

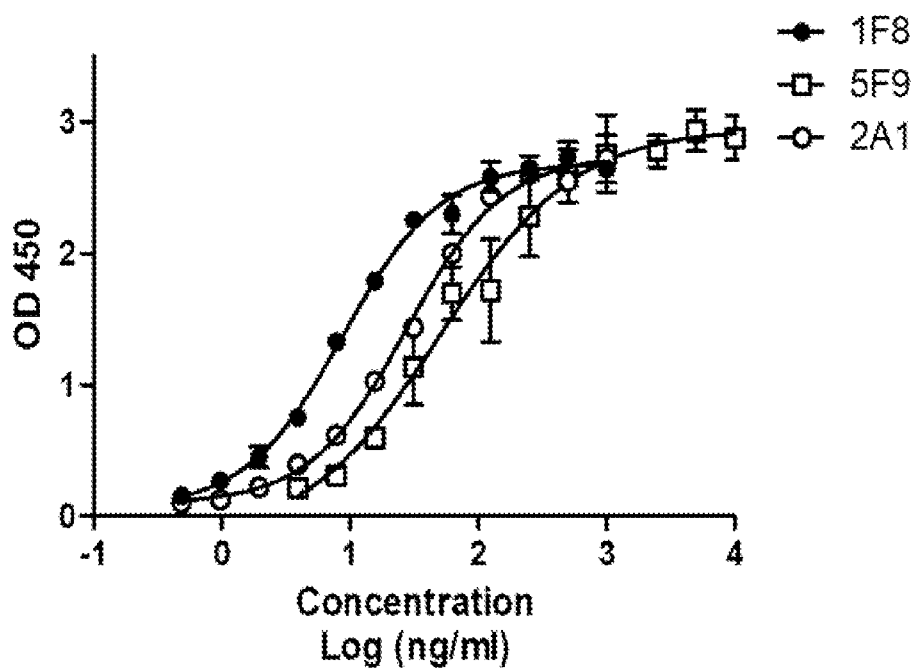


Fig. 1

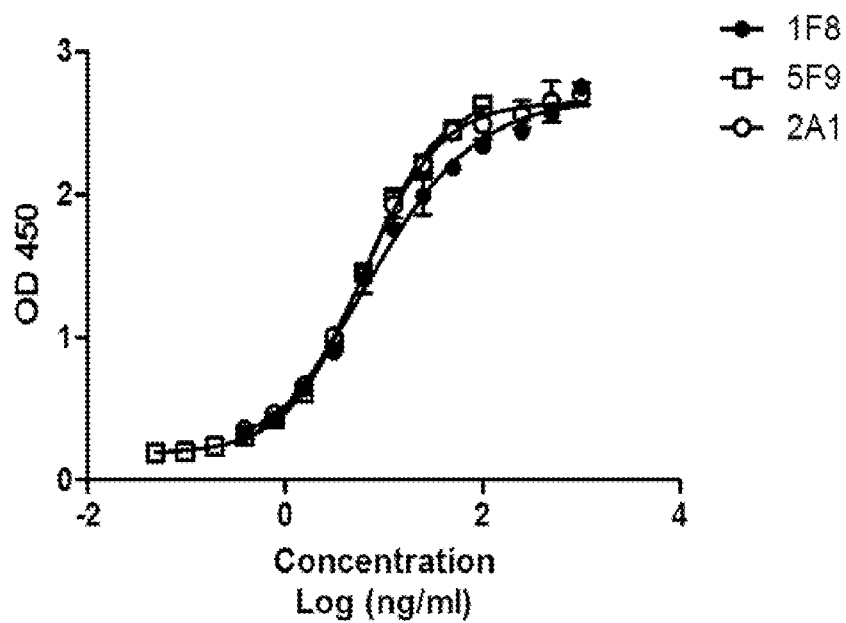


Fig. 2a

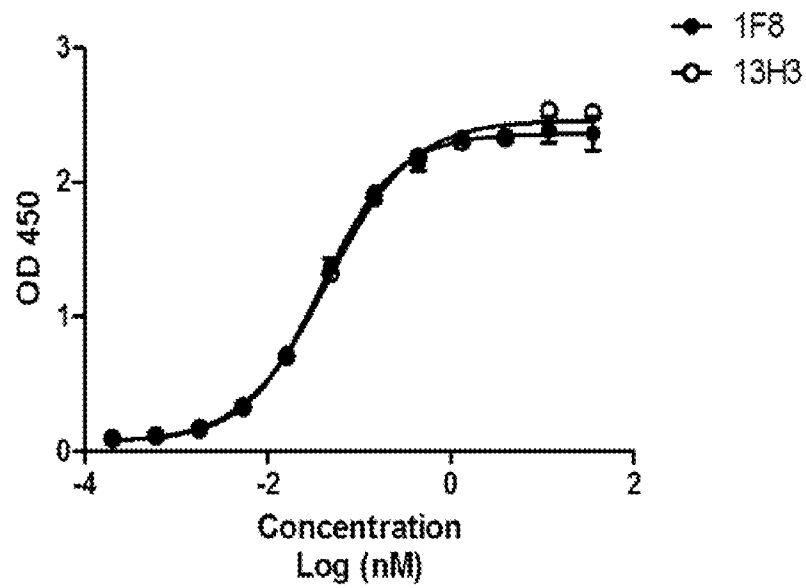


Fig. 2b

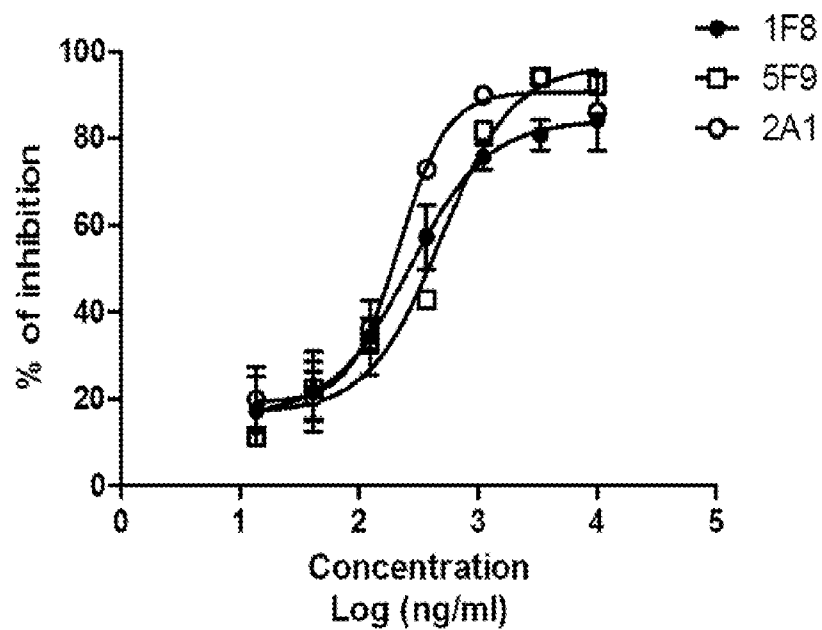


Fig. 3a

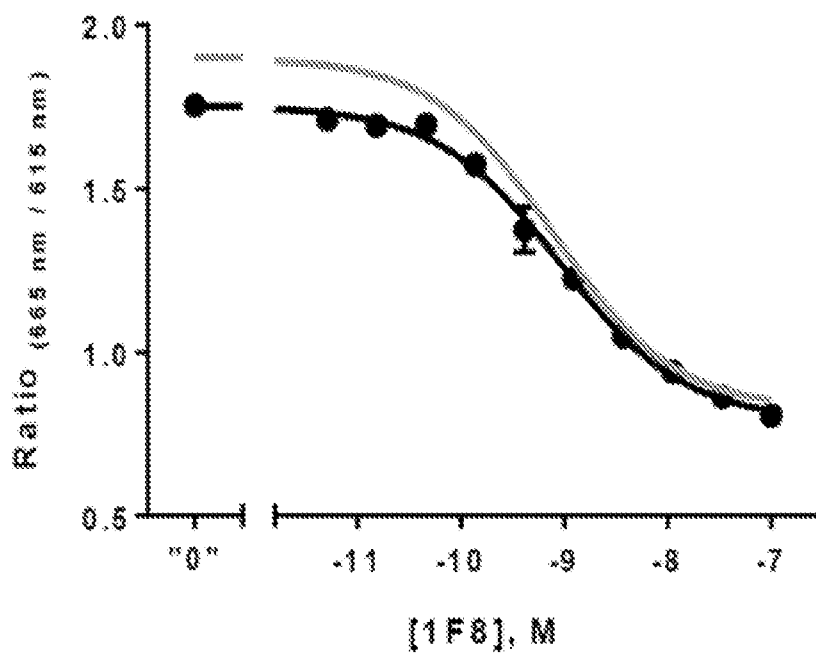
1F8 ($IC_{50} = 0.78$ nM)

Fig. 3b

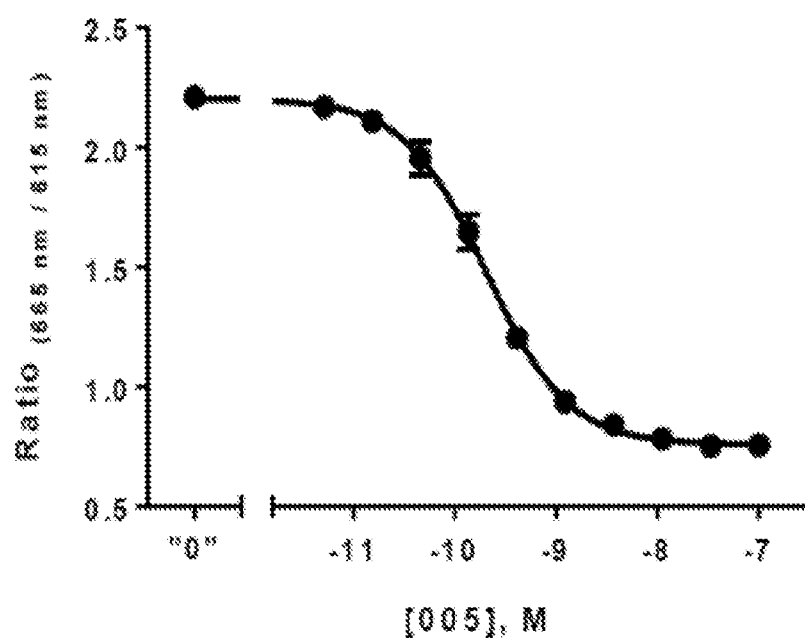
13H3 $IC_{50} = 0.20$ nM

Fig. 3c

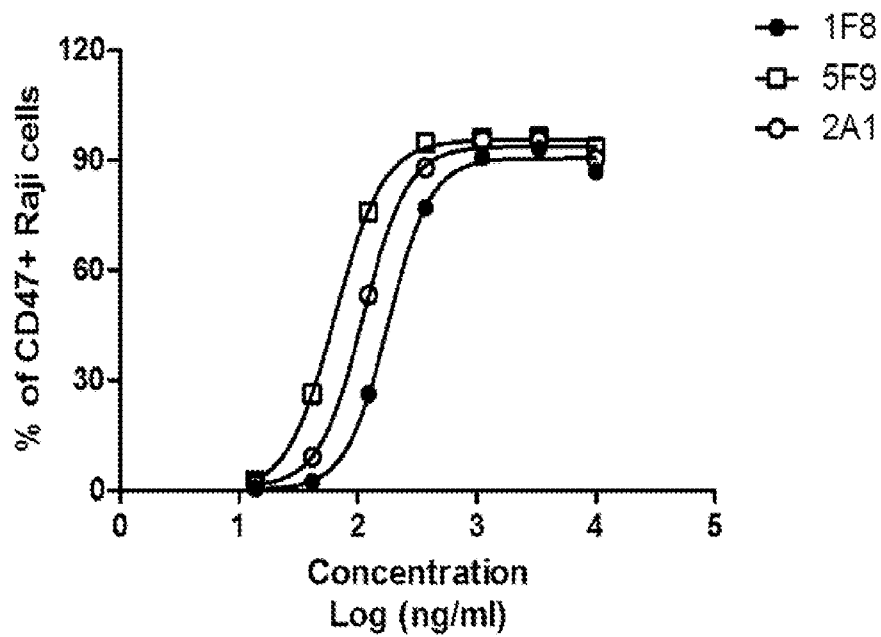


Fig. 4a

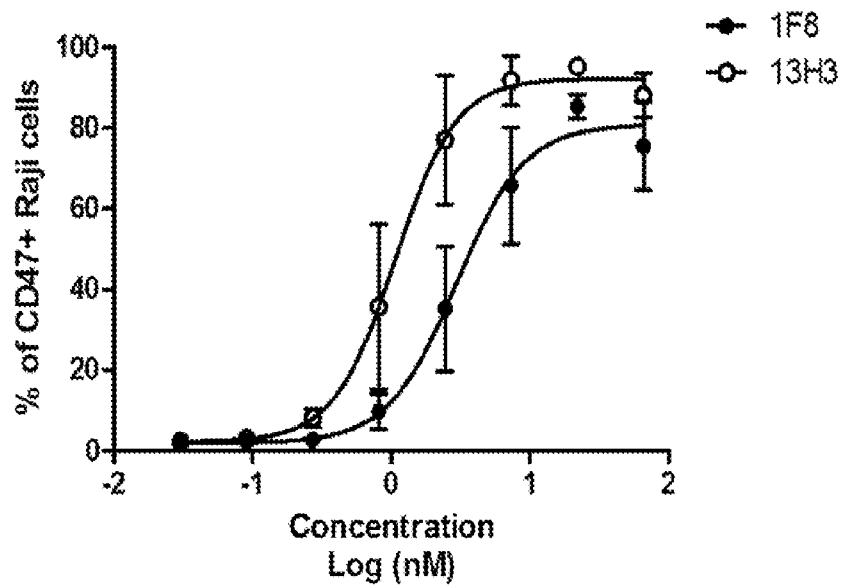


Fig. 4b

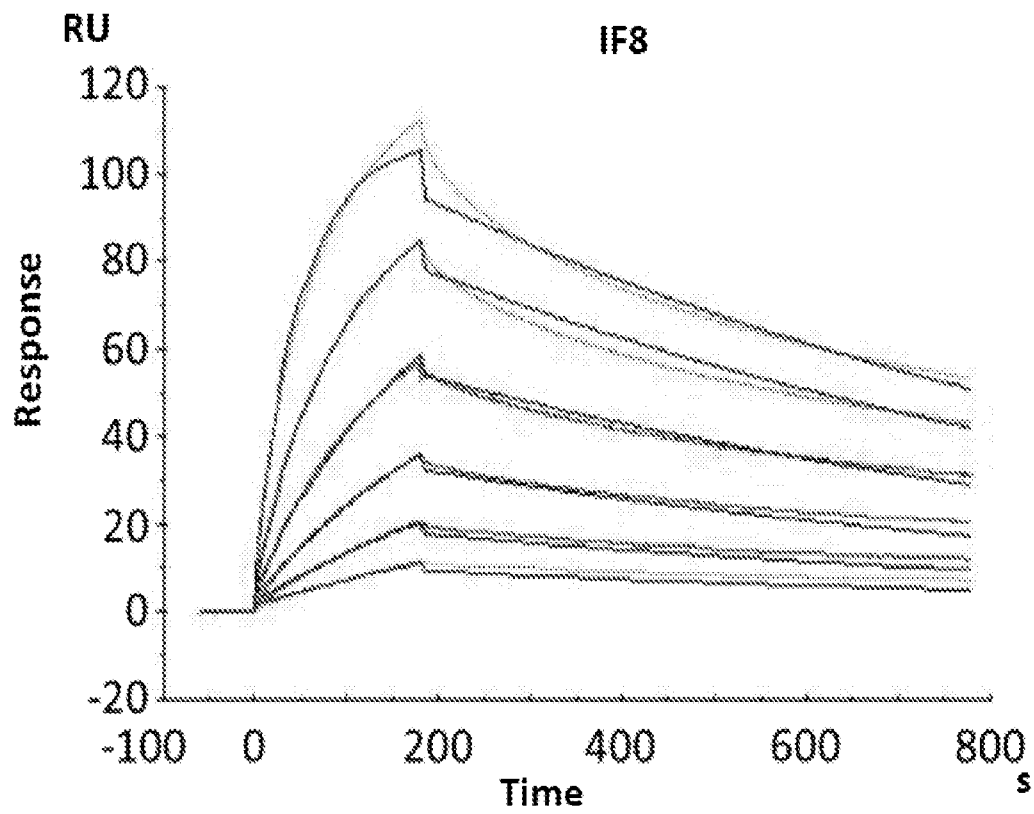


Fig. 4c

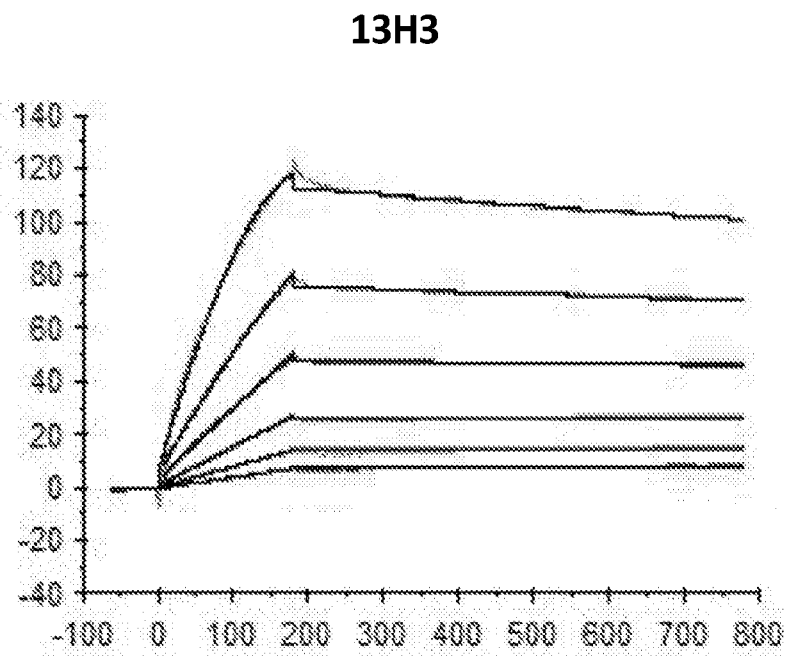


Fig. 4d

Sample	k_a (1/Ms)	k_d (1/s)	KD (M)
1F8	3.75E+05	1.04E-03	2.8E-09
13H3	5.33E+05	2.47E-04	4.6E-10

