

# Project Name: SAP-887-PCT

Status: warnings

Creation date: 2023-08-23

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## General Information

### Current application

Application number: before

IP Office: WO

Application number:

Filing date: 2023-08-28

Applicant file reference: SAP-887-PCT

### Earliest priority application

IP Office: JP

Application number: 2022135598

Filing date: 2022-08-29

### Priority Identification

| IP Office | Application number | Filing date |
|-----------|--------------------|-------------|
| JP        | 2022135598         | 2022-08-29  |

### Invention Title

| Language | Invention title                             |
|----------|---------------------------------------------|
| ja       | 変異Fc領域を含む抗体薬物コンジュゲート                        |
| en       | ANTIBODY-DRUG CONJUGATE HAVING FC MUTATIONS |

### Applicant & Inventor:

Applicant name: 第一三共株式会社

Language: ja

Name Latin: DAIICHI SANKYO COMPANY, LIMITED

Residence Address:

Correspondence Address:

### Sequences

Sequence 1: "Amino acid sequence of human STING WT"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 379    | AA            | Homo sapiens | No                             | No               |

### Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..379           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| MPHSSLHPSI | PCPRGHGAOK | AALVLLSACL | VTLWGLGEPP | EHTLRYLVLH | LASLQLGLLL | 60  |
| NGVCSLAEEL | RHIHSRYRGS | YWRTVRACLG | CPLRRGALLL | LSIYFYSLP  | NAVGPFFTWM | 120 |
| LALLGLSQAL | NILLGLKGLA | PAEISAVCEK | GNFNVAHGLA | WSYYIGYLR  | ILPELOARIR | 180 |
| TYNOHYNNLL | RGAVSORLYI | LLPLDCGVDP | NLSMADPNIR | FLDKLPQOTG | DRAGIKDRVY | 240 |
| SNSIYELLEN | GQRAGTCVLE | YATPLQTLFA | MSQYSQAGFS | REDRLAQAKL | FCRTLEDILA | 300 |
| DAPESQNNCR | LIAYQEPADD | SSFSLSQEV  | RHLRQEEKEE | VTVGS�KTSA | VPSTSTMSQE | 360 |
| PELLISGMEK | PLPLRTDFS  |            |            |            |            | 379 |

Sequence 2: "Nucleotide sequence of human STING WT"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 1140   | DNA           | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                        |
|-------------|------------------|---------------------------------------------------|
| source      | 1..1140          | mol_type = genomic DNA<br>organism = Homo sapiens |

Residues

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| atgcccact   | ccagcctgca  | tccatccatc  | cgtgtccca   | gggtcacgg  | ggcccagaag | 60   |
| gcagccttgg  | tcttgcctgag | tgcctgcctg  | gtgacccttt  | gggggctaag | agagccacca | 120  |
| gagcacactc  | tccggtaacct | ggtgctccac  | ctagccctccc | tgcagctggg | actgctgtta | 180  |
| aacggggctc  | gcagcctggc  | tgaaggactg  | cgccacatcc  | actccaggta | ccggggcagc | 240  |
| tactggagga  | ctgtgcgggc  | ctgcccgggc  | tgcccccctcc | gccgtggggc | cctgttgctg | 300  |
| ctgtccatct  | atttctacta  | ctcccctcca  | aatgccgtcg  | gcccgccctt | cacttggatg | 360  |
| cttgccttcc  | tgggcctctc  | gcaggcactg  | aacatcctct  | tgggcctcaa | gggcctggcc | 420  |
| ccagctgaga  | tctctgcagt  | gtgtgaaaaa  | gggaatttca  | acgtggccca | tgggctggca | 480  |
| tggctcatatt | acatcgagata | ctctgcggctg | atcctgccag  | agctccaggc | ccggattcga | 540  |
| acttacaatc  | agcattacaa  | caacctgcta  | cggggtgcag  | tgaagccagg | gctgtatat  | 600  |
| ctcctcccat  | tggactgtgg  | ggtgcctgat  | aacctgagta  | tggctgacct | caacattcgc | 660  |
| ttcctggata  | aactgcccca  | gcagaccggg  | gaccatgctg  | gcacaaagga | tcgggtttac | 720  |
| agcaacagca  | tctatgagct  | tctggagaa   | gggcagcggg  | cgggcacctg | tgtcctggag | 780  |
| tacgccaccc  | ccttgcagac  | tttgtttgcc  | atgtcacaa   | acagtcaagc | tggcttttag | 840  |
| cgggaggata  | ggcttgagca  | ggccaaaact  | ttctgccgga  | cacttgagg  | catcctggca | 900  |
| gatgccctcg  | agtctcagaa  | caactgccgc  | ctcattgcct  | accaggaacc | tgcagatgac | 960  |
| agcagcttct  | cgctgtccca  | ggaggttctc  | cggcacctgc  | ggcaggagga | aaagggaag  | 1020 |
| gttactgtgg  | gcagcttgaa  | gacctcagcg  | gtgccagta   | cctccacgat | gtcccaagag | 1080 |
| cctgagctcc  | tcatcagtg   | aatggaaaag  | cccctccctc  | tccgcacgga | tttctcttag | 1140 |

