

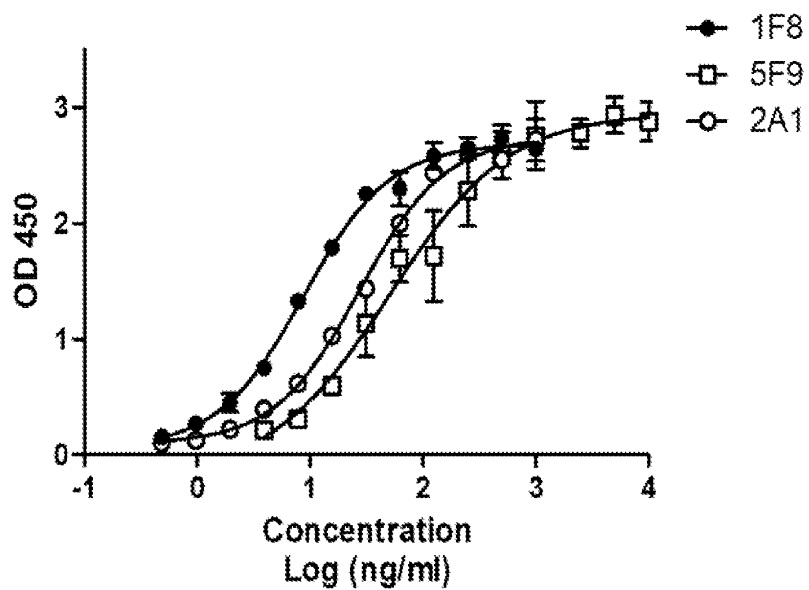


Fig. 1

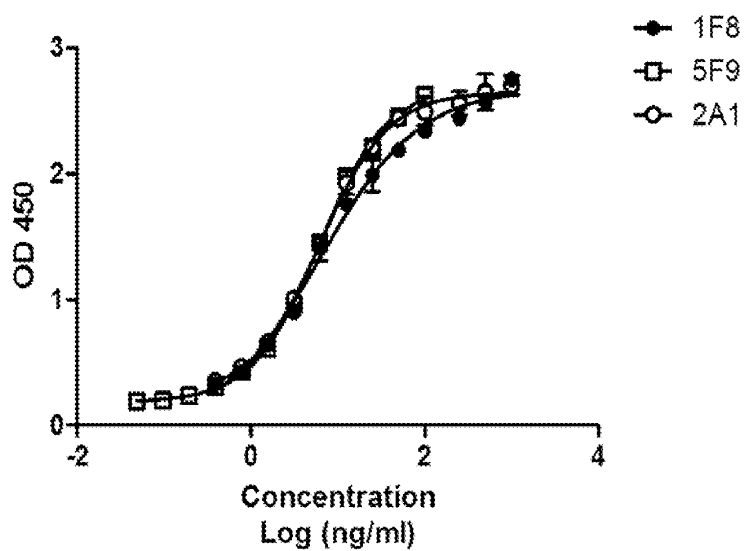


Fig. 2a

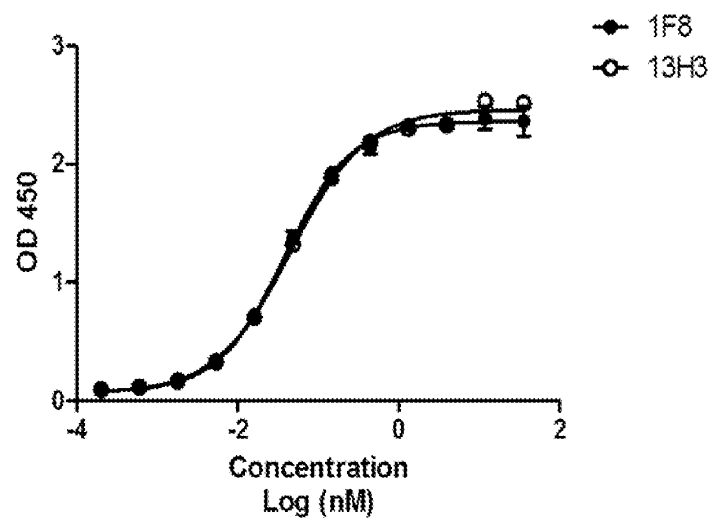


Fig. 2b

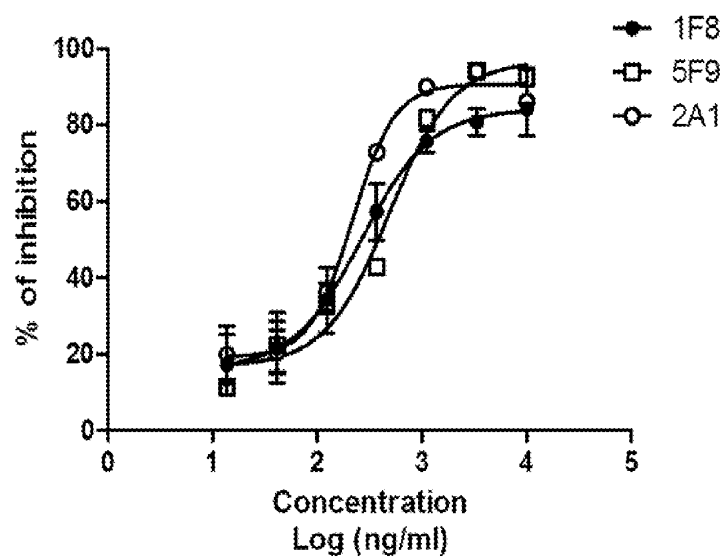


Fig. 3a

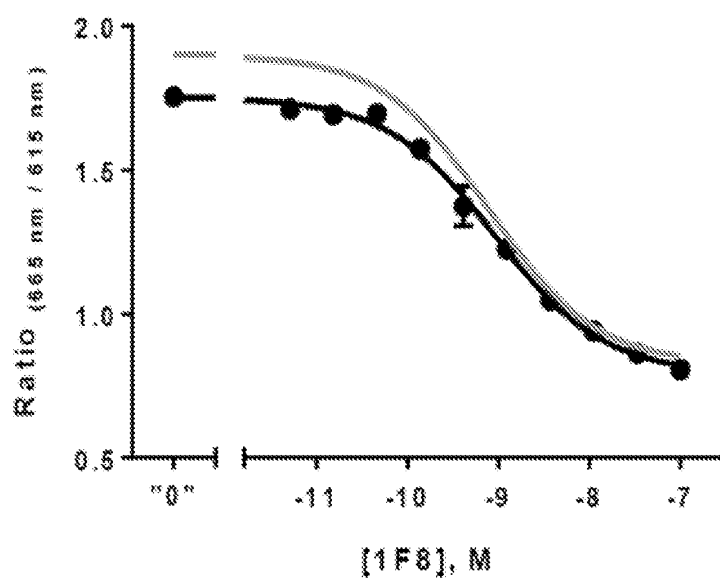
1F8 ($IC_{50} = 0.78 \text{ nM}$)