Fig. 4e

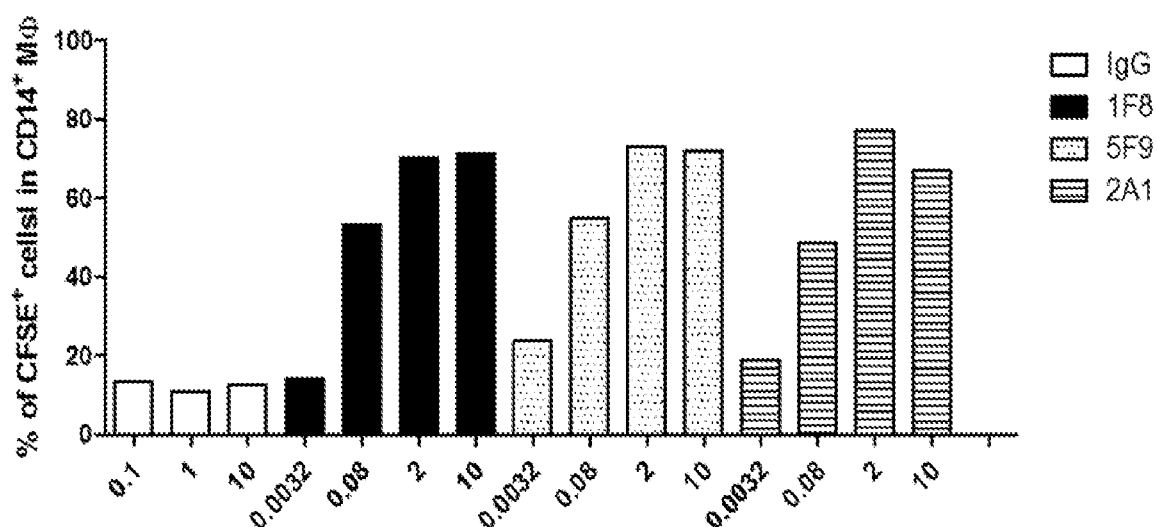


Fig. 5a

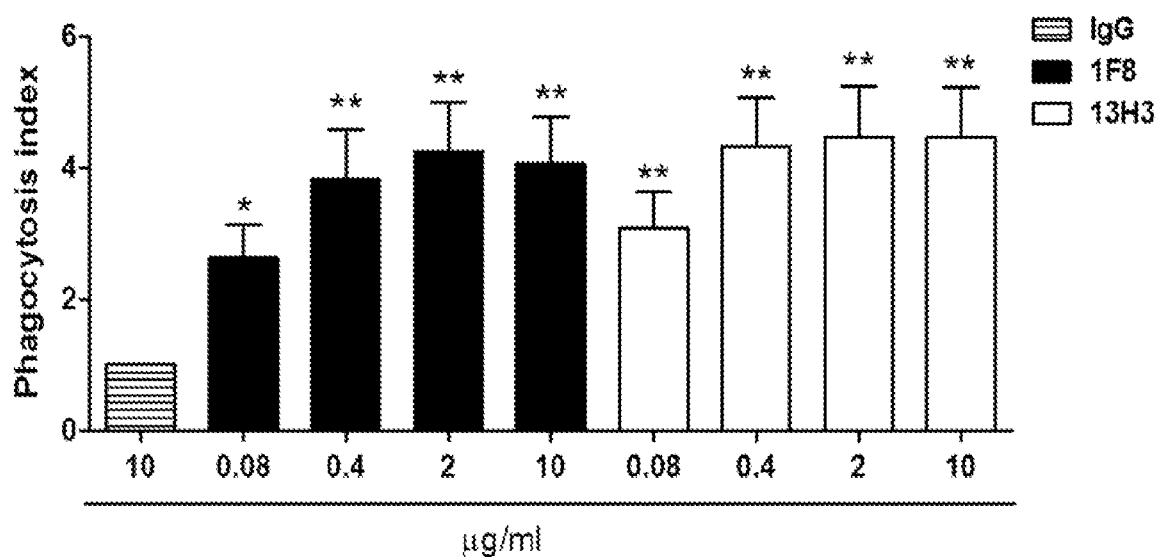


Fig. 5b

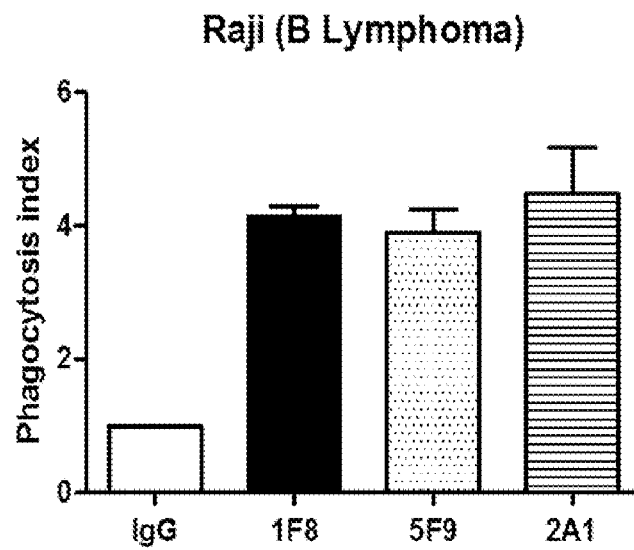


Fig. 6a

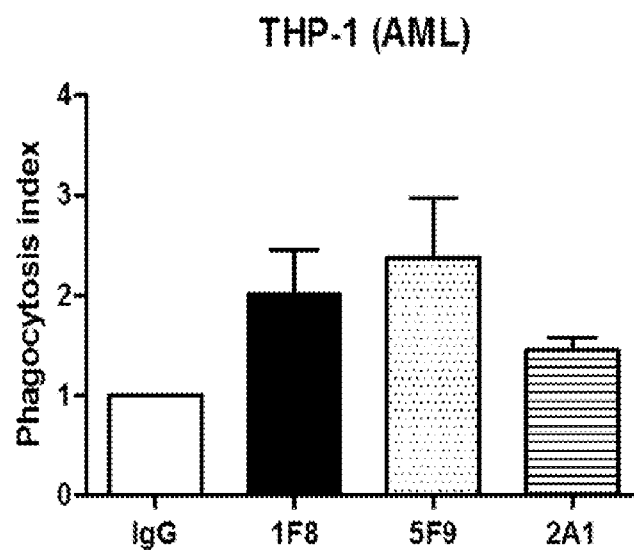


Fig. 6b

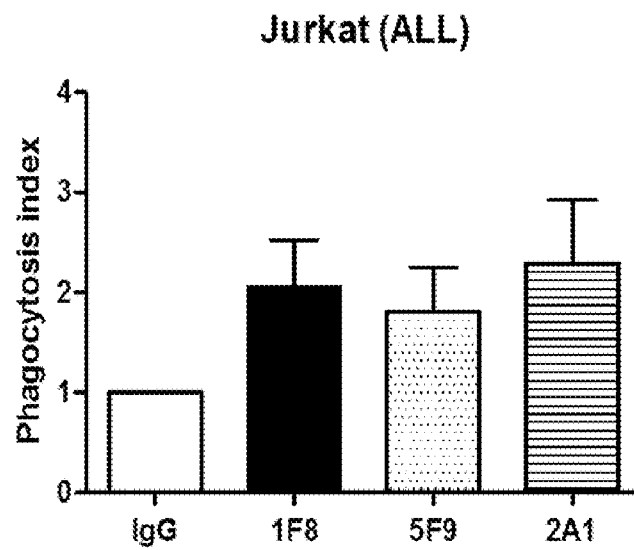


Fig. 6c

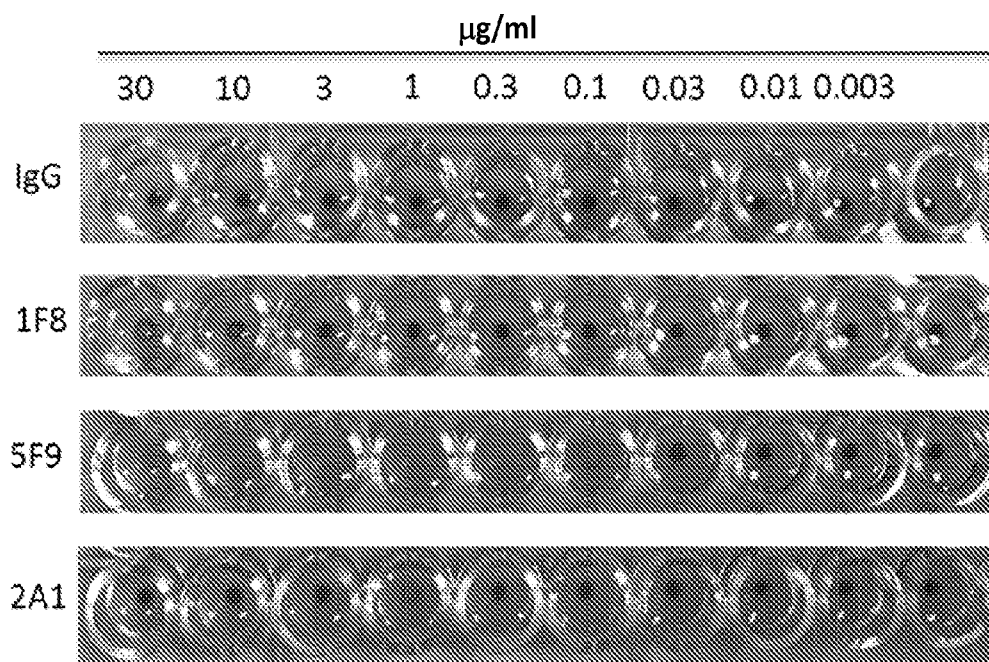


Fig. 7a

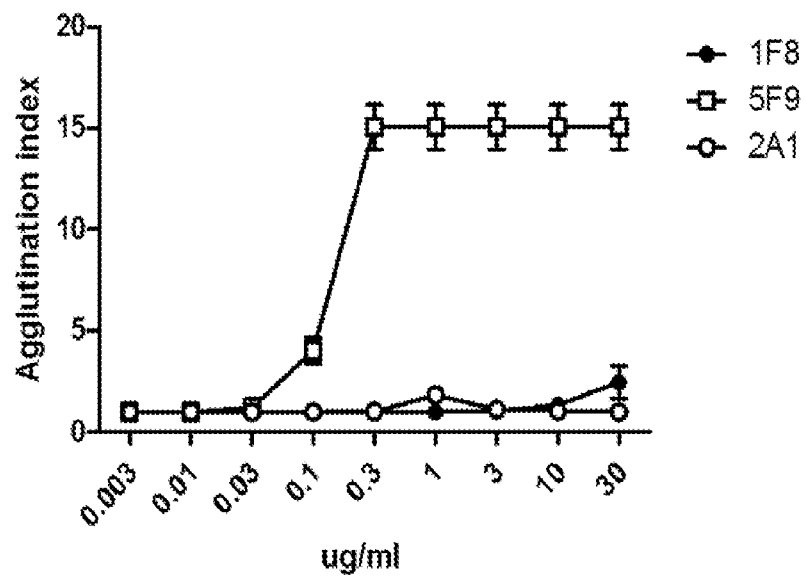


Fig. 7b

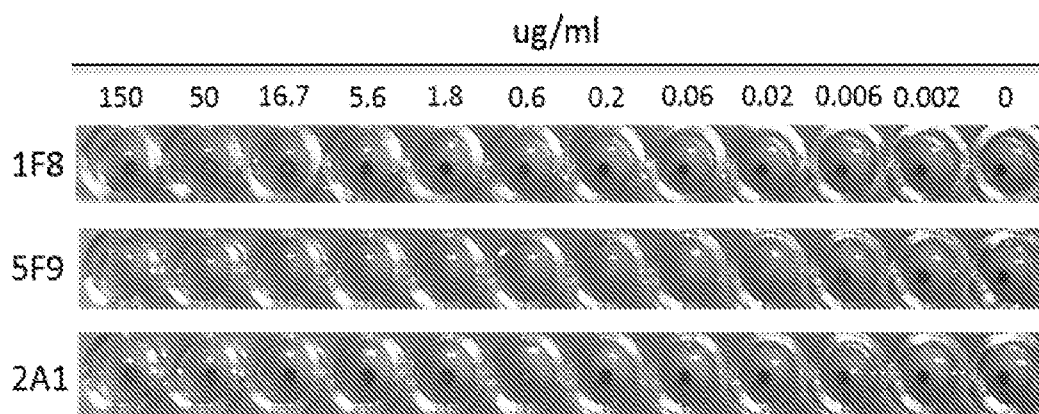


Fig. 8a

