Fig. 1

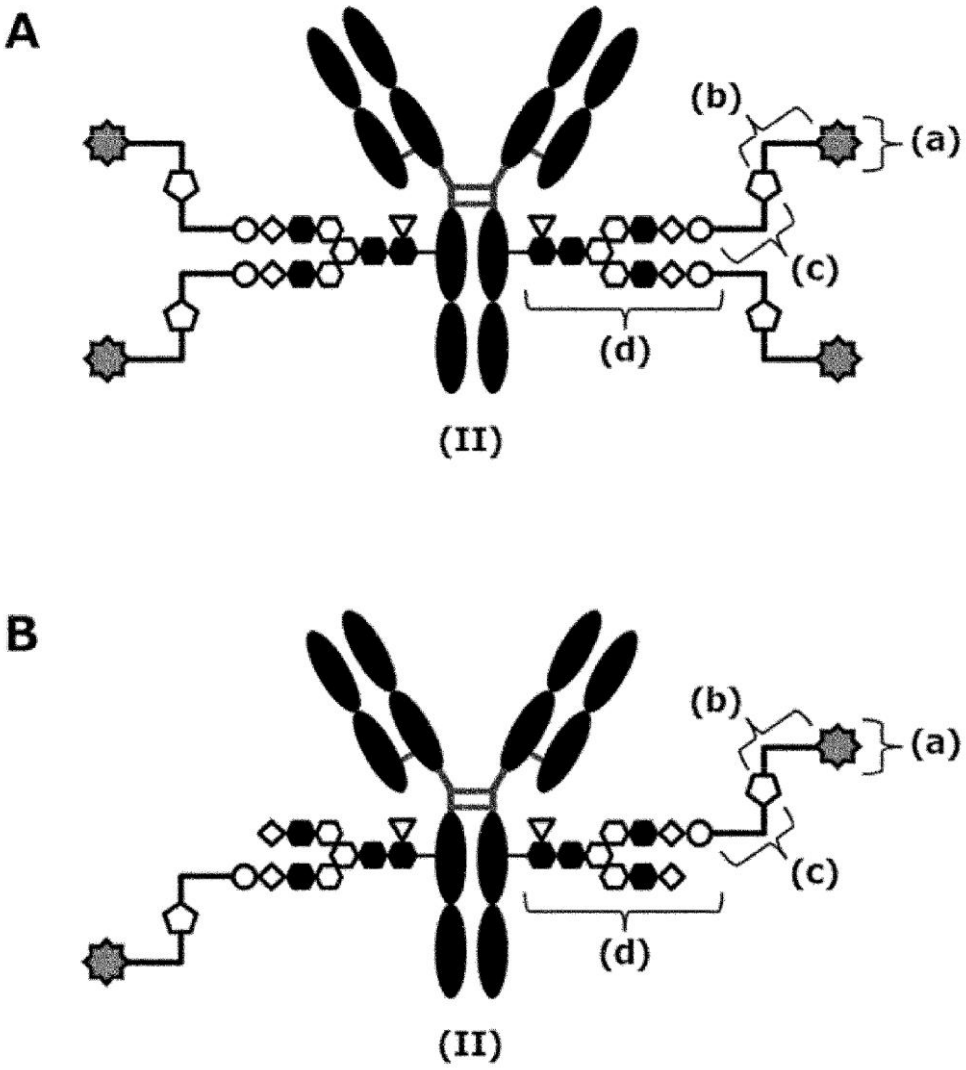


Fig. 2

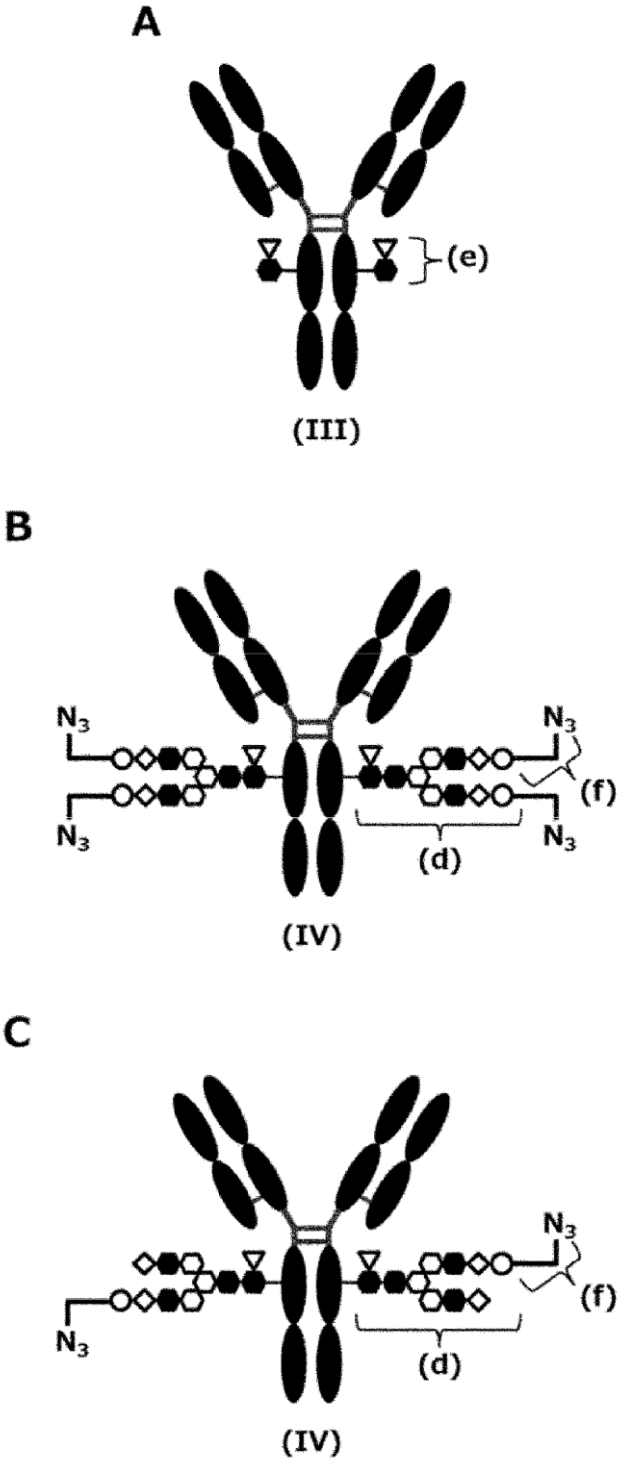


Fig. 3

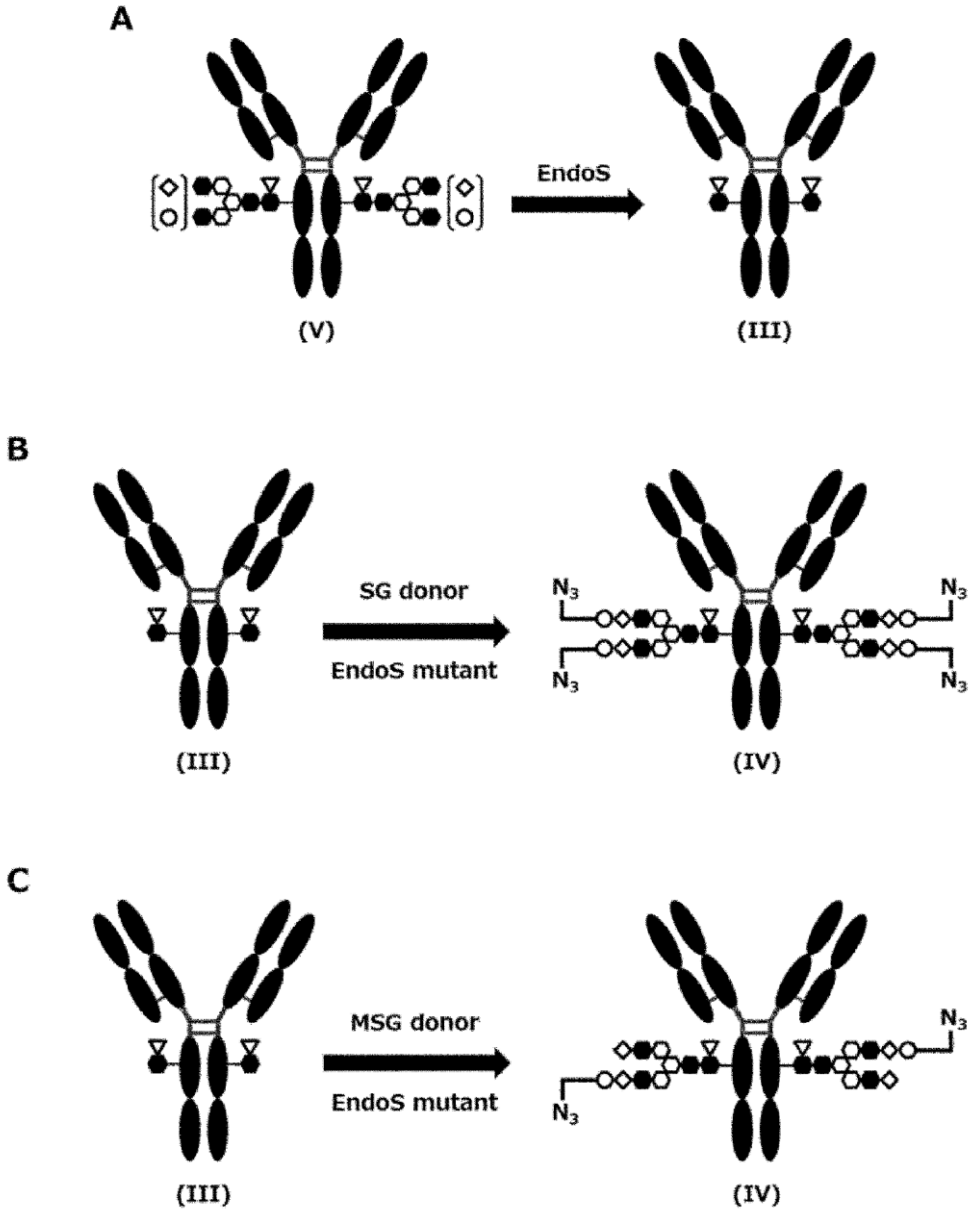

A
EndoS
(V)
(III)
B
SG donor
EndoS mutant
N3
(III)
(IV)
C
MSG donor
EndoS mutant
N3
(III)
(IV)

Fig. 4

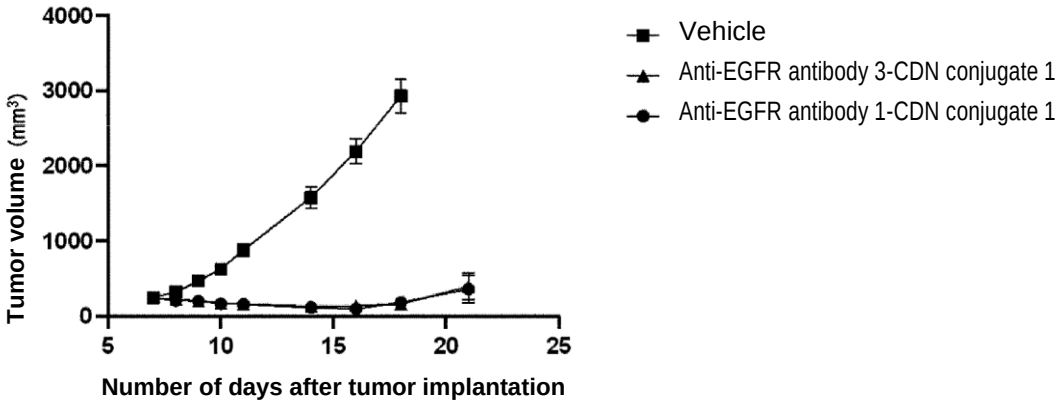

4000
3000
2000
1000
0
Tumor volume (mm3)
5
10
15
20
25
Number of days after tumor implantation
Vehicle
Anti-EGFR antibody 3-CDN conjugate 1
Anti-EGFR antibody 1-CDN conjugate 1