Fig. 3b

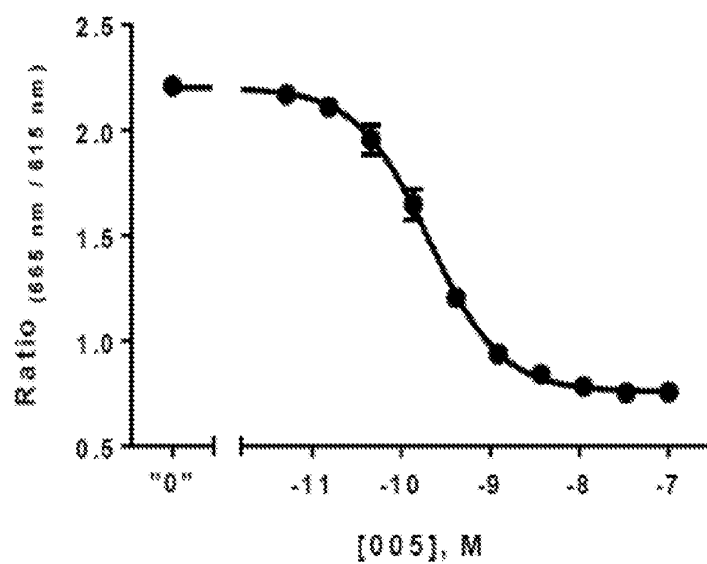
13H3 $IC_{50} = 0.20 \text{ nM}$ 

Fig. 3c

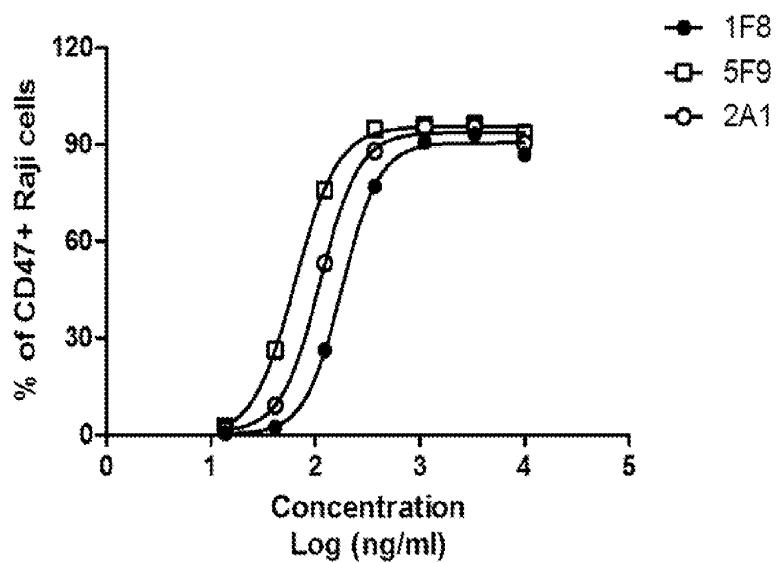


Fig. 4a

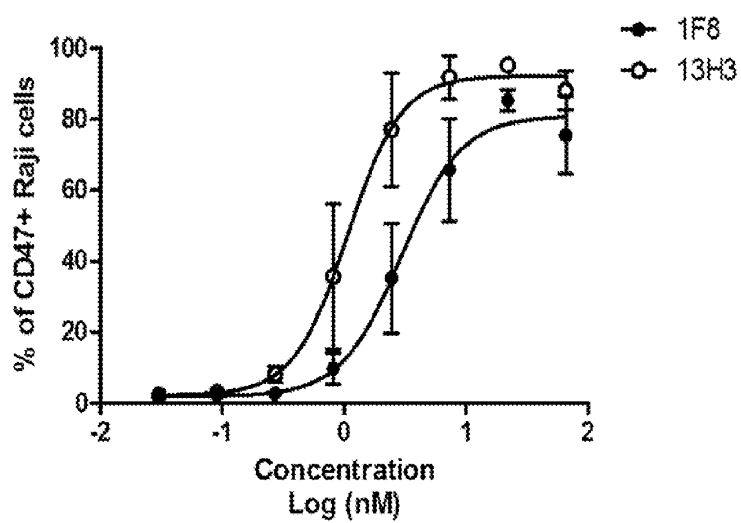


Fig. 4b

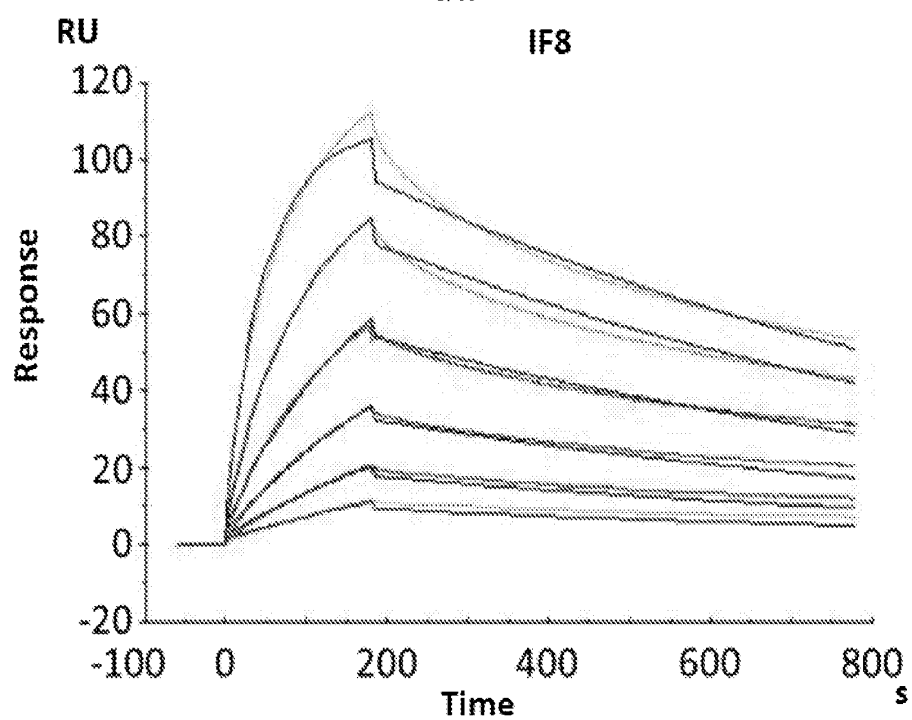


Fig. 4c

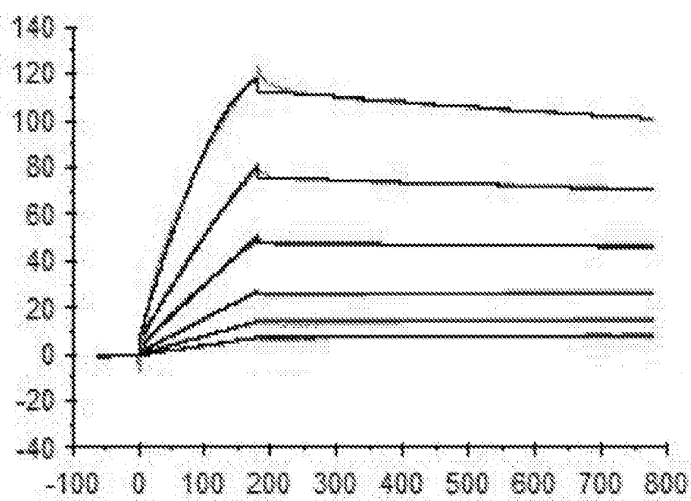
13H3

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

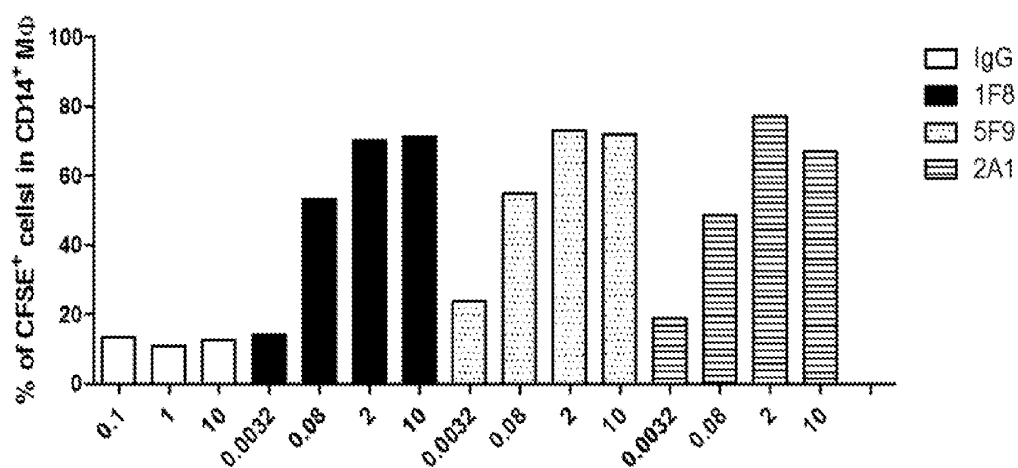


Fig. 5a

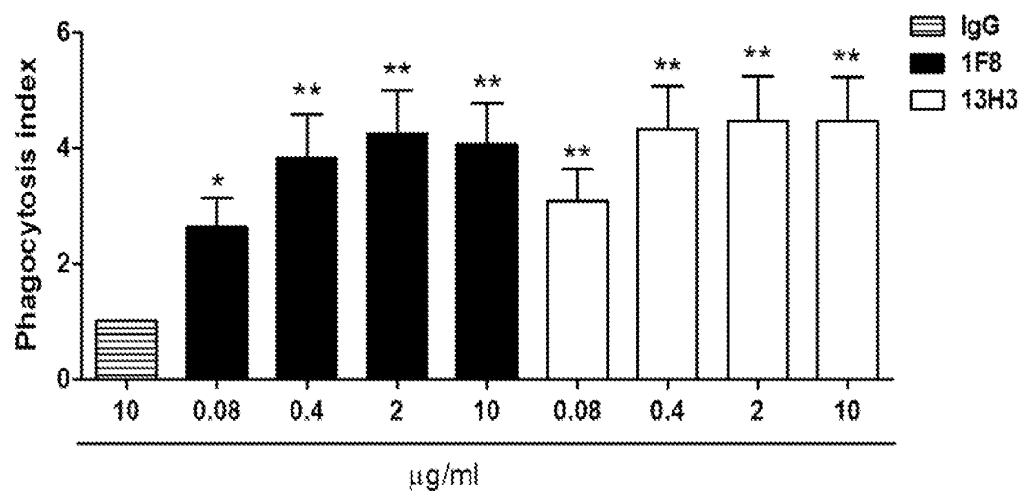


Fig. 5b

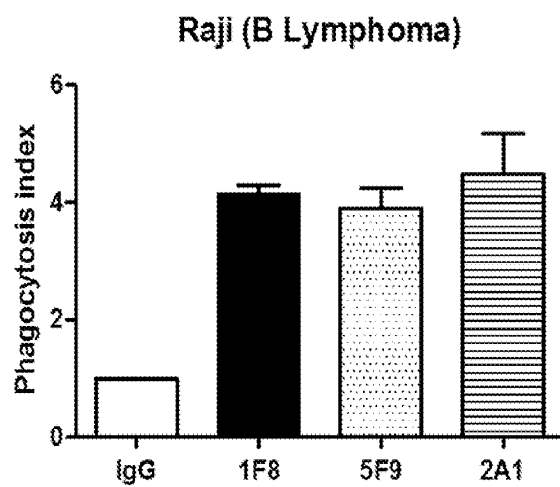


Fig. 6a

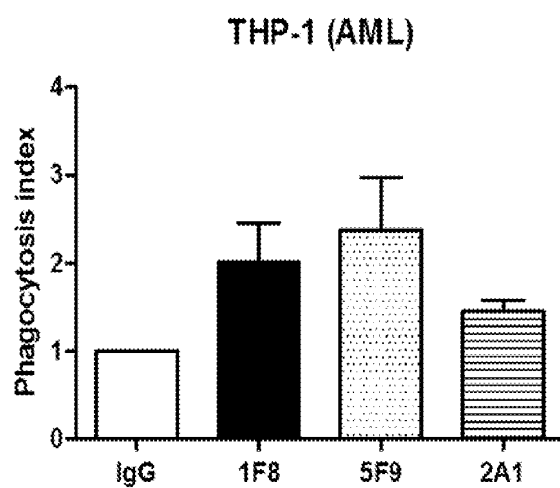


Fig. 6b

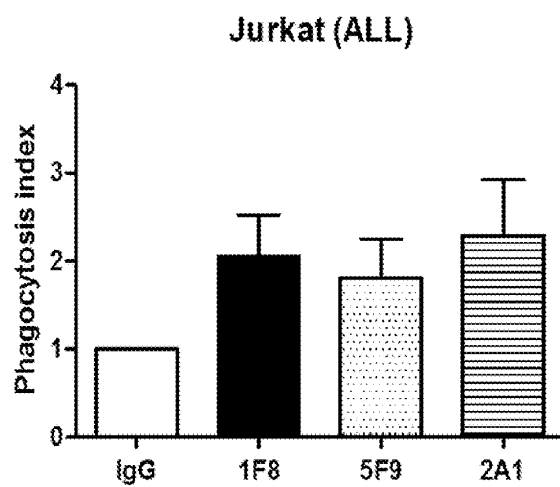


Fig. 6c

