

Fig. 1

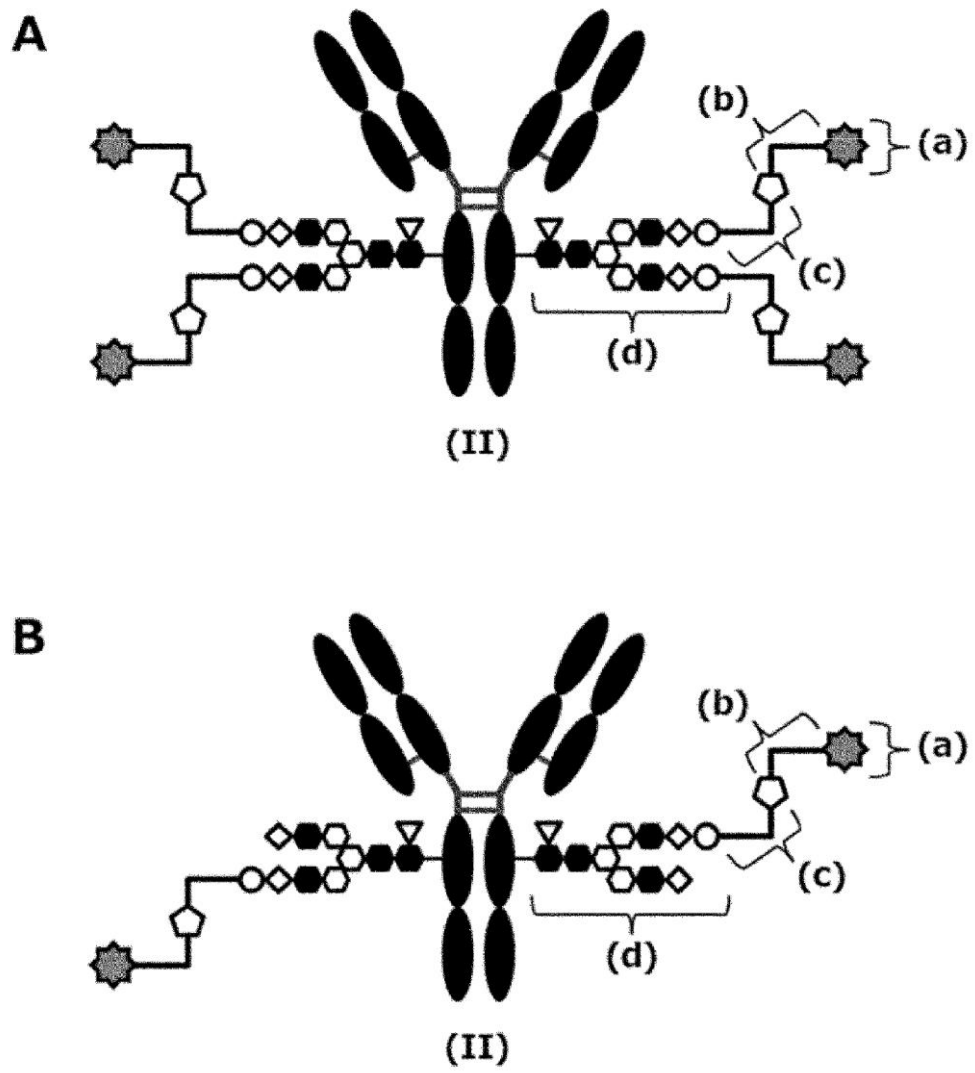


Fig. 2

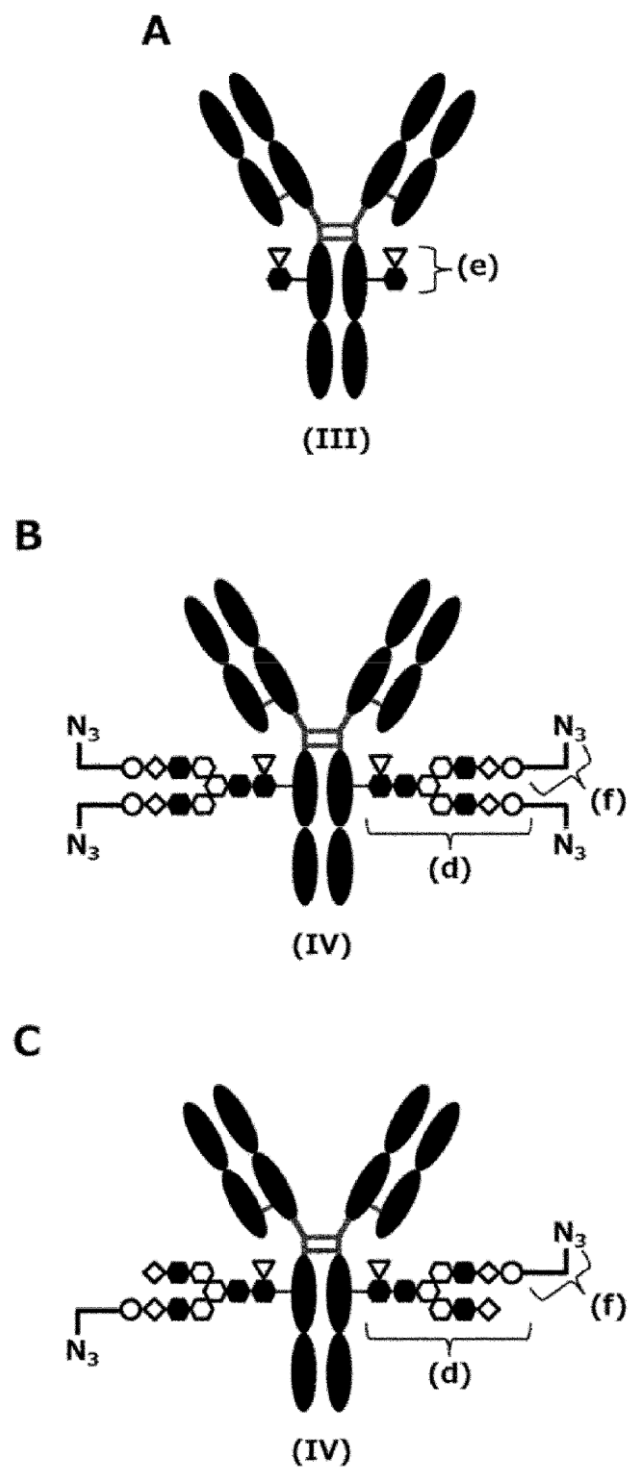


Fig. 3

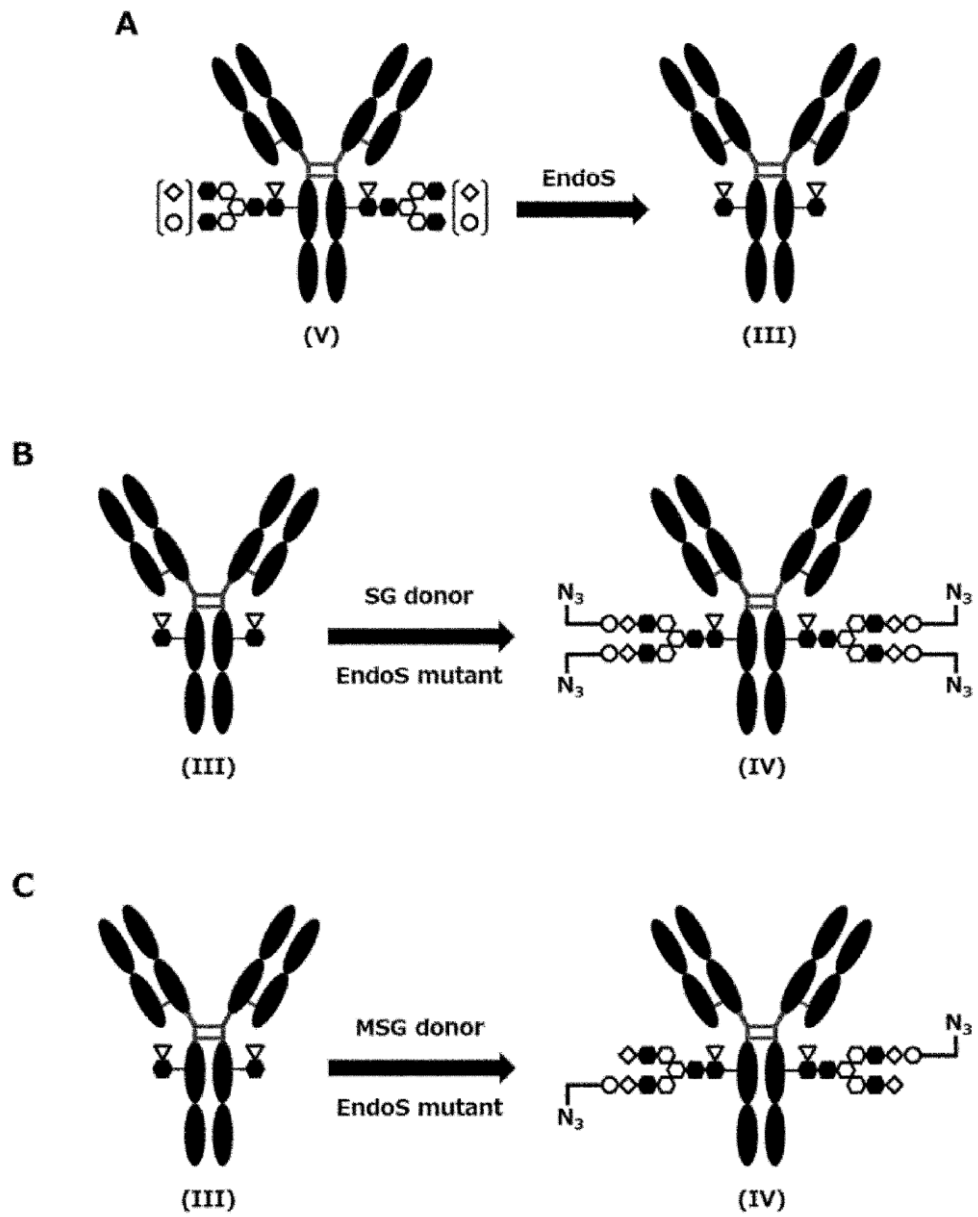


Fig. 4

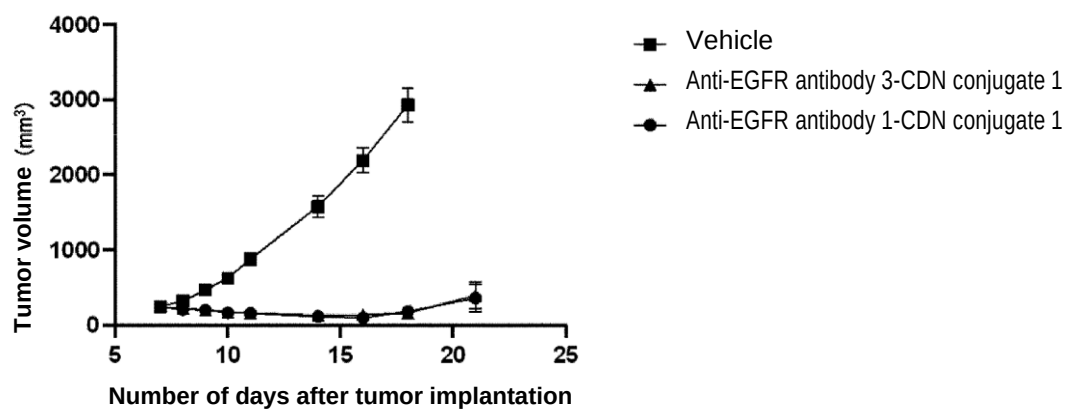


Fig. 5

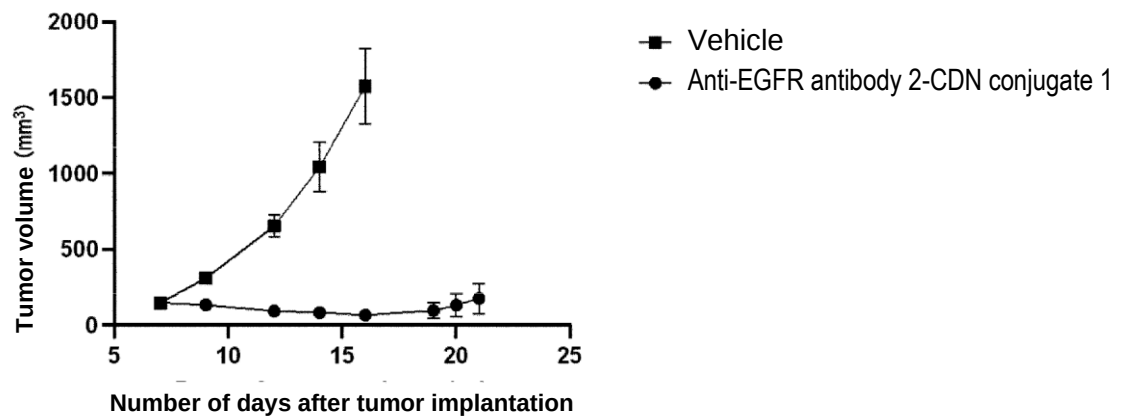


Fig. 6

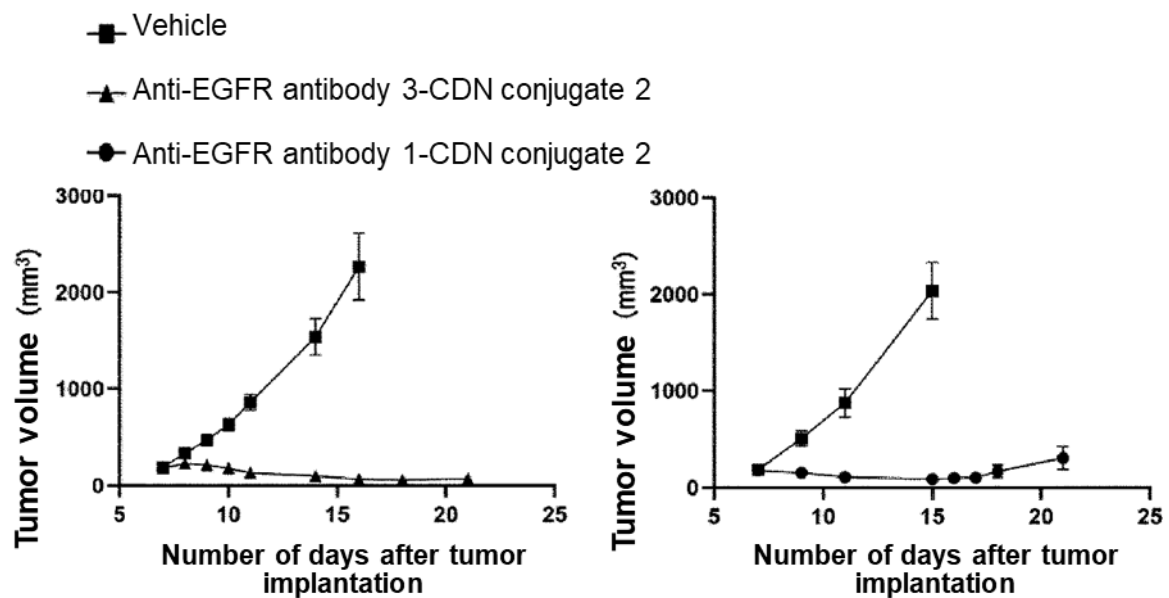