Sequence 3: "Amino acid sequence of human STING H232 (REF) variant"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 379    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..379           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| MPHSSLHPSI | PCPRGHGAOK | AALVLLSACL | VTLWGLGEPP | EHTLRYLVLH | LASLQLGLLL | 60  |
| NGVCSLAEEL | RHIHSRYRGS | YWRTVRACLG | CPLRRGALLL | LSIYFYSLP  | NAVGPFFTWM | 120 |
| LALLGLSQAL | NILLGLKGLA | PAEISAVCEK | GNFNVAHGLA | WSYYIGYLR  | ILPELOARIR | 180 |
| TYNOHYNNLL | RGAVSORLYI | LLPLDCGVDP | NLSMADPNIR | FLDKLPQOTG | DHAGIKDRVY | 240 |
| SNSIYELLEN | GQRAGTCVLE | YATPLQTLFA | MSQYSQAGFS | REDRLAQAKL | FCRTLEDILA | 300 |

Sequence 4: "Nucleotide sequence of human STING H232 (REF) variant"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 1140   | DNA           | Homo sapiens | No                             | No               |

Features

| Feature Key     | Feature Location | Qualifiers                                        |
|-----------------|------------------|---------------------------------------------------|
| source          | 1..1140          | mol_type = genomic DNA<br>organism = Homo sapiens |
| misc_difference | 1..1140          |                                                   |

Residues

|            |            |             |             |            |             |      |
|------------|------------|-------------|-------------|------------|-------------|------|
| atgccccact | ccagcctgca | tccatccatc  | ccgtgtccca  | ggggtcacgg | ggcccagaag  | 60   |
| gcagcccttg | tctctgctag | tgccctgcctg | gtgacccttt  | gggggctaag | agagccacca  | 120  |
| gagcacactc | tccggtacct | gggtgtccac  | ctagcctccc  | tgcagctggg | actgctgtta  | 180  |
| aacgggggtc | gcagcctggc | tgaggagctg  | cgccacatcc  | actccaggta | ccggggcagc  | 240  |
| tactggagga | ctgtgcgggc | ctgcctgggc  | tgccccctcc  | gccgtggggc | cctgtttgctg | 300  |
| ctgtccatct | atttctacta | ctccctccca  | aatgcggtcg  | gccgcgccct | cacttggatg  | 360  |
| cttgccctcc | tgggctcttc | gcaggcactg  | aacatcctcc  | tgggctctca | gggccttgcc  | 420  |
| ccagctgaga | tctctgcagt | gtgtgaaaaa  | gggaatttca  | acgtggccca | tggcttgcca  | 480  |
| tggctcattt | acatcggata | tctgcggctg  | atcctgccag  | agctccaggc | ccggattcga  | 540  |
| acttacaatc | agcattacaa | caacctgcta  | cggggtgcag  | tgagccagcg | gctgtataatt | 600  |
| ctcctcccat | tggactgtgg | gggtgcctgat | aacctgagta  | tggctgaccc | caacattcgc  | 660  |
| ttcctggata | aactgcacca | gcagaccggt  | gaccgtgctg  | gcatcaagga | tcgggttttac | 720  |
| agcaaacagc | tctatgagct | tcttgagaaac | gggcagcggg  | cgggcacctg | tgtcctggag  | 780  |
| tacgccaccc | ccttgcagac | tttgtttgcc  | atgtcacaa   | acagtcaagc | tggcttttag  | 840  |
| cgggaggata | ggcttgagca | ggccaaaact  | ttctgccgga  | cacttgagga | catcctggca  | 900  |
| gatgcccttg | agtctcagaa | caactgccgc  | ctcattgcct  | accaggaacc | tgcagatgac  | 960  |
| agcagcttct | cgctgtccca | ggaggttctc  | cggcacctgc  | ggcaggagga | aaagggaagag | 1020 |
| gttactgtgg | gcagcttgaa | gacctcagcg  | gtgcccagta  | cctccacgat | gtcccaagag  | 1080 |
| cctgagctcc | tcatcagtgg | aatggaaaa   | ccccctccctc | tccgcacgga | tttctcttag  | 1140 |

Sequence 5: "Amino acid sequence of human STING HAQ variant"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 379    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..379           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| MPHSSLHPST | PCPRGHGAQK | AALVLLSACL | VTLWGLGEPP | EHTLRYLVLH | LASLQLGLLL | 60  |
| NGVCSLAEE  | HHIHSRYRGS | YWRTVRACLG | CPLRRGALL  | LSIYFYSLP  | NAVGPPTWM  | 120 |
| LALLGLSOAL | NILLGLKGLA | PAEISAVCEK | GNFNVAHGLA | WSYIYGRLR  | ILPELOARIR | 180 |
| TYNOHYNLL  | RGAVSORLYI | LLPLDCGVPD | NLSMADPNIR | FLDKLPQOTA | DRAGIKDRVY | 240 |
| SNSIYELLEN | GORAGTCVLE | YATPLQTLFA | MSOYSOAGFS | REDRLQAKL  | FCOTLEDILA | 300 |
| DAPESONNCR | LIAYOEPADD | SSFSLSQEVL | RHLRQEEKEE | VTVGSLKTS  | VPSTSTMSQ  | 360 |
| PELLISGMEK | PLPLRTDFS  |            |            |            |            | 379 |