Fig. 5

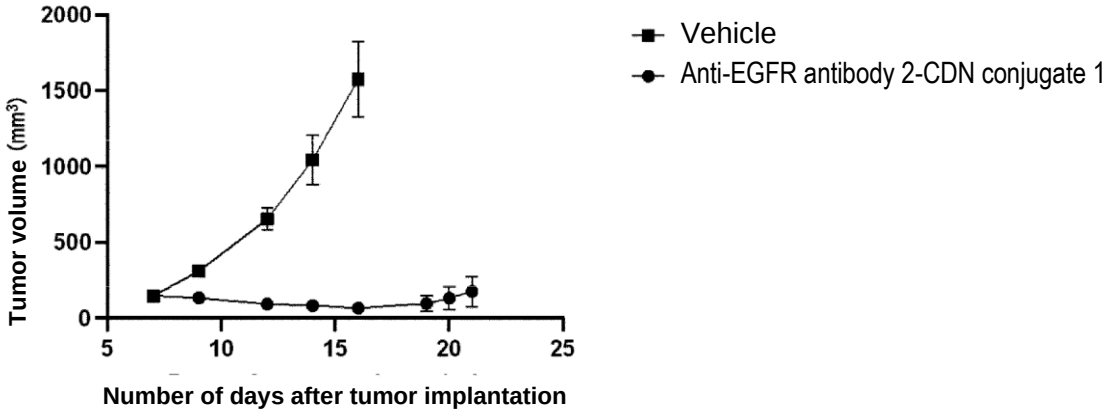


Fig. 6

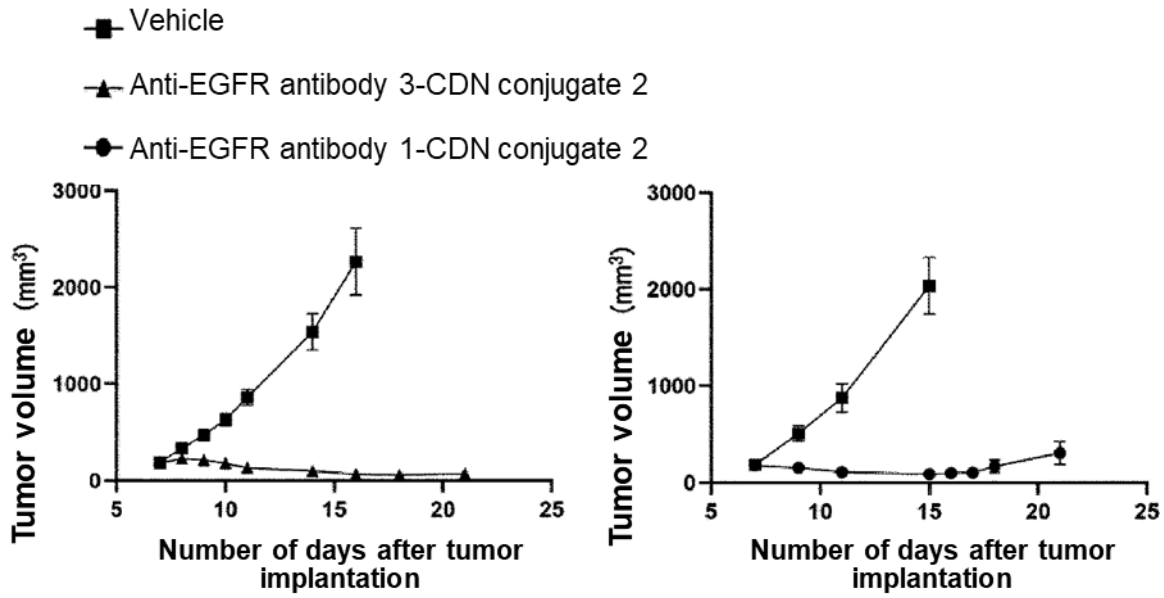


Fig. 7

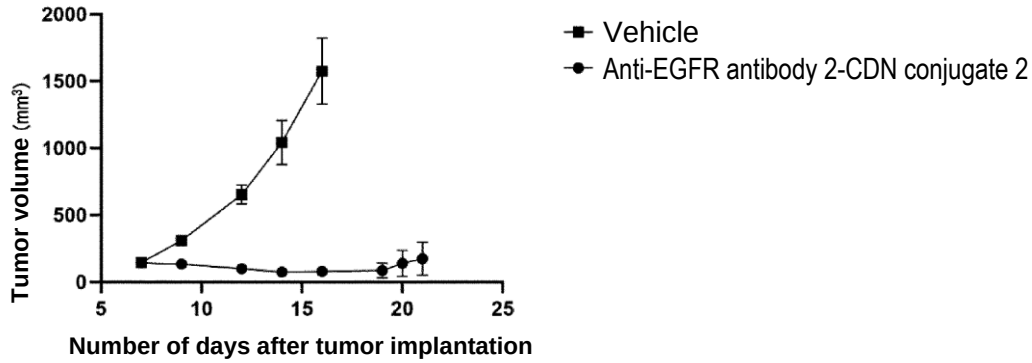


Fig. 8

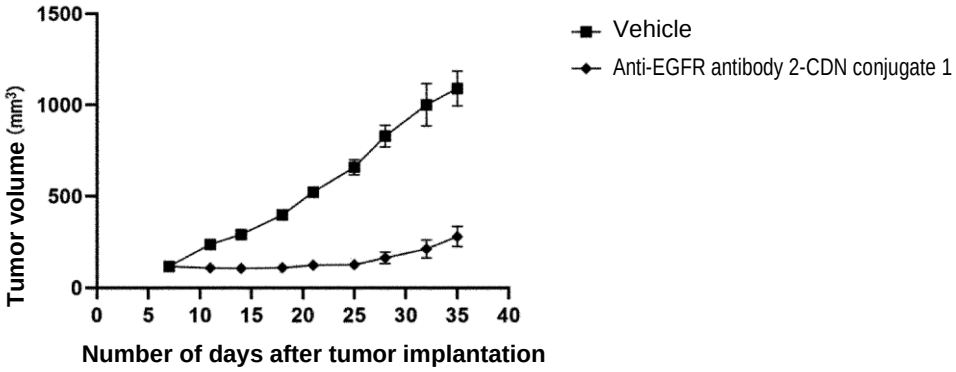

1500
1000
500
0
Tumor volume (mm³)
0
5
10
15
20
25
30
35
40
Number of days after tumor implantation
Vehicle
Anti-EGFR antibody 2-CDN conjugate 1