Fig. 7

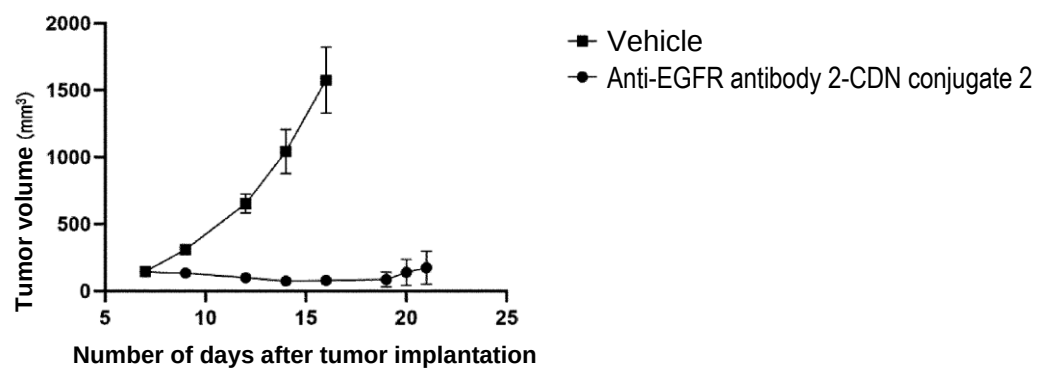


Fig. 8

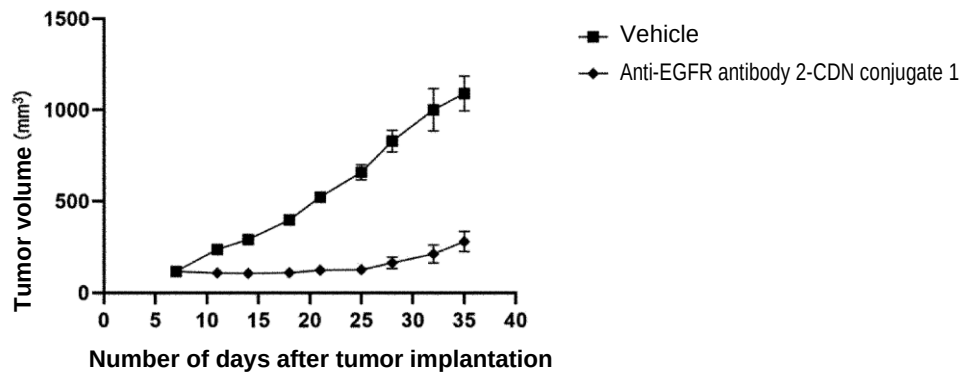


Fig. 9

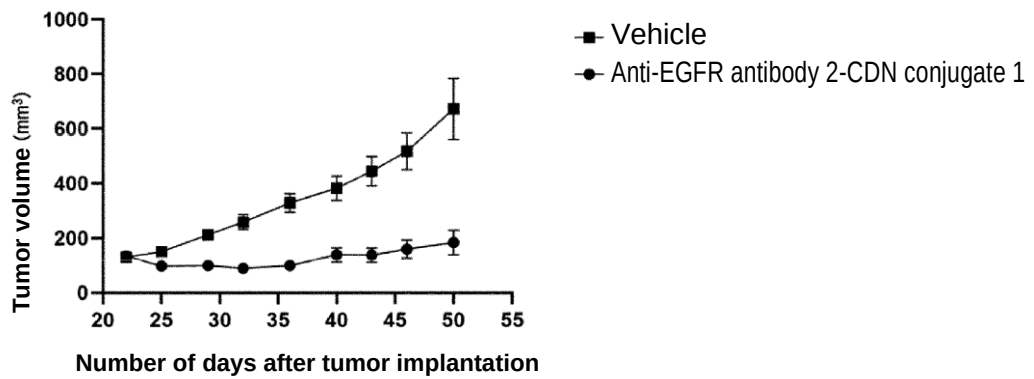


Fig. 10

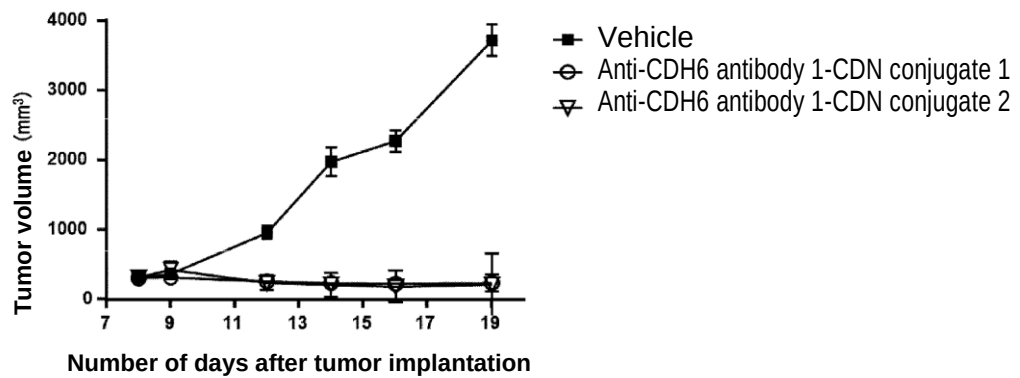


Fig. 11

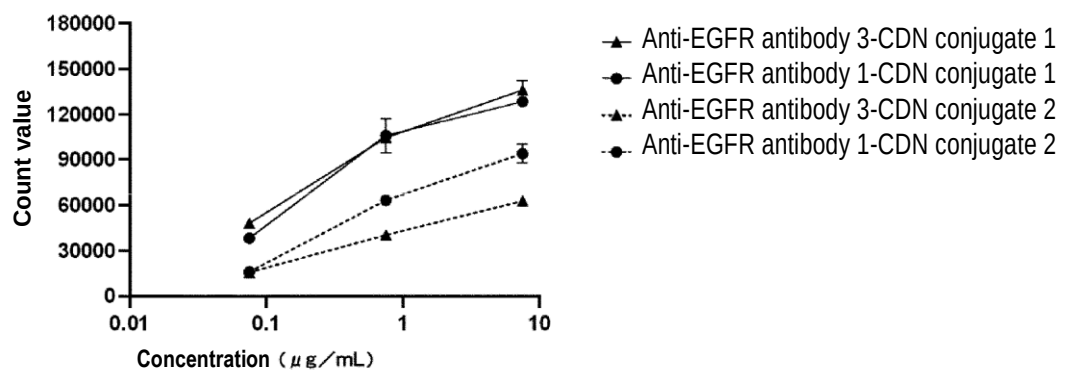


Fig. 12