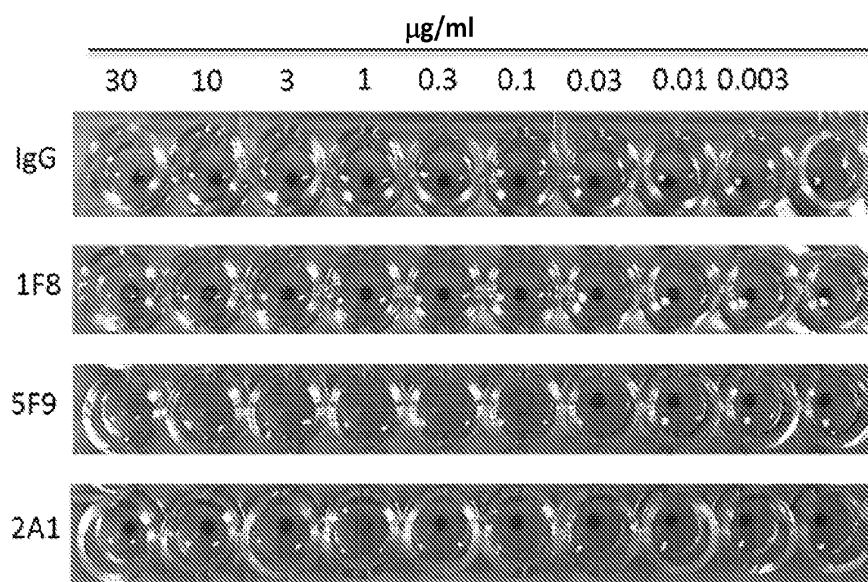


Fig. 7a

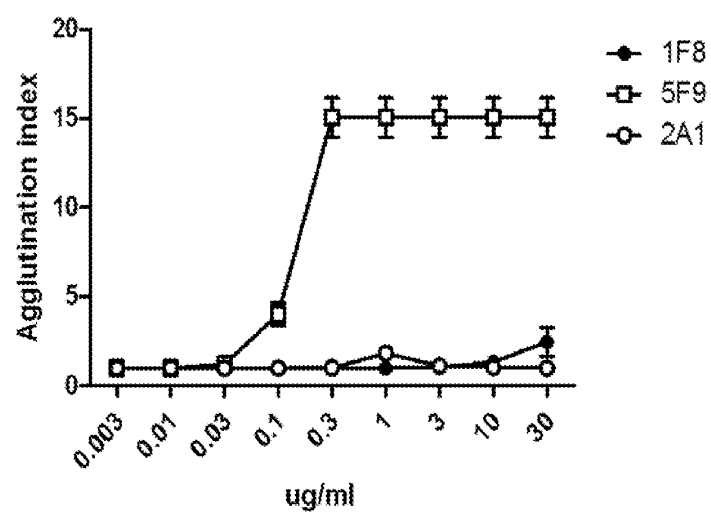


Fig. 7b

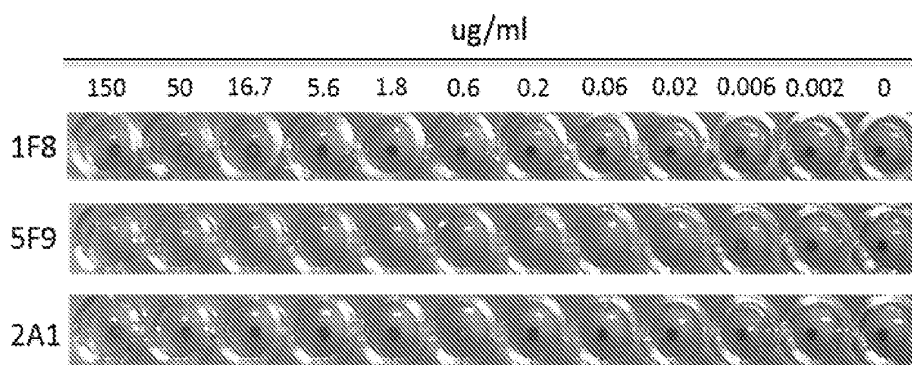


Fig. 8a

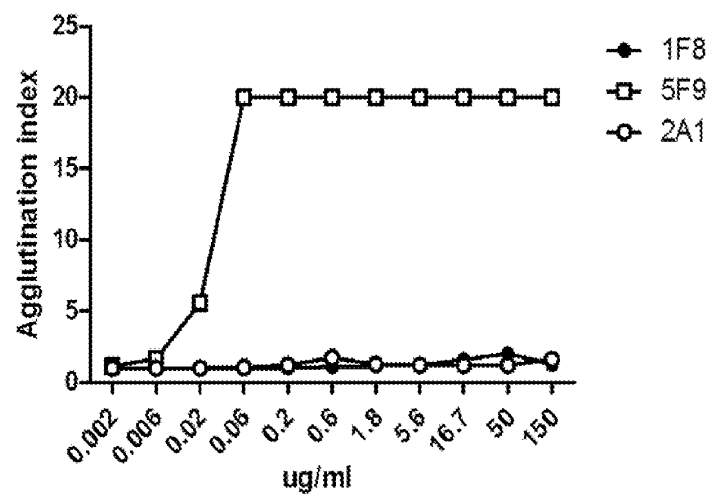


Fig. 8b

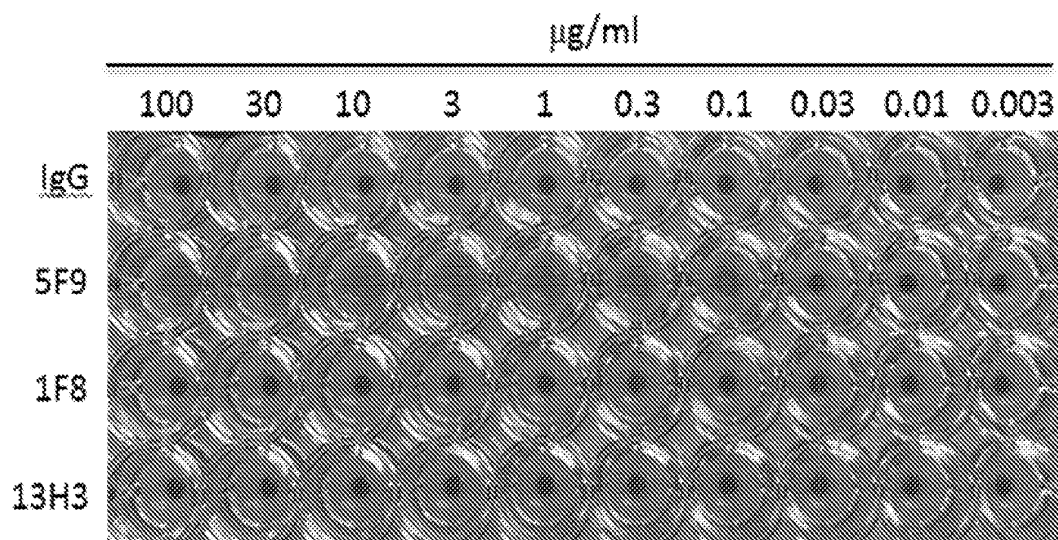


Fig. 8c

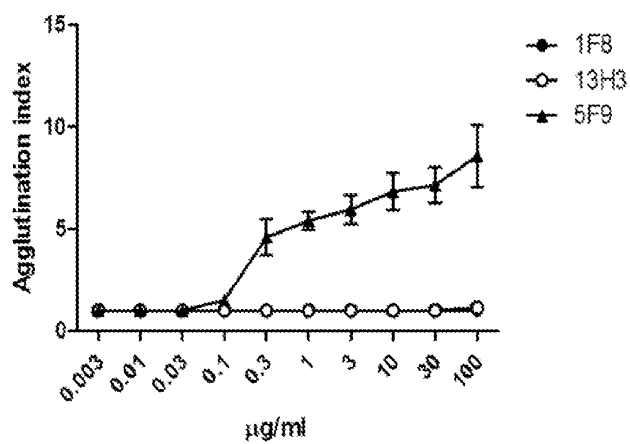


Fig. 8d

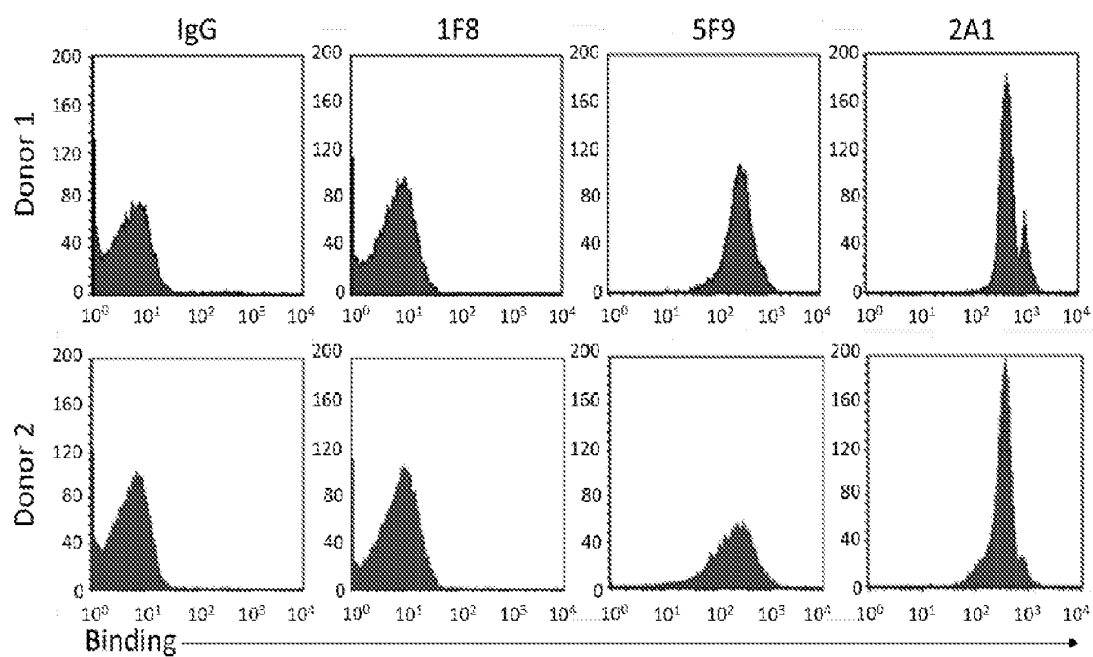


Fig. 9a

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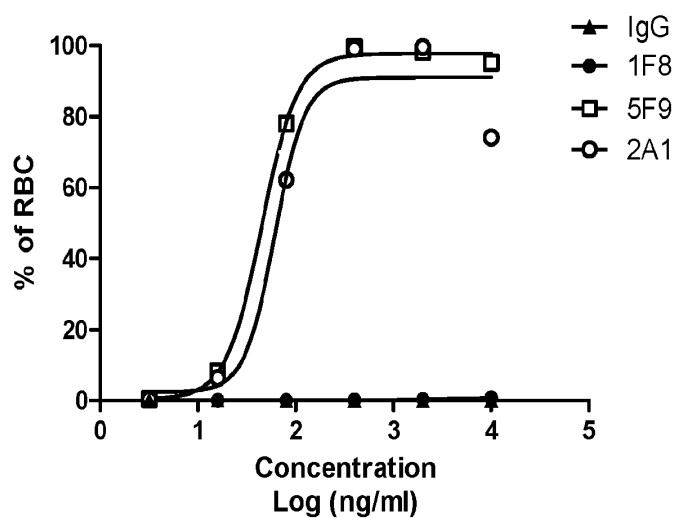


Fig. 9b

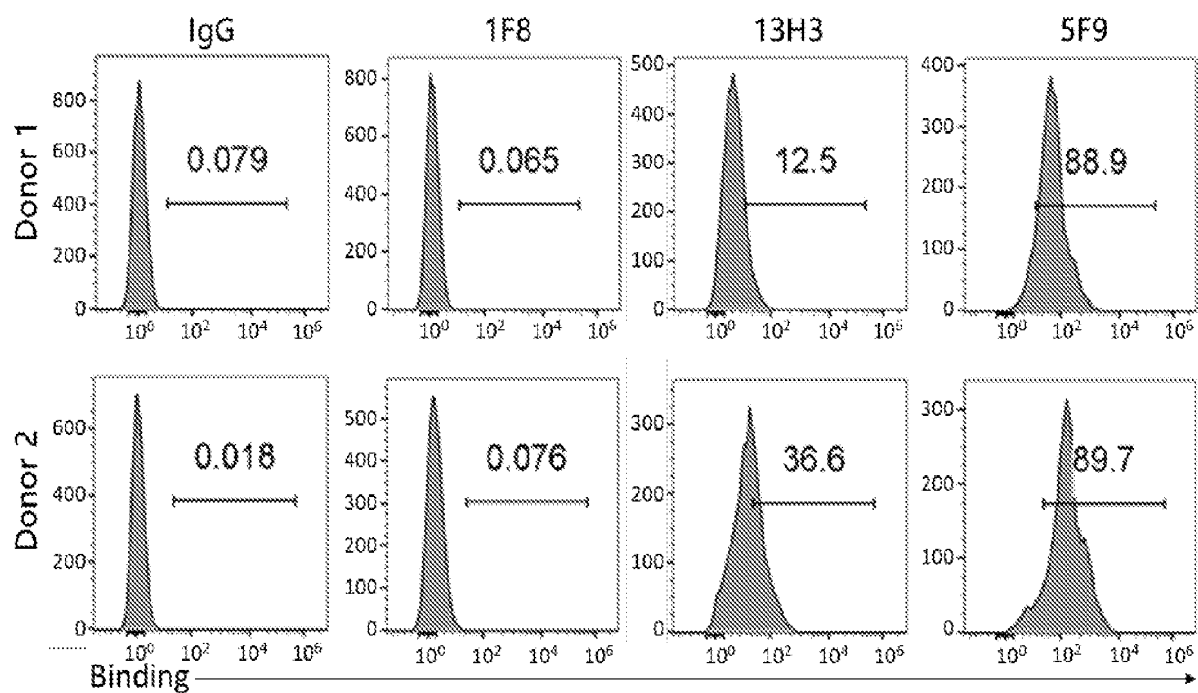


Fig. 9c

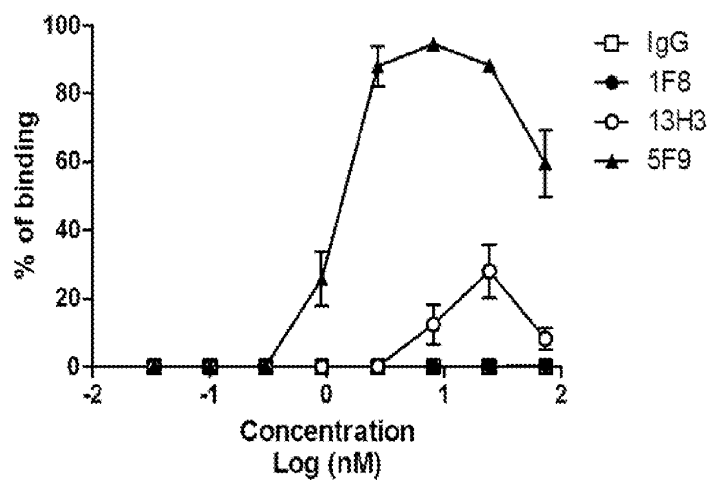


Fig. 9d

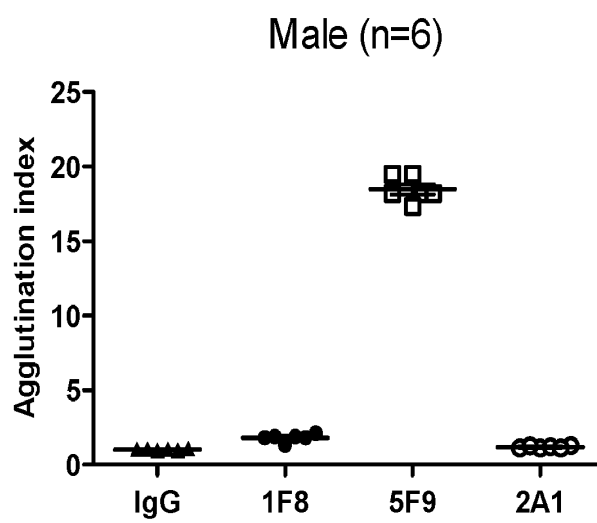


Fig. 10a

Female (n=6)