Sequence 6: "Nucleotide sequence of human STING HAQ variant"

| Length | Molecule Type | Organism | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|----------|--------------------------------|------------------|
|--------|---------------|----------|--------------------------------|------------------|

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 1140   | DNA           | Homo sapiens | No                             | No               |

Features

| Feature Key     | Feature Location | Qualifiers                                      |
|-----------------|------------------|-------------------------------------------------|
| source          | 1..1140          | mol_type = other DNA<br>organism = Homo sapiens |
| misc_difference | 1..1140          |                                                 |

Residues

|             |             |             |            |            |             |      |
|-------------|-------------|-------------|------------|------------|-------------|------|
| atgccccact  | ccagcctgca  | tccatccatc  | ccgtgtccca | ggggtcacgg | ggccccagaag | 60   |
| gcagccttgg  | tcttgctgag  | tgcctgcctg  | gtgaaccttt | gggggctagg | agagccacca  | 120  |
| gagcacacac  | tccggtaacct | gggtgtccac  | ctagcctccc | tgcagctggg | actgctgtta  | 180  |
| aacgggggtct | gcagcctggc  | tgaaggagctg | caccacatcc | actccaggta | ccggggcagc  | 240  |
| tactggagga  | ctgtgcgggc  | ctgcctgggc  | tggcccctcc | gccgtggggc | ccgtttgctg  | 300  |
| ctgttccatct | attttctacta | ctccctccca  | aatgcggtcg | gcccgccctt | cacttggatg  | 360  |
| cttgccctcc  | tgggcctctc  | gcaggcactg  | aacatcctcc | tgggcctcaa | gggcctggcc  | 420  |
| ccagctgaga  | tctctgcagt  | gtgtgaaaaa  | gggaatttca | acgtggccca | tgggctggca  | 480  |
| tgggtcatatt | acatcggata  | tctgcggctg  | atcctgccag | agctccaggc | ccggattcga  | 540  |
| acttacaatc  | agcattacaa  | caacctgcta  | cggggtgcag | tgagccagcg | gctgtatat   | 600  |
| ctcttcccat  | tggactgtgg  | ggtgccctgat | aacctgagta | tggctgacc  | caacattcgc  | 660  |
| ttcctggata  | aactgcctcca | gcagaccgct  | gaccgtgctg | gcatacaagg | tcgggtttac  | 720  |
| agcaaacagca | tctatgagct  | tctggagaa   | gggcagcggg | cgggcacctg | tgtcctggag  | 780  |
| tacgccaccc  | ccttgcagac  | tttgtttggc  | atgtcacaa  | acagtcaagc | tggcttttagc | 840  |
| cgggaggata  | ggccttgadca | ggccaaactc  | ttctgccaga | cacttgagga | catcctggca  | 900  |
| gatgcccttg  | agtctcagaa  | caactgccgc  | ctcattgcct | accaggaaac | tcagatgac   | 960  |
| agcagcttct  | cgctgtccca  | ggaggttctc  | cggcacctgc | ggcaggagga | aaaggaaag   | 1020 |
| gttactgtgg  | gcagcttgaa  | gacctcagcg  | gtgcccagta | cctccacgat | gtcccaagag  | 1080 |
| cctgagctcc  | tcatcagttg  | aatggaaaag  | ccctccctc  | tccgcacgga | tttctcttag  | 1140 |

Sequence 7: "Amino acid sequence of murine STING"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 378    | AA            | Mus musculus | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..378           | mol_type = protein<br>organism = Mus musculus |

Residues

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| MPYSNLHPAI | PRPRGHRSKY | VALIFLVASL | MILWVAKDPP | NHTLKYLAH  | LASHELGLLL | 60  |
| KNLCCLAEEL | CHVQSRYYQS | YWKAVRACLG | CPIHCMAMIL | LSSYFYFLON | TADIYLSWMF | 120 |
| GLLVLYKSL  | MLLGLOSLTP | AEVSAVCEEK | KLNVAGHLAW | SYIIGYLRLI | LPGLQARIRM | 180 |
| FNQLHNNMLS | GAGSRRLYL  | FPLDCGVDPN | LSVVDPNIRF | RDMLPQONID | RAGIKNRVYS | 240 |
| NSVYEILENG | QPAGVCILEY | ATPLQTLFAM | SQDAKAGFSR | EDRLEQAKLF | CRTLEEILED | 300 |
| VPESRNNCRL | IVYQEPDGN  | SFSLSQEVLR | HIRQEEKEEV | TMNAPMTSVA | PPPSVLSQEP | 360 |
| RLGISGMDQP | LPLRTDLI   |            |            |            |            | 378 |