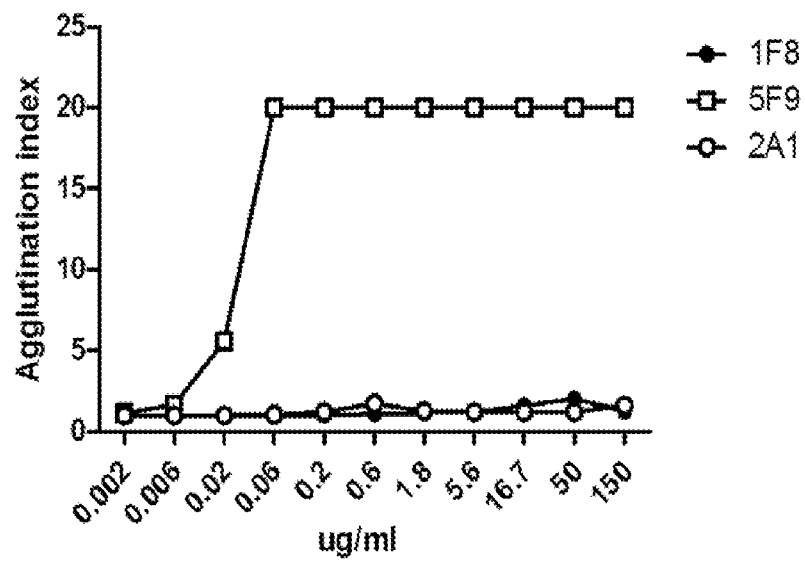


Fig. 8b

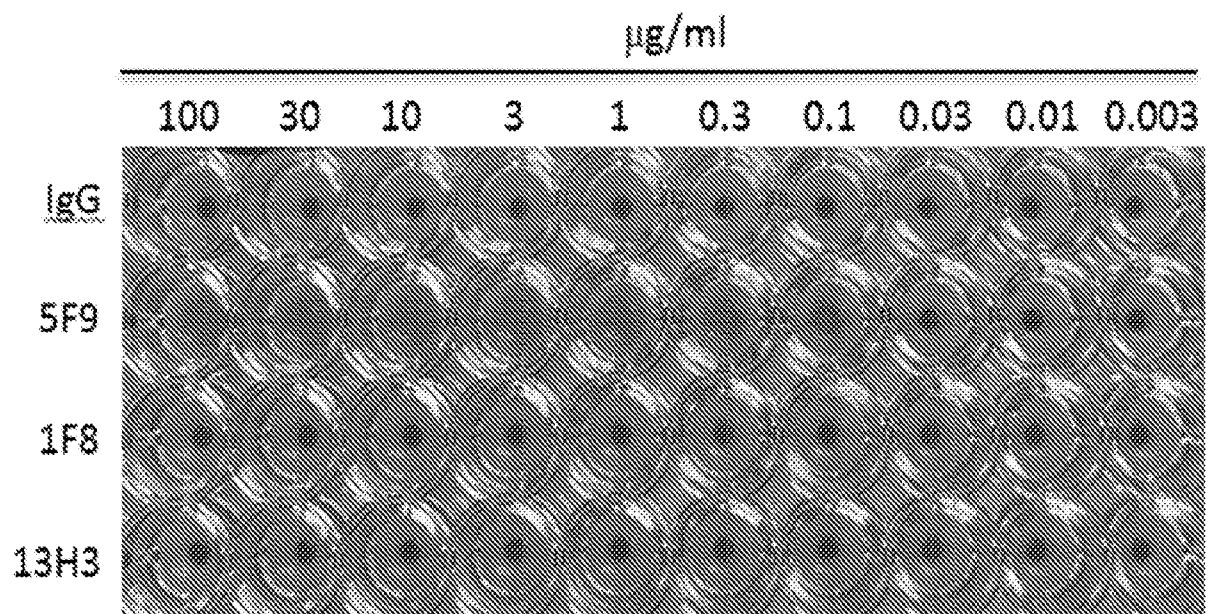


Fig. 8c

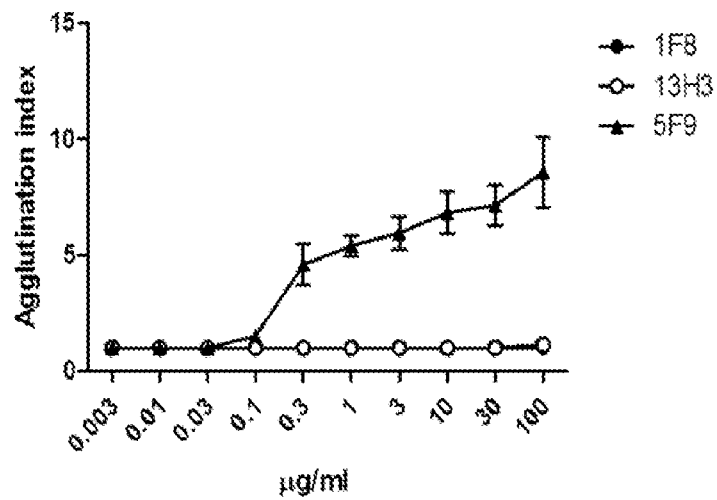


Fig. 8d

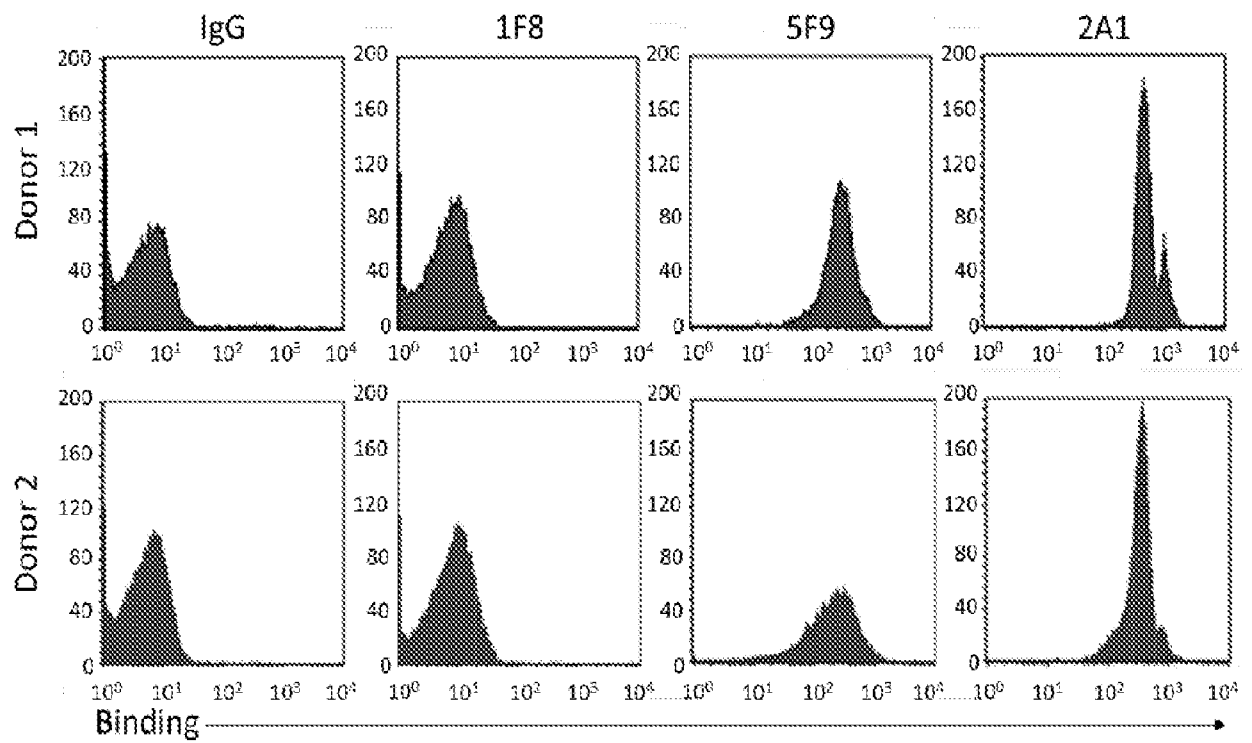


Fig. 9a

12/46

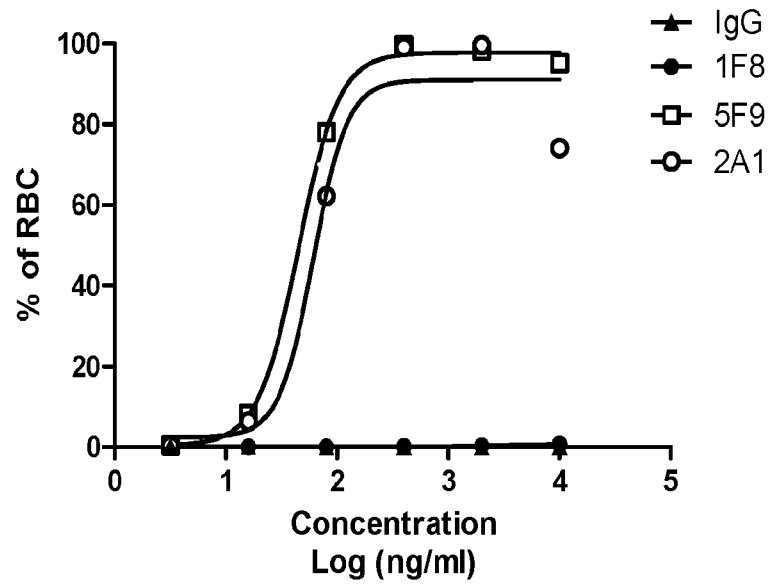


Fig. 9b

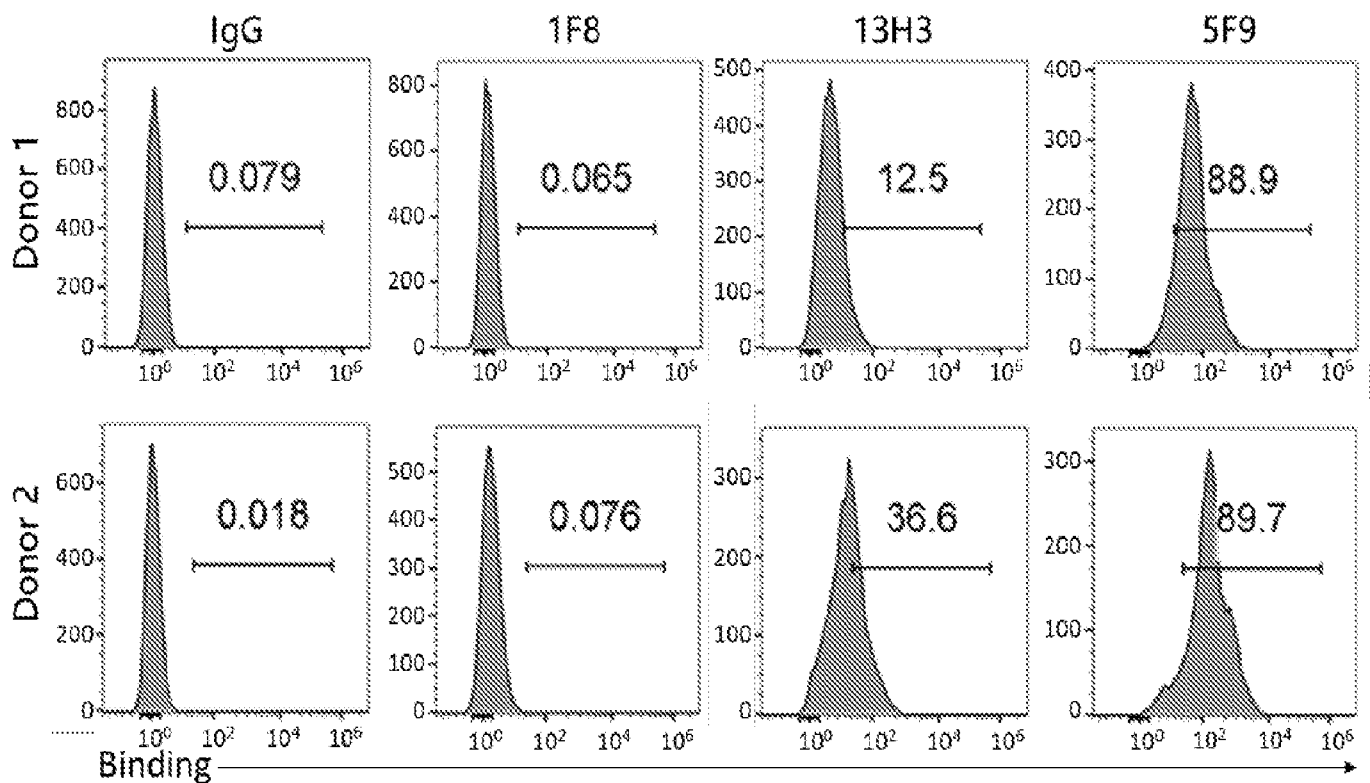


Fig. 9c

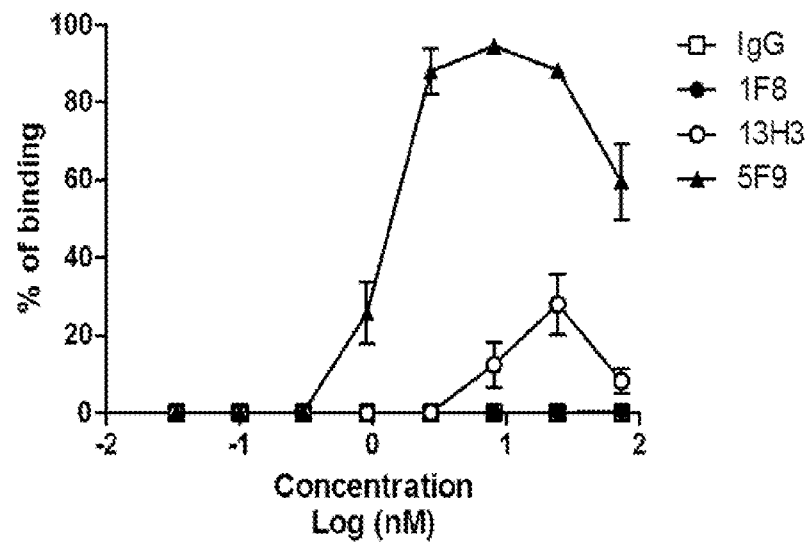


Fig. 9d

Male (n=6)

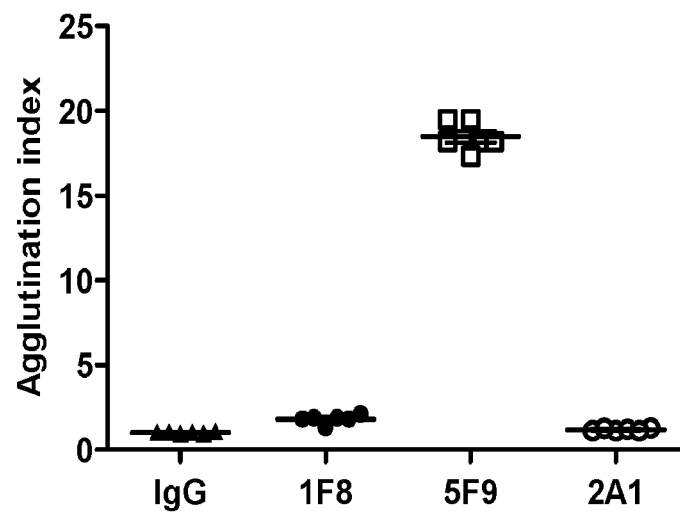


Fig. 10a

Female (n=6)