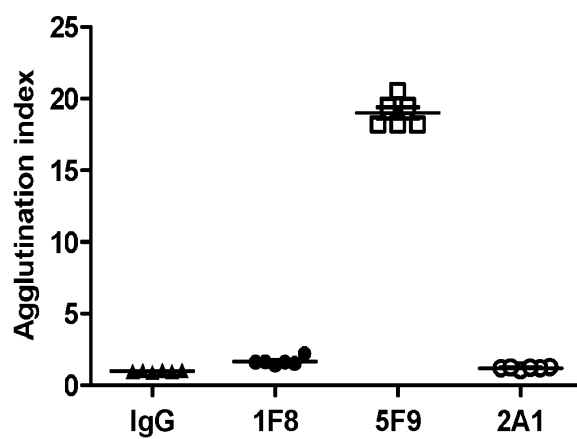


Fig. 10b

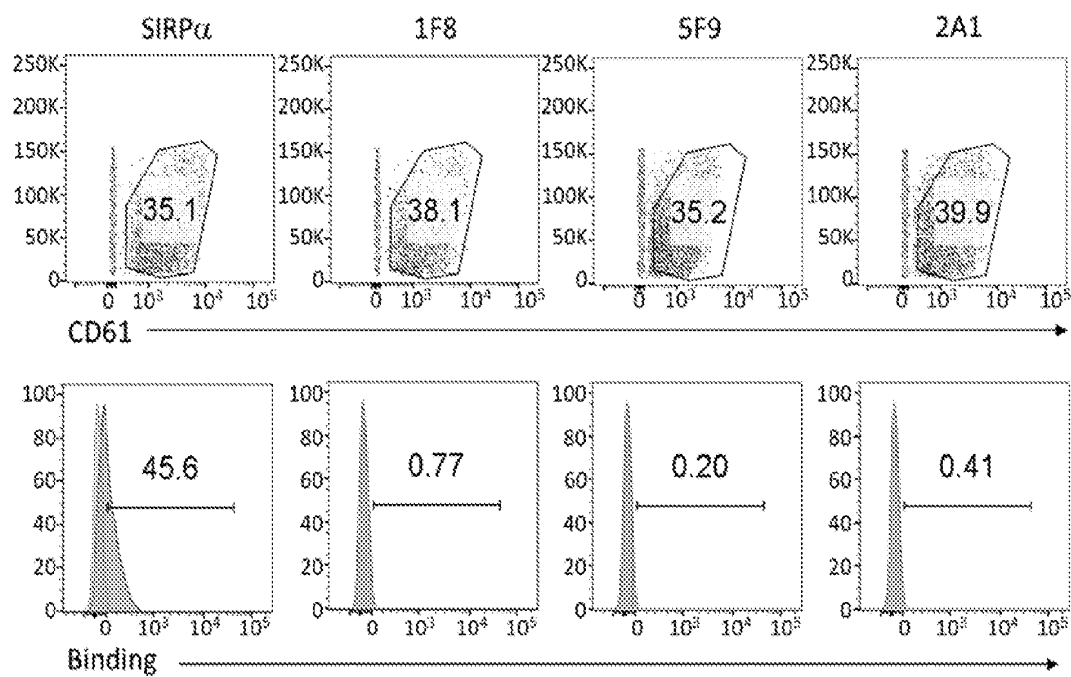


Fig. 11

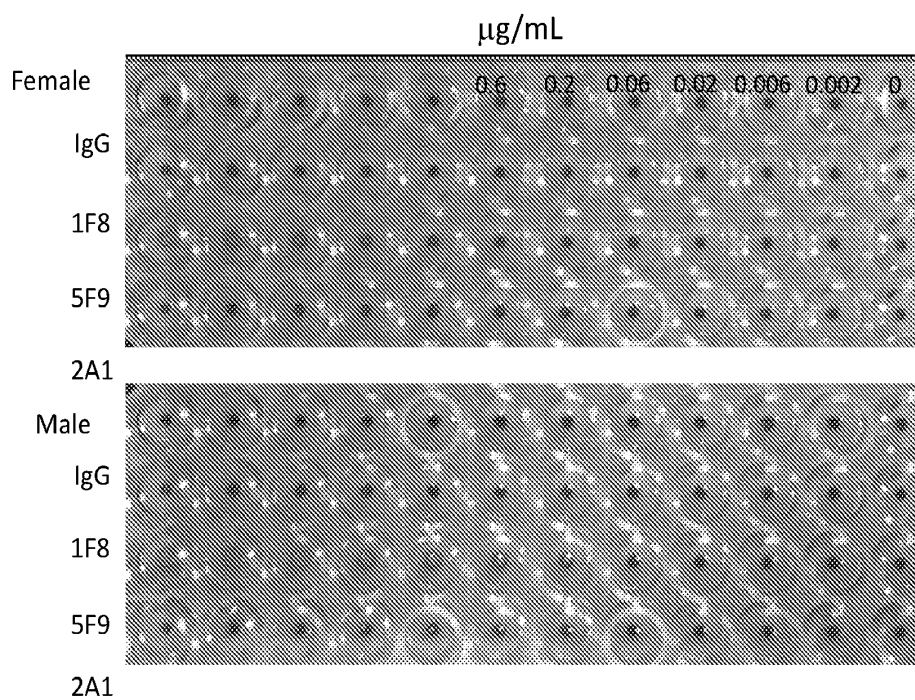


Fig. 12a

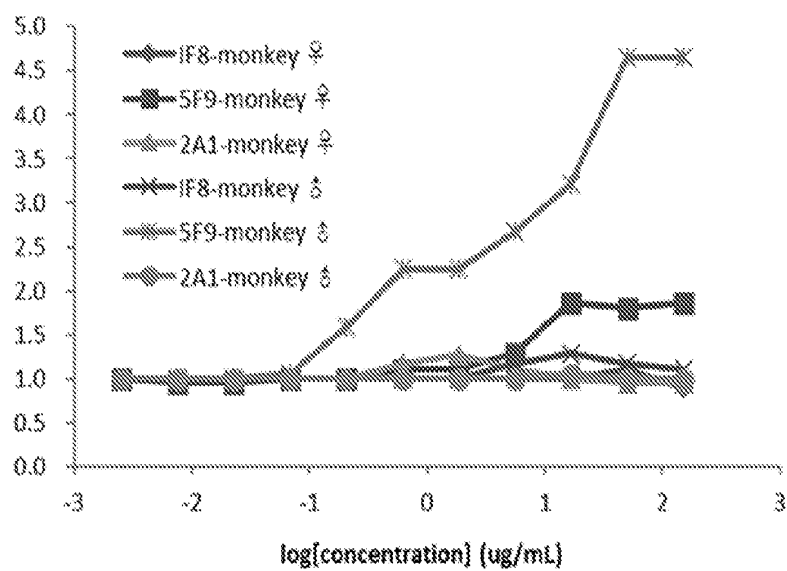
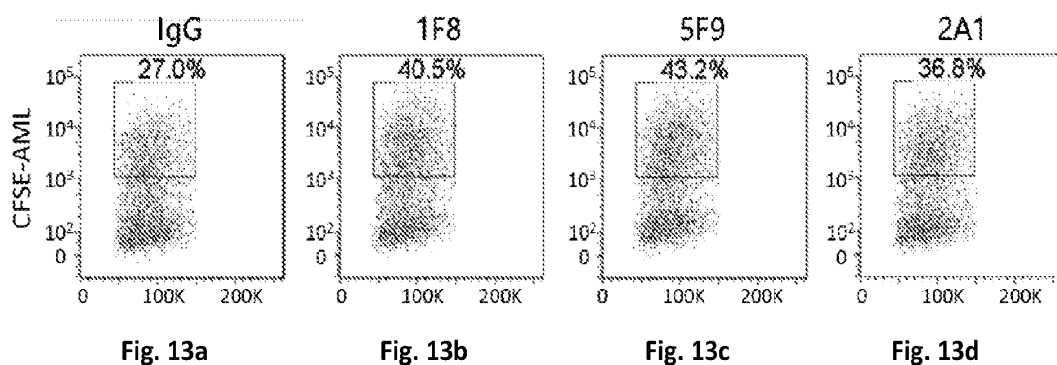


Fig. 12b

Phagocytosis



APC-CD14

AML Binding

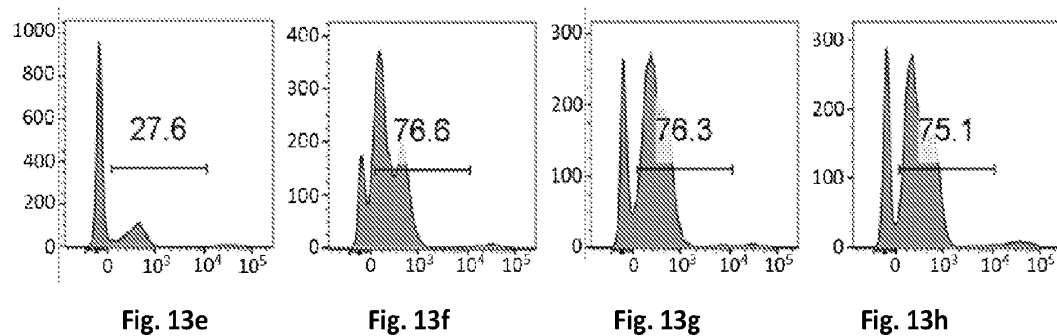
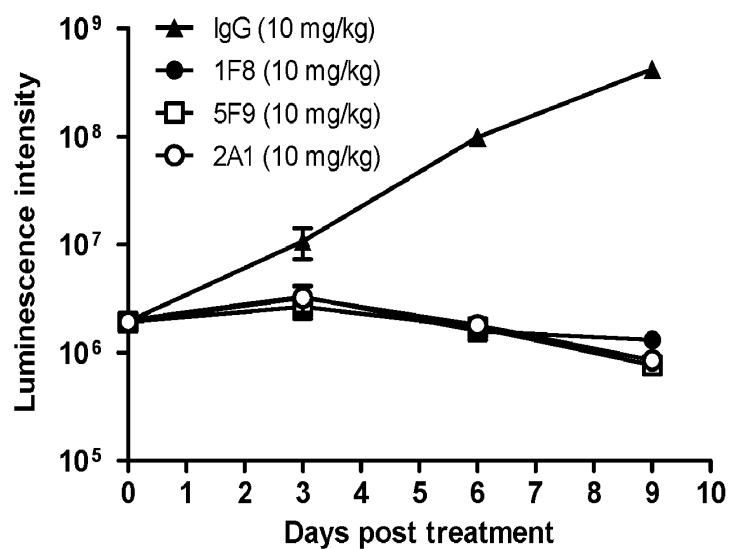