Sequence 8: "Nucleotide sequence of murine STING"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 1137   | DNA           | Mus musculus | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                        |
|-------------|------------------|---------------------------------------------------|
| source      | 1..1137          | mol_type = genomic DNA<br>organism = Mus musculus |

Residues

|             |             |             |            |            |             |      |
|-------------|-------------|-------------|------------|------------|-------------|------|
| atgccatact  | ccaacctgca  | tccagccatc  | ccacggccca | gaggtcac   | ctccaaatat  | 60   |
| gtagccctca  | tctttctggt  | ggccagcctg  | atgatccttt | gggtggcaaa | ggatccacca  | 120  |
| aatcacactc  | tgaagtacct  | agcacttcac  | ctagccctgc | acgaacttgg | actactgttg  | 180  |
| aaaaacctct  | gctgtctggc  | tgaagagctg  | tgccatgtcc | agtccaggta | ccagggcagc  | 240  |
| tactggaagg  | ctgtgcgcgc  | ctgcctggga  | tgcccatcc  | actgtatg   | tatgatctta  | 300  |
| ctatcgtctt  | atttctattt  | ctcccaaaac  | actgctgaca | tatacctcag | ttggatgttt  | 360  |
| ggccttctgg  | tcctctataa  | gtcccctaagc | atgtctctgg | gccttcagag | cttgactcca  | 420  |
| gcggaagtct  | ctgcagtcct  | tgaagaaaaa  | aagttaaatg | ttgcccacgg | gctggcctgg  | 480  |
| tcatactaca  | ttgggtactt  | gcgggtgatc  | ttaccagggc | tccaggcccg | gatccgaatg  | 540  |
| ttcaatcagc  | tacataacaa  | catgctcagt  | gggtcaggga | gccgaagact | gtacatcctc  | 600  |
| tttccattgg  | actgtggggg  | gcctgacaac  | ctgagtgtag | ttgaccccaa | cattcgaattc | 660  |
| cgagatatgc  | tgccccagca  | aaacatcgac  | cgtgctggca | tcaagaatcg | ggtttattcc  | 720  |
| aacagcgtct  | acgagattct  | ggagaaacga  | cagccagcag | gcgtctgtat | cctgggagtac | 780  |
| gccaccctct  | tgcagaccct  | gtttgccatg  | tcacaggatg | ccaaagctgg | cttcagtcgg  | 840  |
| gaggatcggc  | ttgagcaggc  | taaactcttc  | tgccggacac | ttgaggaaat | cctggaagat  | 900  |
| gtccccgagt  | ctcgaataaa  | ctgccgcctc  | attgtctacc | aagaaccac  | agacggaaac  | 960  |
| agttttctcac | tgctctcagga | gggtgtcccg  | cacattcgtc | aggaagaaaa | ggaggaggtt  | 1020 |
| accatgaatg  | cccccatgac  | ctcagtggca  | cctcctccct | ccgtactgtc | ccaagagcca  | 1080 |
| agactcctca  | tcagtgggat  | ggatcagcct  | ctccactcc  | gactgacct  | catctga     | 1137 |

Sequence 9: "Amino acid sequence of HisAviTEV-hSTING (139-342) human WT protein"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 243    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..243           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| MGSSHHHHH  | SSGSLNDIF  | EAQKIEWHEG | GSENLFFOGL | APAEISAVCE | KGNFNVAHGL | 60  |
| AWSYYIGYLR | LILPELQARI | RTYNQHYNNL | LRGAVSORLY | ILLPLDCGVP | DNLSMADPNI | 120 |
| RFLDKLPQOT | GDRAGTKDRV | YSNSIYELLE | NGQRAGTCVL | EYATPLQTLF | AMSQYSQAGF | 180 |
| SREDRLEQAK | LFCRTLEDIL | ADAPESQNNC | RLIAYQEPAD | DSSFSLSQEV | LRHLRQEEKE | 240 |
| EVT        |            |            |            |            |            | 243 |

Sequence 10: "Amino acid sequence of HisAviTEV-hSTING (139-342) human REF variant protein"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 243    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..243           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| MGSSHHHHH  | SSGSLNDIF  | EAQKIEWHEG | GSENLFFOGL | APAEISAVCE | KGNFNVAHGL | 60  |
| AWSYYIGYLR | LILPELQARI | RTYNQHYNNL | LRGAVSORLY | ILLPLDCGVP | DNLSMADPNI | 120 |
| RFLDKLPQOT | GDHAGTKDRV | YSNSIYELLE | NGQRAGTCVL | EYATPLQTLF | AMSQYSQAGF | 180 |
| SREDRLEQAK | LFCRTLEDIL | ADAPESQNNC | RLIAYQEPAD | DSSFSLSQEV | LRHLRQEEKE | 240 |
| EVT        |            |            |            |            |            | 243 |