Fig. 9

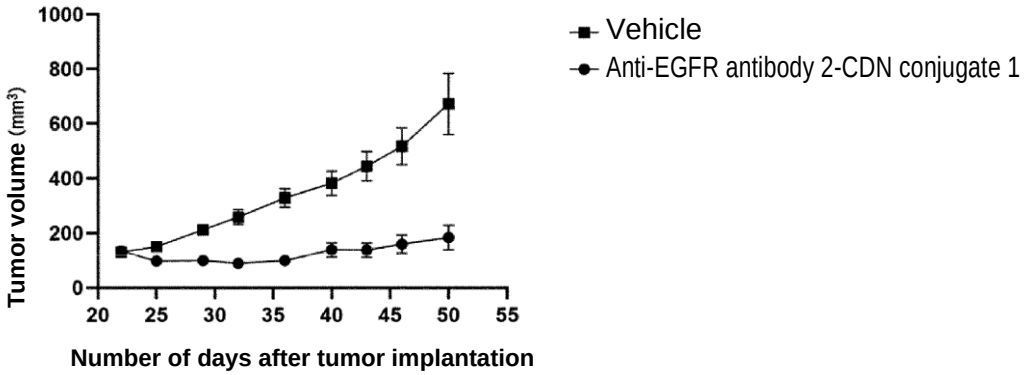


Fig. 10

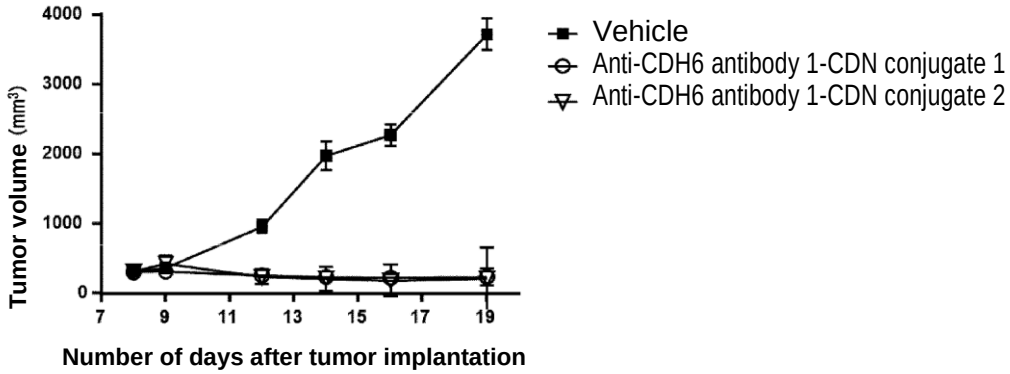


Fig. 11

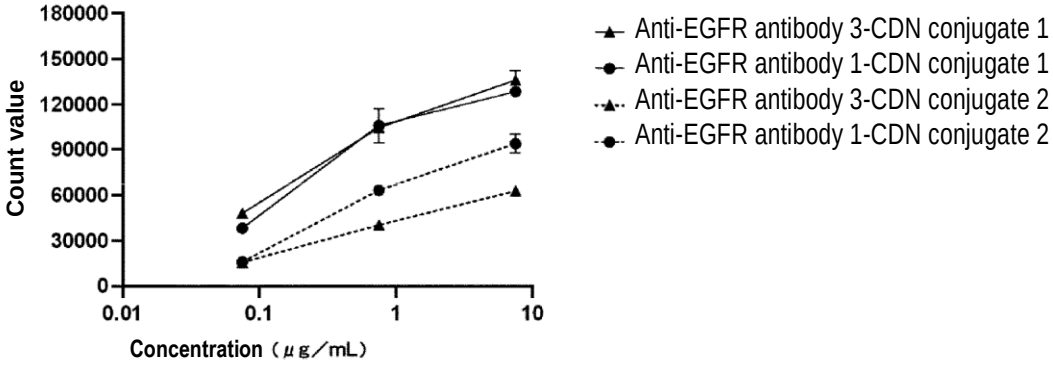


Fig. 12

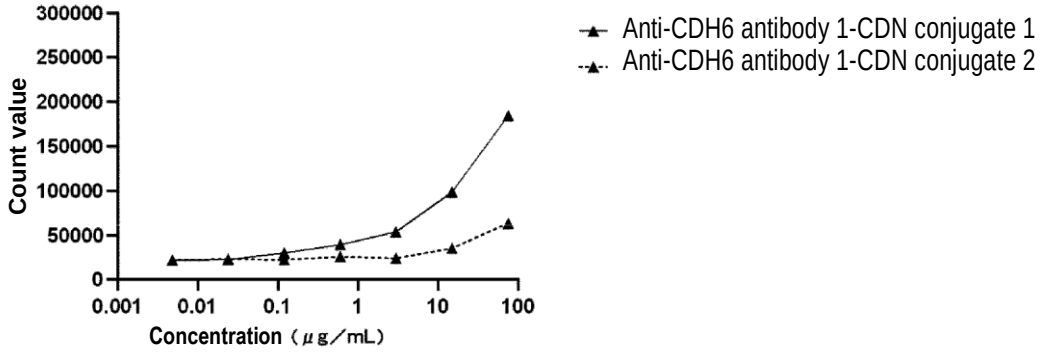


Fig. 13

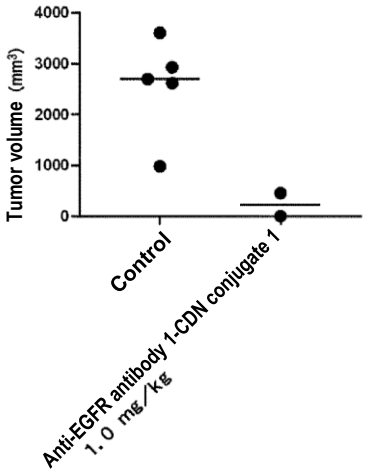


Fig. 14

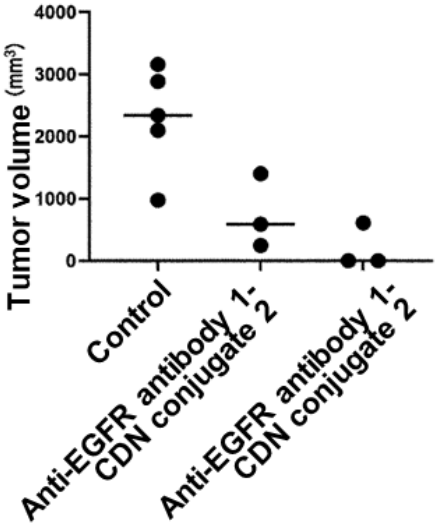


Fig. 15A

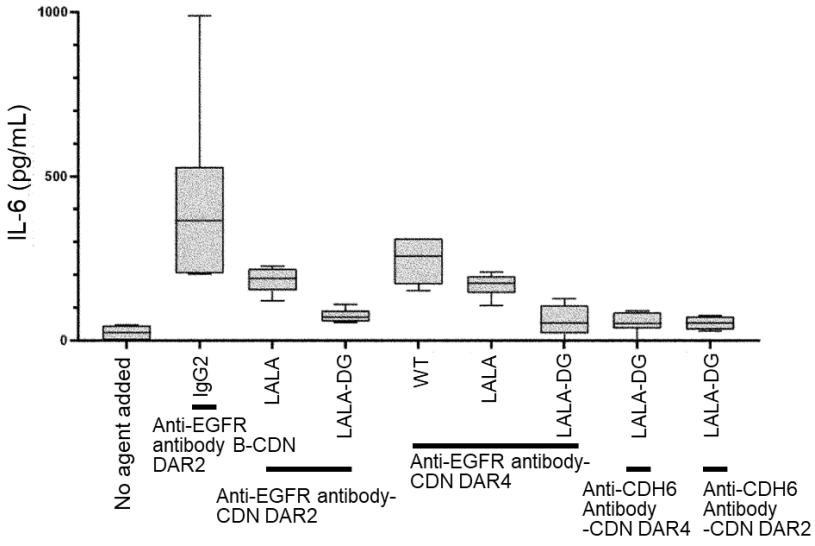


Fig. 15B

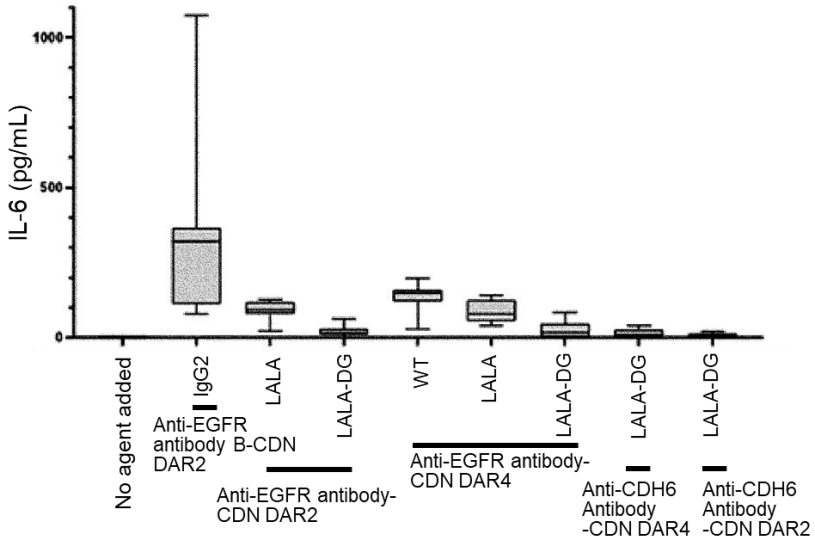


Fig. 16A

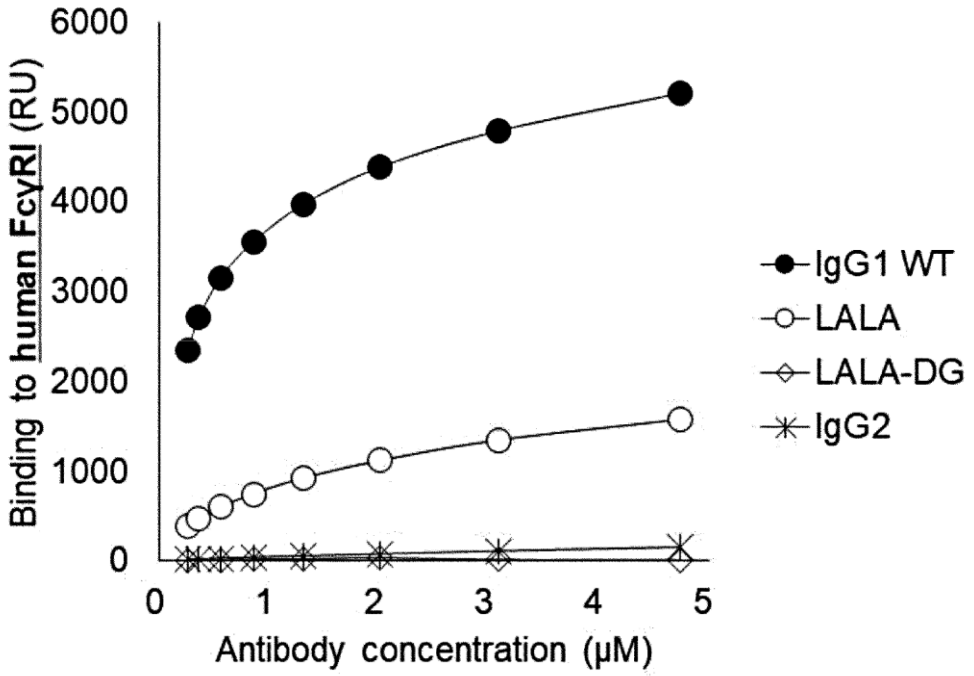


Fig. 16B

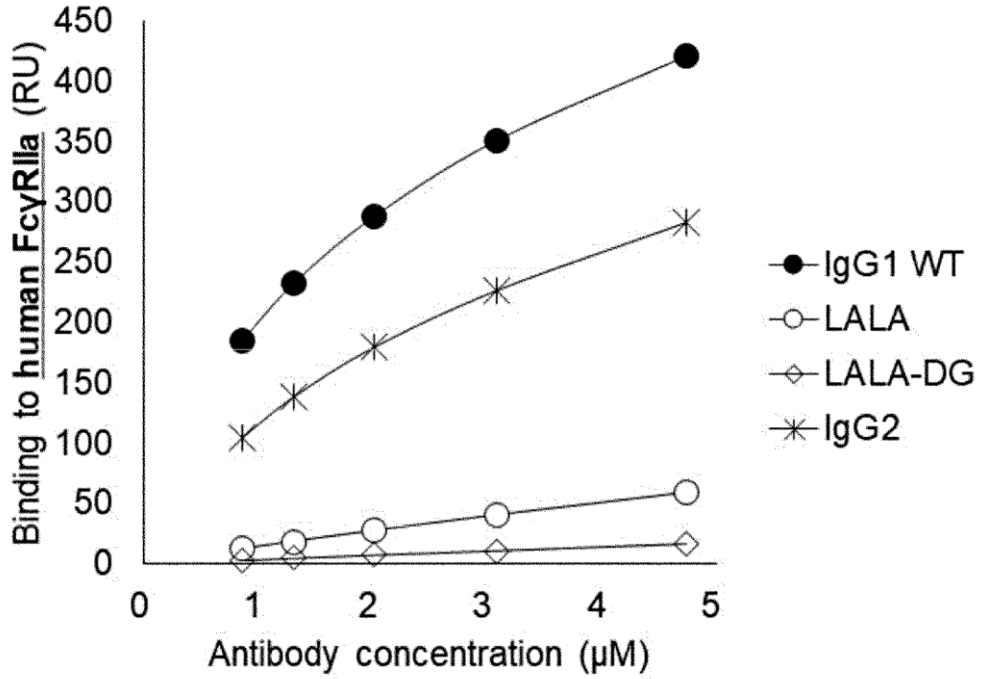


Fig. 16C

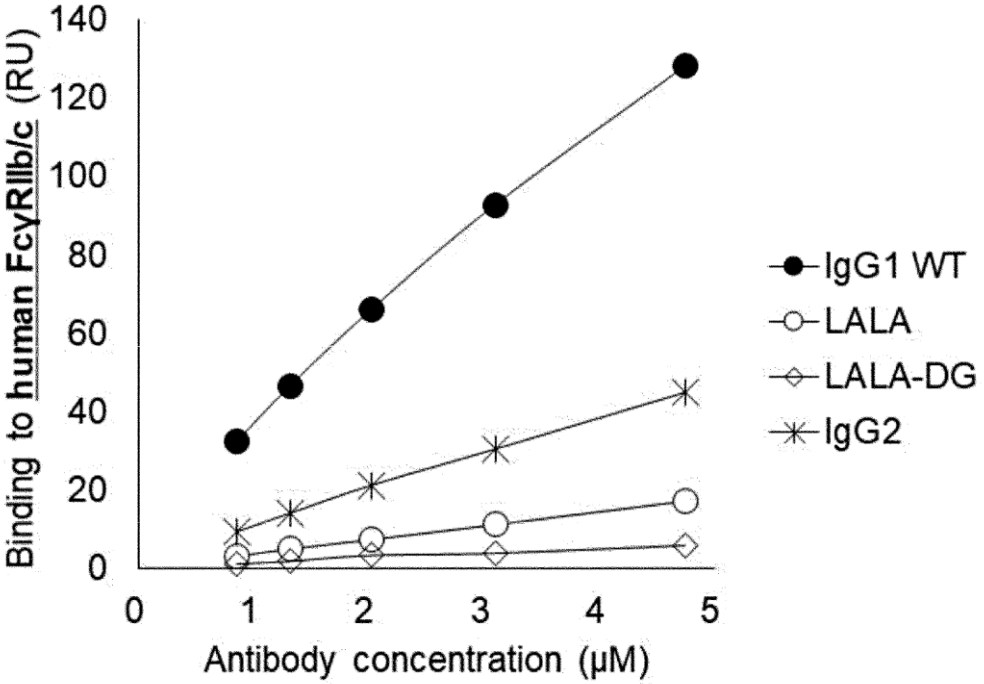


Fig. 16D

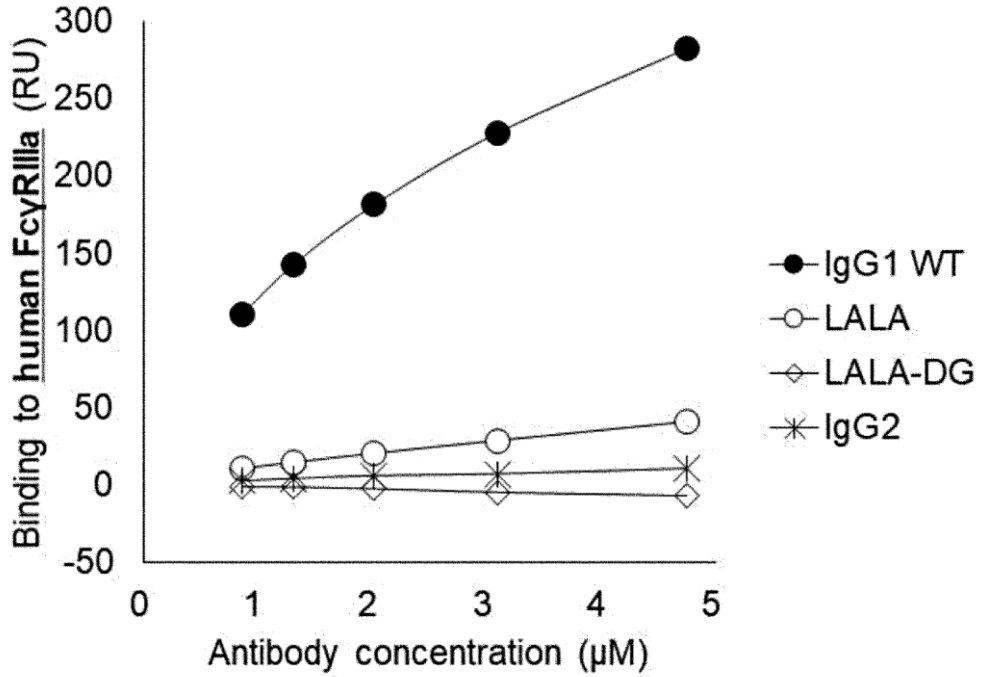


Fig. 16E

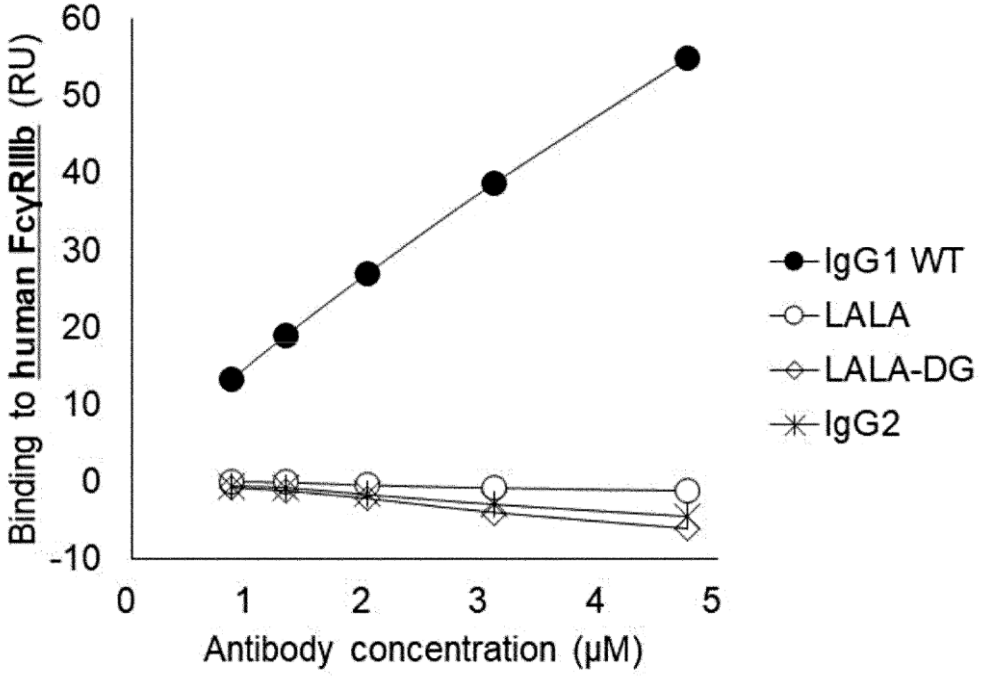


Fig. 17A

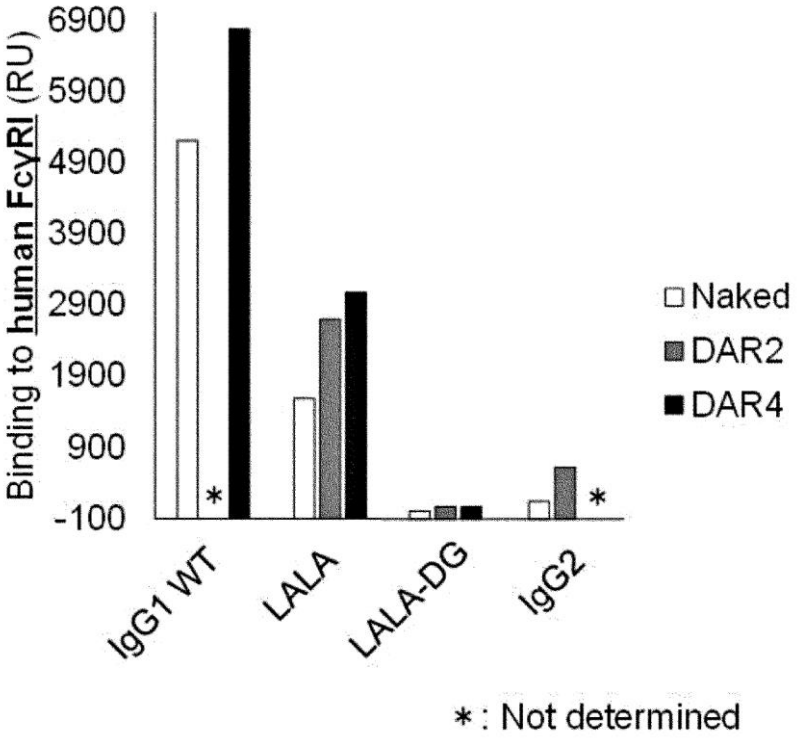


Fig. 17B

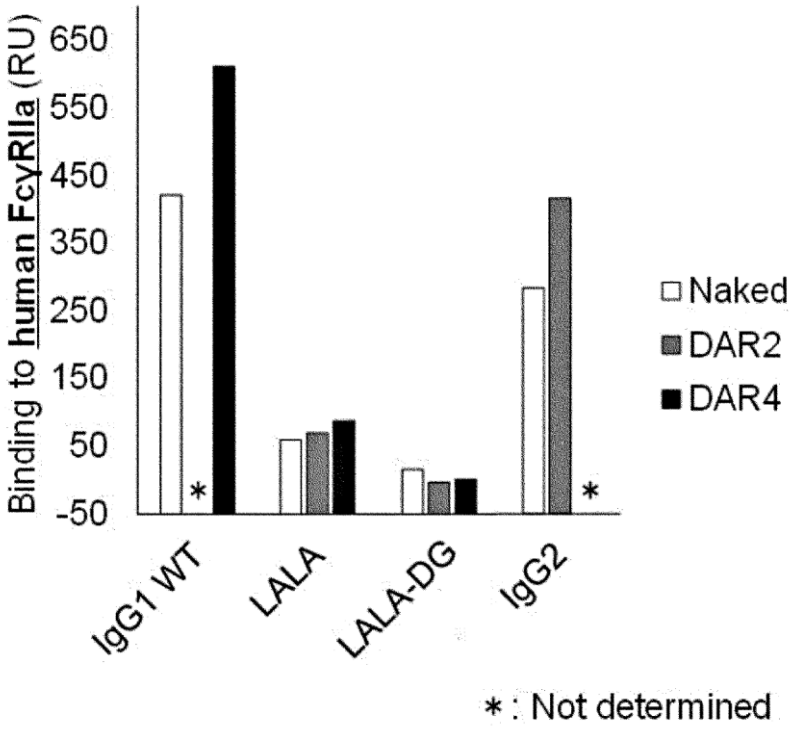


Fig. 17C

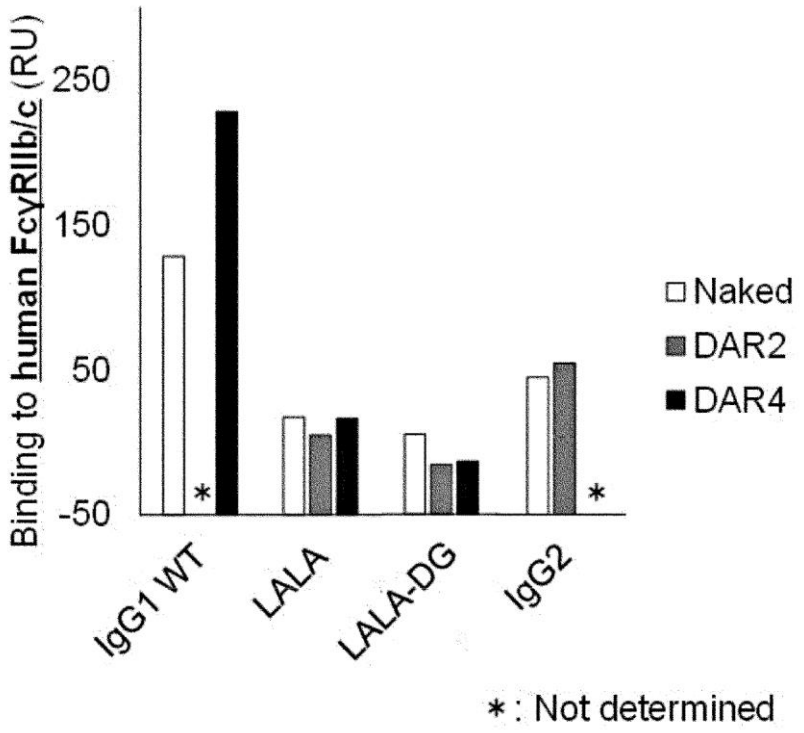


Fig. 17D

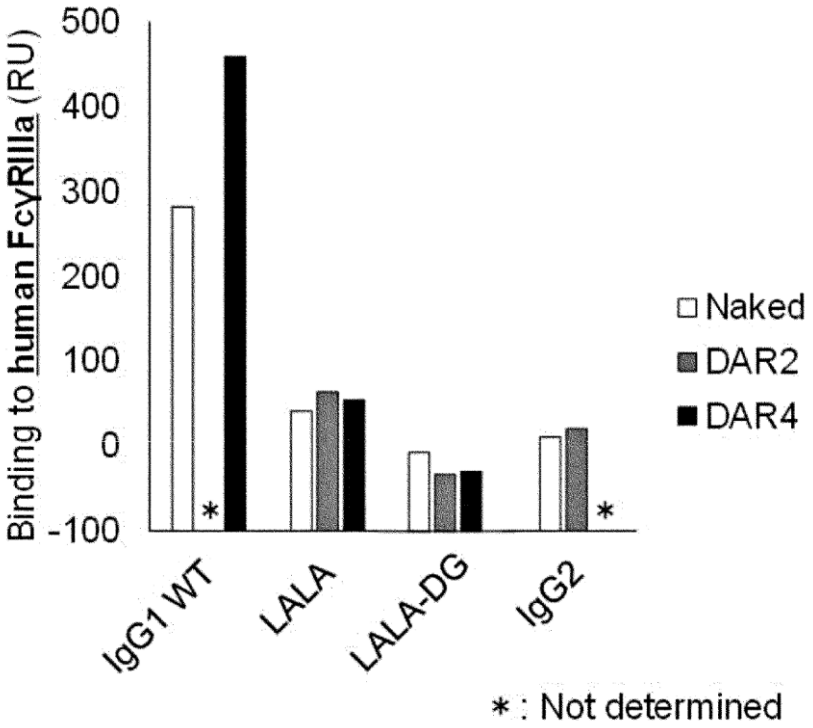


Fig. 17E

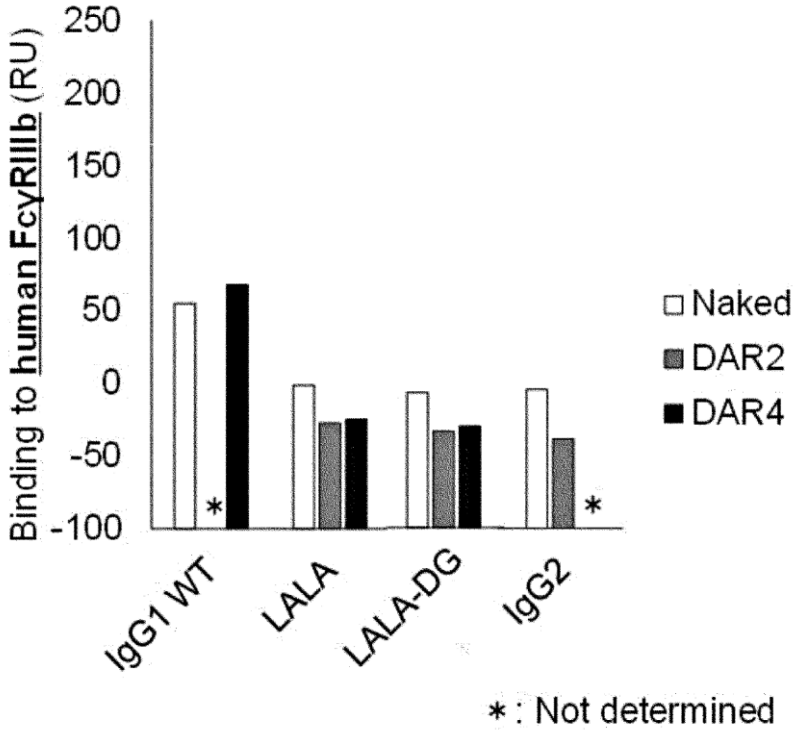


Fig. 18

	CH2 T_m (℃)	ΔT_m (℃)
IgG1 WT	70.6	—
LALA	71.0	+ 0.4
LALA-DG	75.1	+ 4.5

Fig. 19

（a）The amino acid sequence of human wild-type STING (SEQ ID NO: 1)

MPHSSLHPSIPCPRGHGAQKAALVLLSACLVTLWGLGEPPEHTLRYLVLHLASLQLGLLLNGVCSLAEELRHIHS
RYRGSYWRTVRACLGCPLRRGALLLLSIYFYYSLPNAVGPPFTWMLALLGLSQALNILLGLKGLAPAEISAVCEK
GNFNVAHGLAWSYYIGYLRLILPELQARIRTYNQHYNNLLRGAVSQRLYILLPLDCGVPDNLSMADPNIRFLDKL
PQQTGDRAGIKDRVYSNSIYELLENGQRAGTCVLEYATPLQTLFAMSQYSQAGFSREDRLEQAKLFCRTLEDILA
DAPESQNNCRLIAYQEPADDSSFSLSQEVLRHLRQEEKEEVTVGSLKTSAVPSTSTMSQEPELLISGMEKPLPLR
TDFS

（b）The amino acid sequence of human STING REF mutant (R232H) (SEQ ID NO: 3)

MPHSSLHPSIPCPRGHGAQKAALVLLSACLVTLWGLGEPPEHTLRYLVLHLASLQLGLLLNGVCSLAEELRHIHS
RYRGSYWRTVRACLGCPLRRGALLLLSIYFYYSLPNAVGPPFTWMLALLGLSQALNILLGLKGLAPAEISAVCEK
GNFNVAHGLAWSYYIGYLRLILPELQARIRTYNQHYNNLLRGAVSQRLYILLPLDCGVPDNLSMADPNIRFLDKL
PQQTGD<u>H</u>AGIKDRVYSNSIYELLENGQRAGTCVLEYATPLQTLFAMSQYSQAGFSREDRLEQAKLFCRTLEDILA
DAPESQNNCRLIAYQEPADDSSFSLSQEVLRHLRQEEKEEVTVGSLKTSAVPSTSTMSQEPELLISGMEKPLPLR
TDFS

(The site of R232H mutation is underlined.)

（c）The amino acid sequence of human STING HAQ mutant (R71H, G230A, R293Q)

MPHSSLHPSIPCPRGHGAQKAALVLLSACLVTLWGLGEPPEHTLRYLVLHLASLQLGLLLNGVCSLAEEL<u>H</u>HIHS
RYRGSYWRTVRACLGCPLRRGALLLLSIYFYYSLPNAVGPPFTWMLALLGLSQALNILLGLKGLAPAEISAVCEK
GNFNVAHGLAWSYYIGYLRLILPELQARIRTYNQHYNNLLRGAVSQRLYILLPLDCGVPDNLSMADPNIRFLDKL
PQQT<u>A</u>DRAGIKDRVYSNSIYELLENGQRAGTCVLEYATPLQTLFAMSQYSQAGFSREDRLEQAKLFC<u>Q</u>TLEDILA
DAPESQNNCRLIAYQEPADDSSFSLSQEVLRHLRQEEKEEVTVGSLKTSAVPSTSTMSQEPELLISGMEKPLPLR
TDFS

(The three underlines indicate the sites of R71H, G230A, and R293Q mutations, respectively.)

Fig. 20