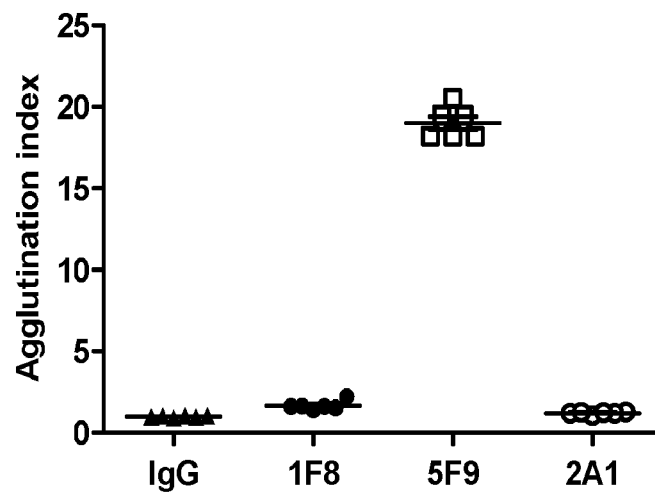


Fig. 10b

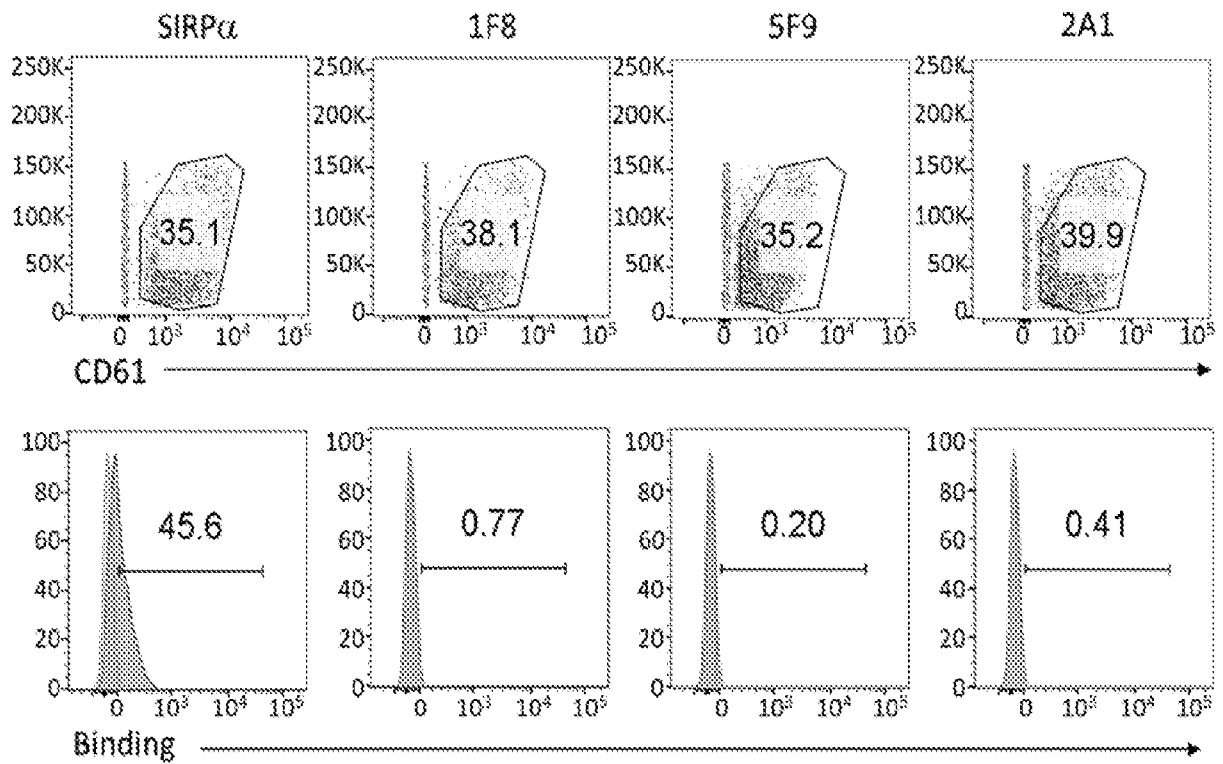


Fig. 11

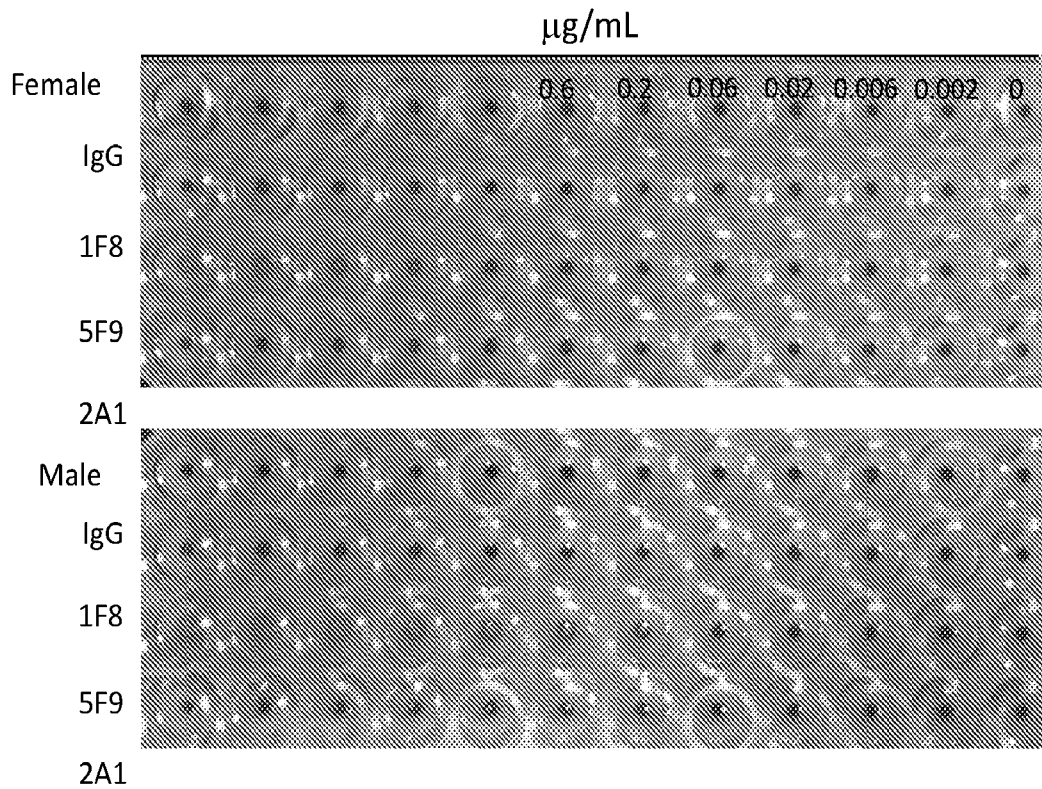


Fig. 12a

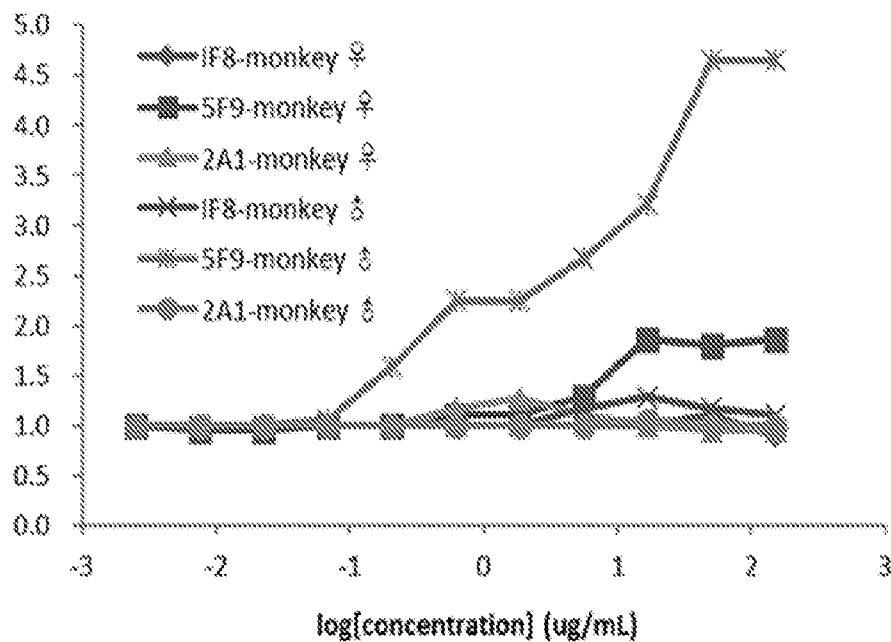
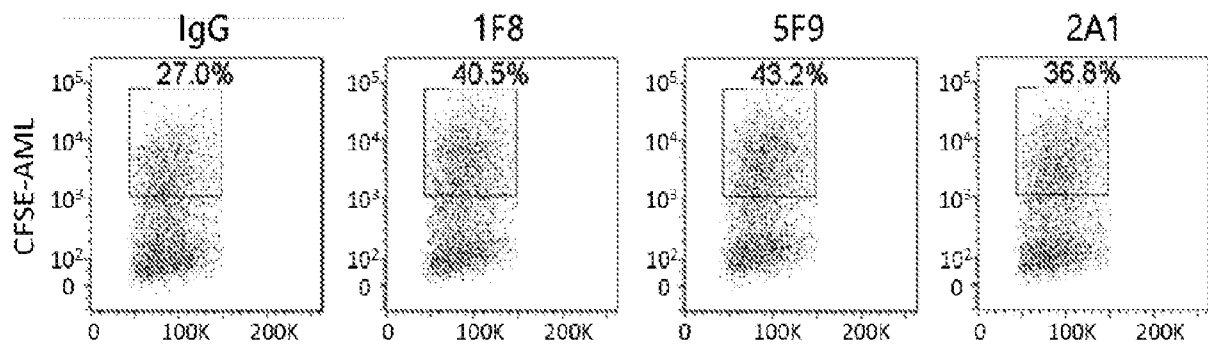


Fig. 12b

Phagocytosis



APC-CD14

AML Binding

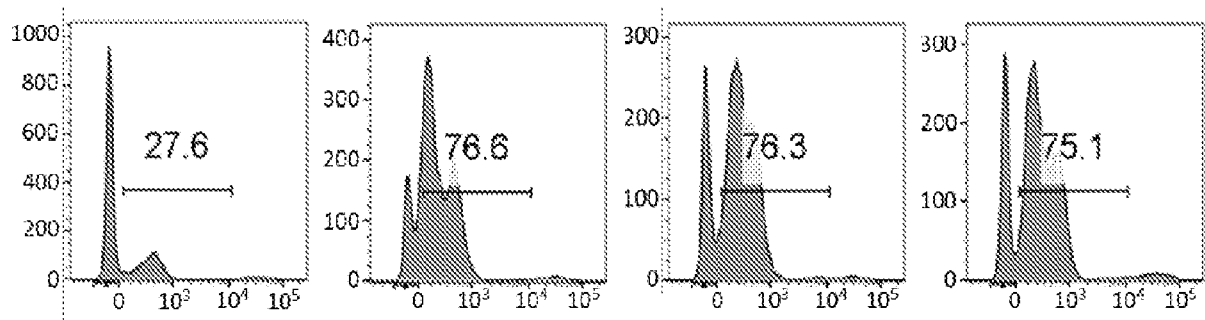


Fig. 13e

Fig. 13f

Fig. 13g

Fig. 13h

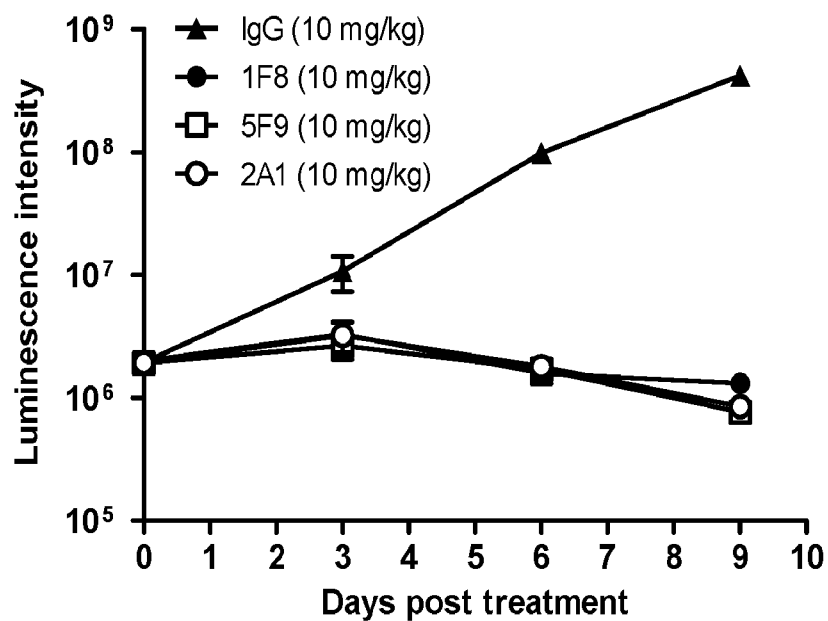


Fig. 14a

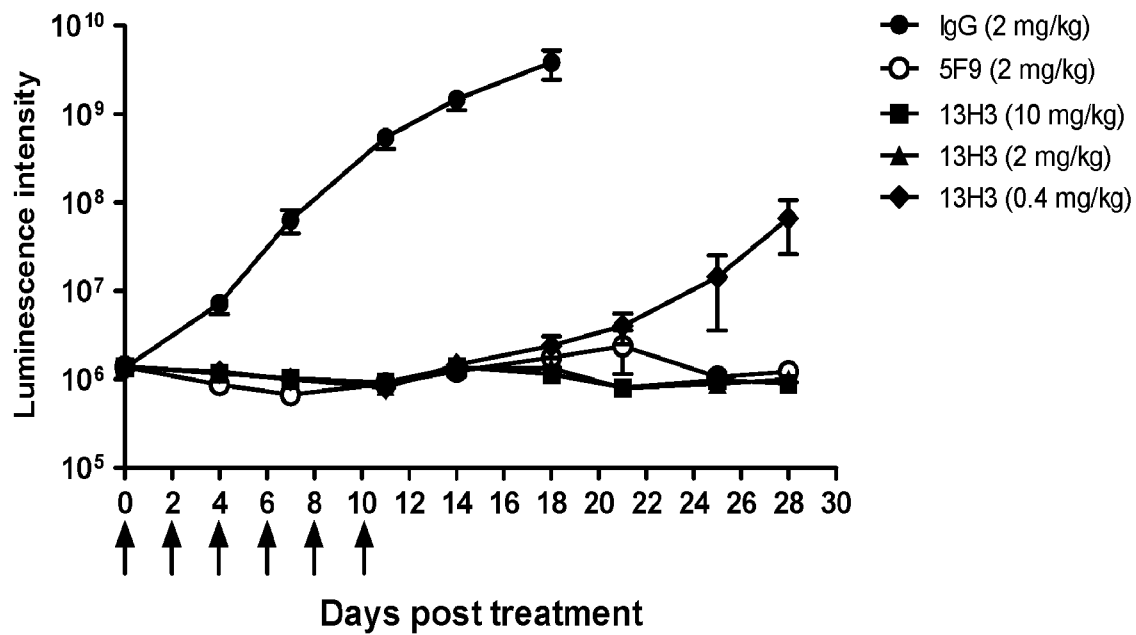


Fig. 14b

M1 MΦ in the spleen

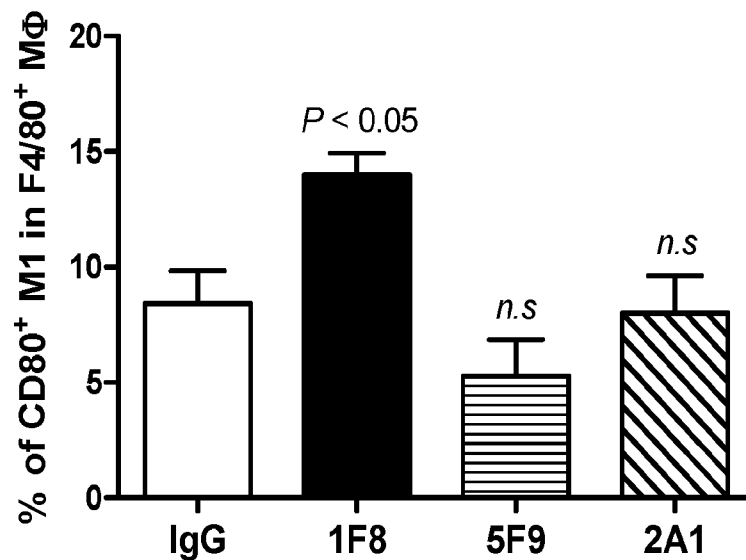


Fig. 15a

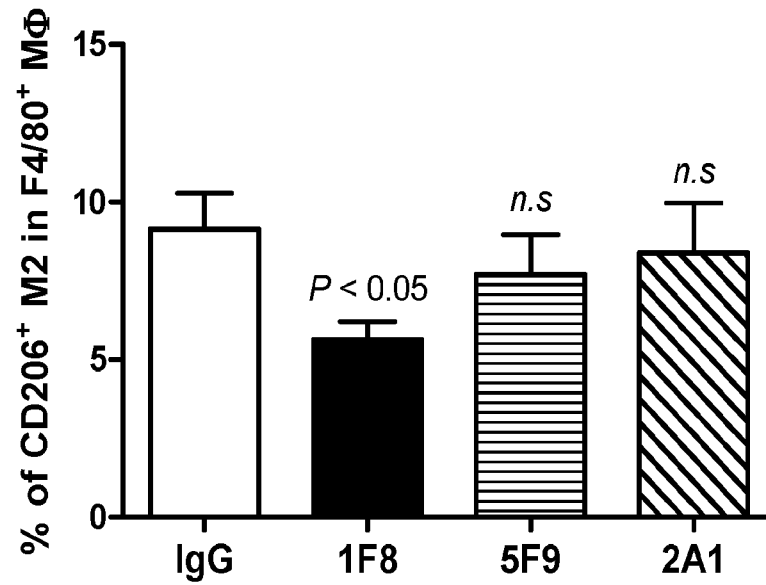
M2 MΦ in the spleen

Fig. 15b

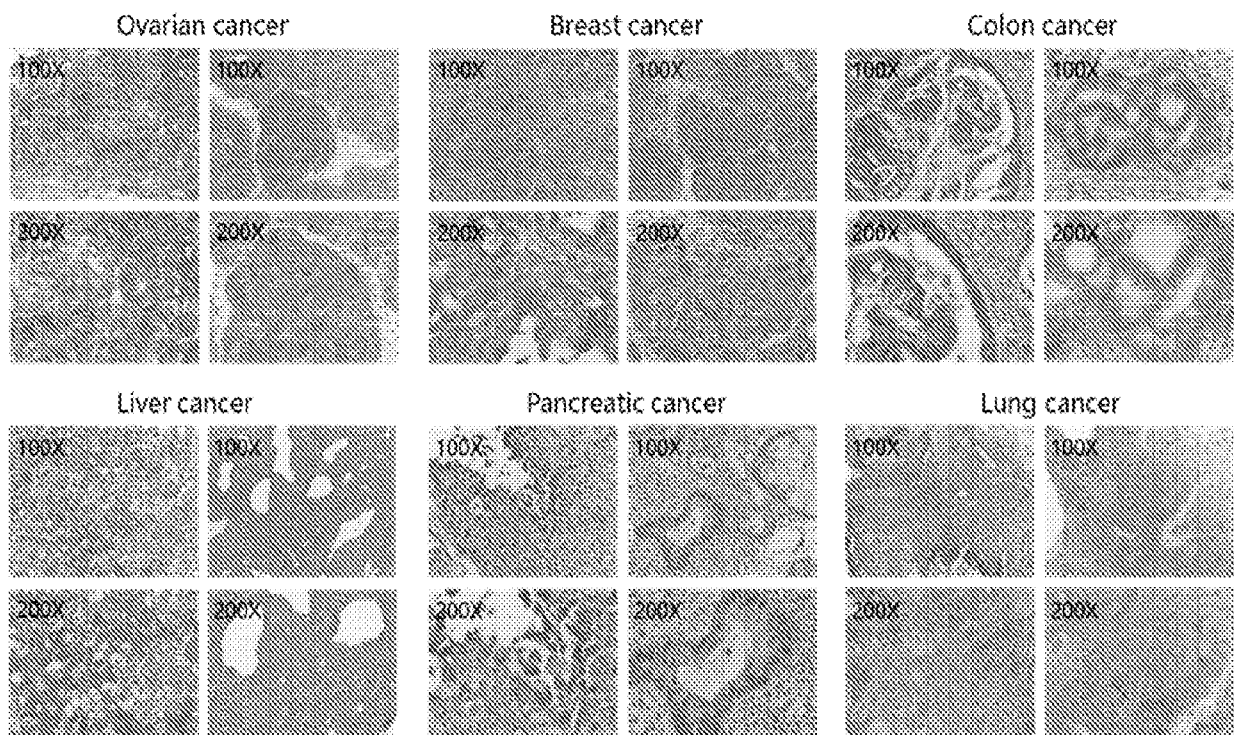


Fig. 16a

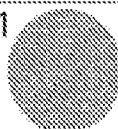
Geometry	Strong stain	Weak stain
Diffuse (all cells)	6 	5 
Moderate (most/many cells)	4 	3 
Focal (few cells)	2 	1 
Negative	0 	