Sequence 11: "Amino acid sequence of HisAviTEV-hSTING (139-342) human HAQ variant protein"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 243    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..243           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| MGSSHHHHHH | SSGSGLNDIF | EAOKIEWHEG | GSENLIFYOGL | APAEISAVCE | KGNFNVAHGL | 60  |
| AWSYYIGYLR | LILPELQARI | RTYNOHYNNL | LRGAVSORLY  | ILLPLDCGVP | DNLSMADPNT | 120 |
| RFLDKLPQOT | ADRAGIKDRV | YSNSIYELLE | NGORAGTCVL  | EYATPLOTLF | AMSQYSQAGF | 180 |
| SREDRLEQAK | LFCQTLEDIL | ADAPESQNNC | RLIAYQEPAD  | DSSFSLSQEV | LRHLRQEEKE | 240 |
| EVT        |            |            |             |            |            | 243 |

Sequence 12: "Amino acid sequence of HisAviTEV-mSTING (138-341) murine WT"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 243    | AA            | Mus musculus | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..243           | mol_type = protein<br>organism = Mus musculus |

Residues

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| MGSSHHHHHH | SSGSGLNDIF | EAOKIEWHEG | GSENLIFYOGL | TPAEVSAVCE | EKKLNVAHGL | 60  |
| AWSYYIGYLR | LILPGLOARI | RMFNQLHNNM | LSGAGSRRLY  | ILFPLDCGVP | DNLSVDDPNT | 120 |
| RFRDMLPOON | IDRAGIKNRV | YSNSVYEILE | NGOPAGVCIL  | EYATPLOTLF | AMSQDAKAGF | 180 |
| SREDRLEQAK | LFCRTLEEIL | EDVPESRNNC | RLIVYQEPTD  | GNSFSLSQEV | LRHIRQEEKE | 240 |
| EVT        |            |            |             |            |            | 243 |

Sequence 13: "Primer: H232R (WT) fwd"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 27     | DNA           | synthetic construct | No                             | No               |

Features

| Feature Key  | Feature Location | Qualifiers                                             |
|--------------|------------------|--------------------------------------------------------|
| misc_feature | 1..27            | note = primer                                          |
| source       | 1..27            | mol_type = other DNA<br>organism = synthetic construct |

## Residues

cggtgctggca tcaaggatcg ggtttac

27

### Sequence 14: "Primer: H232R (WT) rev"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 27     | DNA           | synthetic construct | No                             | No               |

## Features

| Feature Key  | Feature Location | Qualifiers                                             |
|--------------|------------------|--------------------------------------------------------|
| misc_feature | 1..27            | note = primer                                          |
| source       | 1..27            | mol_type = other DNA<br>organism = synthetic construct |

## Residues

gtcaccggtc tgctggggca gttttac

27

### Sequence 15: "Primer: H232R/G230A fwd"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 33     | DNA           | synthetic construct | No                             | No               |

## Features

| Feature Key  | Feature Location | Qualifiers                                             |
|--------------|------------------|--------------------------------------------------------|
| misc_feature | 1..33            | note = primer                                          |
| source       | 1..33            | mol_type = other DNA<br>organism = synthetic construct |

## Residues

gctgaccgtg ctggcatcaa ggatcggggtt tac

33

### Sequence 16: "Primer: H232R/G230A rev"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 25     | DNA           | synthetic construct | No                             | No               |

## Features

| Feature Key  | Feature Location | Qualifiers                                             |
|--------------|------------------|--------------------------------------------------------|
| misc_feature | 1..25            | note = primer                                          |
| source       | 1..25            | mol_type = other DNA<br>organism = synthetic construct |

## Residues

ggtctgctgg ggcagtttat ccagg

25

### Sequence 17: "Primer: R71H fwd"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 24     | DNA           | synthetic construct | No                             | No               |

## Features

| Feature Key  | Feature Location | Qualifiers                                             |
|--------------|------------------|--------------------------------------------------------|
| misc_feature | 1..24            | note = primer                                          |
| source       | 1..24            | mol_type = other DNA<br>organism = synthetic construct |

## Residues

caccacatcc actccaggta ccgg

24

### Sequence 18: "Primer: R71H rev"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 24     | DNA           | synthetic construct | No                             | No               |

## Features

| Feature Key  | Feature Location | Qualifiers                                             |
|--------------|------------------|--------------------------------------------------------|
| misc_feature | 1..24            | note = primer                                          |
| source       | 1..24            | mol_type = other DNA<br>organism = synthetic construct |

## Residues

cagctcctca gccaggctgc agac

24

### Sequence 19: "Primer: R293Q fwd"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 25     | DNA           | synthetic construct | No                             | No               |

## Features

| Feature Key  | Feature Location | Qualifiers                                             |
|--------------|------------------|--------------------------------------------------------|
| misc_feature | 1..25            | note = primer                                          |
| source       | 1..25            | mol_type = other DNA<br>organism = synthetic construct |

## Residues

cagacacttg aggacatcct ggcag

25

### Sequence 20: "Primer: R293Q rev"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 23     | DNA           | synthetic construct | No                             | No               |

## Features

| Feature Key  | Feature Location | Qualifiers                                             |
|--------------|------------------|--------------------------------------------------------|
| misc_feature | 1..23            | note = primer                                          |
| source       | 1..23            | mol_type = other DNA<br>organism = synthetic construct |