The amino acid sequence of CDRL1 of anti-EGFR antibodies (modified anti-EGFR antibodies 1 to 3) (SEQ ID NO: 23)

QASQDISNYLN

The amino acid sequence of CDRL2 of anti-EGFR antibodies (modified anti-EGFR antibodies 1 to 3) (SEQ ID NO: 24)

DASNLET

The amino acid sequence of CDRL3 of anti-EGFR antibodies (modified anti-EGFR antibodies 1 to 3) (SEQ ID NO: 25)

QHFDHLPLA

The amino acid sequence of CDRH1 of anti-EGFR antibodies (modified anti-EGFR antibodies 1 to 3) (SEQ ID NO: 26)

SGDYYWT

The amino acid sequence of CDRH2 of anti-EGFR antibodies (modified anti-EGFR antibodies 1 to 3) (SEQ ID NO: 27)

HIYYSGNTNYNPSLKS

The amino acid sequence of CDRH3 of anti-EGFR antibodies (modified anti-EGFR antibodies 1 to 3) (SEQ ID NO: 28)

DRVTGAFDI

Fig. 21-1

The amino acid sequence of the light chain variable region of anti-EGFR antibodies (modified anti-EGFR antibodies 1 to 3) (SEQ ID NO: 29)

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS
RFSGSGSGTDFTFTISSLQPEDIATYFCQHFDHLPLAFGGGTKVEIKR

The amino acid sequence of the light chain of anti-EGFR antibodies (modified anti-EGFR antibodies 1 to 3) (SEQ ID NO: 30)

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS
RFSGSGSGTDFTFTISSLQPEDIATYFCQHFDHLPLAFGGGTKVEIKRTVAAPSVFIFPP
SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT
LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

The amino acid sequence of the heavy chain variable region of anti-EGFR antibodies (modified anti-EGFR antibodies 1 to 3) (SEQ ID NO: 31)

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTN
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMVTVSS

Fig. 21-2

The amino acid sequence of the heavy chain of a LALA-DG mutant anti-EGFR antibody (modified anti-EGFR antibody 1) (SEQ ID NO: 32)

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTN
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMVTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGP
SVFLFPPKPKDTLMISRTPEVTCVVVGVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

The amino acid sequence of the heavy chain of a LALA-DG mutant anti-EGFR antibody (modified anti-EGFR antibody 2) (SEQ ID NO: 33)

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTN
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMVTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGP
SVFLFPPKPKDTLMISRTPEVTCVVVGVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

The amino acid sequence of the heavy chain of anti-EGFR antibody A (SEQ ID NO: 34)

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTN
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMVTVSS
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Fig. 21-3