Fig. 14a

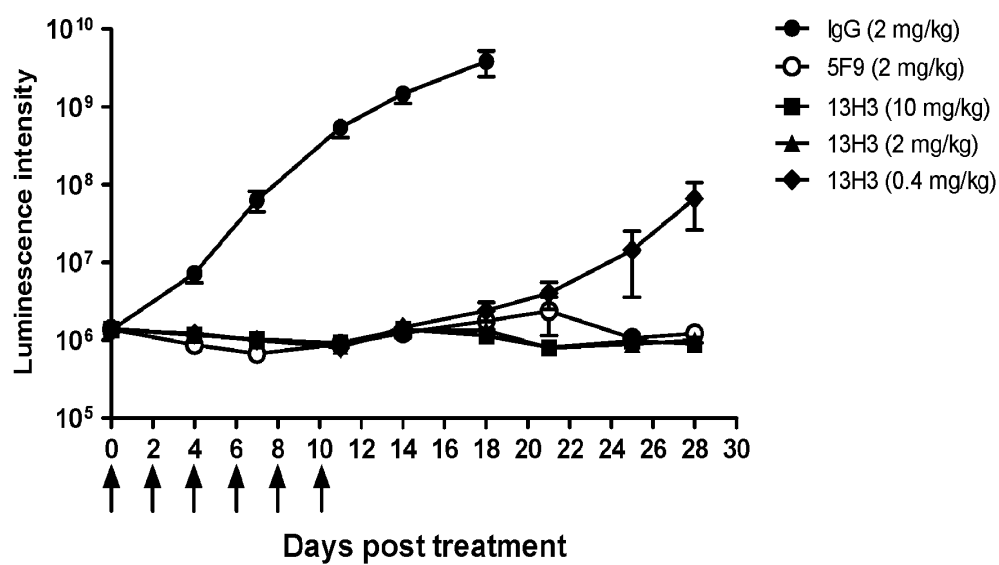


Fig. 14b

M1 MΦ in the spleen

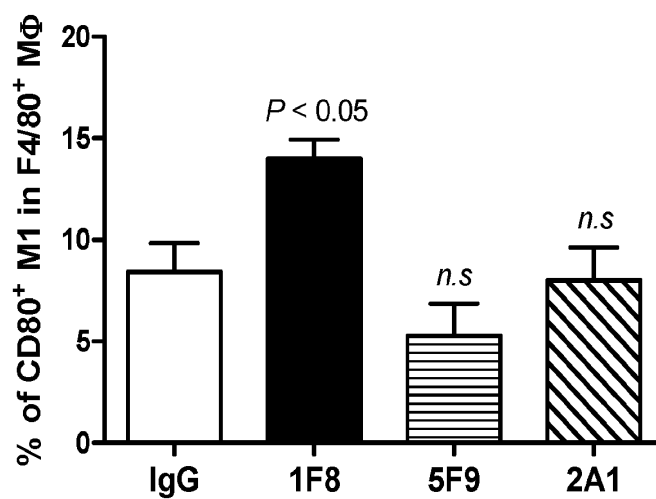


Fig. 15a

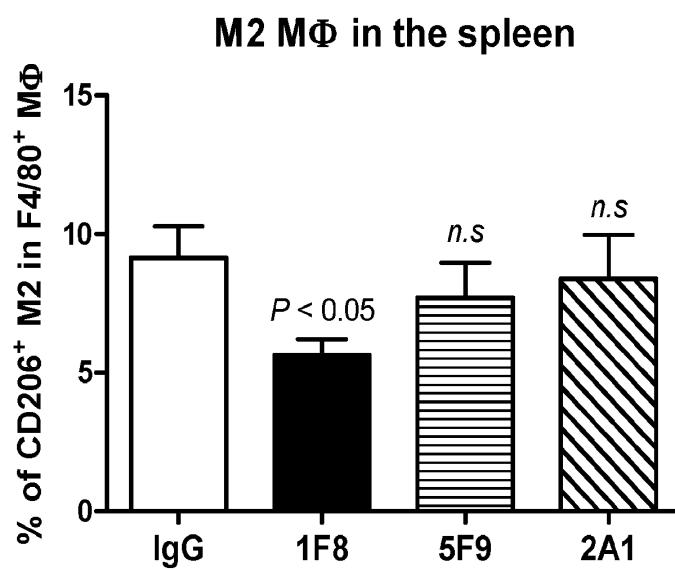


Fig. 15b

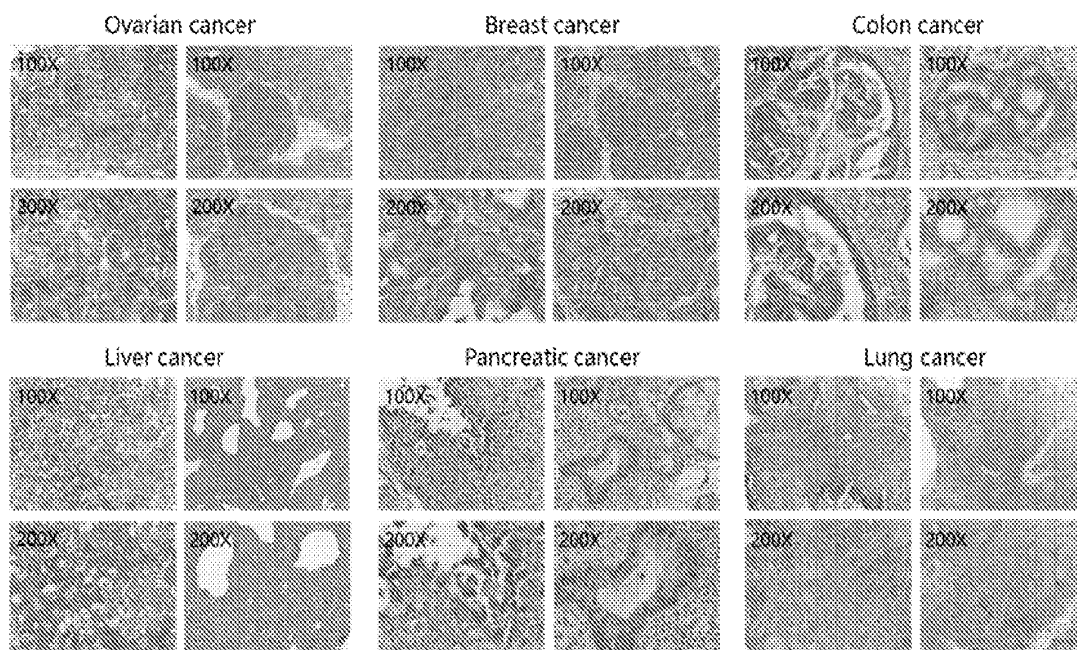


Fig. 16a

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

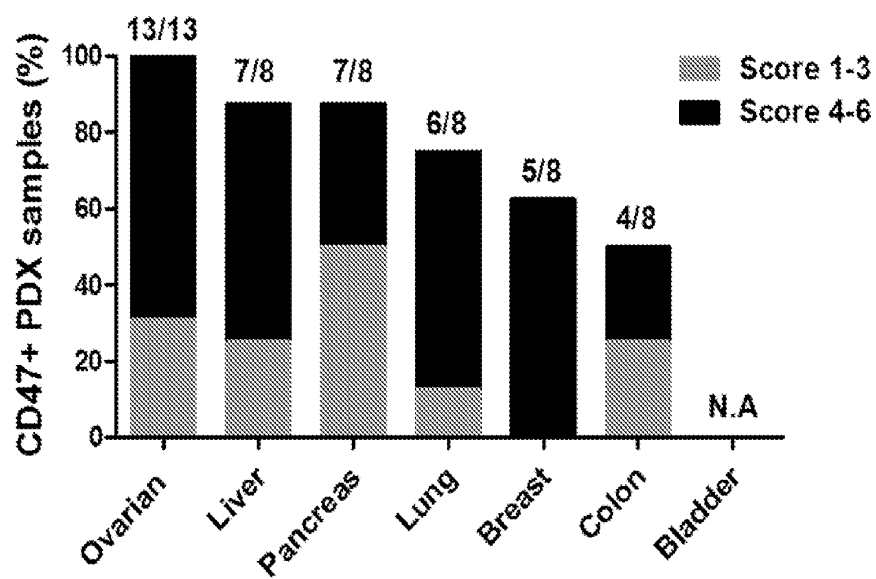


Fig. 16c

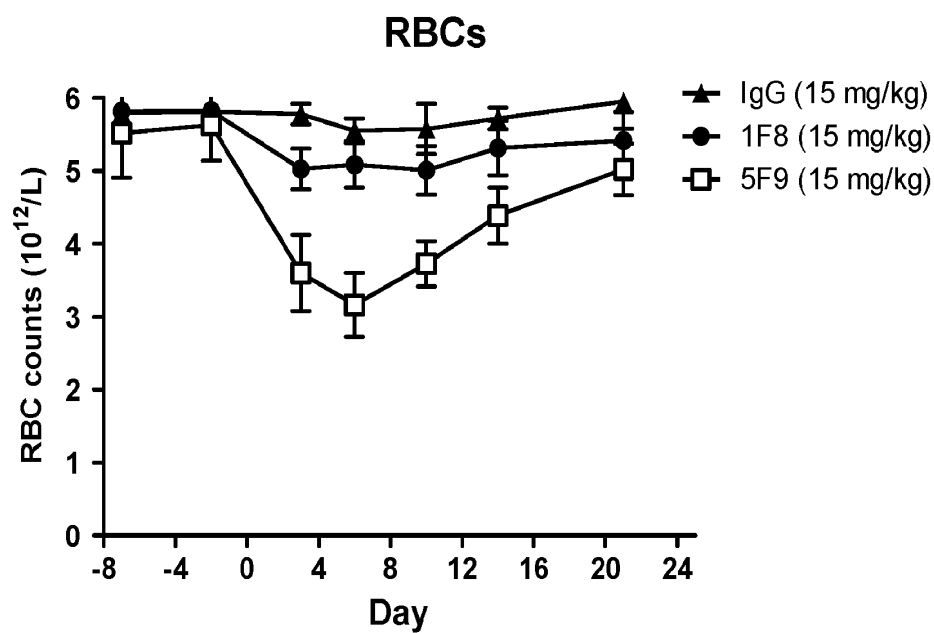


Fig. 17a

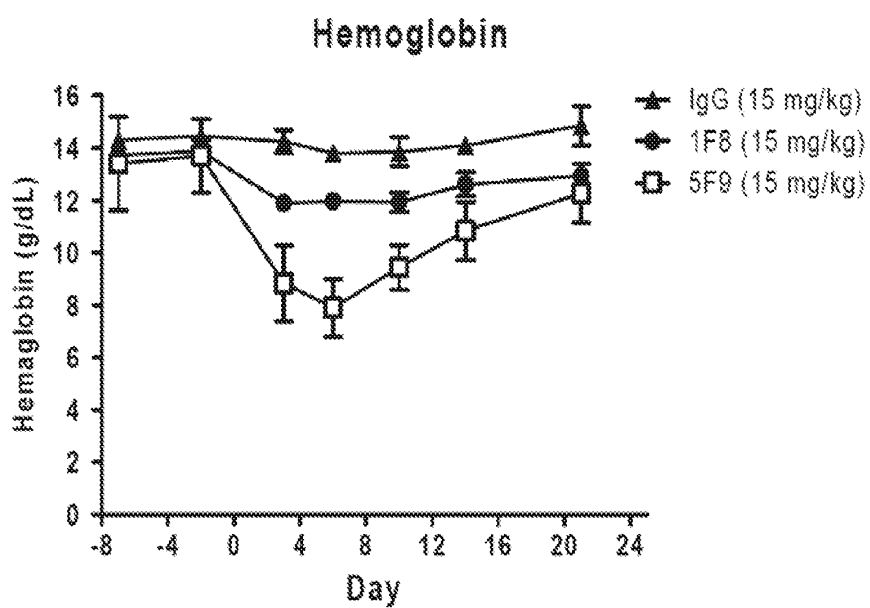


Fig. 17b

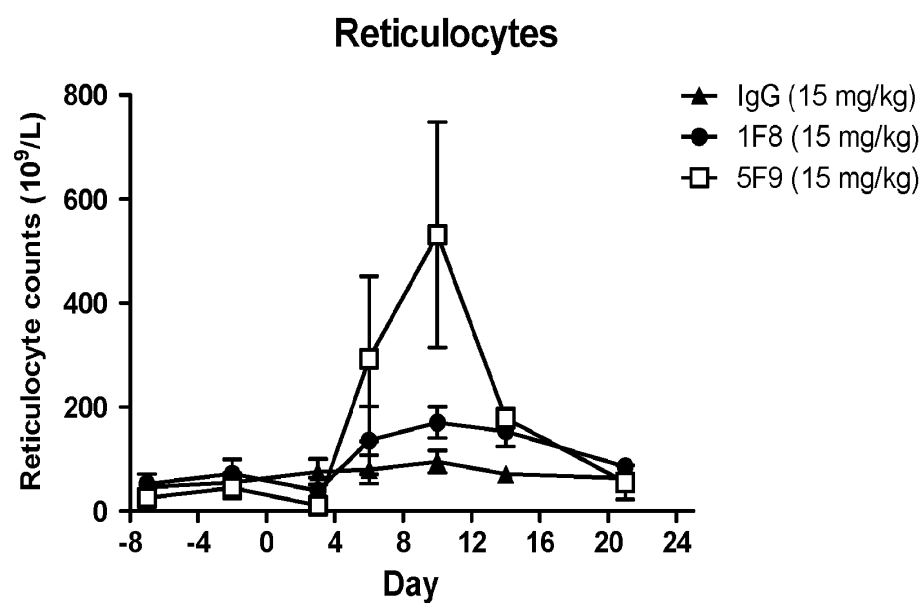


Fig. 17c

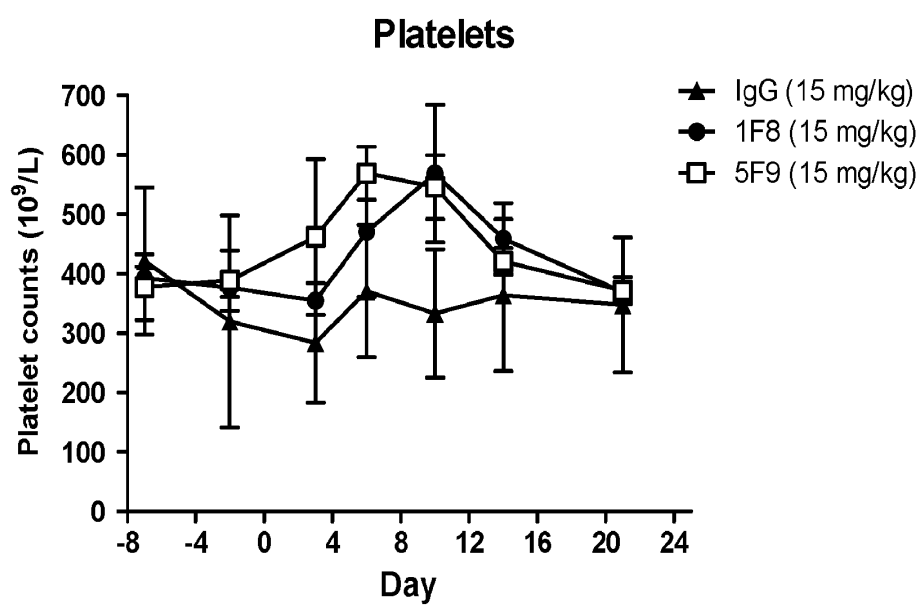


Fig. 17d

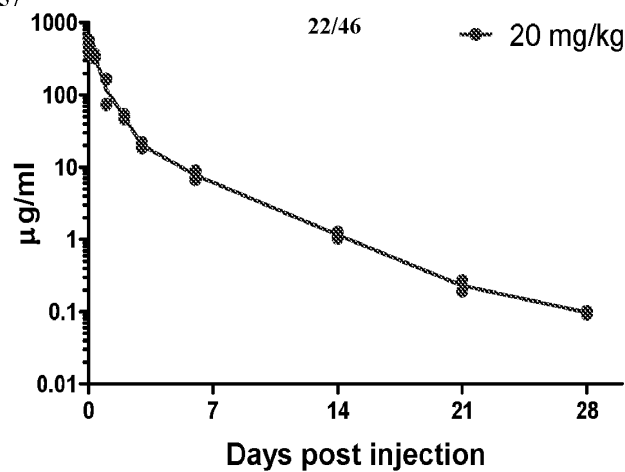


Fig. 17e

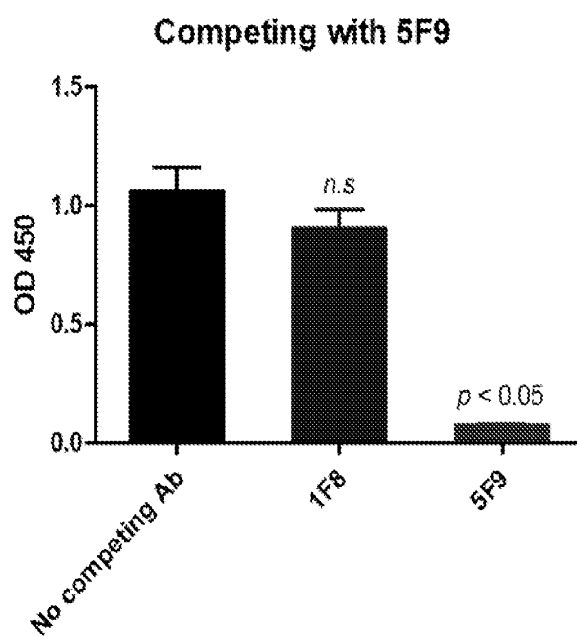


Fig. 18a

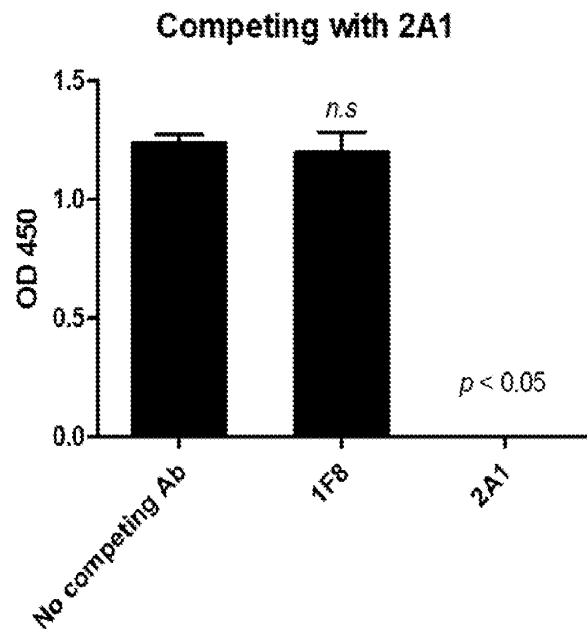


Fig. 18b

Structure of 5F9/CD47 complex



Fig. 18c

Structure of 1F8/CD47 complex



Fig. 18d

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

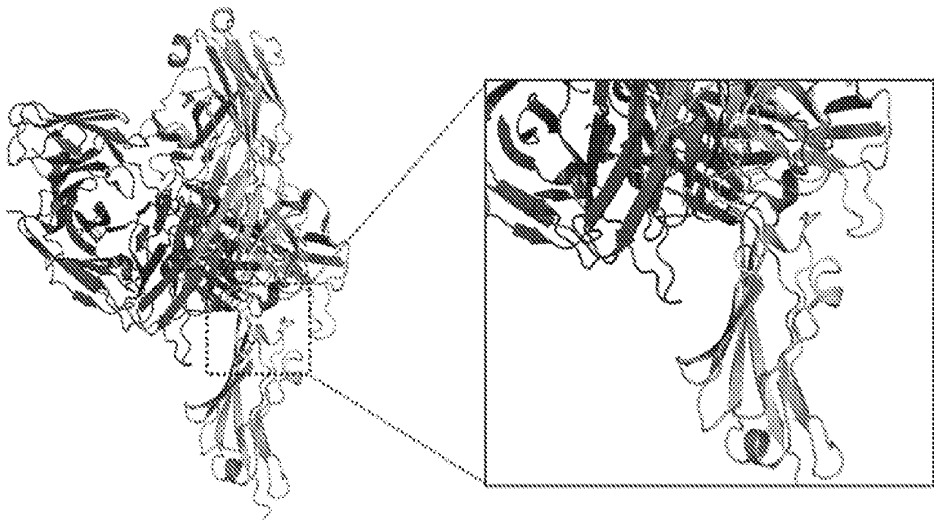


