
Query 481	TDQEIKILFEENKELENALKNIQLPKEEIKKLEVDITLWYKMLPPFRDRSKKYPILLIQV	540			
Seqct 481	TDQEIKILFEENKELENALKNIQLPKEEIKKLEVDITLWYKMLPPFRDRSKKYPILLIQV	540			
Query 541	YGGPCSQSVKSVFSIMNISVLASKEGIVIALVQGRGTAYQSDKLLYAVYKLGWYVEDQ	600			
Seqct 541	YGGPCSQSVKSVFSIMNISVLASKEGIVIALVQGRGTAYQSDKLLYAVYKLGWYVEDQ	600			
Query 601	ITIVAKFIEMGFIDEKRIALNGKSYGGVSSALASGTLGFKCGIAPAVPVSSEYVASYI	660			
Seqct 601	ITIVAKFIEMGFIDEKRIALNGKSYGGVSSALASGTLGFKCGIAPAVPVSSEYVASYI	660			
Query 661	TERFVGLPTKIQNILEHYKISTVMAAEYFRINOVYLLIHGTADDWVHFQISAQIAKALVIA	720			
Seqct 661	TERFVGLPTKIQNILEHYKISTVMAAEYFRINOVYLLIHGTADDWVHFQISAQIAKALVIA	720			
Query 721	QVDFQWYSDQIHGIPGLSSKHLTYRTHFLKQCFSLSD	760			
Seqct 721	QVDFQWYSDQIHGIPGLSSKHLTYRTHFLKQCFSLSD	760			