## Residues

gcagaagagt ttggcctgct caa

23

### Sequence 21: "Primer: hST Fw\_V2"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 39     | DNA           | synthetic construct | No                             | No               |

## Features

| Feature Key  | Feature Location | Qualifiers                                             |
|--------------|------------------|--------------------------------------------------------|
| misc_feature | 1..39            | note = primer                                          |
| source       | 1..39            | mol_type = other DNA<br>organism = synthetic construct |

## Residues

acctgtattt tcagggcctg gccccagctg agatctctg

39

### Sequence 22: "Primer: hST Rv\_V3"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 44     | DNA           | synthetic construct | No                             | No               |

## Features

| Feature Key  | Feature Location | Qualifiers                                             |
|--------------|------------------|--------------------------------------------------------|
| misc_feature | 1..44            | note = primer                                          |
| source       | 1..44            | mol_type = other DNA<br>organism = synthetic construct |

## Residues

cagaattcgc aagcttttaa gtaacctctt ctttttctc ctgc

44

### Sequence 23: "Amino acid sequence of CDRL1 of anti-EGFR antibody (mutated anti-EGFR antibodies 1-3)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 11     | AA            | Homo sapiens | No                             | No               |

## Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..11            | mol_type = protein<br>organism = Homo sapiens |

## Residues

QASQDISNYL N

11

### Sequence 24: "Amino acid sequence of CDRL2 of anti-EGFR antibody (mutated anti-EGFR antibodies 1-3)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 7      | AA            | Homo sapiens | No                             | No               |

## Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..7             | mol_type = protein<br>organism = Homo sapiens |

## Residues

DASNLET

7

### Sequence 25: "Amino acid sequence of CDRL3 of anti-EGFR antibody (mutated anti-EGFR antibodies 1-3)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 9      | AA            | Homo sapiens | No                             | No               |

## Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..9             | mol_type = protein<br>organism = Homo sapiens |

## Residues

QHFDHLPLA

9

**Sequence 26: "Amino acid sequence of CDRH1 of anti-EGFR antibody (mutated anti-EGFR antibodies 1-3)"**

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 7      | AA            | Homo sapiens | No                             | No               |

**Features**

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..7             | mol_type = protein<br>organism = Homo sapiens |

**Residues**

SGDYWT

7

**Sequence 27: "Amino acid sequence of CDRH2 of anti-EGFR antibody (mutated anti-EGFR antibodies 1-3)"**

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 16     | AA            | Homo sapiens | No                             | No               |

**Features**

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..16            | mol_type = protein<br>organism = Homo sapiens |

**Residues**

HIYYSGNTNY NPSLKS

16

**Sequence 28: "Amino acid sequence of CDRH3 of anti-EGFR antibody (mutated anti-EGFR antibodies 1-3)"**

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 9      | AA            | Homo sapiens | No                             | No               |

**Features**

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..9             | mol_type = protein<br>organism = Homo sapiens |

**Residues**

DRVTGAFDI

9

**Sequence 29: "Amino acid sequence of light chain variable region of anti-EGFR antibody (mutated anti-EGFR antibodies 1-3)"**

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 108    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..108           | mol_type = protein<br>organism = Homo sapiens |

Residues

DIQMTQSPSS
LSASVGDRVT
ITCOASQDIS
NYLNWYQOKP
GKAPKLLIYD
ASNLETGVPS
RFSGSGSGTD
FTFTISSLQP
EDIATYFCQH
FDHLPLAFGG
GTKVEIKR

60
108

Sequence 30: "Amino acid sequence of light chain of anti-EGFR antibody (mutated anti-EGFR antibodies 1-3)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 214    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..214           | mol_type = protein<br>organism = Homo sapiens |

Residues

DIQMTQSPSS
LSASVGDRVT
ITCOASQDIS
NYLNWYQOKP
GKAPKLLIYD
ASNLETGVPS
RFSGSGSGTD
FTFTISSLQP
EDIATYFCQH
FDHLPLAFGG
GTKVEIKRTV
AAPSVFIFPP
SDEQLKSGTA
SVVCLLNIFY
PREAKVQWKV
DNALQSGNSQ
ESVTEQDSKD
STYLSSTLT
LSKADYEKHK
VYACEVTHQG
LSSPVTKSFN
RGEK

60
120
180
214

Sequence 31: "Amino acid sequence of heavy chain variable region of anti-EGFR antibody (mutated anti-EGFR antibodies 1-3)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 119    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..119           | mol_type = protein<br>organism = Homo sapiens |

Residues

QVQLQESGPG
LVKPSSETLSL
TCTVSGGSVS
SGDYWTWIR
QSPGKGLEWI
GHIYYSGNTN
YNPSLKSRLL
ISIDTSKTQF
SLKLSSVTAA
DTAIYYCVRD
RVTGAFDIWG
QGTMTVTVSS