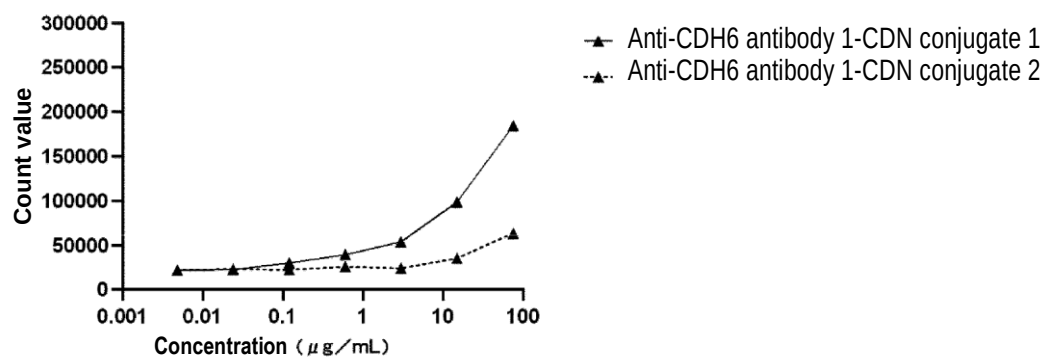


Fig. 13

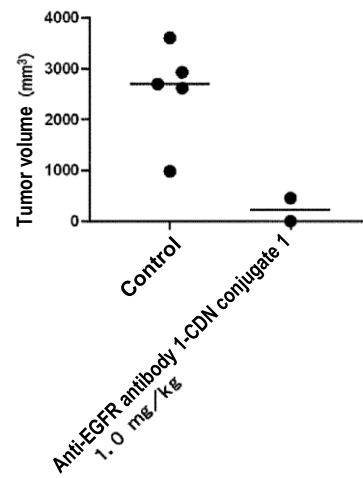


Fig. 14

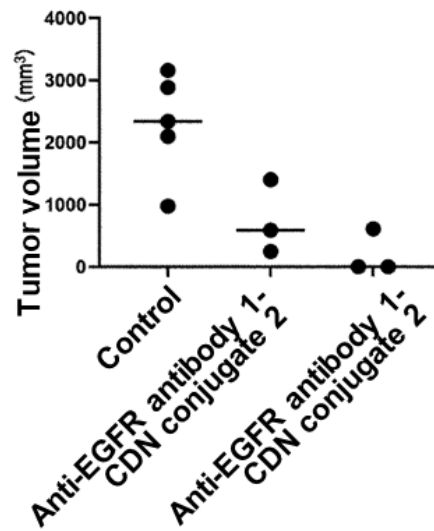


Fig. 15A

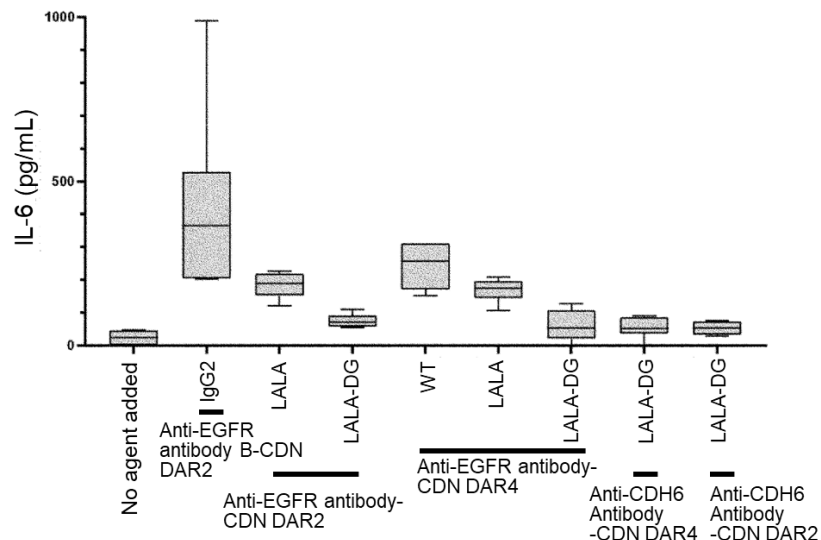


Fig. 15B

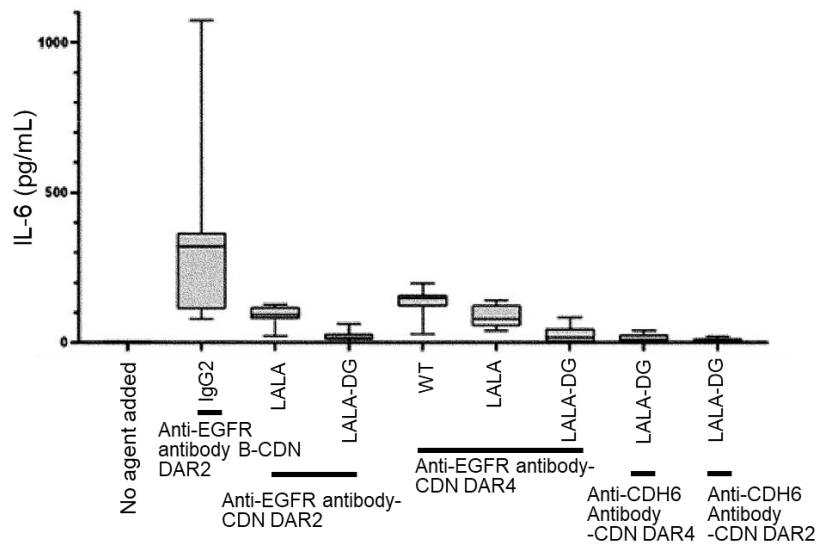
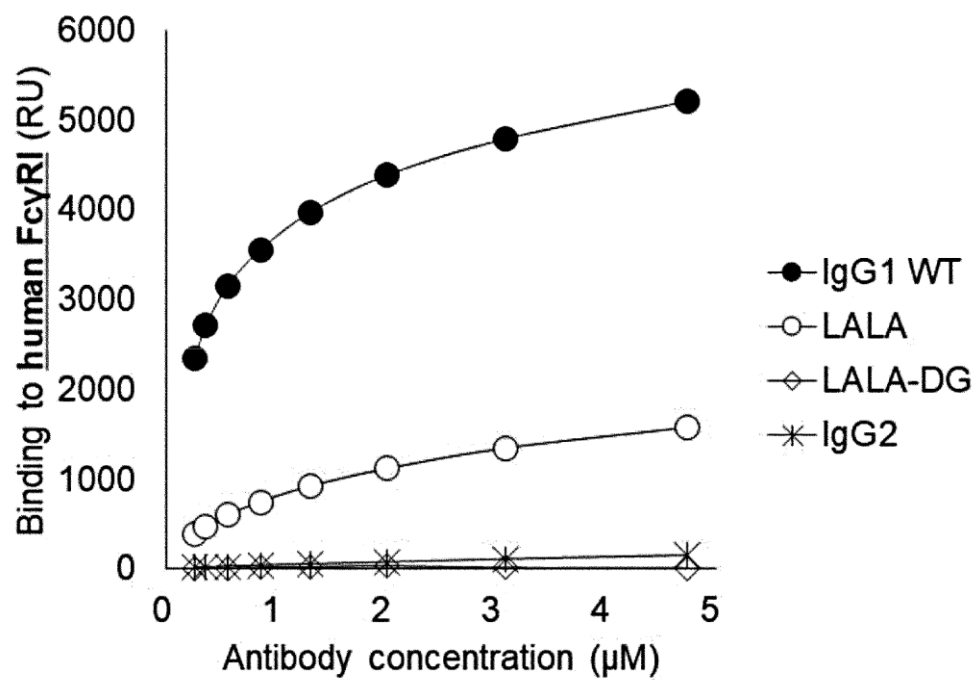