Fig. 16b

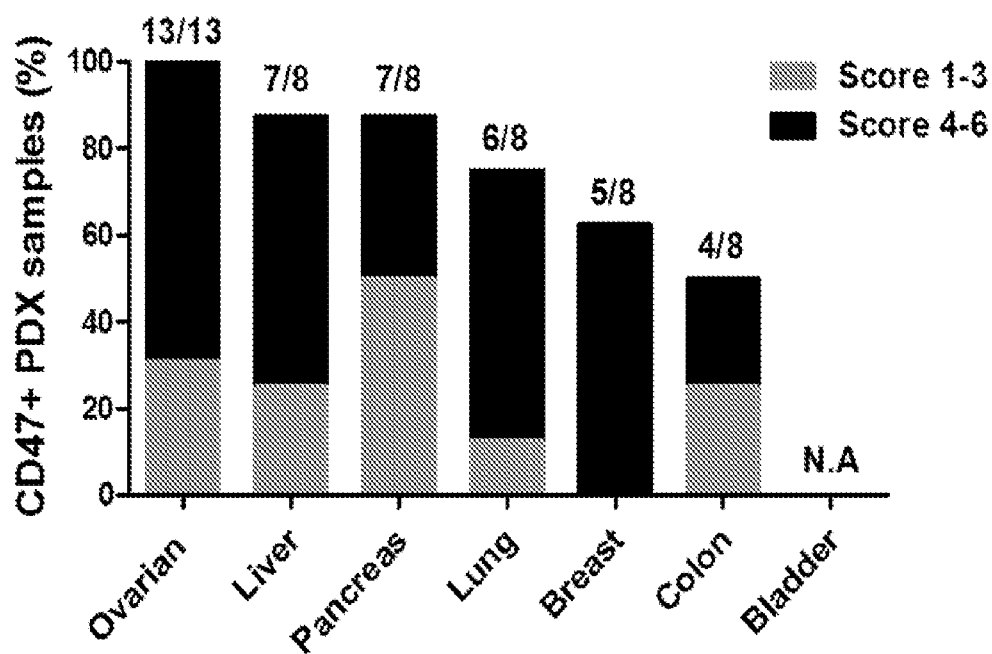


Fig. 16c

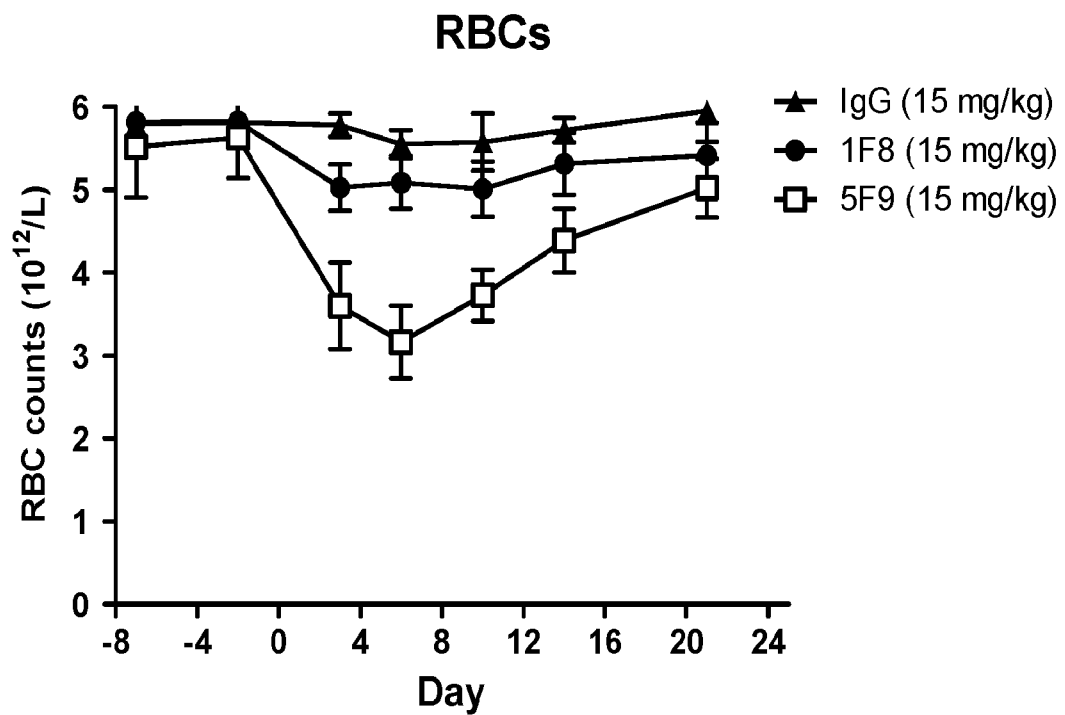


Fig. 17a

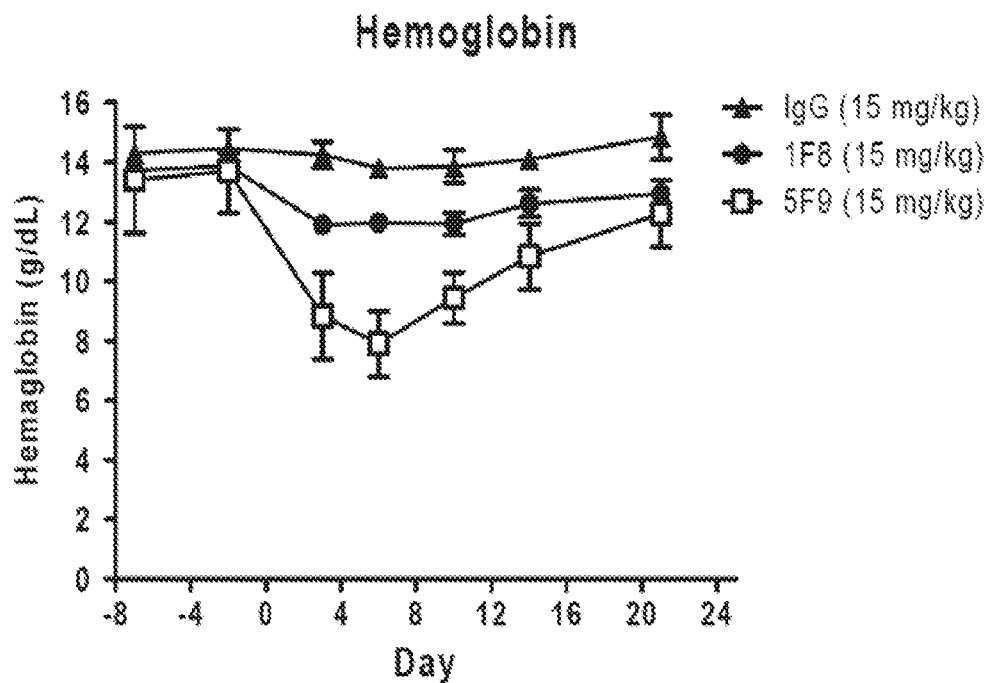


Fig. 17b

Reticulocytes

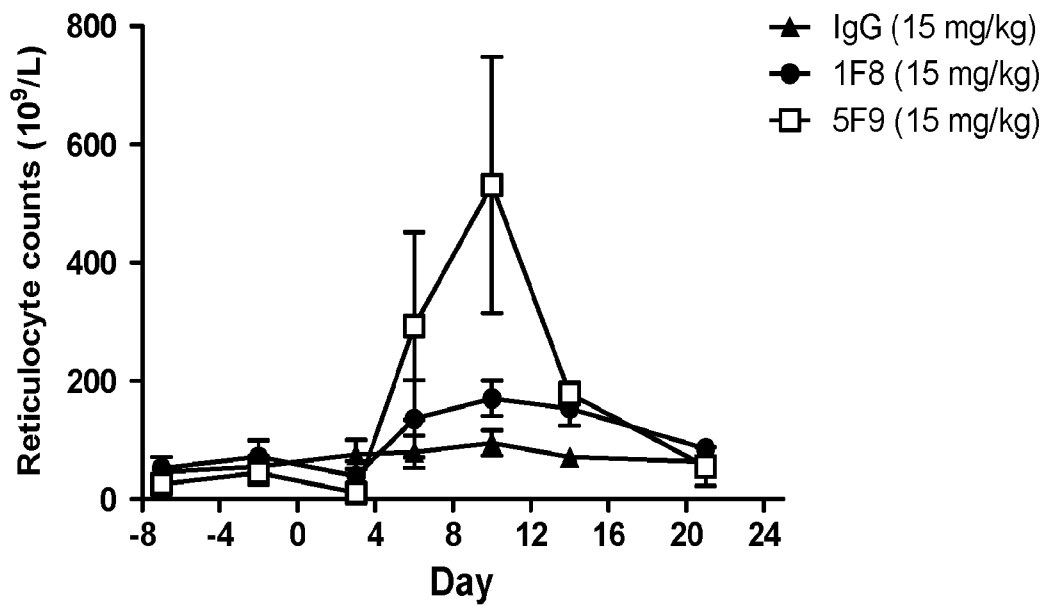


Fig. 17c

Platelets

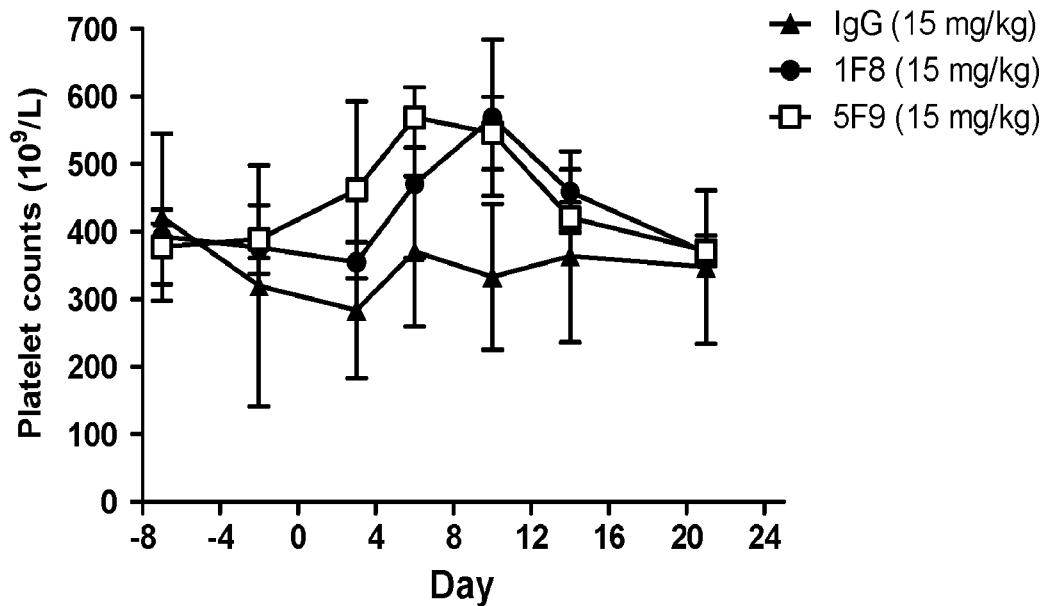


Fig. 17d

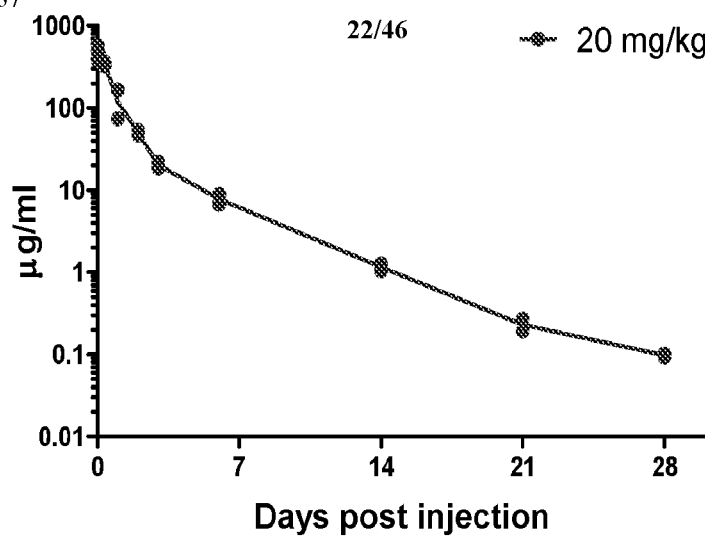


Fig. 17e

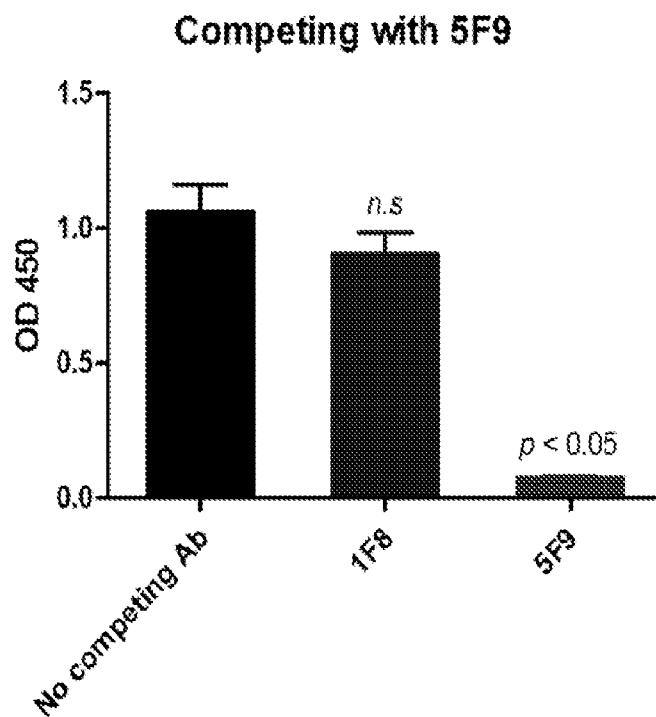


Fig. 18a

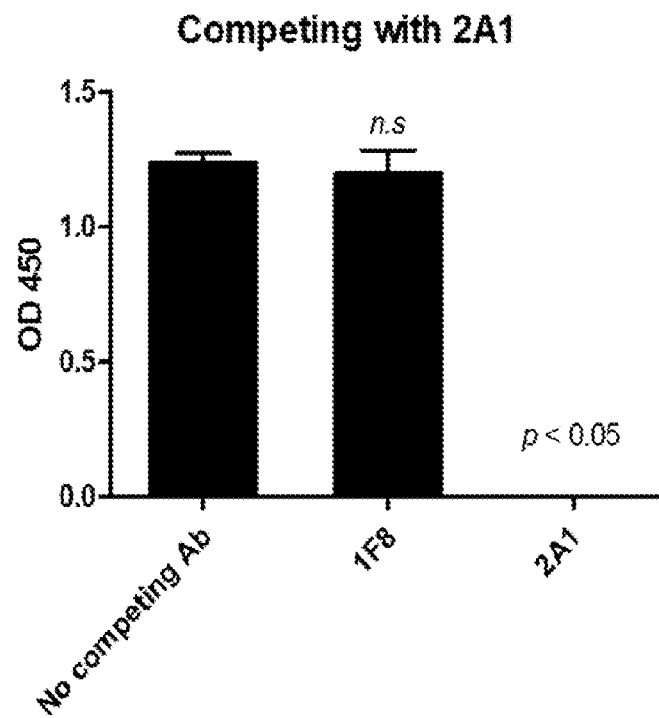


Fig. 18b

Structure of 5F9/CD47 complex



Fig. 18c

Structure of 1F8/CD47 complex



Fig. 18d

Comparison of interaction motif of 5F9 and 1F8 with CD47

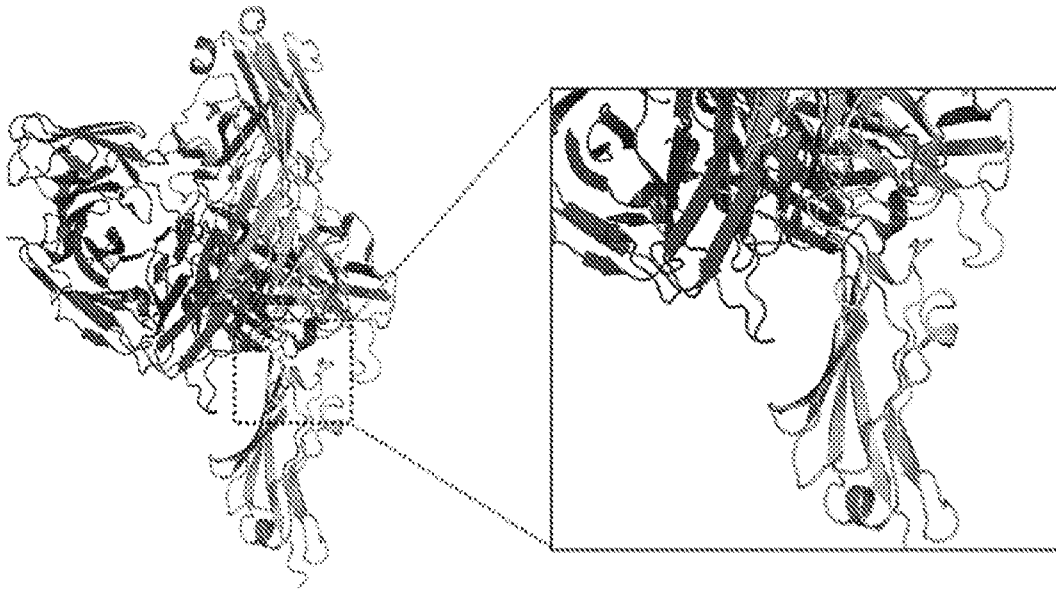


Fig. 18e

Single dose

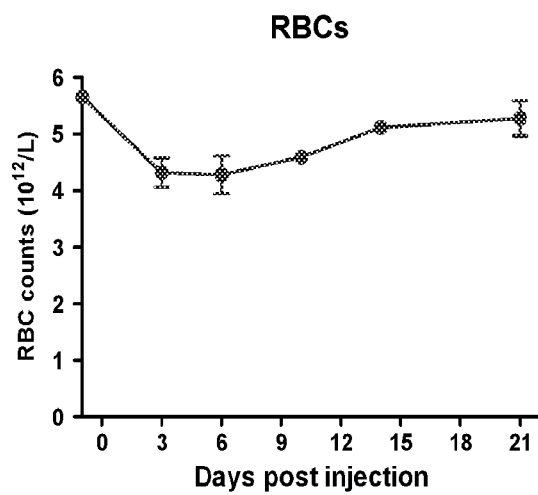


Fig. 19a

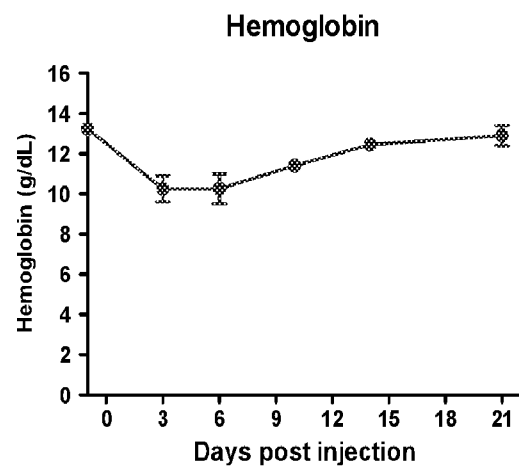


Fig. 19b

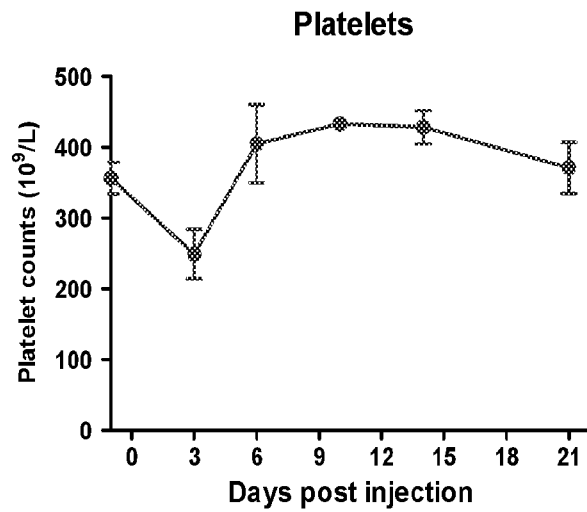


Fig. 19c

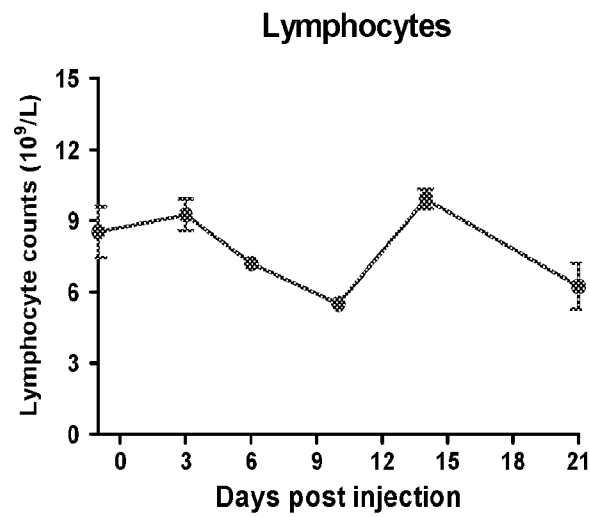


Fig. 19d

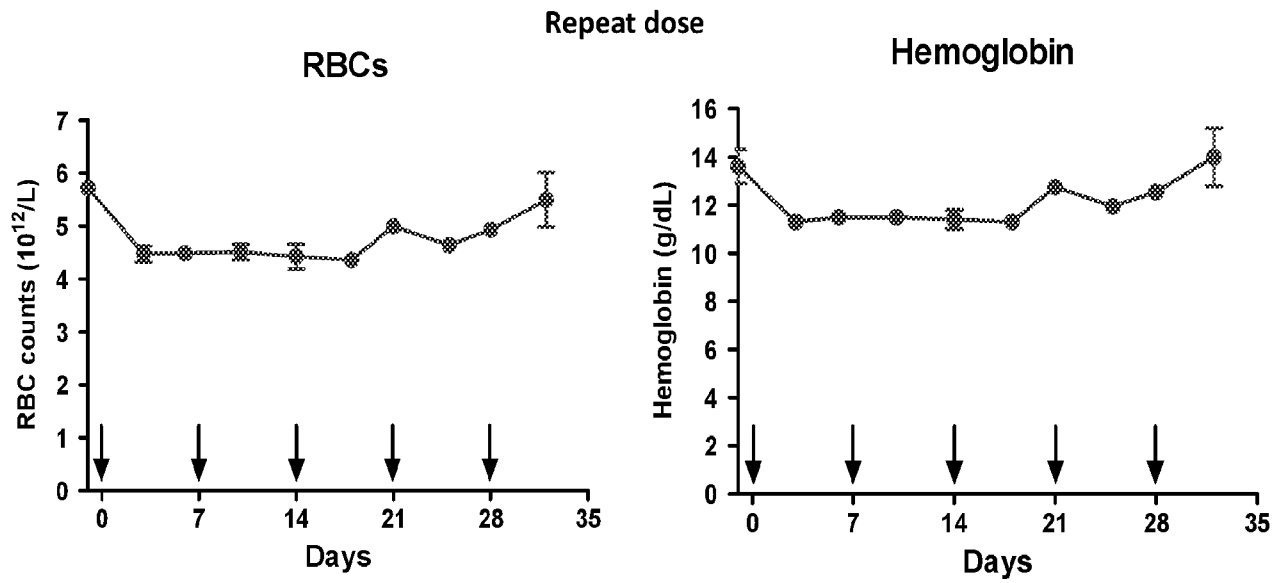


Fig. 19e

Fig. 19f

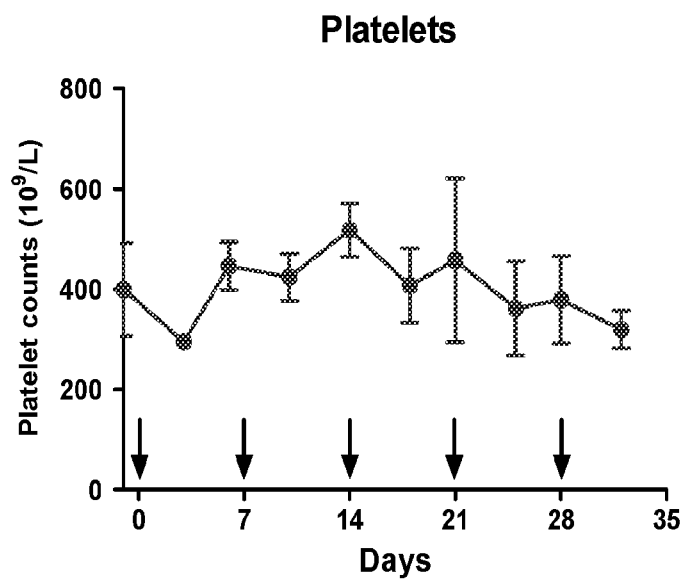


Fig. 19g

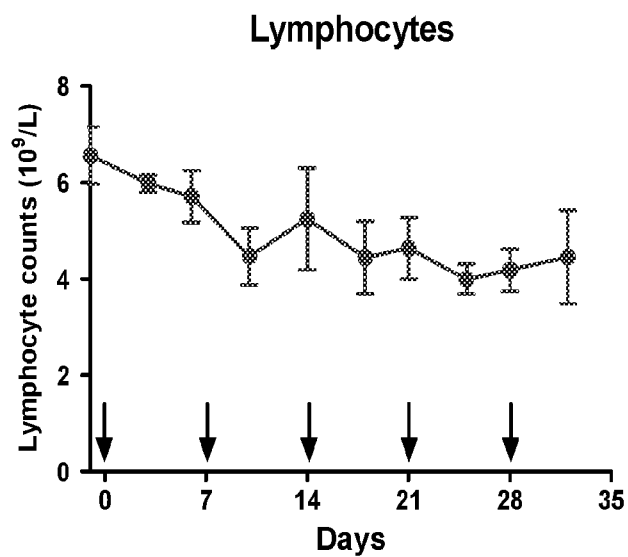


Fig. 19h

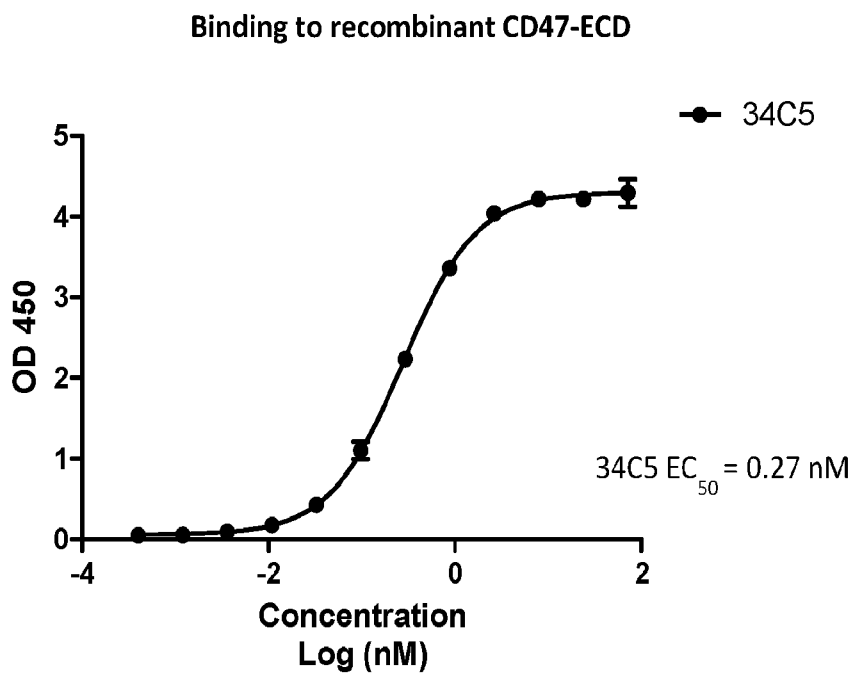


Fig. 20

Binding to CD47-bearing Raji cells

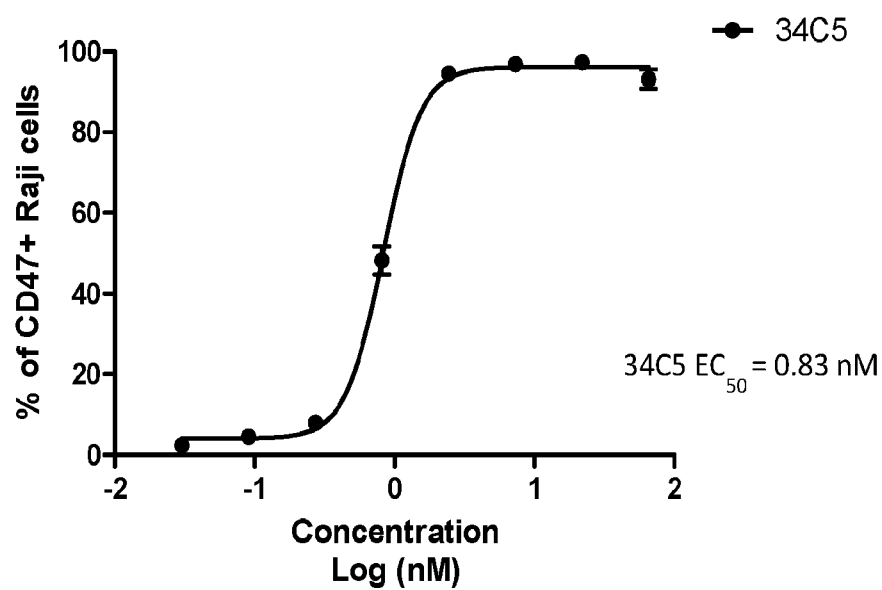


Fig. 21

Blocking of CD47 binding to SIRPa

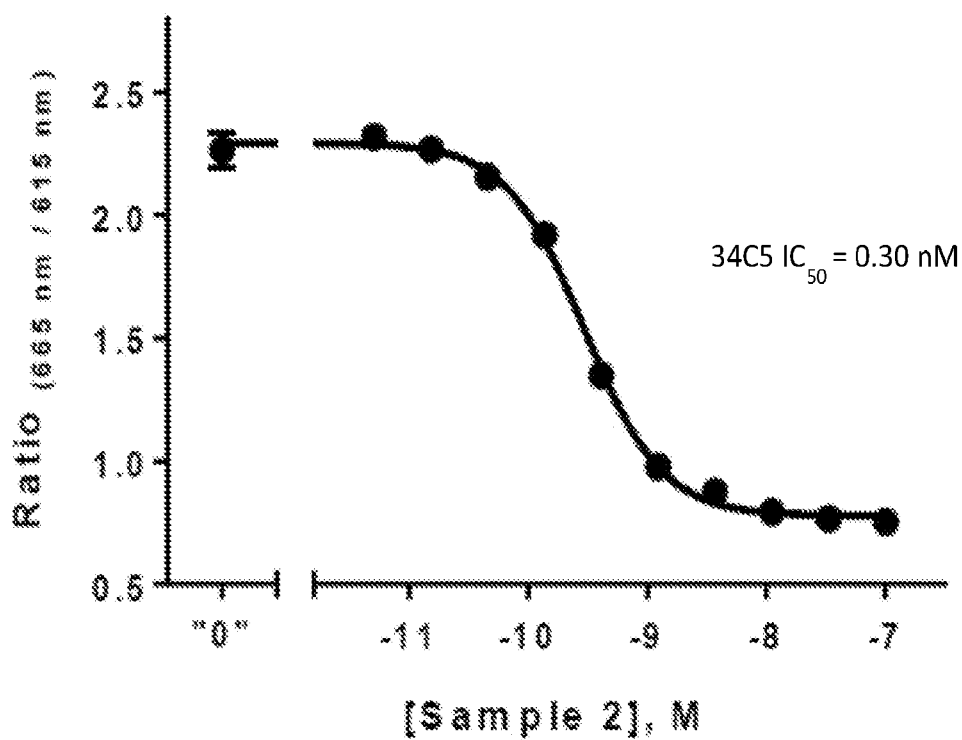


Fig. 22

Phagocytosis of tumor cells by human MΦ

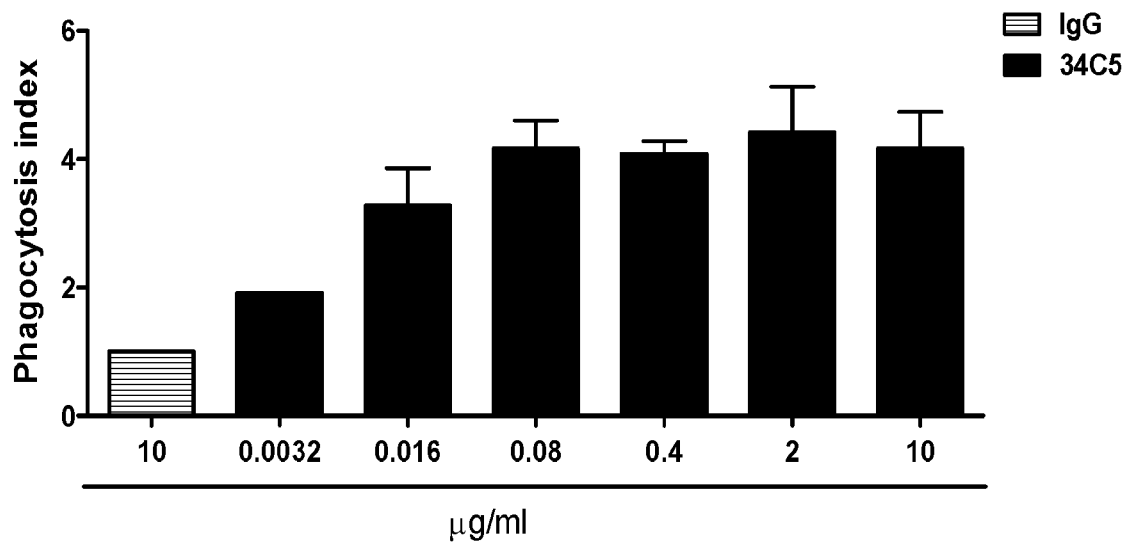


Fig. 23

In vitro RBC agglutination properties

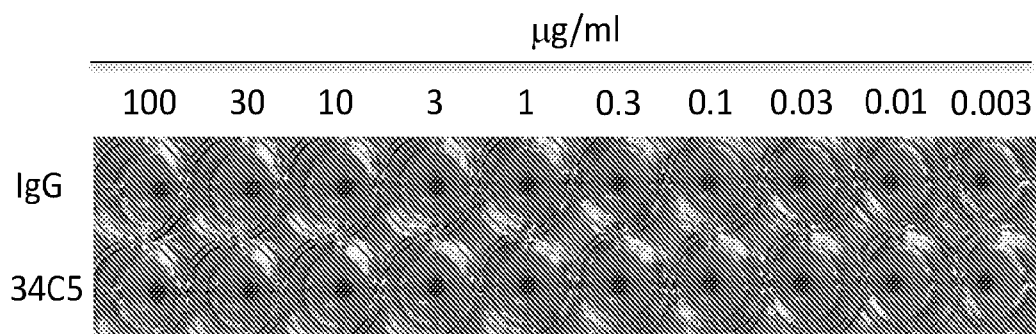


Fig. 24

In vitro RBC binding properties

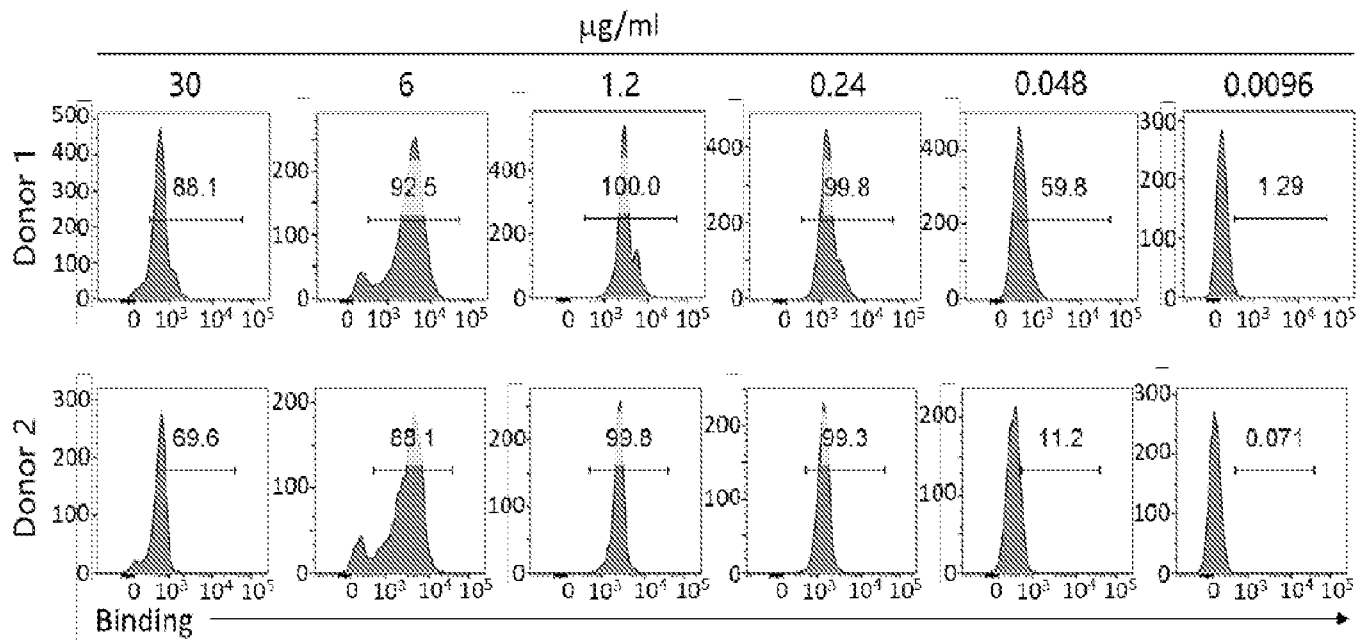


Fig. 25

Amino Acid Sequences:

>CD47-1A1

VH

SEQ ID NO.: 1

QVQLQQSGGGLVQPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN
KNTLYLQMNSLRVEDTAVYYCARYSIGRHTFDHWGQGTLLTVSA

VL

SEQ ID NO.: 2

NFMLTQPHSVSESPGKTVTISCTRSSGGIASNFVQWYQQRPGSVPPTTVIYRDNQRPSGVPDRFSGSVDSSSNSAS
LTISGLKTDDEADYYCQSYDDHNHWVFGGGTKLTVL

>CD47-1F8

VH

SEQ ID NO.: 3

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ ID NO.: 4

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISLHAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-2A11

VH

SEQ ID NO.: 5

QVQLQQSGGGLVQPGGSLRLSCAASGFTFSGYAMTWVRQAPGKGLEWVSAITSTGGRTYYADSVKGRFTTSRDN
RNTLYLQMNSLRAEDTAVYYCARESNFRAFDIWGQGTMTVSA

VL

SEQ ID NO.: 6

EIVLTQSPSLPVTPEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLNNSNRASGVPDRFSGSGSGTD
FTLQISRVEAEDVGVYYCMQALQIPPTFGGGTKVDIK

>CD47-2C2

VH

SEQ ID NO.: 7

EVQLVESGGGLVQPGGSLRLSCAASGFTFIDAWMTWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDN
NTLYLQMNSLRAEDTAVYYCARGARGHPGQDYWGQGTLLTVSA

VL

SEQ ID NO.: 8

NFMLTQPHSVSESPGKTVTISCTRSSGTIASNFVQWYQQRPSSPTPVIFENDRRPSGVPDRFSGSIDSSSNSAS
LTISSLNTEDKADYYCQSYDSSTHGWVFGGGTQLTVL

>CD47-2D7

VH

SEQ ID NO.: 9

QVNLRESGGGLVQPGGSLRLSCAASGFTFSDYYMSWIRQAPGGGLEWVSYSRFGSDTNYADSVKGRFTISRDNV
QNSLYLQMNSLRAEDTAVYYCVRDVHNRDAYWGQGTLLVTVSA

VL

SEQ ID NO.: 10

SYVLTQPPSASGTPGQRTISCSGSSSNIGGNSVSWYQQLPGTAPKLLIYRNHQRP SGVPDRFSGSKSGTSASLA
ISGLRSDDEADYYCATWDFSLSGFVFGTGTKVTVL

>CD47-2G4

VH

SEQ ID NO.: 11

QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN
KNTYYCANTDYYDSSSHTPADYWGQGTLLVTVSA

VL

SEQ ID NO.: 12

ETTLTQSPSSLSASVGDRVTITCRASQDIRNDLDWFQQKPGEAPKRLISAASNLSQGVPSRFSGGSGSEFTLTI
HSLESEDFATYYCQQSYITPPWTFGQGTKLEIK

>CD47-2G11

VH

SEQ ID NO.: 13

QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYGMSWVRQAPGKGLEWVSTISGSGSSTNYADSVKGRFTISRDN
KNTLFLQMNSLRAEDTAVYFCAGRYYYDSLDAFDIWGQGTMTVSA

VL

SEQ ID NO.: 14

EIVLTQSPGTLISLSPGERATLSCRASQEIRTAYLAWYQQKPGQAPRLLIYYASSRATGIPDRFSGSRSGTDFTLT
ISRLEPEDFAVYSCQQYDTSPPTFGQGTRLEIK

>CD47-6F4

VH

SEQ ID NO.: 15

QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGTGGSTYYADSVKGRFTISRDN
KNTLYLQMNSLRAEDTAAYYCAKDKWSSWPTYFYFDYWGQGTLLVTVSA

VL

SEQ ID NO.: 16

NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRP GSSPTTVIYEDNQRP SGVPDRFSGSIDSSSNSAS
LTISGLKTEADYYCQSYDSSNVIFGGGTKVTVL

>CD47-5H1

VH

SEQ ID NO.: 17

QVQLQVSGGGLVQPGGSLRLSCAASGFTFSSYSMAWVRQAPGKGLEWVAAVSNSGVETYYADSVKGRFTISRDN
KNTLYLQMNSLRAEDTAVYYCAKRTRQLLTPREFDYWGQGLVTVLA

VL

SEQ ID NO.: 18

ETTLTQSPSSVSASVGDRVTLTCRASQDITRWLAWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQGSSVPFTFGGGTKVEIK

>CD47-5F6

VH

SEQ ID NO.: 19

QVNLRESGGGLIQPGGSLRLSCAASGFTFTNYAMSWVRQAPGKGLEWVSSVSSAGGSTYYADSVKGRFTISRDN
KNSLYLQMNSLRAEDTAVYYCARRVNRAFDLWGRGTLVTVSA

VL

SEQ ID NO.: 20

DVVMTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLT
ISRLEPEDFAVYYCQQYGSSPPMYTFGQGTKLEIK

>CD47-1F3

VH

SEQ ID NO.: 21

QVQLQESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLVWVGRIKSKTDGGTTDYAAPVKGRFTISR
DSKNTLYLQMNSLKTEDTAVYYCTTDKSYGYTFDYWGQGLVTVSA

VL

SEQ ID NO.: 22

SYVLTPPPSASGTPGQRTISCSGSGSNIGSNSVHWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGISASLA
ISGLQSEDEAVYYCATWDDRLSGPVFAAGTKLTVL

>CD47-2A4

VH

SEQ ID NO.: 23

QVNLRESGGGLVKPGGSLRLSCAASGFTFSSYWMHWVRQAPGKGLEWVSAISGSGAGTYYPDSVKGRFTISRDN
KNTLYLQMNSLRAEDTAVYYCARDRLSFGFDIWGQGLVSVSG

VL

SEQ ID NO.: 24

NFMLTQPHSVSGSPGKTVTISCTRSSGSIGSTYVQWYQQRPGSPPTTVIYKDDQRPSGVPDRFSGSIDGSSNSAS
LTISGLETEDEADYYCQSSDTSNLVFGGGTKVTVL

>CD47-2B12

VH

SEQ ID NO.: 25

QVQLQQSGGGLVQPGGSLRLSCAAPGFTFSRYWMSWVRQAPGKGLEWVANIKGDGSQTYADSVKGRFTISRDNAMKTVYLYQMNSLRAEDTAIYYCAKGAAYHINSWLDPWGQGTLLVTVSA

VL

SEQ ID NO.: 26

ETTLTQSPGTLSPGERVTLSRASQSSISGNLAWYQQRPQGAPRLLIYGAFFRRATGIPDRFSGSGSGTDFTLTITRLEPEDFATYYCQHYNNFPHTFGAGTKVDIK

>CD47-13A11

VH

SEQ ID NO.: 27

KVQLVESGGGLVKPGGSLRLSCAASGITFKHAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISRDSKNTLYLYQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 28

DIVMTQSPDSLAVSLGERATINCKSSQSVLYQVNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGTEFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-15E1

VH

SEQ ID NO.: 29

KVQLVESGGGLVKPGGSLRLSCAASGFTFNNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISRDSKNTLYLYQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 30

DIVMTQSPDSLAVSLGERATINCKSSQTVLYPLNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGTEFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-13H3

VH

SEQ ID NO.: 31

KVQLVESGGGLVKPGGSLRLSCAASGLTFERAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISRDSKNTLYLYQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 32

DIVMTQSPDSLAVSLGERATINCKSSQSVLYAGNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGTEFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-14A8

VH

SEQ ID NO.: 33

KVQLVESGGGLVKPGGSLRLSCAASGFTFPNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA
VL

SEQ. ID NO.: 34

DIVMTQSPDSLAVSLGERATINCKSSQSVLYPGNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDFRSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-16H3