60
119

Sequence 32: "Amino acid sequence of heavy chain of anti-EGFR antibody LALA-DG variant (mutated anti-EGFR

antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 449    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..449           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| QVQLQESGPG | LVKPKSETLSL | TCTVSGGSVS  | SGDYWTWIR  | QSPGKGLEWI  | GHIYYSGNTN | 60  |
| YNPSLKSRLT | ISIDTSKTQF  | SLKLSSVTAA  | DTAIYYCVRD | RVTGAFDIWG  | QGTMTVTSSA | 120 |
| STKGPSVFPL | APSSKSTSGG  | TAALGCLVKD  | YFPEPVTVSW | NSGALTSGVH  | TFPAVLQSSG | 180 |
| LYSLSSVVTV | PSSSLGTQTY  | ICNVNHHKPSN | TKVDKRVEPK | SCDKTHTCPP  | CPAPEAAGGP | 240 |
| SVFLFPPKPK | DTLMISRTP   | VTCVVVGVS   | EDPEVKFNWY | VDGVEVHNAK  | TKPREEOYNS | 300 |
| TYRVVSVLTV | LHODWLNKKE  | YKCKVSNKAL  | PAPIEKTISK | AKGQPREPOV  | YTLPPSREEM | 360 |
| TKNOVSLTCL | VKGFYPSDIA  | VEWESNGOPE  | NNYKTTPPVL | DSDGSFFFLYS | KLTVDKSRWQ | 420 |
| QGNVFSQSV  | HEALHNHYTQ  | KSLSLSPGK   |            |             |            | 449 |

Sequence 33: "Amino acid sequence of heavy chain of anti-EGFR antibody LALA-DG variant (mutated anti-EGFR antibody 2)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 449    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..449           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| QVQLQESGPG | LVKPKSETLSL | TCTVSGGSVS  | SGDYWTWIR  | QSPGKGLEWI  | GHIYYSGNTN | 60  |
| YNPSLKSRLT | ISIDTSKTQF  | SLKLSSVTAA  | DTAIYYCVRD | RVTGAFDIWG  | QGTMTVTSSA | 120 |
| STKGPSVFPL | APSSKSTSGG  | TAALGCLVKD  | YFPEPVTVSW | NSGALTSGVH  | TFPAVLQSSG | 180 |
| LYSLSSVVTV | PSSSLGTQTY  | ICNVNHHKPSN | TKVDKKVEPK | SCDKTHTCPP  | CPAPEAAGGP | 240 |
| SVFLFPPKPK | DTLMISRTP   | VTCVVVGVS   | EDPEVKFNWY | VDGVEVHNAK  | TKPREEOYNS | 300 |
| TYRVVSVLTV | LHODWLNKKE  | YKCKVSNKAL  | PAPIEKTISK | AKGQPREPOV  | YTLPPSREEM | 360 |
| TKNOVSLTCL | VKGFYPSDIA  | VEWESNGOPE  | NNYKTTPPVL | DSDGSFFFLYS | KLTVDKSRWQ | 420 |
| QGNVFSQSV  | HEALHNHYTQ  | KSLSLSPGK   |            |             |            | 449 |

Sequence 34: "Amino acid sequence of heavy chain of anti-EGFR antibody A"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 449    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..449           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| QVQLQESGPG | LVKPSSETLSL | TCTVSGGSVS | SGDYWTWIR  | QSPGKGLEWI | GHIYYSGNTN | 60  |
| YNPSLKSRLT | TSIDTSKTOF  | SLKLSSVTAA | DTAIYVCVRD | RVTGAFDIWG | OGTMVTVSSA | 120 |
| STKGPSVFPL | APSSKSTSGG  | TAALGCLVKD | YFPEPVTVS  | NSGALTSGVH | TTPAVLQSSG | 180 |
| LYSLSSVVT  | PSSSLGTOTY  | ICNVNHKPSN | TKVDKRVEPK | SCDKTHTCPP | CPAPELLGGP | 240 |
| SVFLFPPKPK | DTLMISRTPE  | VTCVVVDVSH | EDPEVKFNWY | VDGVEVHNAK | TKPREEOYNS | 300 |
| TYRVVSVLTV | LHODWLNKGE  | YKCKVSNKAL | PAPIEKTISK | AKGQPREPQV | YTLPPSREEM | 360 |
| TQNQVSLTCL | VKGFIYPSDIA | VEWESNGQPE | NNYKTTTPVL | DSDGSFFLYS | KLTVDKSRWQ | 420 |
| QGNVFCSCVM | HEALHNHYTQ  | KSLSLSPGK  |            |            |            | 449 |