Fig. 16A



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Fig. 16B

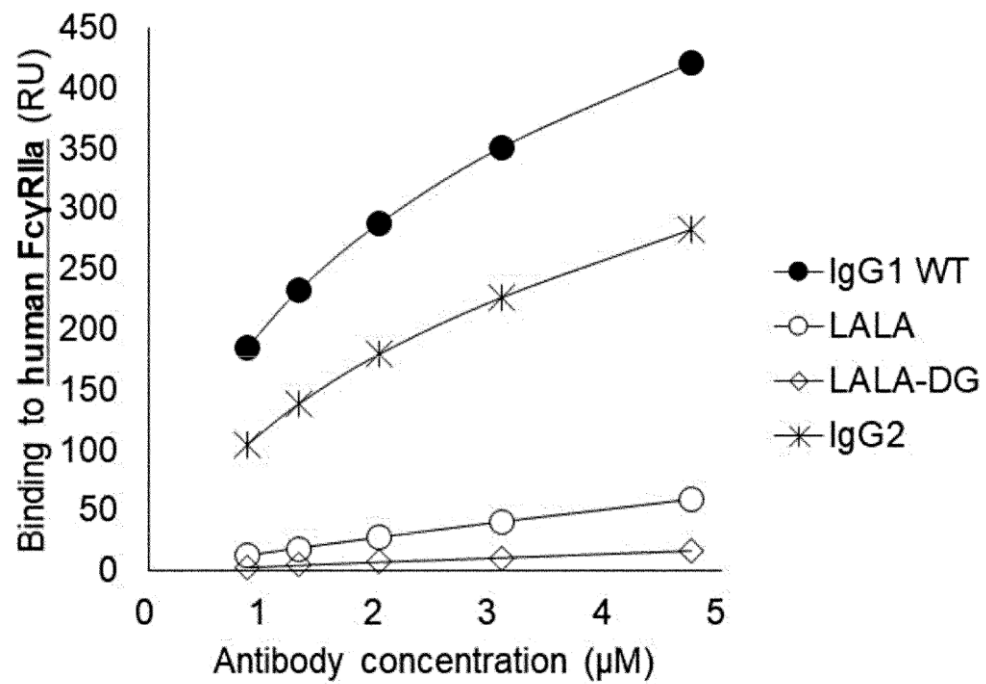


Fig. 16C

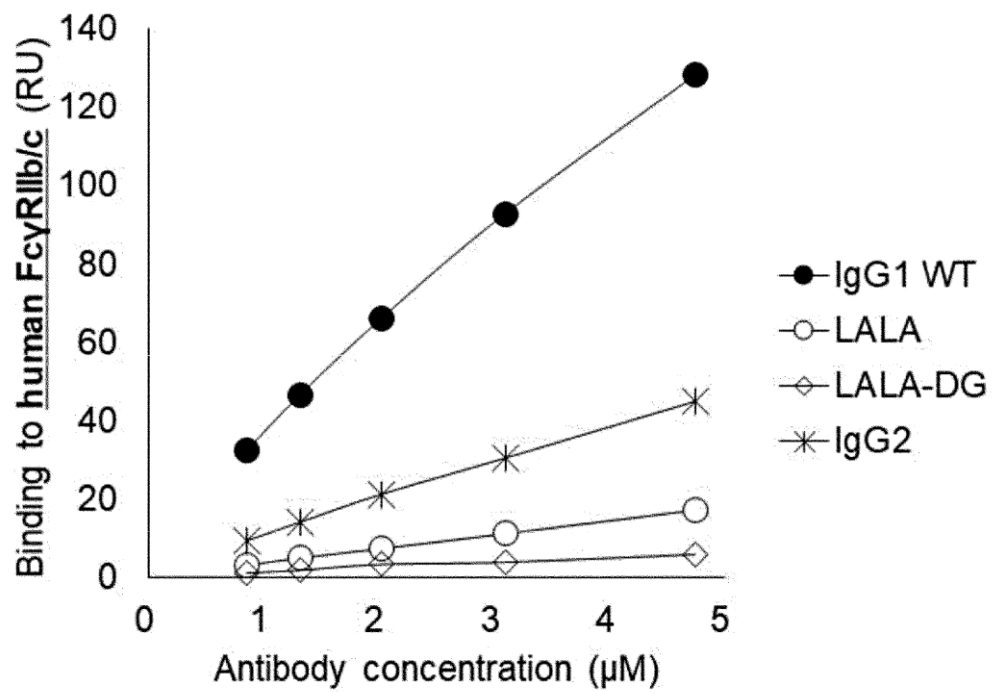


Fig. 16D

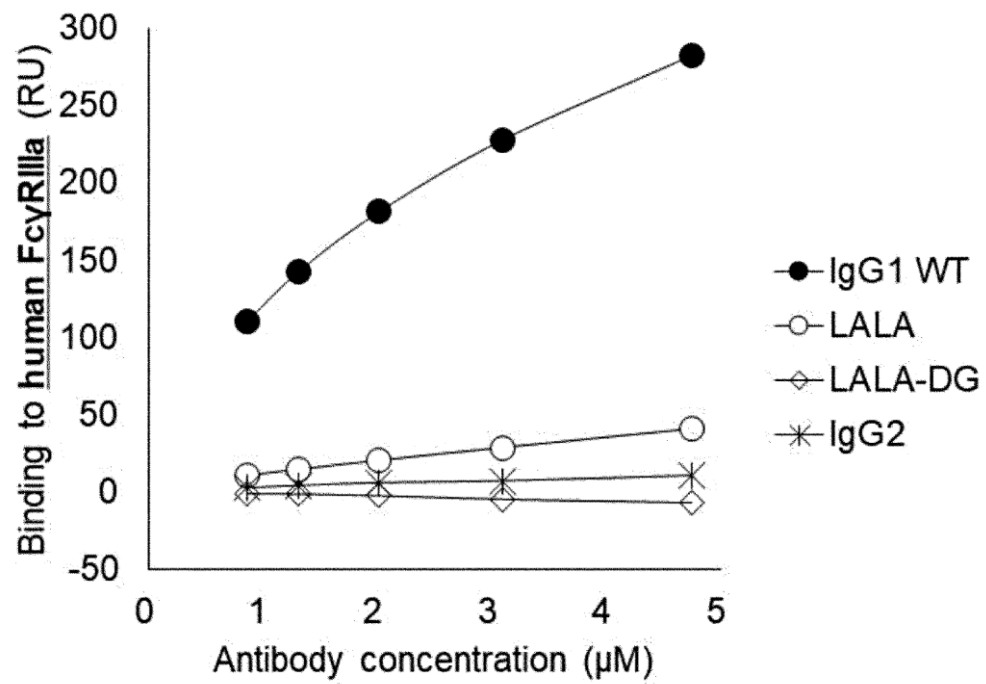


Fig. 16E

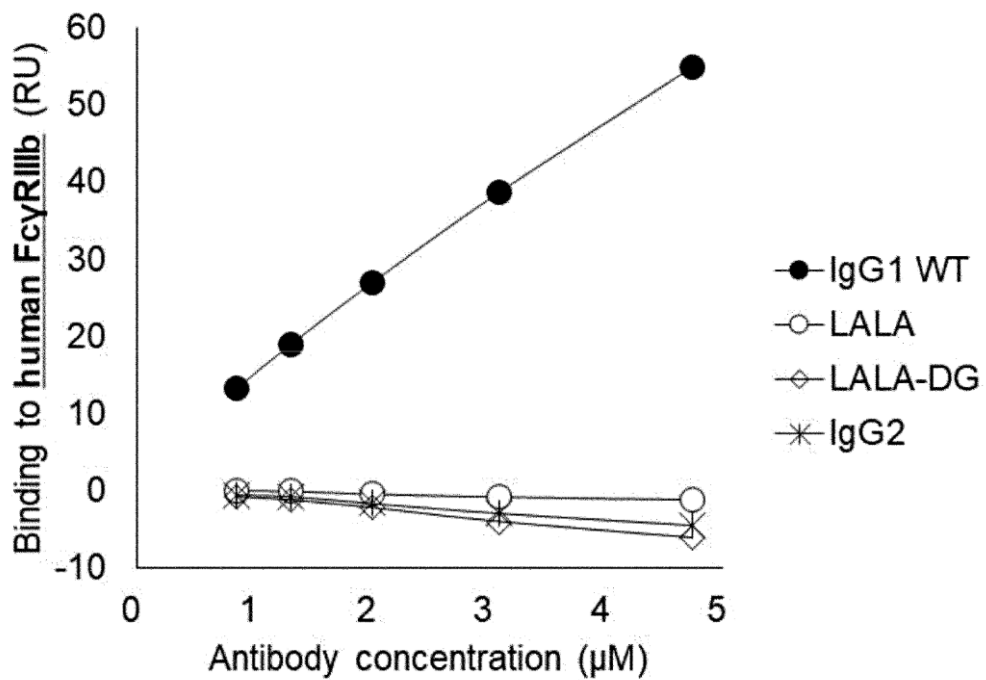


Fig. 17A

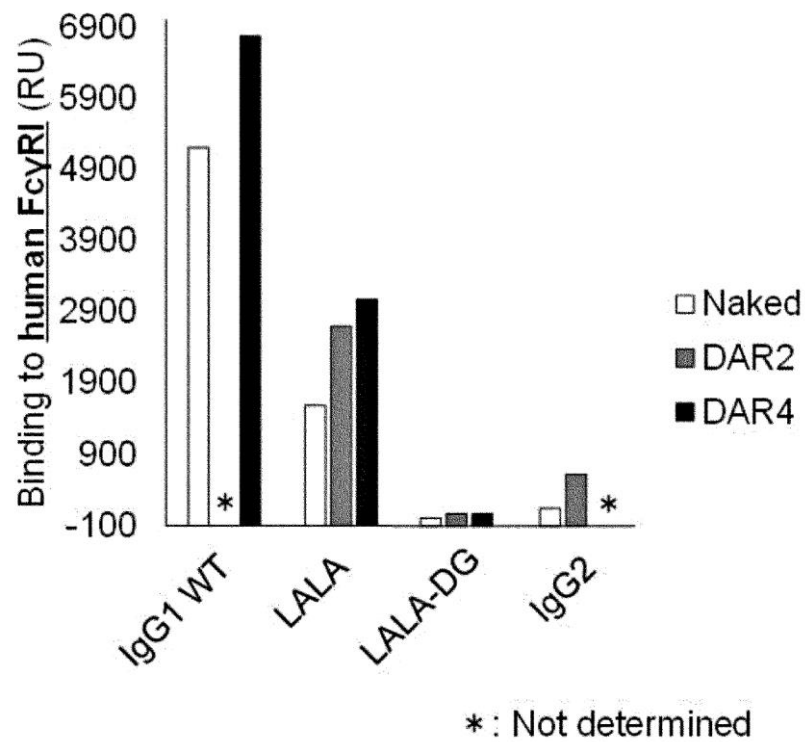


Fig. 17B

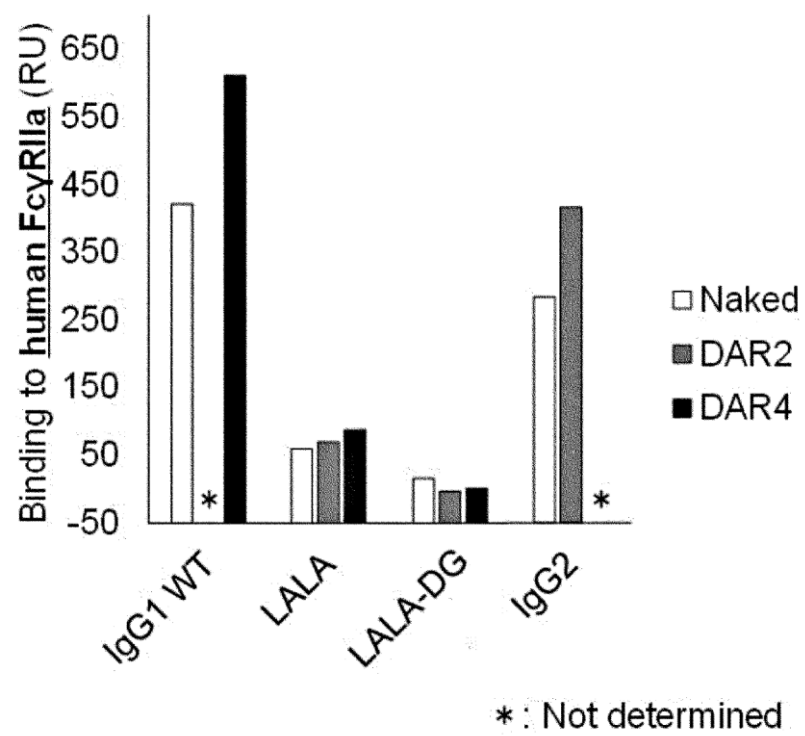


Fig. 17C

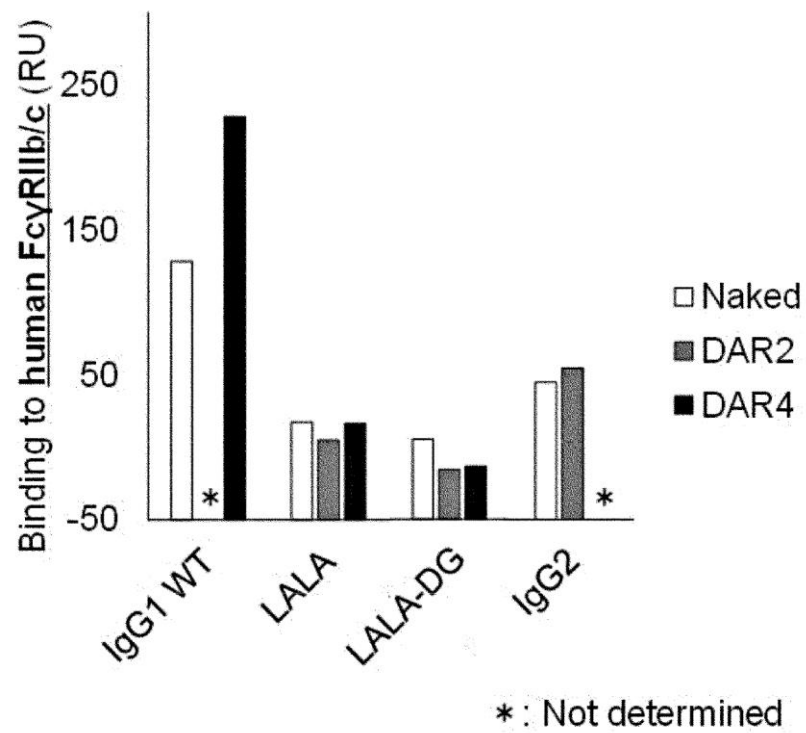


Fig. 17D

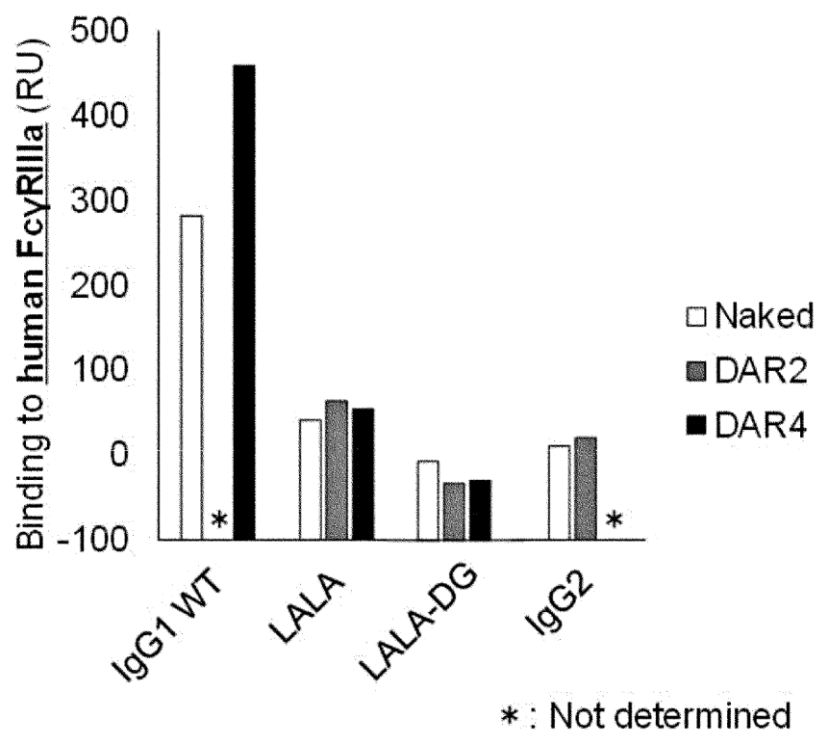


Fig. 17E

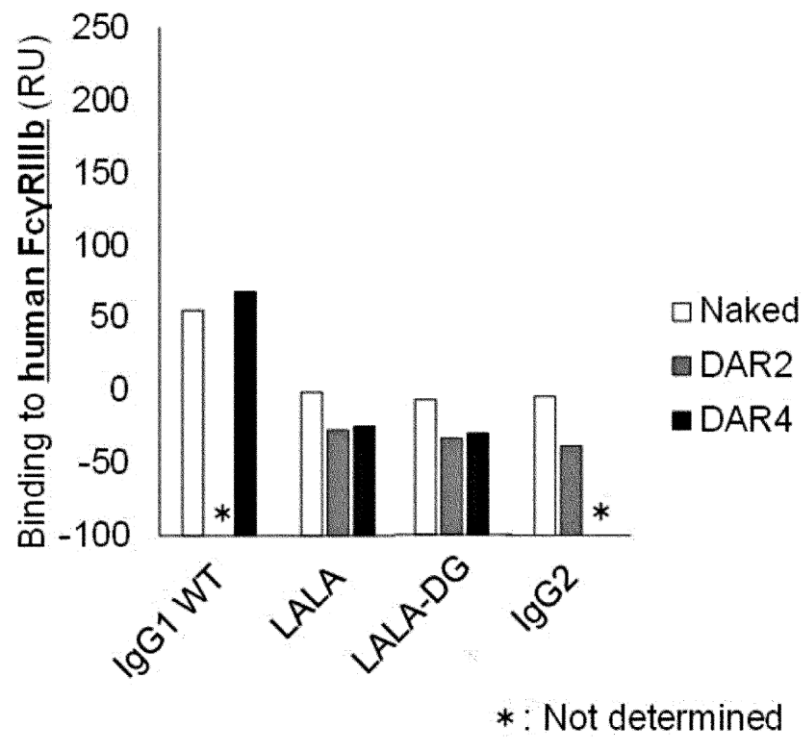


Fig. 18

	CH2 T_m (°C)	ΔT_m (°C)
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)

MPHSSLHPSIPCPRGHGAQKAALVLLSACLVTWGLGEPPEHTLRYLVHLASLQLGLLNGVCSLAEELRHIHS
 RYRGSYWRTVRACLGCP LRRGALLLSIYFYSLPNAVGPPTWMLALLGLSQALNILLGLKGLAPAEISAVCEK