The amino acid sequence of the heavy chain of anti-EGFR antibody B (Vectibix) (SEQ ID NO: 35)

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTN
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFL
FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV
VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ
VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK

The amino acid sequence of the heavy chain of a LALA mutant anti-EGFR antibody (modified anti-EGFR antibody 3) (SEQ ID NO: 36)

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTN
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMVTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

Fig. 22

The amino acid sequence of CDRL1 of anti-CDH6 antibody (modified anti-CDH6 antibody 1) (SEQ ID NO: 37)

KASQNIYKNLA

The amino acid sequence of CDRL2 of anti-CDH6 antibody (modified anti-CDH6 antibody 1) (SEQ ID NO: 38)

DANTLQT

The amino acid sequence of CDRL3 of anti-CDH6 antibody (modified anti-CDH6 antibody 1) (SEQ ID NO: 39)

QQYYSGWA

The amino acid sequence of CDRH1 of anti-CDH6 antibody (modified anti-CDH6 antibody 1) (SEQ ID NO: 40)

RNFMH

The amino acid sequence of CDRH2 of anti-CDH6 antibody (modified anti-CDH6 antibody 1) (SEQ ID NO: 41)

WIYPGDGETEYAQKFQG

The amino acid sequence of CDRH3 of anti-CDH6 antibody (modified anti-CDH6 antibody 1) (SEQ ID NO: 42)

GVYGGFAGGYFDF

Fig. 23

The amino acid sequence of the light chain variable region of anti-CDH6 antibody (modified anti-CDH6 antibody 1) (SEQ ID NO: 43)

DIQMTQSPSSLSASVGDRVTITCKASQNIYKNLAWYQQKPGKAPKLLIYDANTLQTGVPS
RFSGSGSGSDFTLTISSLQPEDFATYFCQQYYSGWAFGQGTKVEIKR

The amino acid sequence of the light chain of anti-CDH6 antibody (modified anti-CDH6 antibody 1) (SEQ ID NO: 44)

DIQMTQSPSSLSASVGDRVTITCKASQNIYKNLAWYQQKPGKAPKLLIYDANTLQTGVPS
RFSGSGSGSDFTLTISSLQPEDFATYFCQQYYSGWAFGQGTKVEIKRTVAAPSVFIFPPS
DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

The amino acid sequence of the heavy chain variable region of anti-CDH6 antibody (modified anti-CDH6 antibody 1) (SEQ ID NO: 45)

EVQLVQSGAEVKKPGASVKVSCKASGYTFTRNFMHWVRQAPGQGLEWMGWIYPGDGETEY
AQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCARGVYGGFAGGYFDFWGQGTLVTV
SS

The amino acid sequence of the heavy chain of a LALA-DG mutant anti-CDH6 antibody (modified anti-CDH6 antibody 1) (SEQ ID NO: 46)

EVQLVQSGAEVKKPGASVKVSCKASGYTFTRNFMHWVRQAPGQGLEWMGWIYPGDGETEY
AQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCARGVYGGFAGGYFDFWGQGTLVTV
SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAA
GGPSVFLFPPKPKDTLMISRTPEVTCVVVGVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Fig. 24