VH

SEQ ID NO.: 35

KVQLVESGGGLVKPGGSLRLSCAASGLTFGNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA
VL

SEQ. ID NO.: 36

DIVMTQSPDSLAVSLGERATINCKSSQSVLYPGNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDFRSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-1A1

VH

SEQ ID NO.: 37

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGNHSSDIWGQGTMTVSA
VL

SEQ. ID NO.: 38

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDFRSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-1A1-A

VH

SEQ ID NO.: 39

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGAHSSDIWGQGTMTVSA
VL

SEQ. ID NO.: 40

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDFRSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-1A1-Q

VH

SEQ ID NO.: 41

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGQHSSDIWGQGMVTVSA
VL

SEQ. ID NO.: 42

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-1A2

VH

SEQ ID NO.: 43

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSAYAFDAWGQGMVTVSA

VL

SEQ. ID NO.: 44

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-1A8

VH

SEQ ID NO.: 45

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSAYAFDSWGQGMVTVSA

VL

SEQ. ID NO.: 46

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-1B1

VH

SEQ ID NO.: 47

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSDRASDKWGQGMVTVSA

SEQ. ID NO.: 48

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-1B2

VH

SEQ ID NO.: 49

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSAYAFDTWGQGMVTVSA

VL

SEQ. ID NO.: 50

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGGTKLEIK

>CD47-1H3

VH

SEQ ID NO.: 51

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGNHSQDIWGQGTMTVSA

VL

SEQ. ID NO.: 52

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGGTKLEIK

>CD47-1H3-Q

VH

SEQ ID NO.: 53

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGQHSQDIWGQGTMTVSA

VL

SEQ. ID NO.: 54

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGGTKLEIK

>CD47-1H3-A

VH

SEQ ID NO.: 55

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGAHSQDIWGQGTMTVSA

VL

SEQ. ID NO.: 56

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGGTKLEIK

>CD47-2A2

VH

SEQ ID NO.: 57

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 58

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLTPPLAFGGGTKLEIK

>CD47-2A3

VH

SEQ ID NO.: 59

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGMVTVSA

VL

SEQ. ID NO.: 60

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLRPPLNFGGGTKLEIK

>CD47-2A6

VH

SEQ ID NO.: 61

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGMVTVSA

VL

SEQ. ID NO.: 62

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLTPPLNFGGGTKLEIK

>CD47-2A10

VH

SEQ ID NO.: 63

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGMVTVSA

VL

SEQ. ID NO.: 64

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQNYLTPPLSFGGGTKLEIK

>CD47-2B1

VH

SEQ ID NO.: 65

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGMVTVSA

VL

SEQ. ID NO.: 66

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLKAPLAFGGGKLEIK

>CD47-2C6

VH

SEQ ID NO.: 67

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISRD
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 68