 GNFNVAHGLAWSYYIGYLRLILPELQARIRTYNQHYNNLLRGAVSQRLYILLPLDCGVPDNL SMADPNIRFLDKL
 PQQTGDRAGIKDRVYSNSIYELLENGQRAGTCVLEYATPLQTLFAMSQYSQAGFSREDRLAQAKLFCRTLEDILA
 DAPESQNNCRLIAYQEPADDSSFSLSQEVLRLRQEEKEEVTGSLKTSAVPSTSTMSQEPELLISGMEKPLPLR
 TDFS

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

MPHSSLHPSIPCPRGHGAQKAALVLLSACLVTWGLGEPPEHTLRYLVHLASLQLGLLNGVCSLAEELRHIHS
 RYRGSYWRTVRACLGCP LRRGALLLSIYFYSLPNAVGPPTWMLALLGLSQALNILLGLKGLAPAEISAVCEK
 GNFNVAHGLAWSYYIGYLRLILPELQARIRTYNQHYNNLLRGAVSQRLYILLPLDCGVPDNL SMADPNIRFLDKL
 PQQTGDHAGIKDRVYSNSIYELLENGQRAGTCVLEYATPLQTLFAMSQYSQAGFSREDRLAQAKLFCRTLEDILA
 DAPESQNNCRLIAYQEPADDSSFSLSQEVLRLRQEEKEEVTGSLKTSAVPSTSTMSQEPELLISGMEKPLPLR
 TDFS

(The site of R232H mutation is underlined.)