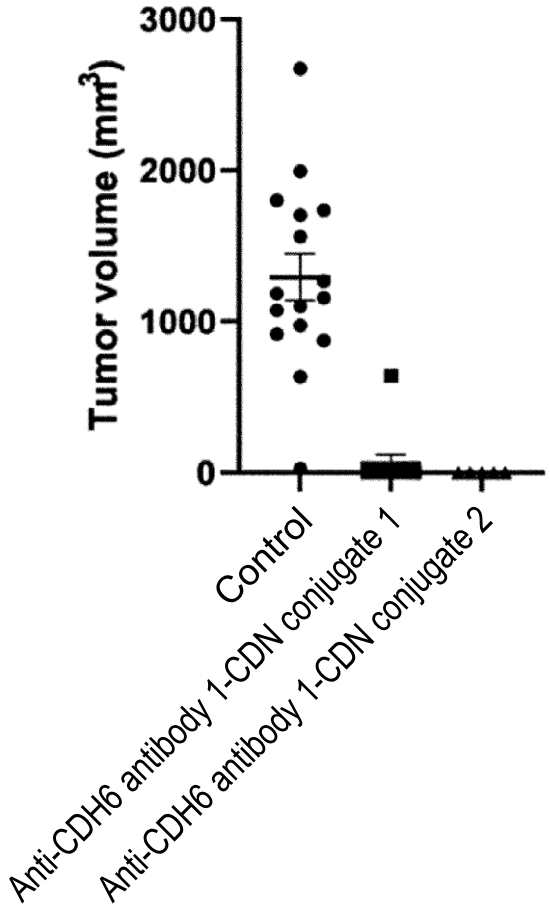

Tumor volume (mm3)
3000
2000
1000
0
Control
Anti-CDH6 antibody 1-CDN conjugate 1
Anti-CDH6 antibody 1-CDN conjugate 2

Fig. 25

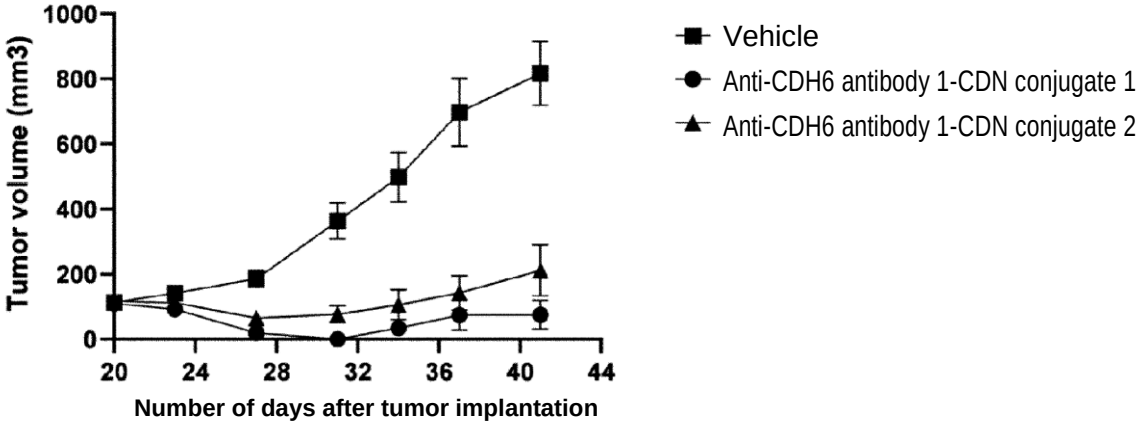

Tumor volume (mm3)
1000
800
600
400
200
0
20
24
28
32
36
40
44
Number of days after tumor implantation
Vehicle
Anti-CDH6 antibody 1-CDN conjugate 1
Anti-CDH6 antibody 1-CDN conjugate 2

Fig. 26

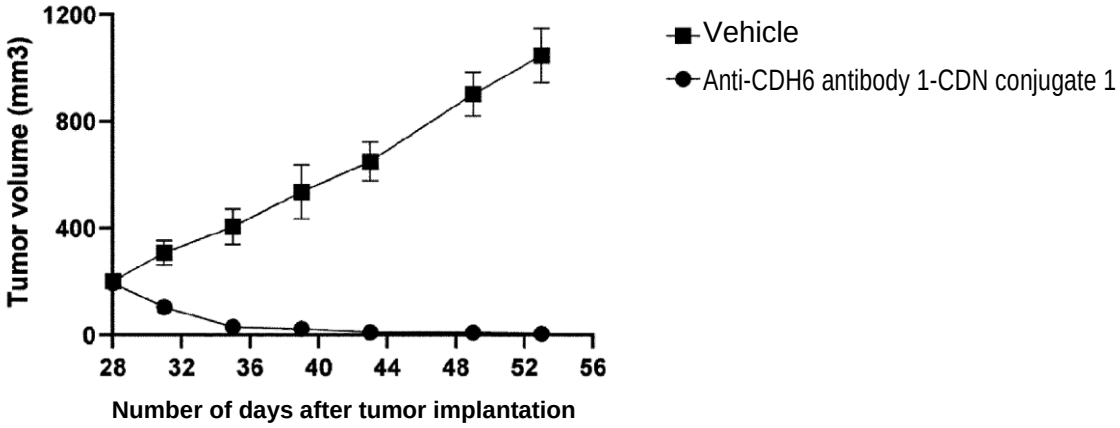


Fig. 27

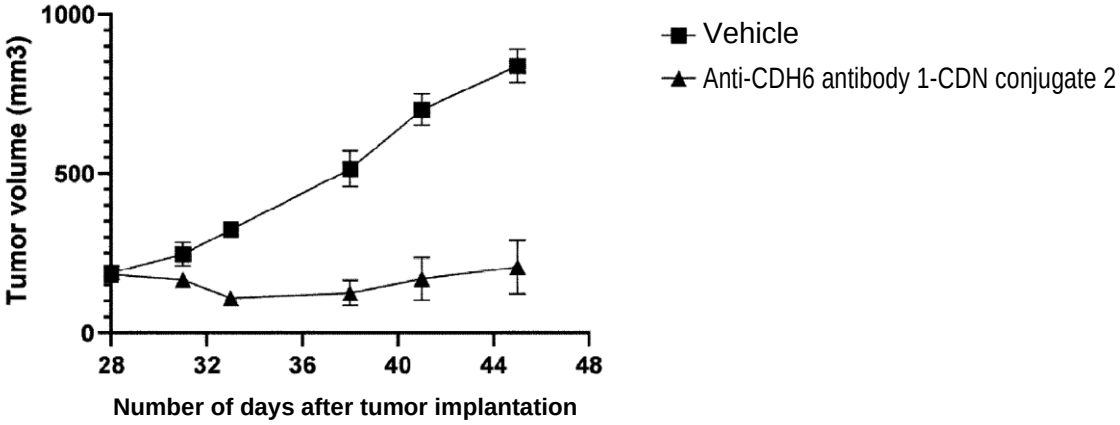


Fig. 28

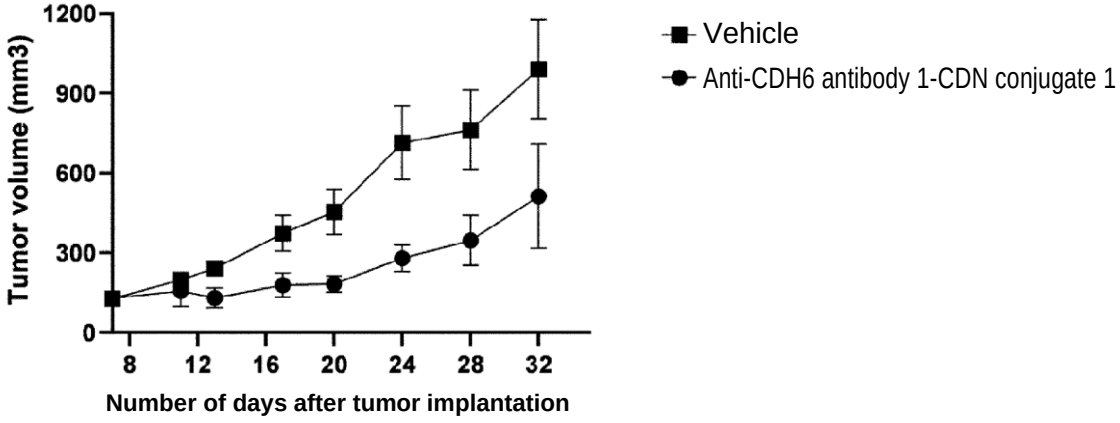


Fig. 29

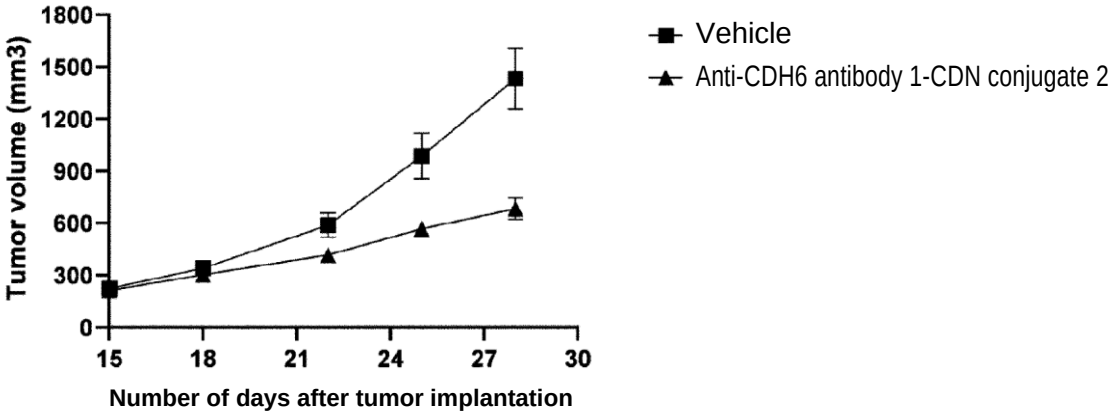


Fig. 30

SEQ ID NO: 47 the amino acid sequence of wild-type Endo-S **NCBI Accession number: AAK34539.1**

```
1   MDKHLLVKRT LGCVCAATLM GAALATHHDS LNTVKAEEKT VQVQKGLPSI 50
51  DSLHYLSENS KKEFKEELSK AGQESQKVKE ILAKAQQADK QAQELAKMKI 100
101 PEKIPMKPLH GPLYGGYFRT WHDKTSDPTE KDKVNSMGEL PKEVDLAFIF 150
151 HDWTKDYSLF WKELATKHVP KLNKQGTRVI RTIPWRFLAG GDNSGIAEDT 200
201 SKYPNTPEGN KALAKAIVDE YVYKYNLDGL DVDVEHDSIP KVDKKEDTAG 250
251 VERSIQVFEE IGKLIGPKGV DKSRLFIMDS TYMADKNPLI ERGAPYINLL 300
301 LVQVYGSQGE KGGWEPVSNR PEKTMEERWQ GYSKYIRPEQ YMIGFSFYEE 350
351 NAQEGNLWYD INSRKDEDKA NGINTDITGT RAERYARWQP KTGGVKGGIF 400
401 SYAIDRDGVA HQPKKYAKQK EFKDATDNIF HSDYSVSKAL KTVMLKDKSY 450
451 DLIDEKDFPD KALREAVMAQ VGTRKGDLER FNGTLRLDNP AIQSLEGLNK 500
501 FKKLAQLDLI GLSRITKLDR SVLPANMKPG KDTLETVLET YKKDNKEEPA 550
551 TIPPVSLKVS GLTGLKELDL SGFDRETLAG LDAATLTSLE KVDISGNKLD 600
601 LAPGTENRQI FDTMLSTISN HVGSNEQTVK FDKQKPTGHY PDTYGKTSLR 650
651 LPVANEKVDL QSQLLFGTVT NQGTLINSEA DYKAYQNHKI AGRSFVDSNY 700
701 HYNNFKVSYE NYTVKVTDST LGTTTDKTLA TDKEETYKVD FFSPADKTKA 750
751 VHTAKVIVGD EKTMMVNLAE GATVIGGSAD PVNARKVFDG QLGSETDNIS 800
801 LGWDSKQSII FKLKEDGLIK HWRFFNDSAR NPETTNKPIQ EASLQIFNIK 850
851 DYNLDNLLEN PNKFDDEKYW ITVDTYSAQG ERATAFSNTL NNITSKYWRV 900
901 VFDTKGDRYS SPVVPELQIL GYPLPNADTI MKTVTTAKEL SQQKDKFSQK 950
951 MLDELKIKEM ALETSLNSKI FDVTAINANA GVLKDCIEKR QLLKK      995
```