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLNAPLHFGGGKLEIK

>CD47-2E7

VH

SEQ ID NO.: 69

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISRD
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 70

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLEAPLVFGGGKLEIK

>CD47-2E9

VH

SEQ ID NO.: 71

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISRD
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 72

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLKAPLHFGGGKLEIK

>CD47-2F1

VH

SEQ ID NO.: 73

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISRD
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 74

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQRLLIAPPFTFGGGTKLEIK

>CD47-2F3

VH

SEQ ID NO.: 75

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGMVTVSA

VL

SEQ. ID NO.: 76

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQNYLTPPLAFGGGTKLEIK

>CD47-34C5

VH

SEQ. ID NO.: 77

CAGGTCCAACCTGGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGTCTTCAGTGAAGGTGTCCTGCAAGGCTTCT
GGCTACACCTTCAGCAGCTACTATATGCACTGGGTGAGGCAGGCTCCTGGACAAGGCCTTGAGTGGATGGGAGAG
ATTAATCCCAACAATGCCCCGTATTAACCTCAATGAAAAGTTCAAGACCAGGGTCACACTCACTGTGGACAAATCC
ACCAGCACAGCATACATGGAGCTCAGCAGCCTGAGATCTGAGGACACCGCGGTCTATTACTGTACCAGAGGATAC
TATAGGTACGGGGCCTGGTTTGGTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTTCA

>CD47-34C5

VL

SEQ. ID NO.: 78

GATATCCAGATGACACAGTCTCCATCCTCCCTGTCTGCCTCTGTGGGAGACAGAGTCACCATCACTTGCAGGGCA
AGTCAGGACATTAGCGATTATTTGAACTGGTATCAACAGAAACCAGGCAAGGCTCCTAAACTCCTGATCTACTAC
ATATCAAGATTACACTCAGGAGTCCCATCACGCTTCAGTGGCAGTGGGTCTGGAACAGATTATACTCTCACCATT
AGCTCCCTGCAGCCAGAAGATTTTGCCACTTACTATTGCCAACAGGGTCATACACTTCCGTGGACCTTCGGTGGA
GGCACCAAGGTGGAAATCAAA

NUCLEOTIDE SEQUENCES OF VH:

>CD47-1A1_VH

SEQ ID NO.: 79

CAGGTACAGCTGCAGCAGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTAAGACTCTCCTGTACAGCCTCT
GGATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCA
ATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGTCGAGGACACGGCCGTATATTACTGTGCGAGATATAGT
ATTGGTAGACACACCTTTGACCACTGGGGCCAGGGCACCTGGTCAACCGTCTCGGCC

>CD47-1F8_VH

SEQ ID NO.: 80

AAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGGTCCCTTAGACTCTCCTGTGCAGCCTCT
GGTTTCACTTTTCAGTAACGCCTGGATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTGGCCGT
ATTAAAAGGAAAACCTGATGGTGAGACAACAGACTACGCTGCACCCGTGAAAGGCAGATTTCAGCATCTCAAGAGAT
GATTCAAAAAACACCCTGTATCTGCAAATGAACAGCTTGAAAACCGAGGACACAGCCGTGTATTACTGCGCTGGC
AGTAACCGAGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTGCC

>CD47-2A11_VH

SEQ ID NO.: 81

CAGGTACAGCTGCAGCAGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTAGCGGCTATGCCATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT
ATTACTTCTACTGGTGGTCTGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCACCTCCAGAGACAATTCC
AGGAACACGTTGTATCTGCAAATGAACAGCCTGAGAGCCGAAGACACGGCCGTATATTACTGTGCGAGAGAGTCA
AACTTCAGGGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTGCC

>CD47-2C2_VH

SEQ ID NO.: 82

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTTAGACTCTCCTGTGCAGCCTCT
GGATTCACTTTTCATTGACGCCTGGATGACCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGTT
ATTTATAGCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGGGGCTAGG
GGCCATCCCGGGCAGGACTACTGGGGGCAGGGCACCCCTGGTCACCGTCTCTGGCC

>CD47-2D7_VH

SEQ ID NO.: 83

CAGGTCAACTTAAGGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTCAGTGACTACTACATGAGCTGGATCCGCCAGGCTCCAGGGGGGGGGCTGGAGTGGGTTTCATAC
ACTAGTCGTTTTGGTAGTGACACAACTACGCAGACTCTGTGAAGGGCCGATTACCATCTCCAGAGACAACGTC
CAGAACTCACTATATCTGCAAATGAACAGCCTGAGGGCCGAGGACACGGCTGTTTATTACTGTGTGAGAGATGTA
CATAACAGGGATGCCTACTGGGGCCAGGGCACCCCTGGTCACCGTCTCTGGCC

>CD47-2G4_VH

SEQ ID NO.: 84

CAGGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT
ATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAACACAGAT
TACTATGATAGTAGTAGCCATACCCCCGCTGACTACTGGGGCCAGGGCACCCCTGGTCACCGTCTCTGGCC

>CD47-2G11_VH

SEQ ID NO.: 85

CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTAGTAGCTATGGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAACT
ATCAGTGGCAGTGGTAGTAGCACAACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTATTTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTTCTGTGCGAAAGGCCGA
TATTACTATGATAGTCTTGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTGCC

>CD47-6F4_VH

SEQ ID NO.: 86

CAGGTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT
ATTAGTGGTACTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGCATATTACTGTGCGAAAGATAAA
TGGAGCAGCTGGCCCACTTACTACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCGGCC

>CD47-5H1_VH

SEQ ID NO.: 87

CAGGTGCAGCTGCAGGTGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTCAGTAGCTATAGCATGGCCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTCGCGGCT
GTTAGTAATAGTGGTGTGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATTTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAACGAACT
AGACAACTGCTAACTCCGCGGGAGTTTGACTACTGGGGCCAGGGCACCCCTGGTCACCGTCTTGGCC

>CD47-5F6_VH

SEQ ID NO.: 88

CAGGTCAACTTAAGGGAGTCTGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTACCAATTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAAGT
GTTAGTAGTGCTGGTGGTAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAACGCC
AAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTTTATTACTGTGCGAGACGAGTC
AATCGGGCCTTCGATCTCTGGGGCCGTGGAACCCCTGGTCACCGTCTCGGCC

>CD47-1F3_VH

SEQ ID NO.: 89

CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTTAGACTCTCCTGTGCAGCCTCT
GGATTCACTTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGTGTGGGTGGCCGT
ATTAAAAGCAAACTGATGGTGGGACAACAGACTACGCTGCACCCGTGAAAGGCAGATTACCATCTCAAGAGAT
GATTCAAAAAACACGCTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACCACA
GATAAGAGCTATGGTTACACATTTGACTACTGGGGCCAGGGCACCCCTGGTCACCGTCTCGGCC

>CD47-2A4_VH

SEQ ID NO.: 90

CAGGTCAACTTAAGGGAGTCTGGGGGAGGCTTGGTAAAGCCGGGGGGGTCCCTTAGACTCTCCTGTGCAGCCTCT
GGATTACCTTCAGTAGCTACTGGATGCACTGGGTCCGCCAAGCCCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT
ATCAGTGGTAGTGGTGCCGGCACATACTACCCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGATCGG
TCCTTATCTTTTGGTTTTGATATTTGGGGCCAAGGCACCTGGTCTCCGTCTCTGGC

>CD47-2B12_VH

SEQ ID NO.: 91

CAGGTACAGCTGCAGCAGTCAGGGGGAGGCTTGGTCCAGCCGGGGGGGTCACTGAGACTCTCCTGTGCAGCCCCCT
GGATTACCTTTAGTAGATATTGGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGACTGGAGTGGGTGGCCAAC
ATAAAGGGAGATGGAAGTCAGACATACTATGCGGACTCTGTGAAGGGCCGATTACCATCTCCAGAGACAACGCC
ATGAAAACAGTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCATATATTACTGTGCGAAAGGGGCT
GCTTATCACATTAACAGCTGGCTCGACCCCTGGGGCCAGGGCACCTGGTCACCGTCTCGGCC

NUCLEOTIDE SEQUENCES OF VL:

>CD47-1A1_VL

SEQ ID NO.: 92

AATTTTATGCTGACTCAGCCCCACTCTGTGTGCGAGTCTCCGGGGAAGACGGTAACCATCTCCTGCACCCGCAGC
AGTGGCGGCATTGCCAGTAACCTTTGTGCACTGGTACCAGCAGCGCCCGGGCAGTGTCCCCACCACTGTGATCTAT
AGGGATAACCAAAGACCCCTCTGGAGTCCCTGATCGGTTCTCTGGCTCCGTGACAGCTCCTCCAATTCTGCCTCC
CTCACCATCTCTGGGCTGAAGACTGACGATGAGGCTGACTATTATTGTGAGTCCTATGATGACCACAATCATTGG
GTGTTGCGGCGGCGGGACCAAGCTGACCGTCCTA

>CD47-1F8_VL

SEQ ID NO.: 93

GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCC
AGCCAGAGTGTTTTATACAGCTCCAACAATAGGAACTACCTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCT
AAGCTGCTCATTAACCAGGCATCTACCCGGGCATCCGGCGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACA
GAGTTCACTCTCATCATCAGCAGCCTGCAGGCTGAAGATGTGGCGATTATTACTGTGAGCAATATTATACTCCT
CCCCTCGCTTTCGGCGGAGGGACCAAGCTGGAGATCAAA

>CD47-2A11_VL

SEQ ID NO.: 94

GAAATTGTGTTGACGCAGTCTCCACTCTCCCTGCCCCTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCT
AGTCAGAGCCTCCTGCACAGTAATGGATACAACCTATTTGGATTGGTACCTGCAGAAACCAGGGCAGTCTCCACAG
CTCCTGATCTATTTGAATTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGTACAGAT
TTTACACTGCAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTACTACTGTATGCAAGCTCTACAAATTCCT
CCCACTTTCGGCGGAGGGACCAAGTGGATATCAAA

>CD47-2C2_VL

SEQ ID NO.: 95

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGAAAGACGGTAACCATCTCCTGCACCCGCAGC
AGTGGCACCATTGCCAGCAACTTTGTGCAGTGGTATCAACAGCGCCCGGGCAGTTCGCCACCCCAGTGATCTTT
GAGAATGACCGAAGACCCTCTGGGGTCCCTGATCGGTTCTCTGGCTCCATCGACAGCTCCTCCAATTCTGCCTCC
CTCACCATTTCTGCTACTGAACACTGAGGACAAGGCTGACTACTACTGTCAGTCCTATGATAGCAGCACTCATGGG
TGGGTGTTTGGCGGAGGGACCCAGCTCACCGTTTTA

>CD47-2D7_VL

SEQ ID NO.: 96

TCCTATGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTCTGGAAGC
AGCTCCAACATCGGCGGTAATTCTGTATCCTGGTACCAGCAACTCCCAGGAACGGCCCCCAAGCTCCTCATCTAT
AGGAATCATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCC
ATCAGTGGGCTCCGGTCCGACGACGAGGCTGATTATTATTGTGCAACATGGGATTTACGCCTGAGTGGTTTTGTCT
TTCGGAACCTGGGACCAAGGTCACCGTCCTA

>CD47-2G4_VL

SEQ ID NO.: 97

GAAACTACACTCACGCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCC
AGTCAGGACATCAGAAATGATTTAGACTGGTTTCAACAAAAACCAGGCGAAGCCCCCTAAACGCCTGATCTCTGCT
GCATCTAATTTGCAGAGTGGGGTCCCCCTCACGATTCAGCGGCGGTGGCTCTGGCTCCGAATTCACCTCTCACAATC
CACAGCCTGGAGTCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACATTACCCCTCCTTGGACGTTTCGGC
CAAGGGACCAAGCTGGAGATCAAA

>CD47-2G11_VL

SEQ ID NO.: 98

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCC
AGTCAGGAAATTAGGACCGCCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
TATGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTACGCGGCAGTAGGTCTGGGACAGACTTCACCTCTCACC
ATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTCCTGTCTCAGCAGTATGATACCTCACCTCCCACCTTCGGC
CAAGGGACACGACTGGAGATTAAA

>CD47-6F4_VL

SEQ ID NO.: 99

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAACCATCTCCTGCACCCGCAGC
AGTGGCAGCATTTGCCAGCAACTATGTGCAGTGGTACCAACAGCGCCCGGGCAGTTCCCCCACCAGTGTGATCTAT
GAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCTGGCTCCATCGACAGCTCCTCCAACCTCTGCCTCC
CTCACCATCTCTGGACTGAAGACTGAGGACGAGGCTGACTACTACTGTCAGTCTTATGATAGCAGCAATGTGATA
TTCGGCGGAGGGACCAAGGTCACCGTCCTA

>CD47-5H1_VL

SEQ ID NO.: 100

GAAACTACACTCACGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCCTCACTTGTCGGGCG
AGTCAGGATATCACAAAGGTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGAT
GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC
AGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAACAGGGTTCCAGTGTTCCTTTCACTTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

>CD47-5F6_VL

SEQ ID NO.: 101

GATGTTGTGATGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCC
AGTCAGAGTGTAGCAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
GGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC
ATCAGCAGACTGGAGCCTGAAGATTTTGCACTGTATTACTGTGACAGTATGGTAGCTCACCTCCTATGTACACT
TTTGGCCAGGGGACCAAGCTGGAGATCAAA

>CD47-1F3_VL

SEQ ID NO.: 102

TCCTATGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGT
GGCTCCAACATCGGAAGTAATTCTGTTCACTGGTACCAGCAACTCCAGGAACGGCCCCCAAACCTCCTCATCTAT
ACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCATTTCAGCCTCCCTGGCT
ATCAGTGGGCTCCAGTCTGAGGATGAGGCTGTTTATTACTGTGCAACGTGGGATGACAGACTGAGTGGTCCGGTG
TTCGCCGCAGGGACCAAGCTGACCGTCCTA

>CD47-2A4_VL

SEQ ID NO.: 103

AATTTTATGCTGACTCAGCCCCACTCTGTGTGCGGGTCTCCGGGGAAGACGGTAACCATCTCCTGCACCCGCAGC
AGTGGCAGCATTTGGCAGCACCTATGTGCAGTGGTACCAACAGCGCCCGGGCAGTCCCCCACCCTGTGATCTAT
AAGGATGACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCTGGCTCCATCGACGGCTCCTCCAACCTCTGCCTCC
CTCACCATCTCTGGACTGGAGACTGAGGACGAGGCTGACTACTACTGTGAGTCTTCTGATACCAGCAATCTGGTC
TTCGGCGGAGGGACCAAGGTCACCGTCCTA

>CD47-2B12_VL

SEQ ID NO.: 104

GAAACTACACTCACGCAGTCTCCAGGCACCCTGTCTGTTTCTCCGGGGGAAAGAGTTACCCTCTCCTGCAGGGCC
AGTCAGAGTATTAGCGGTAATTACTTAGCCTGGTACCAGCAGAGACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
GGGGCATTCAGGAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC
ATCACCAGACTGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACACTATAATAATTTCCCCACACTTTTCGGC
GCAGGGACCAAAGTGGATATCAAA

>CD47-34C5_VH

SEQ ID NO.: 105

QVQLVQSGAEVKKPGSSVKVSCKASGYTFSSYYMHWRQAPGQGLEWMGEINPNNARINFNEKFKTRVTLTVDKS
TSTAYMELSSLRSED TAVYYCTRGYYRYGAWFGYWGQGLTVTVSS

>CD47-34C5_VL

SEQ ID NO.: 106

DIQMTQSPSSLSASVGRVTITCRASQDISDYLNWYQQKPGKAPKLLIYYISRLHSGVPSRFSGSGSGTDYTLTI
SSLQPEDFATYYCQQGHTLPWTFGGGTKVEIK

Fig. 26

>CD47

SEQ ID NO.: 107

QLLFNKTksVEF TFCNDTVVIP CFVTNMEAQN TTEVYVKWKF KGRDIYTFDG
ALNKSTVPTD FSSAKIEVSQ LLKGDASLKM DKSDAVSHTG NYTCEVTELT
REGETIIELK YRVVSWFSPNE

Fig. 27