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

MPHSSLHPSIPCPRGHGAQKAALVLLSACLVTWGLGEPPEHTLRYLVHLASLQLGLLNGVCSLAEELHHIHS
 RYRGSYWRTVRACLGCP LRRGALLLSIYFYSLPNAVGPPTWMLALLGLSQALNILLGLKGLAPAEISAVCEK
 GNFNVAHGLAWSYYIGYLRLILPELQARIRTYNQHYNNLLRGAVSQRLYILLPLDCGVPDNL SMADPNIRFLDKL
 PQQTADRAGIKDRVYSNSIYELLENGQRAGTCVLEYATPLQTLFAMSQYSQAGFSREDRLAQAKLFCQTLEDILA
 DAPESQNNCRLIAYQEPADDSSFSLSQEVLRLRQEEKEEVTGSLKTSAVPSTSTMSQEPELLISGMEKPLPLR
 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)

HIYYSGNTNYP SLKS

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
RFSGSGSGTDFTFTISSLQPEDIATYFCQHFDHLPLAFGGGKVEIKR

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

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS
RFSGSGSGTDFTFTISSLQPEDIATYFCQHFDHLPLAFGGGKVEIKRTVAAPSVFIFPP
SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSLT
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)

QVQLQESGPGLVKPSSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTN
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMTVSS

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
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMTVSSA
 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
 LYSLSVVVTPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGP
 SVFLFPPKPKDTLMISRTPEVTCVVVGVSHPEDPEVKFNWYVDGVEVHNAKTKPREEQNS
 TYRVSVLTTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM
 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ
 QGNVFSCSVMEALHNHYTQKSLSLSPGK

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
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMTVSSA
 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
 LYSLSVVVTPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPEAAGGP
 SVFLFPPKPKDTLMISRTPEVTCVVVGVSHPEDPEVKFNWYVDGVEVHNAKTKPREEQNS
 TYRVSVLTTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM
 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ
 QGNVFSCSVMEALHNHYTQKSLSLSPGK

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

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTN
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMTVSS
 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSVVVTPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
 STYRVSVLTTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW
 QGNVFSCSVMEALHNHYTQKSLSLSPGK

Fig. 21-3

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

QVQLQESGPGGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTN
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMTVSSA
 STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
 LYSLSVVTVPSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPGPCAPPVAGPSVFL
 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV
 VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ
 VSLTCLVKGFIYPSDIAVEWESNGQPENNYKTPPMLDSGGSFFLYSKLTVDKSRWQQGNV
 FSCSVMEALHNHYTQKSLSLSPGK

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

QVQLQESGPGGLVKPSETLSLTCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTN
YNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYCVRDRVTGAFDIWGQGTMTVSSA
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 LYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGP
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 TKNQVSLTCLVKGFIYPSDIAVEWESNGQPENNYKTPPVLDSDGGSFFLYSKLTVDKSRWQ
 QGNVFSCSVMEALHNHYTQKSLSLSPGK

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
DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT
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
AQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCARGVYGGFAGGYFDWGGQGLVTV
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
AQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCARGVYGGFAGGYFDWGGQGLVTV
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SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAA
GGPSVFLFPPKPKDTLMISRTPEVTCVTVGVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Fig. 24