A603

ATCACACCTGTCTCAGAAAAITCATAGAAA
 |||||
 ATCACACCTGTCTCAGAAAAITCATAGAAA

FIG. 1

FIG. 1

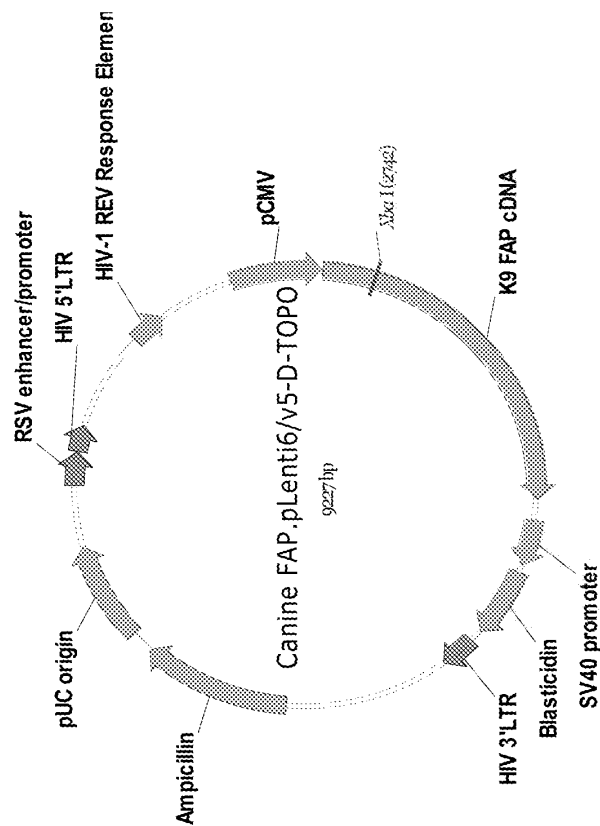


FIG. 2B

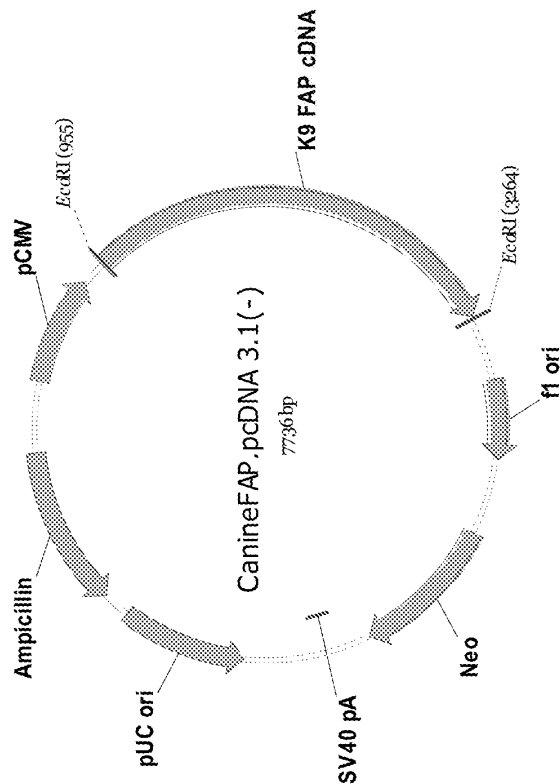


FIG. 2A

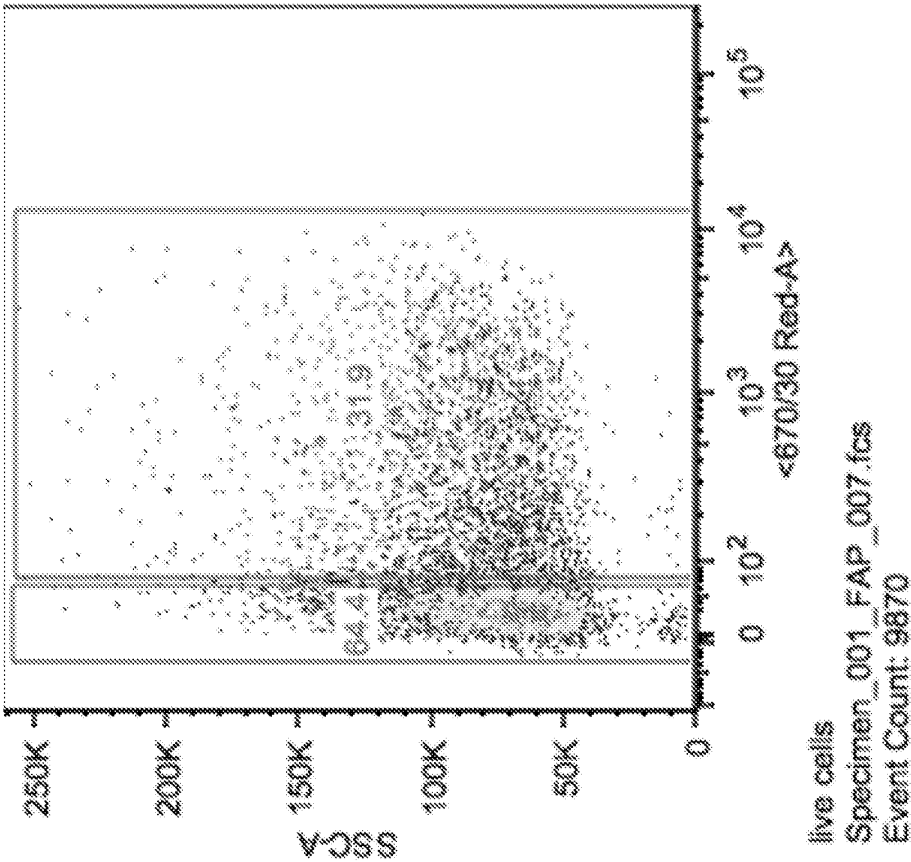


FIG. 2C

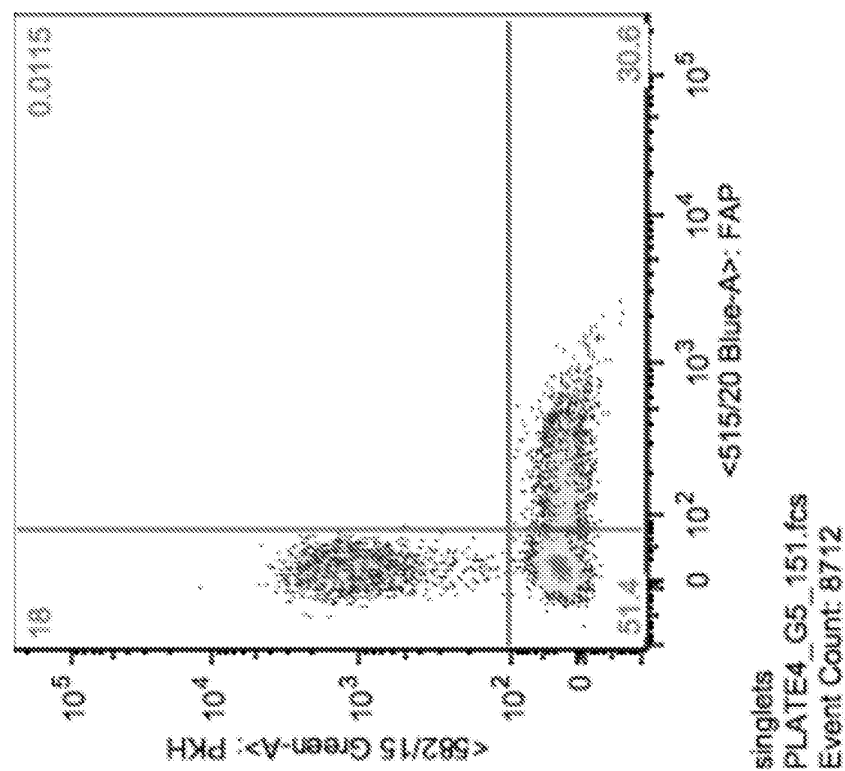


FIG. 3

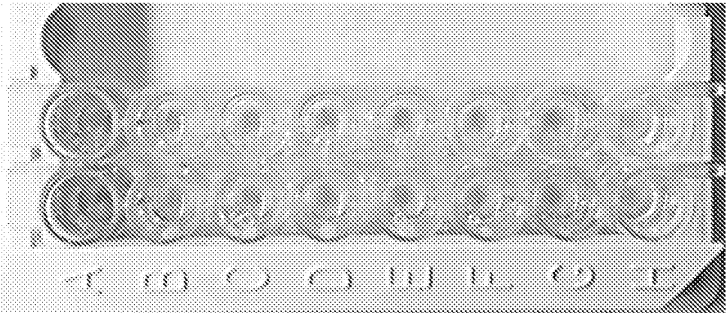


FIG. 4B