Fig. 18e

Single dose

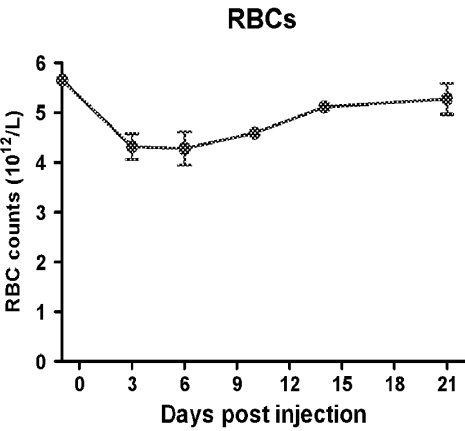


Fig. 19a

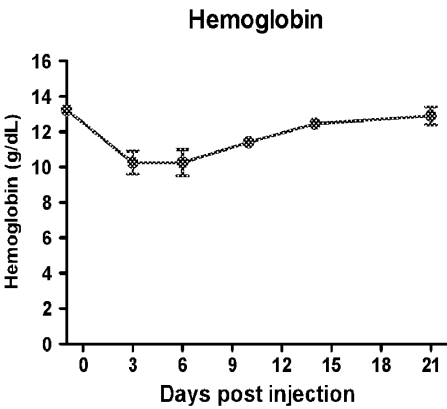


Fig. 19b

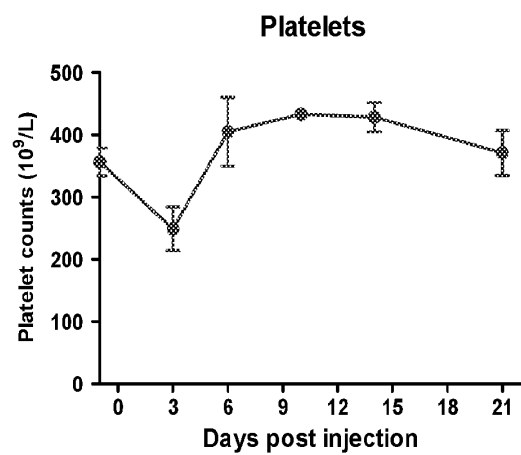


Fig. 19c

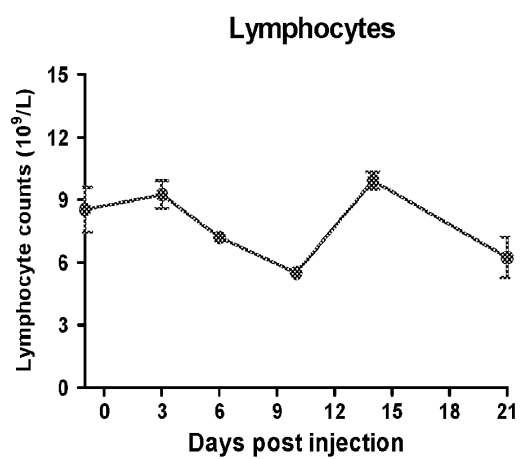


Fig. 19d

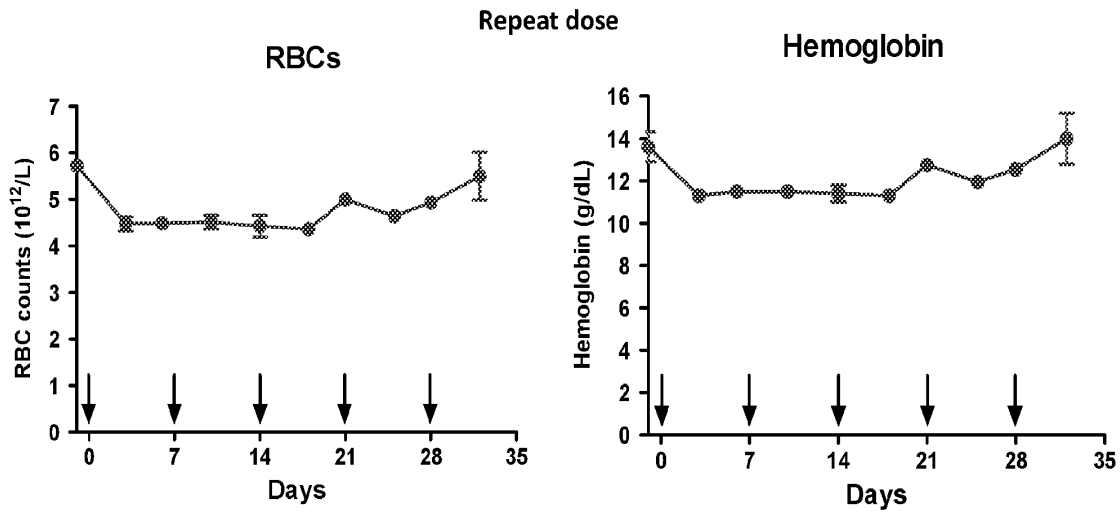


Fig. 19e

Fig. 19f

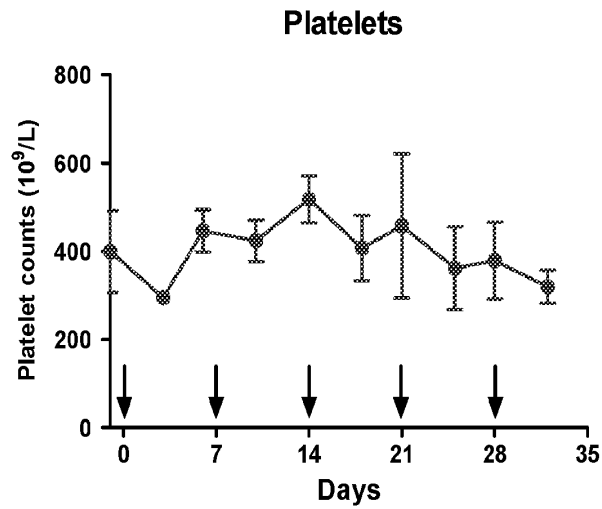


Fig. 19g

Lymphocytes

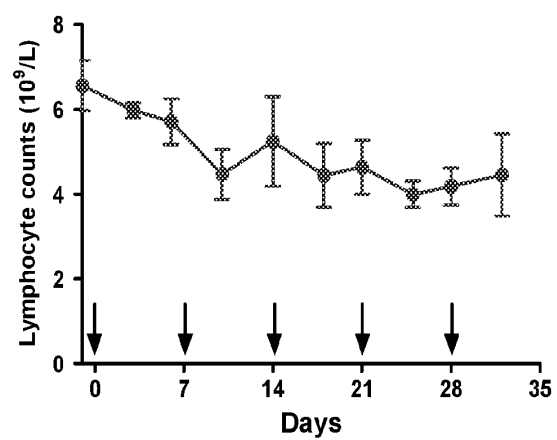


Fig. 19h

Binding to recombinant CD47-ECD

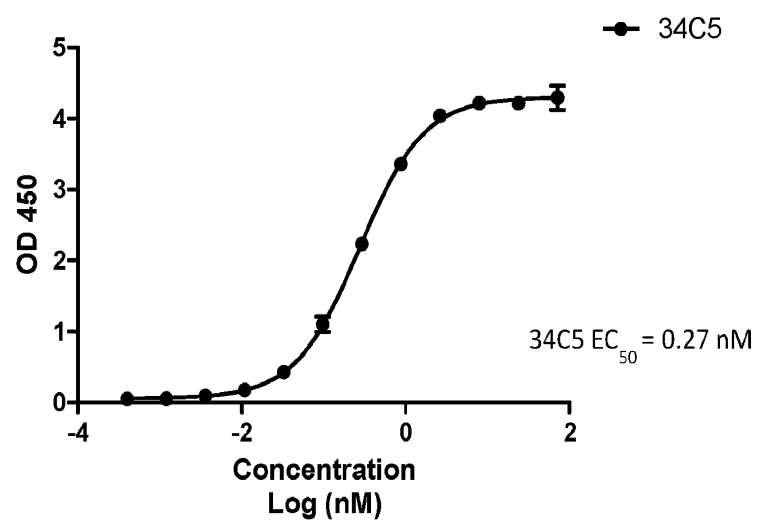


Fig. 20

Binding to CD47-bearing Raji cells

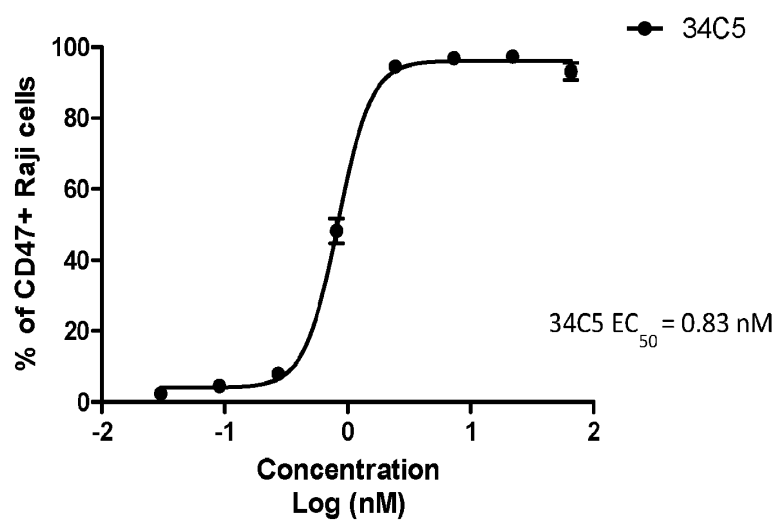


Fig. 21

Blocking of CD47 binding to SIRPa

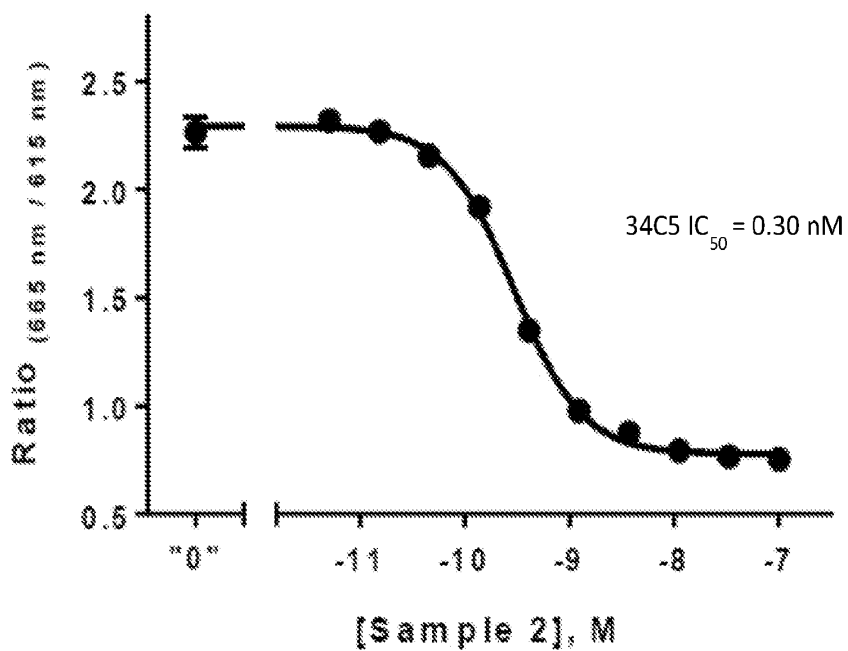


Fig. 22

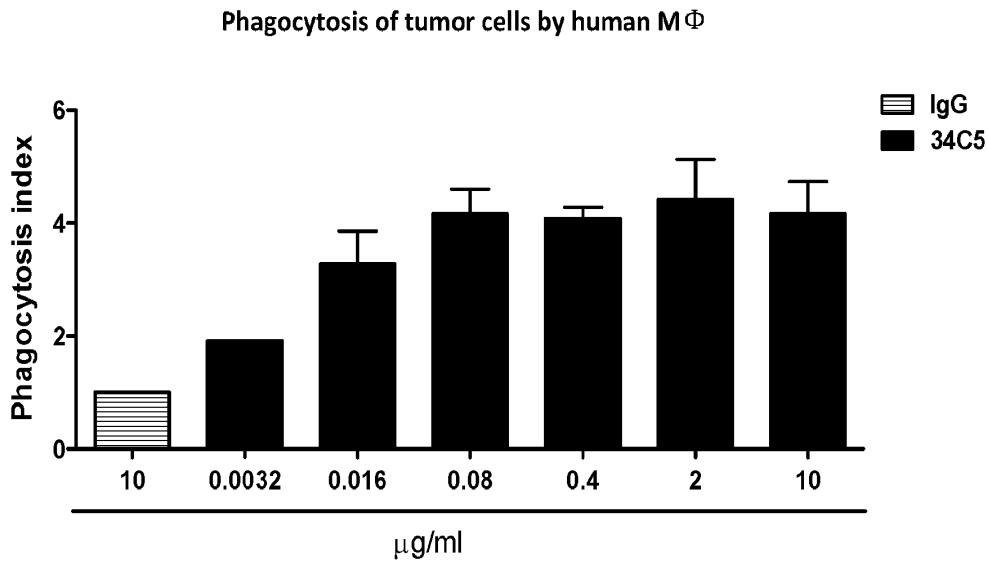


Fig. 23

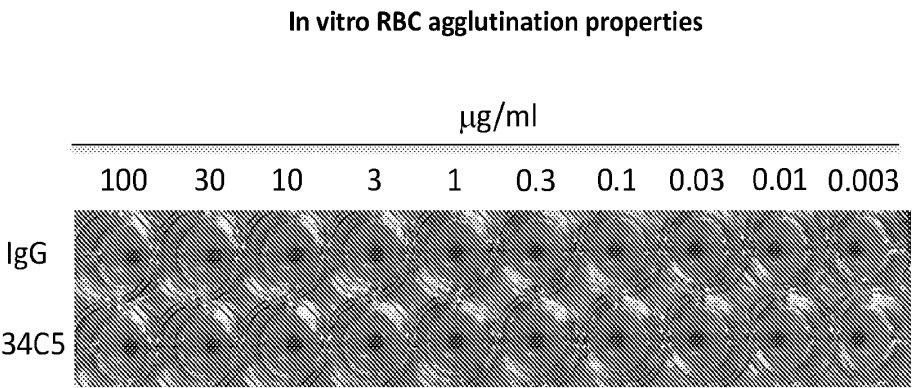


Fig. 24

In vitro RBC binding properties

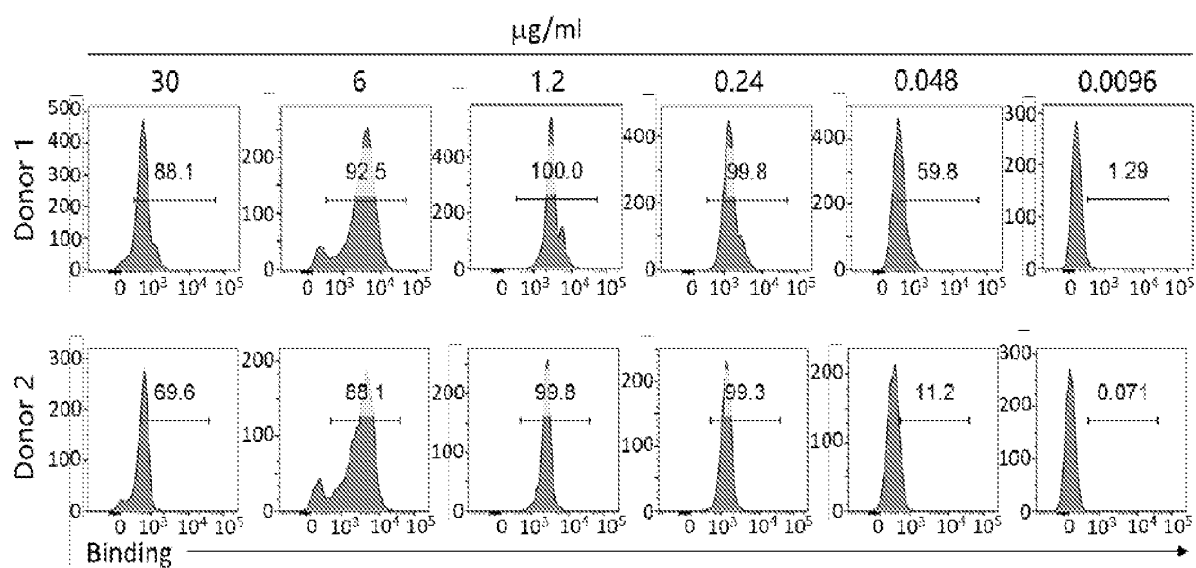


Fig. 25

Amino Acid Sequences:

>CD47-1A1

VH

SEQ ID NO.: 1

QVQLQQSGGGLVQPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN
KNTLYLQMNSLRVEDTAVYYCARYSIGRHTFDHWGQGTLVTVSA

VL

SEQ ID NO.: 2

NFMLTQPHSVSESPGKTVTISCTRSSGGIASNFVQWYQQRPGSVPTTVIYRDNQRPSPGVPDRFSGSVDSSSNSAS
LTISGLKTDDEADYYCQSYDDHNHWVFGGGTKLTVL

>CD47-1F8

VH

SEQ ID NO.: 3

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ ID NO.: 4

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDRFSGSGSGT
EFTLIISLHAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-2A11

VH

SEQ ID NO.: 5

QVQLQQSGGGLVQPGGSLRLSCAASGFTFSGYAMTWVRQAPGKGLEWVSAITSTGGRTYYADSVKGRFTTSRDN
RNTLYLQMNSLRAEDTAVYYCARESNFRAFDIWGQGTMTVSA

VL

SEQ ID NO.: 6

EIVLTQSPSLPVPVTPGEPASISCRSSQSLHSNGYNYLDWYLQKPGQSPQLLIYLSNRRASGVDRFSGSGSGTD
FTLQISRVEAEDVGVYYCMQALQIPPTFGGGTKVDIK

>CD47-2C2

VH

SEQ ID NO.: 7

EVQLVESGGGLVQPGGSLRLSCAASGFTFIDAWMTWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDN
NTLYLQMNSLRAEDTAVYYCARGARGHPGDYWGQGTMTVSA

VL

SEQ ID NO.: 8

NFMLTQPHSVSESPGKTVTISCTRSSGTIASNFVQWYQQRPGSSPTFVIFENDRRPSGVDRFSGSIDSSSNSAS
LTISSLNTEDKADYYCQSYDSSTHGWVFGGGTKLTVL

>CD47-2D7

VH

SEQ ID NO.: 9

QVNLRESGGGLVQPGGSLRLSCAASGFTFSDYYMSWIRQAPGGGLEWVSYTSRFGSDTNYADSVKGRFTISRDNV
QNSLYLQMNSLRAEDTAVYYCVRDVHNRDAYWGQGLVTVSA

VL

SEQ ID NO.: 10

SYVLTQPPSASGTPGQRTISCSGSSSNIGGNSVSWYQQLPGTAPKLLIYRNHQRP SGVPDRFSGSKSGTSASLA
ISGLRSDDEADYYCATWDFSLSGFVFGTGTKVTVL

>CD47-2G4

VH

SEQ ID NO.: 11

QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN
KNTYYCANTDYYDSSHTPADYWGQGLVTVSA

VL

SEQ ID NO.: 12

ETTLTQSPSSLSASVGDRTITCRASQDIRNDLDWFQQKPGEAPKRLISAASNLQSGVPSRFGSGGSGSEFTLTI
HSLSEDFATYYCQQSYITPPWTFGQGTKLEIK

>CD47-2G11

VH

SEQ ID NO.: 13

QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYGMWVRQAPGKGLEWVSTISGSGSSTNYADSVKGRFTISRDN
KNTLFLQMNSLRAEDTAVYFCAKGRYYYDSLDAFDIWGQGMVTVSA

VL

SEQ ID NO.: 14

EIVLTQSPGTLSPGERATLSCRASQEIRTAYLAWYQQKPGQAPRLLIYYASSRATGIPDRFSGSRSGTDFTLT
ISRLEPEDFAVYSCQQYDTSPTFGQGTRLEIK

>CD47-6F4

VH

SEQ ID NO.: 15

QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGTGGSTYYADSVKGRFTISRDN
KNTLYLQMNSLRAEDTAAYYCAKDKWSSWPTYTFDYWGQGLVTVSA

VL

SEQ ID NO.: 16

NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSSPTTVIYEDNQRP SGVPDRFSGSIDSSNSAS
LTISGLKTEADYYCQSYDSSNVIFGGGTVTVL

>CD47-5H1

VH

SEQ ID NO.: 17

QVQLQVSGGGLVQPGGSLRLSCAASGFTFSSYSMAWVRQAPGKGLEWVAAVSNSGVETYYADSVKGRFTISRDN
KNTLYLQMNSLRAEDTAVYYCAKRTRQLLTPREFDYWGQGTLLVTVLA

VL

SEQ ID NO.: 18

ETTLTQSPSSVSASVGDRVTLTCSRASQDITRWLAWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLT
SSLQPEDFATYYCQQGSSVPFTFGGGTKVEIK

>CD47-5F6

VH

SEQ ID NO.: 19

QVNLRESGGGLIQPGGSLRLSCAASGFTFTNYAMSWVRQAPGKGLEWVSSVSSAGGSTYYADSVKGRFTISRDN
KNSLYLQMNSLRAEDTAVYYCARRVNRAFDLWGRGTLTVSA

VL

SEQ ID NO.: 20

DVMTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLT
ISRLEPEDFAVYYCQQYGSSPPMYTFGGGTKLEIK

>CD47-1F3

VH

SEQ ID NO.: 21

QVQLQESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLVWVGRIKSKTDGGTTDYAAPVKGRFTISR
DSKNTLYLQMNSLKTEDTAVYYCTTDKSYGYTFDYWGQGTLLVTVSA

VL

SEQ ID NO.: 22

SYVLTQPPSASGTPGQRTVISCSSGSGSNIGSNSVHWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGISASLA
ISGLQSEDEAVYYCATWDDRLSGPVFAAGTKLTVL

>CD47-2A4

VH

SEQ ID NO.: 23

QVNLRESGGGLVKPGGSLRLSCAASGFTFSSYWMHWVRQAPGKGLEWVSAISGSGAGTYYPDSVKGRFTISRDN
KNTLYLQMNSLRAEDTAVYYCARDRLSFGFDIWGQGTLLVSVSG

VL

SEQ ID NO.: 24

NFMLTQPHSVSGSPGKTVTISCTRSSGSIGSTYVQWYQQRPGSPPTTVIYKDDQRPSGVPDRFSGSIDGSSNSAS
LTISGLETEDEADYYCQSSDTSNLVFGGGTKVTVL

>CD47-2B12

VH

SEQ ID NO.: 25

QVQLQQSGGGLVQPGGSLRLSCAAPGFTFSRYWMSWVRQAPGKGLEWVANIKGDGSQTYADSVKGRFTISRDNAMKTVYQLQMNSLRAEDTAIYYCAKGAAYHINSWLDPWGQGTTLTVSA

VL

SEQ ID NO.: 26

ETTLTQSPGTLSPGERVTLSRASQSIGNYLAWYQQRPQGAPRLLIYGAFRRATGIPDRFSGSGSGTDFTLTITRLEPEDFATYYCQHYNFPHTFGAGTKVDIK

>CD47-13A11

VH

SEQ ID NO.: 27

KVQLVESGGGLVKPGGSLRLSCAASGITFKHAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISRDSKNTLYQLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 28

DIVMTQSPDSLAVSLGERATINCKSSQSVLYQVNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGTEFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-15E1

VH

SEQ ID NO.: 29

KVQLVESGGGLVKPGGSLRLSCAASGFTFNNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISRDSKNTLYQLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 30

DIVMTQSPDSLAVSLGERATINCKSSQTVLYPLNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGTEFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-13H3

VH

SEQ ID NO.: 31

KVQLVESGGGLVKPGGSLRLSCAASGLTFERAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISRDSKNTLYQLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 32

DIVMTQSPDSLAVSLGERATINCKSSQSVLYAGNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGTEFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGKLEIK

>CD47-14A8

VH

SEQ ID NO.: 33

KVQLVESGGGLVKPGGSLRLSCAASGFTFPNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWQGTMVTVSA
VL

SEQ. ID NO.: 34

DIVMTQSPDSLAVSLGERATINCKSSQSVLYPGNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGGTKLEIK

>CD47-16H3

VH

SEQ ID NO.: 35

KVQLVESGGGLVKPGGSLRLSCAASGLTFGNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWQGTMVTVSA
VL

SEQ. ID NO.: 36

DIVMTQSPDSLAVSLGERATINCKSSQSVLYPGNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGGTKLEIK

>CD47-1A1

VH

SEQ ID NO.: 37

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGNHSSDIWQGTMVTVSA
VL

SEQ. ID NO.: 38

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGGTKLEIK

>CD47-1A1-A

VH

SEQ ID NO.: 39

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGAHSSDIWQGTMVTVSA
VL

SEQ. ID NO.: 40

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGGTKLEIK

>CD47-1A1-Q

VH

SEQ ID NO.: 41

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGQHSSDIWGQGTMTVSA

VL

SEQ. ID NO.: 42

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGTKLEIK

>CD47-1A2

VH

SEQ ID NO.: 43

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSAYAFDAWGQGTMTVSA

VL

SEQ. ID NO.: 44

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGTKLEIK

>CD47-1A8

VH

SEQ ID NO.: 45

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSAYAFDSWGQGTMTVSA

VL

SEQ. ID NO.: 46

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGTKLEIK

>CD47-1B1

VH

SEQ ID NO.: 47

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSDRASDKWGQGTMTVSA

SEQ. ID NO.: 48

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGTKLEIK

>CD47-1B2

VH

SEQ ID NO.: 49

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSAYAFDTWGQGTMTVSA

VL

SEQ. ID NO.: 50

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGTKLEIK

>CD47-1H3

VH

SEQ ID NO.: 51

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGNHSQDIWGQGTMTVSA

VL

SEQ. ID NO.: 52

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGTKLEIK

>CD47-1H3-Q

VH

SEQ ID NO.: 53

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGQHSQDIWGQGTMTVSA

VL

SEQ. ID NO.: 54

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGTKLEIK

>CD47-1H3-A

VH

SEQ ID NO.: 55

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGGAHSQDIWGQGTMTVSA

VL

SEQ. ID NO.: 56

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYYTPPLAFGGGTKLEIK

>CD47-2A2

VH

SEQ ID NO.: 57

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 58

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLTPPLAFGGGKLEIK

>CD47-2A3

VH

SEQ ID NO.: 59

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 60

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLRPPLNFGGGKLEIK

>CD47-2A6

VH

SEQ ID NO.: 61

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 62

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLTPPLNFGGGKLEIK

>CD47-2A10

VH

SEQ ID NO.: 63

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 64

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQNYLTPPLSFGGGKLEIK

>CD47-2B1

VH

SEQ ID NO.: 65

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 66

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLKAPLAFGGGTKLEIK

>CD47-2C6

VH

SEQ ID NO.: 67

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 68

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLNAPLHFGGGTKLEIK

>CD47-2E7

VH

SEQ ID NO.: 69

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 70

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLEAPLVFGGGTKLEIK

>CD47-2E9

VH

SEQ ID NO.: 71

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 72

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISSLQAEDVAIYYCQQYLKAPLHFGGGTKLEIK

>CD47-2F1

VH

SEQ ID NO.: 73

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGTMTVSA

VL

SEQ. ID NO.: 74

DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISLQAEDVAIYYCQRLIAPPFTFGGGTKLEIK

>CD47-2F3

VH

SEQ ID NO.: 75

KVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEWVGRIKRKTDGETTDYAAPVKGRFSISR
DSKNTLYLQMNSLKTEDTAVYYCAGSNRAFDIWGQGMVTVSA

VL

SEQ. ID NO.: 76

DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNRNYLAWYQQKPGQPPKLLINQASTRASGVDPDRFSGSGSGT
EFTLIISLQAEDVAIYYCQNYLTPPLAFGGGTKLEIK

>CD47-34C5

VH

SEQ. ID NO.: 77

CAGGTCCAACCTGGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGTCTTCAGTGAAGGTGTCCTGCAAGGCTTCT
GGCTACACCTTCAGCAGCTACTATATGCACTGGGTGAGGCAGGCTCCTGGACAAGGCCTTGAGTGGATGGGAGAG
ATTAATCCCAACAATGCCCGTATTAACCTCAATGAAAAGTTCAAGACCAGGGTCACACTCACTGTGGACAAATCC
ACCAGCACAGCATACATGGAGCTCAGCAGCCTGAGATCTGAGGACACCGCGGTCTATTACTGTACCAGAGGATAC
TATAGGTACGGGGCTGGTTTGGTTACTGGGGCCAAGGGAATCTGGTCACTGTCTCTTCA

>CD47-34C5

VL

SEQ. ID NO.: 78

GATATCCAGATGACACAGTCTCCATCCTCCCTGTCTGCCTCTGTGGGAGACAGAGTCACCATCACTTGCAGGGCA
AGTCAGGACATTAGCGATTATTTGAACTGGTATCAACAGAAACCAGGCAAGGCTCCTAACTCCTGATCTACTAC
ATATCAAGATTACACTCAGGAGTCCCATCACGCTTCAGTGGCAGTGGGTCTGGAACAGATTATACTCTCACCATT
AGCTCCCTGCAGCCAGAAGATTTTGCCACTTACTATTGCCAACAGGGTCATACACTTCCGTGGACCTTCGGTGGA
GGCACCAAGGTGGAAATCAA

NUCLEOTIDE SEQUENCES OF VH:

>CD47-1A1_VH

SEQ ID NO.: 79

CAGGTACAGCTGCAGCAGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTAAGACTCTCCTGTACAGCCTCT
GGATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGTCTCAGCA
ATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGTCGAGGACACGGCCGTATATTACTGTGCGAGATATAGT
ATTGGTAGACACACCTTTGACCACTGGGGCCAGGGCACCTGGTCACCGTCTCGGCC

>CD47-1F8_VH

SEQ ID NO.: 80

AAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGGTCCCTTAGACTCTCCTGTGCAGCCTCT
GGTTTCACTTTTCAGTAACGCCTGGATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTGGCCGT
ATTAAAAGGAAAACCTGATGGTGAGACAACAGACTACGCTGCACCCGTGAAAGGCAGATTACAGCATCTCAAGAGAT
GATTCAAAAAACACCCTGTATCTGCAAATGAACAGCTTGAAAACCGAGGACACAGCCGTGTATTACTGCGCTGGC
AGTAACCGAGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTGCC

>CD47-2A11_VH

SEQ ID NO.: 81

CAGGTACAGCTGCAGCAGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTAGCGGCTATGCCATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT
ATTACTTCTACTGGTGGTTCGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCACCTCCAGAGACAATTCC
AGGAACACGTTGTATCTGCAAATGAACAGCCTGAGAGCCGAAGACACGGCCGTATATTACTGTGCGAGAGAGTCA
AACTTCAGGGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTGCC

>CD47-2C2_VH

SEQ ID NO.: 82

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTTAGACTCTCCTGTGCAGCCTCT
GGATTCACTTTTCATTGACGCCTGGATGACCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGTT
ATTTATAGCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGGGGCTAGG
GGCCATCCCGGGCAGGACTACTGGGGGCAGGGCACCCCTGGTCACCGTCTCTGGCC

>CD47-2D7_VH

SEQ ID NO.: 83

CAGGTCAACTTAAGGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTCAGTGACTACTACATGAGCTGGATCCGCCAGGCTCCAGGGGGGGGCTGGAGTGGGTCTCAGT
ACTAGTCGTTTTGGTAGTGACACAACTACGCAGACTCTGTGAAGGGCCGATTACCATCTCCAGAGACAACGTC
CAGAACTCACTATATCTGCAAATGAACAGCCTGAGGGCCGAGGACACGGCTGTTTATTACTGTGTGAGAGATGTA
CATAACAGGGATGCCTACTGGGGCCAGGGCACCCCTGGTCACCGTCTCTGGCC

>CD47-2G4_VH

SEQ ID NO.: 84

CAGGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT
ATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAACACAGAT
TACTATGATAGTAGTAGCCATACCCCGCTGACTACTGGGGCCAGGGCACCCCTGGTCACCGTCTCTGGCC

>CD47-2G11_VH

SEQ ID NO.: 85

CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTAGTAGCTATGGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCAACT
ATCAGTGGCAGTGGTAGTAGCACAACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTATTTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTTCTGTGCGAAAGGCCGA
TATTACTATGATAGTCTTGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTGCCC

>CD47-6F4_VH

SEQ ID NO.: 86

CAGGTACAGCTGGTGGAGTCTGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCAGCT
ATTAGTGGTACTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGCATATTACTGTGCGAAAGATAAA
TGGAGCAGCTGGCCCCACTTACTACTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCGGCC

>CD47-5H1_VH

SEQ ID NO.: 87

CAGGTGCAGCTGCAGGTGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTCAGTAGCTATAGCATGGCCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCGCGCT
GTTAGTAATAGTGGTGGTGGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATTTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAACGAACT
AGACAACTGCTAACTCCGCGGGAGTTTGACTACTGGGGCCAGGGCACCCCTGGTCACCGTCTTGGCC

>CD47-5F6_VH

SEQ ID NO.: 88

CAGGTCAACTTAAGGGAGTCTGGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTACCAATTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCAAGT
GTTAGTAGTGCTGGTGGTAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAACGCC
AAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTTTATTACTGTGCGAGACGAGTC
AATCGGGCCTTCGATCTCTGGGGCCGTGGAACCCCTGGTCACCGTCTCGGCC

>CD47-1F3_VH

SEQ ID NO.: 89

CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTTAGACTCTCCTGTGCAGCCTCT
GGATTCACTTTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGTGTGGGTGGCCGT
ATTAAAAGCAAACTGATGGTGGGACAACAGACTACGCTGCACCCGTGAAAGGCAGATTACCATCTCAAGAGAT
GATTCAAAAAACACGCTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACCACA
GATAAGAGCTATGGTTACACATTTGACTACTGGGGCCAGGGCACCCCTGGTCACCGTCTCGGCC

>CD47-2A4_VH

SEQ ID NO.: 90

CAGGTCAACTTAAGGGAGTCTGGGGGAGGCTTGGTAAAGCCGGGGGGGTCCCTTAGACTCTCCTGTGCAGCCTCT
GGATTCACCTTCAGTAGCTACTGGATGCACTGGGTCCGCCAAGCCCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT
ATCAGTGGTAGTGGTGCCGGCACATACTACCCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGATCGG
TCCTTATCTTTTGGTTTTGATATTTGGGGCCAAGGCACCCTGGTCTCCGTCTCTGGC

>CD47-2B12_VH

SEQ ID NO.: 91

CAGGTACAGCTGCAGCAGTCAGGGGAGGCTTGGTCCAGCCGGGGGGGTCACTGAGACTCTCCTGTGCAGCCCCCT
GGATTCACCTTTAGTAGATATTGGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGACTGGAGTGGGTGGCCAAC
ATAAAGGGAGATGGAAGTCAGACATACTATGCGGACTCTGTGAAGGGCCGATTACCATCTCCAGAGACAACGCC
ATGAAAACAGTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCATATATTACTGTGCGAAAGGGGCT
GCTTATCACATTAACAGCTGGCTCGACCCCTGGGGCCAGGGCACCCCTGGTCACCGTCTCGGCC

NUCLEOTIDE SEQUENCES OF VL:

>CD47-1A1_VL

SEQ ID NO.: 92

AATTTTATGCTGACTCAGCCCCACTCTGTGTGCGAGTCTCCGGGGAAGACGGTAACCATCTCCTGCACCCGCAGC
AGTGGCGGCATTGCCAGTAACTTTGTGCAGTGGTACCAGCAGCGCCCGGGCAGTGTCCCCACCACTGTGATCTAT
AGGGATAACCAAAGACCCTCTGGAGTCCCTGATCGGTTCTCTGGCTCCGTCGACAGCTCCTCCAATTCTGCCTCC
CTCACCATCTCTGGGCTGAAGACTGACGATGAGGCTGACTATTATTGTGAGTCCTATGATGACCACAATCATTTGG
GTGTTTCGGCGGCGGGACCAAGCTGACCGTCCTA

>CD47-1F8_VL

SEQ ID NO.: 93

GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCC
AGCCAGAGTGTTTTATACAGCTCCAACAATAGGAATACCTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCT
AAGCTGCTCATTAACCAGGCATCTACCCGGGCATCCGGCGTCCCTGACCGATTGAGTGGCAGCGGGTCTGGGACA
GAGTTCACTCTCATCATCAGCAGCCTGCAGGCTGAAGATGTGGCGATTTATTACTGTGAGCAATATTATACTCCT
CCCCTCGCTTTCGGCGGAGGGACCAAGCTGGAGATCAAA

>CD47-2A11_VL

SEQ ID NO.: 94

GAAATTGTGTTGACGCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCT
AGTCAGAGCCTCCTGCACAGTAATGGATACAATATTTGGATTGGTACCTGCAGAAACCAGGGCAGTCTCCACAG
CTCCTGATCTATTTGAATTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGTACAGAT
TTTACACTGCAAATCAGCAGAGTGGAGGCTGAGGATGTGGGGTTTACTACTGTATGCAAGCTCTACAAATTCCT
CCCCTTTCGGCGGAGGGACCAAGTGGATATCAAA

>CD47-2C2_VL

SEQ ID NO.: 95

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGAAAGACGGTAACCATCTCCTGCACCCGCAGC
AGTGGCACCATTGCCAGCAACTTTGTGCAGTGGTATCAACAGCGCCCGGGCAGTTCGCCCACCCAGTGATCTTT
GAGAATGACCGAAGACCCTCTGGGGTCCCTGATCGGTTCTCTGGCTCCATCGACAGCTCCTCCAATTCTGCCTCC
CTCACCATTTCGTCACTGAACACTGAGGACAAGGCTGACTACTACTGTCAAGTCCATGATAGCAGCACTCATGGG
TGGGTGTTTGGCGGAGGGACCCAGCTCACCGTTTTA

>CD47-2D7_VL

SEQ ID NO.: 96

TCCTATGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTCTGGAAGC
AGCTCCAACATCGGCGGTAATTCTGTATCCTGGTACCAGCAACTCCCAGGAACGGCCCCAAGCTCCTCATCTAT
AGGAATCATCAGCGGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCC
ATCAGTGGGCTCCGGTCCGACGACGAGGCTGATTATTATTGTGCAACATGGGATTTAGCCTGAGTGGTTTTGTCT
TTCGGAAGTGGGACCAAGGTCACCGTCCTA

>CD47-2G4_VL

SEQ ID NO.: 97

GAAACTACACTCAGCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCC
AGTCAGGACATCAGAAATGATTTAGACTGGTTTCAACAAAAACCAGGCGAAGCCCCATAACGCCTGATCTCTGCT
GCATCTAATTTGCAGAGTGGGGTCCCCCTCAGATTACGCGCGGTGGCTCTGGCTCCGAATTCATCTCACAAATC
CACAGCCTGGAGTCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACATTACCCCTCCTTGGACGTTCCGGC
CAAGGGACCAAGCTGGAGATCAAA

>CD47-2G11_VL

SEQ ID NO.: 98

GAAATTGTGTTGACGAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCC
AGTCAGGAAATTAGGACCGCCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
TATGCATCCAGCAGGGCCACTGGCATCCAGACAGGTTTCAGCGGCAGTAGGTCTGGGACAGACTTCACTCTCACC
ATCAGCAGACTGGAGCCTGAAGATTTTGCAAGTGTATTCCTGTGACAGTATGATACCTCACCTCCACCTTCGGC
CAAGGGACACGACTGGAGATTAAA

>CD47-6F4_VL

SEQ ID NO.: 99

AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCTCCGGGGAAGACGGTAACCATCTCCTGCACCCGCAGC
AGTGGCAGCATTGCCAGCAACTATGTGCAGTGGTACCAACAGCGCCCGGGCAGTTCACCCACCACTGTGATCTAT
GAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCTGGCTCCATCGACAGCTCCTCCAATCTGCCTCC
CTCACCATCTCTGGACTGAAGACTGAGGACGAGGCTGACTACTACTGTCAAGTCTTATGATAGCAGCAATGTGATA
TTCGGCGGAGGGACCAAGGTCACCGTCCTA

>CD47-5H1_VL

SEQ ID NO.: 100

GAAACTACACTCAGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCCTCACTTGTCTGGGCG
AGTCAGGATATCACAAGGTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGAT
GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC
AGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAACAGGGTTCCAGTGTTCCTTTCACTTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

>CD47-5F6_VL

SEQ ID NO.: 101

GATGTTGTGATGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCC
AGTCAGAGTGTAGCAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
GGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC
ATCAGCAGACTGGAGCCTGAAGATTTTGCAAGTGTATTACTGTGTCAGCAGTATGGTAGCTCACCTCCTATGTACACT
TTTGGCCAGGGGACCAAGCTGGAGATCAAA

>CD47-1F3_VL

SEQ ID NO.: 102

TCCTATGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTCTGGAAGT
GGCTCCAACATCGGAAGTAATTCTGTTCACTGGTACCAGCAACTCCCAGGAACGGCCCCAAACTCCTCATCTAT
ACTAATAATCAGCGGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCATTTCAGCCTCCCTGGCT
ATCAGTGGGCTCCAGTCTGAGGATGAGGCTGTTTATTACTGTGCAACGTGGGATGACAGACTGAGTGGTCCGGTG
TTCGCCGCAGGGACCAAGCTGACCGTCCTA

>CD47-2A4_VL

SEQ ID NO.: 103

AATTTTATGCTGACTCAGCCCCACTCTGTGTCTGGGGTCTCCGGGGAAGACGGTAACCATCTCCTGCACCCGCAGC
AGTGGCAGCATTTGGCAGCACCTATGTGCAGTGGTACCAACAGCGCCCGGGCAGTCCCCCACCCTGTGATCTAT
AAGGATGACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCTGGCTCCATCGACGGCTCCTCCAACCTCTGCCTCC
CTCACCATCTCTGGACTGGAGACTGAGGACGAGGCTGACTACTACTGTCACTTCTTGATACCAGCAATCTGGTC
TTCGGCGGAGGGACCAAGGTACCGTCCTA

>CD47-2B12_VL

SEQ ID NO.: 104

GAAACTACACTCAGCAGTCTCCAGGCACCCTGTCTGTTTCTCCGGGGGAAAGAGTTACCCTCTCCTGCAGGGCC
AGTCAGAGTATTAGCGGTAATTACTTAGCCTGGTACCAGCAGAGACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
GGGGCATTGAGGAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC
ATCACCAGACTGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACACTATAATAATTTCCCCACACTTTTCGGC
GCAGGGACCAAAGTGGATATCAAA

>CD47-34C5_VH

SEQ ID NO.: 105

QVQLVQSGAEVKKPGSSVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGEINPNNARINFNEKFKTRVTLTVDKS
TSTAYMELSSLRSEDTAVYYCTRGYYRYGAWFGYWGQGTLLTVSS

>CD47-34C5_VL

SEQ ID NO.: 106

DIQMTQSPSSLSASVGDRVTITCRASQDISDYLNWYQQKPGKAPKLLIYYISRLHSGVPSRFSGSGSGTDYTLTI
SSLQPEDFATYYCQQGHTLPWTFGGGTKVEIK

Fig. 26

>CD47

SEQ ID NO.: 107

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

Fig. 27