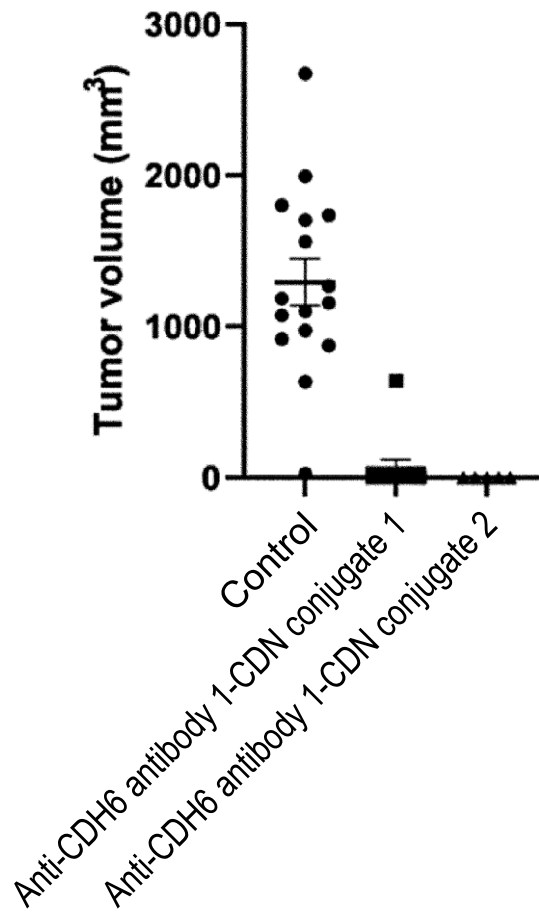


Fig. 25

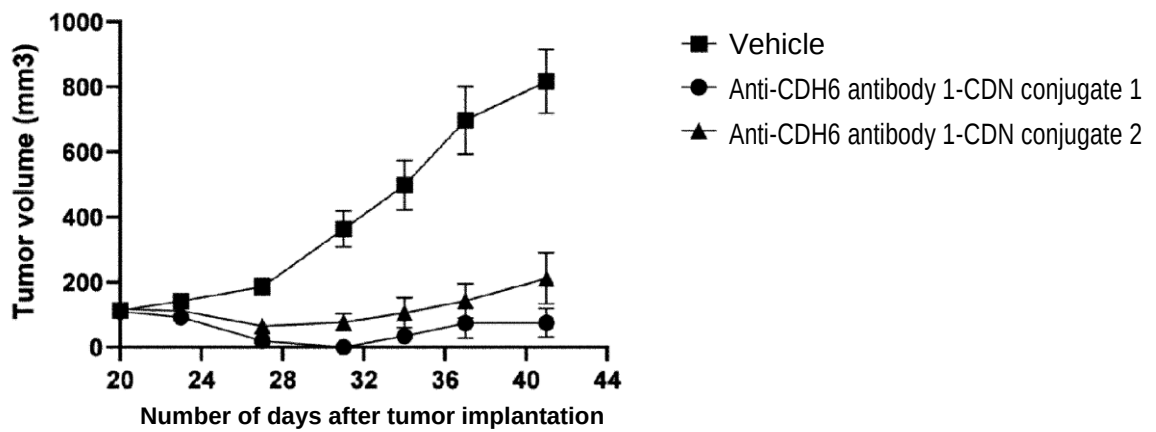


Fig. 26

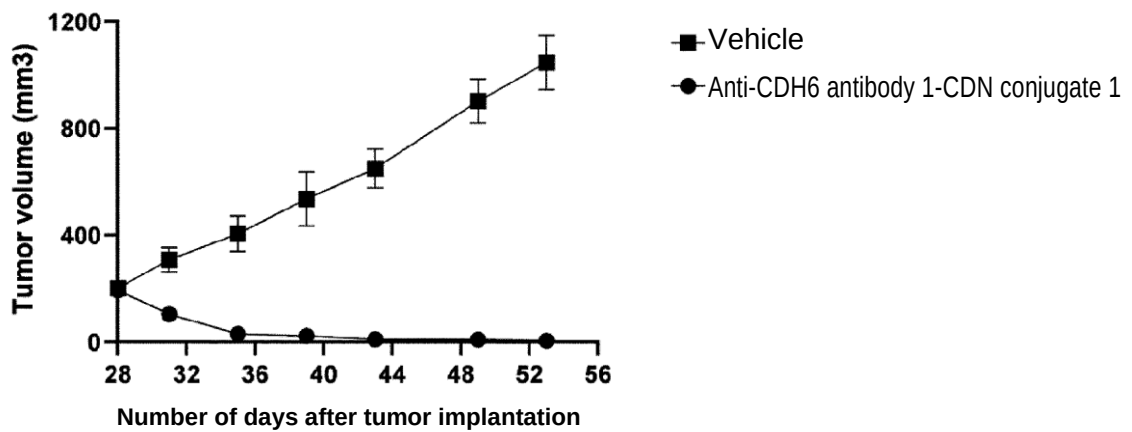


Fig. 27

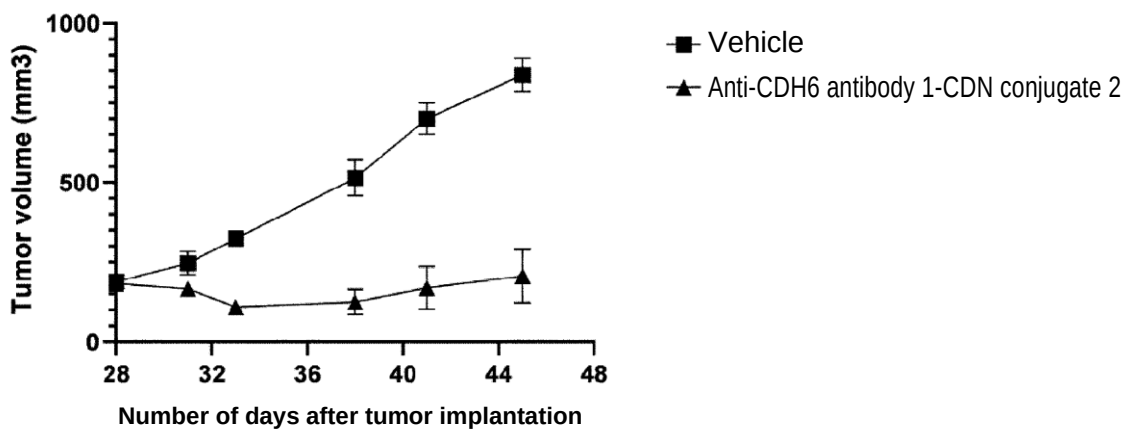


Fig. 28

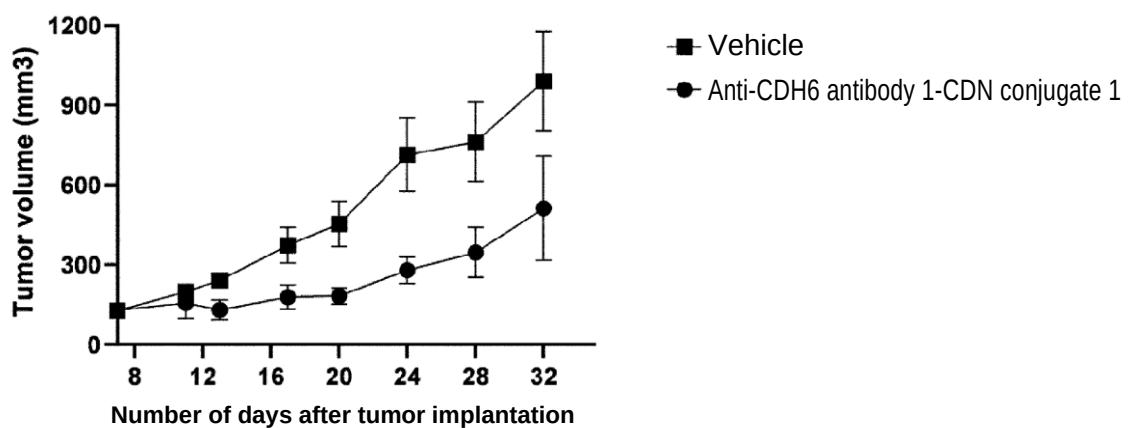


Fig. 29

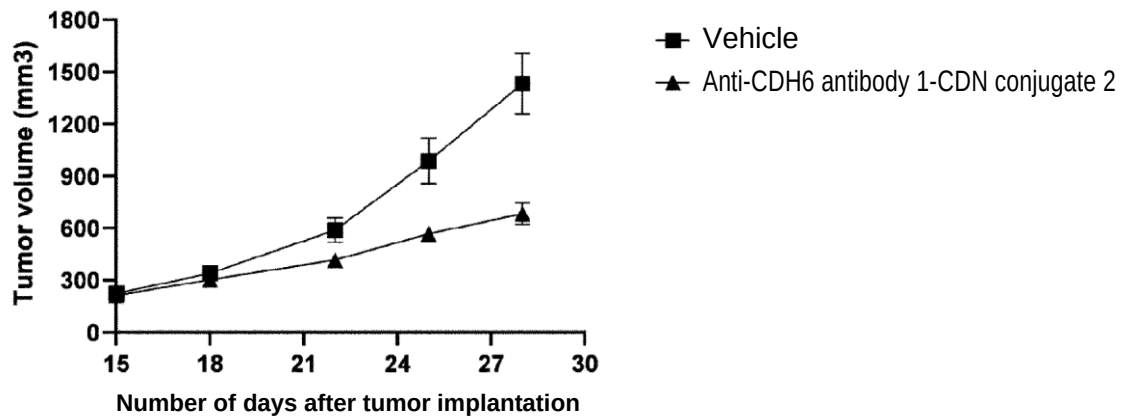


Fig. 30

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

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1   MDKHL LVKRT  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  KTVMLKD KSY  450
451 DLIDEKDFPD  KALREAVMAQ  VGTRKGD LER  FNGTLRLDNP  AIQSLEGLNK  500
501 FKKLAQLDLI  GLSRITKLDR  SVLPANMKPG  KDTLETVLET  YKKDNKEEPA  550
551 TIPPVSLKVS  GLTGLKELDL  SGFDRETLAG  LDAATLTSLE  KVDISGNKLD  600
601 LAPGTENRQI  FDTMLSTISN  HVGSNEQTVK  FDKQKPTGHY  PDTYGKTS LR  650
651 LPVANEKV DL  QSQLLFGTVT  NQGT LINSEA  DYKAYQNHKI  AGRSFVDSNY  700
701 HYNFKVSYE  NYT VKVTDST  LGTTT DKTLA  TDKEETYKVD  FFSPADKTKA  750
751 VHTAKVIVGD  EKTMMVNLA E  GATVIGGSAD  PVNARKVFDG  QLGSETDNIS  800
801 LGWDSKQSI I  FKLKEDGLIK  HWRFFNDSAR  NPETTNKPIQ  EASLQIFNIK  850
851 DYNLDN LLEN  PNKFDDEKYW  ITVD TYSAQG  ERATAFSNTL  NNITSKYWRV  900
901 VFDTKGDRYS  SPVVP ELQIL  GYPLPNADTI  MKTVTTAKEL  SQQKDKFSQK  950
951 MLDELKIKEM  ALETSLNSKI  FDVTAINANA  GVLKDCIEKR  QLLKK  995

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Fig. 31

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

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1   MDKHLIVKRT LGCVCAATLM GAALATHHDS LNTVKAEECT 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 YYGSQGGAE VDTINSDWNQ YQNYIDASQF MIGFSFFES ASKGNLWFDV 300
301 NEYDPNNPEK GKDIEGTRAK KYAEWQPSTG GLKAGIFSYA IDR DGVAHVP 350
351 STYKNRTSTN LQRHEVDNIS HTDYTVSRKL KTLMTEDKRY DVIDQKDIPD 400
401 PALREQIIQQ VGQYKGDLE R YNKTLVLTGD KIQLNKGLEK 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

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Fig. 32

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

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1   MNKRLLVKRT FGCVCAAAIL GVAPLSHPTI VEAREELKMP NGLEQSIADV 50
51  EAKIDALTYL SKNSKDEFKH SMYEIPSNRE HKPVSPKQAL QNAKKADAQA 100
101 ERLAKMTIPK KEELKALEGP LYGGYFRTWQ DKTSDPTETN KVNSFGELPK 150
151 EVDLAFVFHD YTKDYSFLWE 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 YMVGFSFYEK KDFNNRWKDI NEEDPSDPHI GEKIQGTRAE RYAKWQPKTG 400
401 GLKGGLFSYA IDR DGVAQPK 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

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Fig. 33

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

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1   MPSLQLQPDD KLAPVSFALK SMNELRDWTP DEKIKFNVSS VALQPRVKNA 50
51  LKPQLLLTHD MAGGYKEDKN IQGNNYKDIY NIQYWHLADT FVYFSHERVS 100
101 IPPVNWTNAC HRNGVKCLGT FLVEGNNQMH EMEALLHGPP LLNNTDDPMR 150
151 LWSPYYADQL VAIKHYGFD GWLFNIECEF FPFPTNPKFK AEELAKFLHY 200
201 FKEKLHNEIP GSQLIWYDSM TNEGEIHWQN QLTWKNELFF KNTDGIFLNY 250
251 WWKKEYPEMA RRVAEGIGRS GLEVYFGTDV WGRHTYGGGG FKSYPGVKTA 300
301 YSAMTSSALF GMAWTYEHFE KSEFEKMDRL FWCGGKYSDY PPPPKNPDD 350
351 EKEVESDDSE DELMYGHKKG IADTVESIPV PGTDWFTVNF DRGFGNRFYY 400
401 RGKRLSQPW SHLSHQAILP NKSYPNPEIY PTDQNIKITS SLDCDHGAFL 450
451 GGTSIIKQ RFNHRESHDV ETEISIPLYK LSLDASKGCS LRYIYRTLLM 500
501 KDVKLTVACH FSLKTND SVN FFKVWQPDEN FSFEYDDGMR ATVTTENSTE 550
551 SRCFLLRTE EDTGENDWIT KTINVPVPE GSQLYITRLE VSVVLDTAGL 600
601 VGLVNQVIAC LGYISIIPTI NSGIKTDSSR IIQDLFWKDQ KYTKIGKESL 650
651 DDIAQEEVHR YYGTNLWENT ANVVNAWEEI DYYNVFYKES DDSATRIFLG 700
701 TAFCNQFRVS GLDIILSKLP KIVIEAVNKE GYISSSGSID LSLN 744