Fig. 31

SEQ ID NO: 48 the amino acid sequence of wild-type Endo-S2 **NCBI Accession number: ACI61688.1**

```
1   MDKHLLVKRT LGCVCAATLM GAALATHHDS LNTVKAEEKT VQTGKTDQQV 50
51  GAKLVQEIRE GKRGPLYAGY FRTWHDRAST GIDGKQQHPE NTMAEVPKEV 100
101 DILFVFHDHT ASDSPFWSEL KDSYVHKLHQ QGTALVQTIG VNELNGRTGL 150
151 SKDYPDTPEG NKALAAAIVK AFVTDRGVDG LDIDIEHEFT NKRTPEEDAR 200
201 ALNVFKEIAQ LIGKNGSDKS KLLIMDTTLS VENNPIFKGI AEDLDYLLRQ 250
251 YYGSQGGEAE VDTINSDWNQ YQNYIDASQF MIGFSFFESS ASKGNLWFDV 300
301 NEYDPNNPEK GKDIEGTRAK KYAEWQPSTG GLKAGIFSYA IDRDGVAHVP 350
351 STYKNRTSTN LQRHEVDNIS HTDYTVSRKL KTLMTEDKRY DVIDQKDIPD 400
401 PALREQIIQQ VGQYKGDLER YNKTLVLTGD KIQNLKGLEK LSKLQKLELR 450
451 QLSNVKEITP ELLPESMKKD AELVMVGMTG LEKLNLSGLN RQTLDGIDVN 500
501 SITHLTSFDI SHNSLDLSEK SEDRKLLMTL MEQVSNHQKI TVKNTAFENQ 550
551 KPKGYYPQTY DTKEGHYDVD NAEHDILTDF VFGTVTKRNT FIGDEEAFAI 600
601 YKEGAVDGRQ YVSKDYTYEA FRKDYKGYKV HLTASNLGET VTSKVTATTD 650
651 ETYLVDVSDG EKVVHHMKLN IGSGAIMMEN LAKGAKVIGT SGDFEQAKKI 700
701 FDGEKSDRFF TWGQTNWIAF DLGEINLAKE WRLFNAETNT EIKTDSSLNV 750
751 AKGRLQILKD TTIDLEKMDI KNRKEYLSND ENWTDVAQMD DAKAIFNSKL 800
801 SNVLSRYWRF CVDGGASSYY PQYTELQILG QRLSNDVANT LKD         843
```

Fig. 32

SEQ ID NO: 49 the amino acid sequence of wild-type Endo-Si **NCBI Accession number: EKB52062.1**

```
1   MNKRLLVKRT FGCVCAAAIL GVAPLSHPTI VEAREELKMP NGLEQSIADV 50
51  EAKIDALTYL SKNSKDEFKH SMYEIPSNRE HKPVSPKQAL QNAKKADAQA 100
101 ERLAKMTIPK KEELKALEGP LYGGYFRTWQ DKTSDPTETN KVNSFGELPK 150
151 EVDLAFVFHD YTKDYSLFWE ELATKQVPKL NKQGTRVIRT IPWRFLSGAD 200
201 HSDISADKEK FPNTEAGNKA LAKAIVDEYV YKYNLDGLDI DIERDSVPKV 250
251 NDKEDPEALA RTVEVFKEIG KLIGANGADK SRLLIMDTTY TAEENPLIKE 300
301 TAQYLNLLLV QVYGFSGENG NYLHHKNILD ETSSMEGRWQ GYSKYIRPEQ 350
351 YMVGFSFYEE KDFNNRWKDI NEEDPSDPHI GEKIQGTRAE RYAKWQPKTG 400
401 GLKGGLFSYA IDRDGVAQPK QKTEHPELDK IVKSEYKVSK ALKKLMMTDD 450
451 QYQPIDQSDF PDKALRESII KQVGTRRGDL ERFKGTLRLD NPEIKDLTGL 500
501 NKLKRVAKLE LINLPKITKI DKDDLPQNLK PLTDNQKSNL EIKGTYDDSK 550
551 LYKDIPAFDL VISGLSGLES LDISGHQRDT LSGIDASTLP SLKAINISDN 600
601 HFDLAQGTEN RHILDTILAT LAKNGASTAS FDKQKPKGLY PESYSTAPLH 650
651 LQVGQGKINV IDDLIFGTRT NQNTLINTEN DFEAYKEQTI QGKPFIAPDY 700
701 LYDNFKVSYK EYSASIVDST LAETTDKTID TAKAETYQVT VSNKDGKTVH 750
751 SVKVIVGDEK PMMVNLAQDA KIIGTDNMTQ SAKVFDGQKD QFLLSWNKDS 800
801 SVIFELKTPG TAKHWRFFDD GKNDSVTLSV FKGDASNFET EKDKAENWVE 850
851 ITKDSRKNDD KVFSSPLEVD NAKYLKVTIK KEAKYIYFNE LQILGYPGVV 900
901 AKKTADDLRP TEADKSDDKS DKNDTEAK                         928
```

Fig. 33

SEQ ID NO: 50 the amino acid sequence of wild-type Endo-M **NCBI Accession number: BAB43869.1**

```
1   MPSLQLQPDD KLAPVSFALK SMNELRDWTP DEKIKFNVSS VALQPRVKNA 50
51  LKPQLLLTHD MAGGYKEDKN IQGNNYKDIY NIQYWHLADT FVYFSHERVS 100
101 IPPVNWTNAC HRNGVKCLGT FLVEGNNQMH EMEALLHGPP LLNNTDDPMR 150
151 LWSPYYADQL VAIAKHYGFD GWLFNIECEF FPFPTNPKFK AEELAKFLHY 200
201 FKEKLHNEIP GSQLIWYDSM TNEGEIHWQN QLTWKNELFF KNTDGIFLNY 250
251 WWKKEYPEMA RRVAEGIGRS GLEVYFGTDV WGRHTYGGGG FKSYKGVKTA 300
301 YSAMTSSALF GMAWTYEHFE KSEFEKMDRL FWCGGKYSDY PPPPPKNPDD 350
351 EKEVESDDSE DELMYGHKKG IADTVESIPV PGTDWFVTNF DRGFGNRFYY 400
401 RGKRLLSQPW SHLSHQAILP NKSYRNPEIY PTDQNIKITS SLDCDHGAFL 450
451 GGTSLIIKGQ RFNHRESHDV ETEISIPLYK LSLDASKGCS LRYIYRTLLM 500
501 KDVKLTVACH FSLKTNDSVN FFKVWQPDEN FSFEYDDGMR ATVTTENSTE 550
551 SRCFLLRTTE EDTGENDWIT KTINVPAVPE GSQLYITRLE VSVVLDTAGL 600
601 VGLVNQVIAC LGYISIIPTI NSGIKTDSSR IIQDLFWKDQ KYTKIGKESL 650
651 DDIAQEEVHR YYGTLNWENT ANVVNAWEEI DYYNVFYKES DDSATRIFLG 700
701 TAFCNQFRVS GLDIILSKLP KIVIEAVNKE GYISSSGSID LSLN       744
```

Fig. 34

SEQ ID NO: 51 the amino acid sequence of wild-type Endo-Rp **NCBI Accession number:** unregistered *

```
1   MPSLELQQAA DTRLFESMPL QTMNELGSWE PSNASRANIA TIPLHQRSNL 50
51  DPAEPRLIVT HDMAGGYKED SNIQGNTYDT IYSCQYWQYV DTFIYFSHHR 100
101 VTIPPVNWIN ACHRNGVKTL GTFIVEGAAG MFALERFVYG PEPGQRNSWS 150
151 PYYADKLVDI AEFYGFDGWL LNIESDFFPL YRNPSLKAIH LAKLLRYLKN 200
201 AMHARVPGSE IIWYDSMTTN GSVQWQNNIT PKNSIFFEAA DGIFLNYWWN 250
251 ATVPPLALQV AHRLGRQGSD VYFGTDVWGR GTFGGGGFDS YLAVGTARAF 300
301 KTSSALFGTA WIYEHFGKKD FELMDRLLWL GGDQSEYPAQ EGEQNRTVKV 350
351 TSHLGRHPGI ADVSPVRSAP GKTWFATWFD RGYGTGFYYQ GKKLLSQPWS 400
401 HLSHQSIPPN LIARLQREEN HGLSYFLADD DAYIGGTSLL IAAEITQERQ 450
451 LPLYQLEYDV TEGCEVQFIY KSPEPDMQGK IDIYLNLQVT DILPDELAFY 500
501 WQDVTDASSQ ADATTAMRLY LNENTVIYLK PSRKQELAEG WLLCSVRVPP 550
551 TYPLGIATIK ELGIHVDGKE TVLFRLGLLT IIPLGDAPSA LSRITQVQLQ 600
601 RDEDIHSKCP SSSCELWATL SWMMEHNSKE DWDQVDHYMI FFKNVDSKAE 650
651 PIFLGTSFST EYRISGLEIK KHGNSIEIWA VNRLGTVIAR QDIDIQ     696
```

Fig. 35

SEQ ID NO: 52 the amino acid sequence of wild-type Endo-CC **NCBI Accession number: EAU82416.1**

```
1   MPIAGKKFHP RALPEFWRTF REMDEWRATQ TGPQARPAEG ILKYVPRKIR 50
51  PADIAGKGRL LVSHDYKGGY VEDPFSKSYS FNWWFSTDSF NYFAHHRITI 100
101 PPPEWINAAH RQGVPILGTI IFEGGSDEDI LRMVIGKTPG STSNFHAERN 150
151 AEYTVPVSSY YAELFADLAV ERGFDGWLLN VEIGLQGGSE QARGLAAWVA 200
201 LLQQEVLKKV GPHGLVIWYD SVTVRGDLWW QDRLNAFNLP FFLNSSGIFT 250
251 NYWWYNDAPQ KQIDFLSRVD PNLTGQTAEP HQYNLQKTIQ DIYIGVDVWG 300
301 RGSHGGGGFG AYKAIEHADP KGLGFSVALF AQGWTWETEE EKPGWNWAQF 350
351 WDYDSKLWVG PPGVVEAPDH TVKPGEYPCV HGPFQPISSF FLTYPPPDPL 400
401 DLPFYTNFCP GIGDAWFVEG KEVFRSETGW TDMDKQTTVG DLVWPRPKIY 450
451 DLPSQNASQA TLNAAFNFND AWNGGNSLQI NLTVPGGATT YGAYWVPIQT 500
501 FTFSSRRQYE ASIVYKPGLS GKTRFDAKYE VGIRTITGED QGKIISNTTT 550
551 EVGNGWRKVH ILFEIETPVE GGSIIVPSSI GLVIAVSNVS TTEQFEFPFL 600
601 VGQITIHPHL PDRYKEFKPA LLWLLFTPSA GTNSLDGTLT WDVVAAIERP 650
651 PPVEINNPDD AQIPWNLQPT KQEWFPDFLY FNVYVLELLD GGGQGPPQWI 700
701 GTTGYDGEKK RFFIYDESLP PTSGLRRFTF QIEGVLETGE STHWYDAPAA 750
751 PSATAGGEQK RTRRTSLKSV LSPLRRKKSK GDISVAK              787
```