Isotyping (Thermo Fisher Rapid ELISA Mouse mAb Isotyping Kit #37503)		
Run information		
A	2.30701	2.05944
B	0.128739	0.134897
C	0.061526	0.083505
D	0.053079	0.070057
E	0.054464	0.074575
F	0.048878	0.064709
G	0.280926	0.302431
H	0.05484	0.067141

FIG. 4A

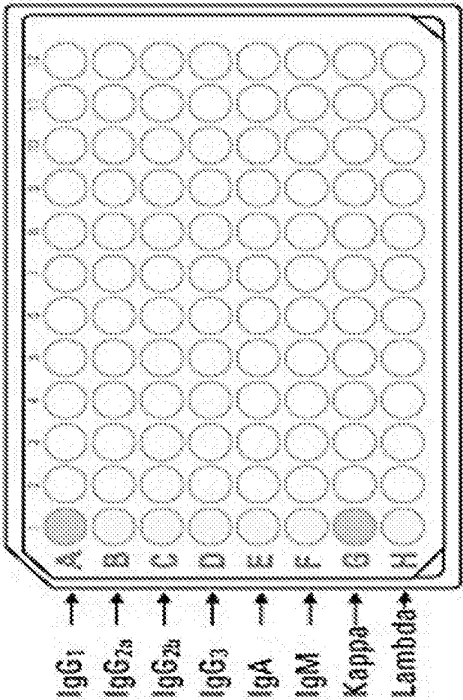


FIG. 4C

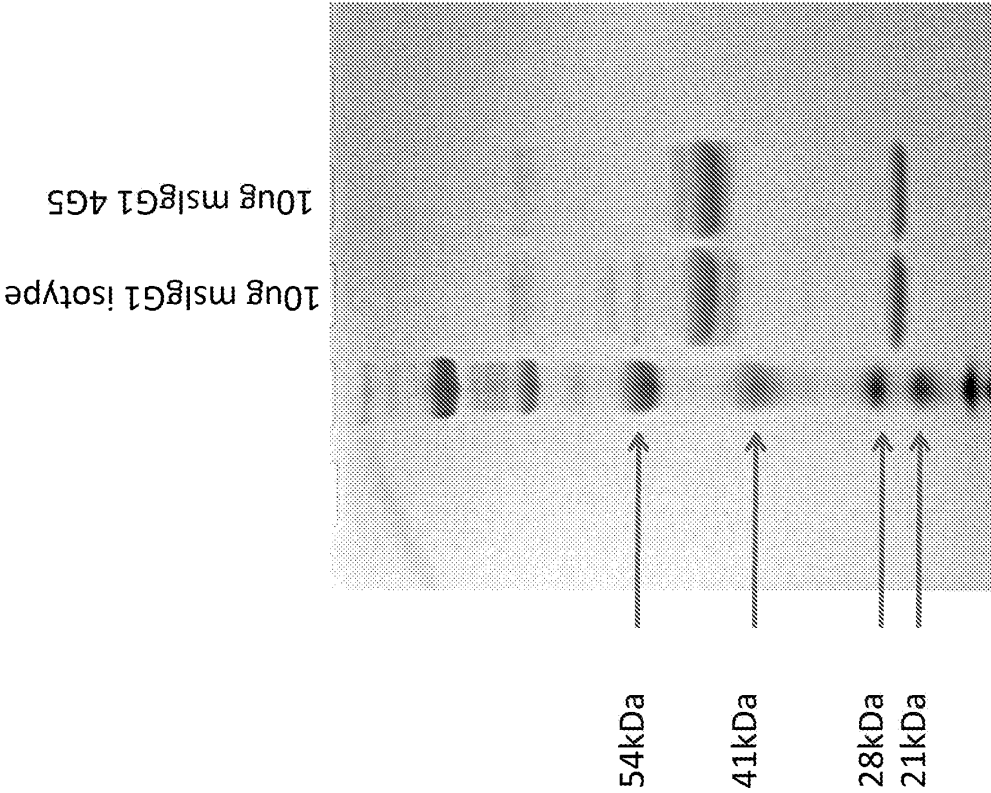


FIG. 5