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Fig. 34

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

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1   MPSLELQQA DTRLFESMPL QTMNELGSWE PSNASRANIA TIPLHQRSNL 50
51  DPAEPRLIVT HDMAGGYKED SNIQGNTYDT IYSCQYWQYV DTFIYFSHR 100
101 VTIPPVNWIN ACHRNKVKTL GTFIVEGAAG MFALERFVYG PEPGQRNSWS 150
151 PYYADKLVDI AEFYGF DGWL LNIESDFFPL YRNPSLKAIH LAKLLRYLKN 200
201 AMHARVPGSE IIWYDSMTN GSVQWQNNIT PKNSIFFEAA DGIFLNYWWN 250
251 ATPPPLALQV AHRLGRQGS VYFGTDVWGR GTFGGGGFDS YLAVGTARAF 300
301 KTSSALFGTA WIYEHFGKKD FELMDRLLWL GGDQSEYPAQ EGEQNRTVKV 350
351 TSHLGRHPGI ADVSPVRSAP GKTWFATWFD RGYGTGFYYQ GKKLLSQPWS 400
401 HLSHQSI PPN LIARLQREEN HGLSYFLADD DAYIGGTSLL IAAEITQERQ 450
451 LPLYQLEYDV TEGCEVQFIY KSPEPDMQ GK IDIYLNQVT DILPDELAFY 500
501 WQDVTDASSQ ADATTAMRLY LNENTVIYK PSRKQELAEG WLLCSVRVPP 550
551 TYPLGIATIK ELGIHVDGKE TVLFRLGLLT IIPLGDAPSA LSRITQVQLQ 600
601 RDEDIHSCP SSSCELWATL SWMMEHNSKE DWDQVDHYMI FFKNVDSKAE 650
651 PIFLGTSFST EYRISGLEIK KHGNSIEIWA VNRLGTVIAR QDIDIQ 696

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Fig. 35

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

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1   MPIAGKKFHP RALPEFWRTF REMDEWRATQ TGPQARPAEG ILKYVPRKIR 50
51  PADIAGKGRL LVSHDYKGGY VEDPFSKSYS FNWWFSTDSE NYFAHHRITI 100
101 PPPEWINAAH RQGVPI LGTI IFEGGSDEDI LRMVIGKTPG STSNFHAERN 150
151 AEYTPVPSSY YAE LFADLAV ERGFDGWLLN VEIGLQGGSE QARGLAAWVA 200
201 LLQQEVLKKV GPHGLVIWYD SVTVRGDLWW QDR LNAFNLP FFLNSSGIFT 250
251 NYWWYNDAPQ KQIDFLSRVD PNL TGQTAE P HQYNLQKTIQ DIYIGVDVWG 300
301 RGS HGGGFG 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 LSPLRRKSKS GDISVAK 787

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Fig. 36

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

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1   MAQSQLLGGA VRPVFFDKLE ELRRWHTQSA NLSRESELD LNVATEPFSS 50
51  YERAQTGSGS RSSEPVPGDK EDPPIKLMVC HDFKGGYQDY EDAQPLGYFP 100
101 HPTGSR YFLQ YPQLIDQFVY FSHHRVTVPP VNWINEFCHRN GIKCFGT VIF 150
151 EGNASKDFEE LDRLVSRDEK GDFVFVDALI KLA AHYGFDG YLLNIETTFS 200
201 NTKIAADLEP FAEQLKSG LH CLDSKNE LIW YDSYVFPANK VSYTNGVTES 250
251 NYNFFSLSDA FFSNYWWNIK NLQENIKNVG VLG VQKKIYV GYDVWGRGTL 300
301 VGKGGFDSSL ACKMIAKFS NVALFAPAWT YESLGPKDFN QNDARFWIGL 350
351 FENESSISST VPPHSSAVYK INESSFIFYT NFSSGEGNRF FSKGSEVYRK 400
401 NWVNGSLQFD LPIDLHRKDK NGLQWALDKS DAFHGGACLE IKYSEIKDEN 450
451 GYQIFNNQMV SDFTLFNFTK ECHFTVNVK VTYKLNHGTK STF KIKIKYI 500
501 IERRFRSVQT VRTGYLTIPL LSTSGKWFTV EESFQINLQT SHEYIVLESA 550
551 HVTYDEDRSA DSFFRSYIVE DSAITSVIDN EEYEKLINSE IYNDEDEDW 600
601 ILVPSDVSIS SSESQSNDSK TQYLGRKLFG NKSTPKTRTL EGTAPLLRIG 650
651 EFAIISANNY PSSNFLAVTS VKSIESSRLE GDSLVL LNWQ VEGEHQKGVC 700
701 YYIIYVNGAV VGLSVAPKFI YQDTELASEN SASARSNYKK SGLGSSSDRK 750
751 SKVRVDSVDK LGNVFTGSEV WV 772

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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	T IPWRFLAGG	DNSGIAEDAS	200
201	KYPNTPEGNK	ALAKAIVDEY	VYKYNLDGLD	V DIHDSIPK	VNGEASDENL	250
251	KRSIDVFEEI	GKLIGPKGAD	KSRLFIM DST	YMADKNPLIE	RGAPYIDLLL	300
301	VQ VYGSQGEQ	GEFQNDTKSV	TKTPEERWQG	YSKYIRPEQY	MIGFSFYEE K	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	DISDNKDLA	PKTENRQIFD	VMLSTVNNNA	GISEQSIKFD	NQKPAGNYPQ	650
651	TYGATNLQLP	VRQEKIDLQH	QLLFGTITNQ	GTLINSEADY	KTYRNQKIAG	700
701	RNFVDPDYPY	NNFKVSHDNY	TVKVTDSLGL	TTTDKMLATD	KEETYKVDFE	750
751	SPTDKTKAVH	TAKVIVGDEK	TMMVNLAEGA	TVIKSENDEN	AQKVFNIGME	800
801	YNPLSFNNKS	SIIFEIKDPS	LAKYWRLFND	SSKDKKDYIK	EAKLEVFTGQ	850
851	LNAEADVVTI	LEKPDNWVTV	STYSGEEKVF	SHSLDNISAK	YWRVTVDNKK	900
901	DQYGYVSLPE	LQILGYPLPN	ADTIMKTVTV	AKELSQQQDK	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	VEKAQPEKLE	EIVSKAQQAD	KQAKTLAEMK	100
101	VPEKIPMKPL	KGPLYGGYFR	TWHDKTSDPA	EKDKVNSMGE	LPKEVDLAFV	150
151	FHDWTKDYSL	FWQELATKHV	PTLNKQGTRV	IR T IPWRFLA	GGDHSGIAED	200
201	AQKYPNTPEG	NKALAKAIVD	EYVYKYNLDG	LDVD IERDSI	PKVNKEESKE	250
251	GIERSIQVFE	EIGKLIGPKG	ADKSRLFIM D	STY MADKNPL	IERGAPYIDL	300
301	LLV Q VYGTQG	EKGGFDMANH	KAVDTMEERW	ESYSKYIRPE	QYMGFSFYE	350
351	E KANSNLWY	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	TENRQILDLM	LATVTKHGGV	SEKTFVFDHQ	KPTGLYPDTY	GTKSLQLPVA	650
651	NDTIDLQAKL	LFGTVTNQGT	LINSEADYKA	YQEQEIAGHR	FVDSSYDYKA	700
701	FAVTYKDYKI	KVTDSTLGV	DHKLSTLSKE	ETYKVEFFSP	INSTKPVHEA	750
751	KIVVGEEKTM	MVNLAEGATI	IGGDADPTNA	KKVFDGLLNN	DTTTLSTSNK	800
801	ASIIIFELKEP	GLVKHWRFFN	DSKISKADYI	KEAKLEAFVG	HLEDSSKVKD	850
851	SLEKSTEWVT	VSDYSGEAQE	FSQPLNNIGA	KYWRITIDNK	KSQYGYVSLP	900
901	ELQIIGHRLP	EAATVMTTMA	AAEELSQQKD	KFSQEQQLKEL	EVKVAALKAA	950
951	LDNKMFNADT	INASFADVKA	YIDKLLADAA	GKKTTLGKATK	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	KKEFK EGLSK	AGEVPEKLD	ILSKAQQADK	QAKVLAEMKV	100
101	PEKIAMKPLK	GPLYGGYFRT	WHDKTS DP AE	KDKVNSMGEL	PKEVDLAFVF	150
151	HDWTKDYSFF	WQELATKHVP	TLNKQGTRVI	RTIPWRFLAG	GDHSGIAEDT	200
201	QKYPNTPEGN	KALAKAIVDE	YVYKYNLDGL	DVDIERDSIP	KVNGKESNEN	250
251	IQRSI AVFEE	IGKLIGPKGA	DKSRLFIMDS	TYMADKNPLI	ERGAQYIDLL	300
301	LVQVYGTQGE	KGDWDPVARK	PEKTMEERWE	SYSKYIRPEQ	YMGFSFYEE	350
351	NAGSGNLWYD	INERKDDHNP	LNSEIAGTRA	ERYAKWQPKT	GGVKG GIFS Y	400
401	AIDRDGVAHQ	PKKVS DDEKR	TNKA IKDITD	GIVKSDYKVS	KALKKVMEND	450
451	KSYELIDQKD	FPDKALREAV	IAQVGSRRGD	LERFNGTLRL	DNPDIKSLEG	500
501	LNKLKKLAKL	ELIGLSQITK	LD SLVLPANA	KPTKDTLANV	LEAYDSAKKE	550
551	ETKAIPQVAL	TISGLTGLKE	LNLAGFDRDS	LAGIDAASLT	SLEKVDLSSN	600
601	KLDLAAGTEN	RQILD TMLAT	VTKHGGVSEK	TFVFDHQKPT	GLYPTYGTK	650
651	SLQLPVANDT	IDLQAKLLFG	TVTNQGTLIN	SEADYKAYQE	QEIAGHRFVD	700
701	SSYDYKAF AV	TYKDYKIKVT	DSTLGVT D HK	DLSTSKEETY	KVEFFSPTNS	750
751	TKPVHEAKVV	VGA EKTMMVN	LAEGATVIGG	DADPTNAKKV	FDGLLNNDTT	800
801	ILSTSNKASI	IFELKEPGLV	KYWRFFNDSK	ISKADCIKEA	KLEAFVGHLE	850
851	AGSKVKDSLE	KSSKWVTVSD	YSGEDQEFSQ	PLNNIGAKYW	RITVDTKGGR	900
901	YNWPSLP ELQ	IIGYQLPAAD	LVMAMLATAE	ELSQQKDKFS	QEQLKELEV K	950
951	IAALKAALDS	KMFNADAINA	STADLKAYVD	KLLADRTDQE	KVAKAAKVEQ	1000
1001	PVATDIKENT	EPENPKTD				1018