Fig. 36

SEQ ID NO: 53 the amino acid sequence of wild-type Endo-Om **NCBI Accession number: BAN20080.1**

```
1   MAQSQLLGGA VRPVFFDKLE ELRRWHTQSA NLSRESELDS LNVATEPFSS 50
51  YERAQTGSGS RSSEPVPGDK EDPPIKLMVC HDFKGGYQDY EDAQPLGYFP 100
101 HPTGSRYFLQ YPQLIDQFVY FSHHRVTVPP VNWINFCHRN GIKCFGTVIF 150
151 EGNASKDFEE LDRLVSRDEK GDFVFVDALI KLAAHYGFDG YLLNIETTFS 200
201 NTKIAADLEP FAEQLKSGLH CLDSKNELIW YDSYVFPANK VSYTNGVTES 250
251 NYNFFSLSDA FFSNYWWNIK NLQENIKNVG VLGVQKKIYV GYDVWGRGTL 300
301 VGKGGFDSSL ACKMIAKFKS NVALFAPAWT YESLGPKDFN QNDARFWIGL 350
351 FENESSISST VPPHSSAVYK INESSFIFYT NFSSGEGNRF FSKGSEVYRK 400
401 NWVNGSLQFD LPIDLHRKDK NGLQWALDKS DAFHGGACLE IKYSEIKDEN 450
451 GYQIFNNQMV SDFTLFNFTK ECHFPTVNVK VTYKLNHKTK STFKIKIKYI 500
501 IERRFRSVQT VRTGYLTIPL LSTSGKWFTV EESFQINLQT SHEYIVLESA 550
551 HVTYDEDRSA DSFFRSYIVE DSAITSVIDN EEYEKLINSE IYNDDEDEDW 600
601 ILVPSDVSIS SSESQSNDSK TQYLGRKLFG NKSTPKTRTL EGTAPLLRIG 650
651 EFAIISANNY PSSNFLAVTS VKSIESSRLE GDSLVLLNWQ VGEGHQKGVC 700
701 YYIIYVNGAV VGLSVAPKFI YQDTELASEN SASARSNYKK SGLGSSSDRK 750
751 SKVRVDSVDK LGNVFTGSEV WV                              772
```

Fig. 37

SEQ ID NO: 54 the amino acid sequence of wild-type Endo-Sd GenBank Accession number: ANI26082

```
1    MDKRLLVKRT LGCVCSATLM GTILGTHHDS LISVKAEEKI TQVSQTSTSI    50
51   DDLHYLSENS KKEFKEELSK EKVPEKVKEI LSKAQQANKQ AQELAEMKVP   100
101  DKIPMKPLNG PLYGGYFRTW HDKTSDPLEK DKVNSMGELP KEVDLAFVFH   150
151  DWTKDYSLFW KELATKHVPK LNKQGTRVIR TIPWRFLAGG DNSGIAEDAS   200
201  KYPNTPEGNK ALAKAIVDEY VYKYNLDGLD VDIEHDSIPK VNGEASDENL   250
251  KRSIDVFEEI GKLIGPKGAD KSRLFIMDST YMADKNPLIE RGAPYIDLLL   300
301  VQVYGSQGEQ GEFQNDTKSV TKTPEERWQG YSKYIRPEQY MIGFSFYEEK   350
351  AGSGNLWYDI NARKDEDTAN GINDDITGTR AERYARWQPK TGGVKGGIFS   400
401  YAIDRDGVAH QPKQIAEKDK QSVKNNRPLI SEITDNIFHS NYSVSKTLKT   450
451  VMLKDKAYDL IDEKDFPDKA LREAVMAQVG TRKGDLERFN GTLRLDNPAI   500
501  QSLEGLNKFK KLAQLDLIGL SRIIKLDQSV LPANMKPGKD PLETVLETYK   550
551  KNGKEEPAII PPVSLTVSGL TGLKELDLSG FDRETLAGID AATLTSLEKV   600
601  DISDNKLDLA PKTENRQIFD VMLSTVNNNA GISEQSIKFD NQKPAGNYPQ   650
651  TYGATNLQLP VRQEKIDLQH QLLFGTITNQ GTLINSEADY KTYRNQKIAG   700
701  RNFVDPDYPY NNFKVSHDNY TVKVTDSTLG TTTDKMLATD KEETYKVDFF   750
751  SPTDKTKAVH TAKVIVGDEK TMMVNLAEGA TVIKSENDEN AQKVFNGIME   800
801  YNPLSFNNKS SIIFEIKDPS LAKYWRLFND SSKDKKDYIK EAKLEVFTGQ   850
851  LNAEADVKTI LEKPDNWVTV STYSGEEKVF SHSLDNISAK YWRVTVDNKK   900
901  DQYGYVSLPE LQILGYPLPN ADTIMKTVTV AKELSQQKDK FPQQLLDEST   950
951  AKEAVVEASL NSKLFDTGVI NTNVEALKNV VDECLAYEKN KETAFKATED  1000
1001 YRAAVNGVKA ESVTVEEMAQ LKDLIGKAAH LNSKIDAKLA DREYDKDLLG  1050
1051 LIGELTNITR TVKSFVK                                     1067
```

Fig. 38

SEQ ID NO: 55 the amino acid sequence of wild-type Endo-Sz GenBank Accession number: KIS14581.1

```
1    MEKQVLVKKT LKCVCAAALM VAILAAQHDS LIRVKAEDKL VQTSPSVSAI    50
51   DALHYLSENS KKEFKEELSK VEKAQPEKLK EIVSKAQQAD KQAKTLAEMK   100
101  VPEKIPMKPL KGPLYGGYFR TWHDKTSDPA EKDKVNSMGE LPKEVDLAFV   150
151  FHDWTKDYSL FWQELATKHV PTLNKQGTRV IRTIPWRFLA GGDHSGIAED   200
201  AQKYPNTPEG NKALAKAIVD EYVYKYNLDG LDVDIERDSI PKVNKEESKE   250
251  GIERSIQVFE EIGKLIGPKG ADKSRLFIMD STYMADKNPL IERGAPYIDL   300
301  LLVQVYGTQG EKGGFDNANH KAVDTMEERW ESYSKYIRPE QYMVGFSFYE   350
351  EKANSGNLWY DVNVEDDTNP NIGSEIKGTR AERYAKWQPK TGGVKGGIFS   400
401  YGIDRDGVAH PKKNGPKTPD LDKIVKSDYK VSKALKKVME NDKSYELIDQ   450
451  KDFPDKALRE AVIAQVGSRR GNLERFNGTL RLDNPDIKSL EGLNKLKKLA   500
501  KLELIGLSQI TKLDSSVLPE NIKPTKDTLV SVLETYKNDD RKEEAKAIPQ   550
551  VALTISGLTG LKELNLAGFD RDSLAGIDAA SLTSLEKVDL SSNKLDLAAG   600
601  TENRQILDTM LATVTKHGGV SEKTFVFDHQ KPTGLYPDTY GTKSLQLPVA   650
651  NDTIDLQAKL LFGTVTNQGT LINSEADYKA YQEQEIAGHR FVDSSYDYKA   700
701  FAVTYKDYKI KVTDSTLGVT DHKDLSTSKE ETYKVEFFSP INSTKPVHEA   750
751  KIVVGEEKTM MVNLAEGATI IGGDADPTNA KKVFDGLLNN DTTTLSTSNK   800
801  ASIIFELKEP GLVKHWRFFN DSKISKADYI KEAKLEAFVG HLEDSSKVKD   850
851  SLEKSTEWVT VSDYSGEAQE FSQPLNNIGA KYWRITIDNK KSQYGYVSLP   900
901  ELQIIGHRLP EAATVMTTMA AAEELSQQKD KFSQEQLKEL EVKVAALKAA   950
951  LDNKMFNADT INASFADVKA YIDKLLADAA GKKTLGKATK EAQPVATDAK  1000
1001 EKAESENPKA D                                          1011
```

Fig. 39

SEQ ID NO: 56 the amino acid sequence of wild-type Endo-Se GenBank Accession number: CAW92602.1

```
1    MEKQVLVKKT LKCVCAAALM VAILAAQHDS LIRVKAEDKV VQTSPSVSAI   50
51   DDLHYLSENS KKEFKEGLSK AGEVPEKLKD ILSKAQQADK QAKVLAEMKV  100
101  PEKIAMKPLK GPLYGGYFRT WHDKTSDPAE KDKVNSMGEL PKEVDLAFVF  150
151  HDWTKDYSFF WQELATKHVP TLNKQGTRVI RTIPWRFLAG GDHSGIAEDT  200
201  QKYPNTPEGN KALAKAIVDE YVYKYNLDGL DVDIERDSIP KVNGKESNEN  250
251  IQRSIAVFEE IGKLIGPKGA DKSRLFIMDS TYMADKNPLI ERGAQYIDLL  300
301  LVQVYGTQGE KGDWDPVARK PEKTMEERWE SYSKYIRPEQ YMVGFSFYEE  350
351  NAGSGNLWYD INERKDDHNP LNSEIAGTRA ERYAKWQPKT GGVKGGIFSY  400
401  AIDRDGVAHQ PKKVSDDEKR TNKAIKDITD GIVKSDYKVS KALKKVMEND  450
451  KSYELIDQKD FPDKALREAV IAQVGSRRGD LERFNGTLRL DNPDIKSLEG  500
501  LNKLKKLAKL ELIGLSQITK LDSLVLPANA KPTKDTLANV LEAYDSAKKE  550
551  ETKAIPQVAL TISGLTGLKE LNLAGFDRDS LAGIDAASLT SLEKVDLSSN  600
601  KLDLAAGTEN RQILDTMLAT VTKHGGVSEK TFVFDHQKPT GLYPDTYGTK  650
651  SLQLPVANDT IDLQAKLLFG TVTNQGTLIN SEADYKAYQE QEIAGHRFVD  700
701  SSYDYKAFAV TYKDYKIKVT DSTLGVTDHK DLSTSKEETY KVEFFSPTNS  750
751  TKPVHEAKVV VGAEKTMMVN LAEGATVIGG DADPTNAKKV FDGLLNNDTT  800
801  ILSTSNKASI IFELKEPGLV KYWRFFNDSK ISKADCIKEA KLEAFVGHLE  850
851  AGSKVKDSLE KSSKWVTVSD YSGEDQEFSQ PLNNIGAKYW RITVDTKGGR  900
901  YNWPSLPELQ IIGYQLPAAD LVMAMLATAE ELSQQKDKFS QEQLKELEVK  950
951  IAALKAALDS KMFNADAINA STADLKAYVD KLLADRTDQE KVAKAAKVEQ 1000
1001 PVATDIKENT EPENPKTD                                   1018
```