Sequence 35: "Amino acid sequence of heavy chain of anti-EGFR antibody B"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 445    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..445           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| QVQLQESGPG | LVKPSSETLSL | TCTVSGGSVS | SGDYWTWIR  | QSPGKGLEWI | GHIYYSGNTN | 60  |
| YNPSLKSRLT | TSIDTSKTOF  | SLKLSSVTAA | DTAIYVCVRD | RVTGAFDIWG | OGTMVTVSSA | 120 |
| STKGPSVFPL | APSSKSTSGG  | TAALGCLVKD | YFPEPVTVS  | NSGALTSGVH | TTPAVLQSSG | 180 |
| LYSLSSVVT  | PSSSLGTOTY  | ICNVNHKPSN | TKVDKTVERK | CCVECPPCPA | PPVAGPSVFL | 240 |
| FPPKPKDTLM | ISRTPEVTCV  | VVDVSHEDPE | VQFNWYVDGV | EVHNAKTKPR | EEQFNSTFRV | 300 |
| VSVLTVVHOD | WLNGKEYCKK  | VSNKGLPAPI | EKTISKTKGQ | PREPQVYTL  | PSREEMTKNQ | 360 |
| VSLTCLVKGF | YPSDIAVEWE  | SNGQPENNYK | TTTPMLDSDG | SFFLYSKLTV | DKSRWQQGNV | 420 |
| FSCVMHEAL  | HNHYTQKSL   | LSPGK      |            |            |            | 445 |

Sequence 36: "Amino acid sequence of heavy chain of anti-EGFR antibody LALA variant (mutated anti-EGFR antibody 3)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 449    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..449           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| QVQLQESGPG | LVKPSSETLSL | TCTVSGGSVS | SGDYWTWIR  | QSPGKGLEWI | GHIYYSGNTN | 60  |
| YNPSLKSRLT | TSIDTSKTOF  | SLKLSSVTAA | DTAIYVCVRD | RVTGAFDIWG | OGTMVTVSSA | 120 |
| STKGPSVFPL | APSSKSTSGG  | TAALGCLVKD | YFPEPVTVS  | NSGALTSGVH | TTPAVLQSSG | 180 |
| LYSLSSVVT  | PSSSLGTOTY  | ICNVNHKPSN | TKVDKRVEPK | SCDKTHTCPP | CPAPEAAGGP | 240 |
| SVFLFPPKPK | DTLMISRTPE  | VTCVVVDVSH | EDPEVKFNWY | VDGVEVHNAK | TKPREEOYNS | 300 |
| TYRVVSVLTV | LHODWLNKGE  | YKCKVSNKAL | PAPIEKTISK | AKGQPREPQV | YTLPPSREEM | 360 |
| TQNQVSLTCL | VKGFIYPSDIA | VEWESNGQPE | NNYKTTTPVL | DSDGSFFLYS | KLTVDKSRWQ | 420 |
| QGNVFCSCVM | HEALHNHYTQ  | KSLSLSPGK  |            |            |            | 449 |

Sequence 37: "Amino acid sequence of CDRL1 of anti-CDH6 antibody (mutated anti-CDH6 antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 11     | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..11            | mol_type = protein<br>organism = Homo sapiens |

Residues

KASQNIYKNL A

11

Sequence 38: "Amino acid sequence of CDRL2 of anti-CDH6 antibody (mutated anti-CDH6 antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 7      | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..7             | mol_type = protein<br>organism = Homo sapiens |

Residues

DANTLQT

7

Sequence 39: "Amino acid sequence of CDRL3 of anti-CDH6 antibody (mutated anti-CDH6 antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 8      | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..8             | mol_type = protein<br>organism = Homo sapiens |

Residues

QQYYSGWA

8

Sequence 40: "Amino acid sequence of CDRH1 of anti-CDH6 antibody (mutated anti-CDH6 antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 5      | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..5             | mol_type = protein<br>organism = Homo sapiens |

## Residues

RNFMH

5

### Sequence 41: "Amino acid sequence of CDRH2 of anti-CDH6 antibody (mutated anti-CDH6 antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 17     | AA            | Homo sapiens | No                             | No               |

## Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..17            | mol_type = protein<br>organism = Homo sapiens |

## Residues

WIYPGDGETE YAQKFQG

17

### Sequence 42: "Amino acid sequence of CDRH3 of anti-CDH6 antibody (mutated anti-CDH6 antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 13     | AA            | Homo sapiens | No                             | No               |

## Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..13            | mol_type = protein<br>organism = Homo sapiens |

## Residues

GVYGGFAGGY FDF

13

### Sequence 43: "Amino acid sequence of light chain variable region of anti-CDH6 antibody (mutated anti-CDH6 antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 107    | AA            | Homo sapiens | No                             | No               |

## Features

| Feature Key | Feature Location | Qualifiers |
|-------------|------------------|------------|
|-------------|------------------|------------|

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..107           | mol_type = protein<br>organism = Homo sapiens |

Residues

DIQMTQSPSS
LSASVGDVRT
ITCKASONIY
KNLAWYQOKP
GKAPKLLIYD
ANTLQTGVPS
60
RFSGSGSGSD
FTLTISSLQP
EDFATYFCQQ
YYSGWAFGQG
TKVEIKR
107

Sequence 44: "Amino acid sequence of light chain of anti-CDH6 antibody (mutated anti-CDH6 antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 213    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..213           | mol_type = protein<br>organism = Homo sapiens |

Residues

DIQMTQSPSS
LSASVGDVRT
ITCKASONIY
KNLAWYQOKP
GKAPKLLIYD
ANTLOTGVPS
60
RFSGSGSGSD
FTLTISSLQP
EDFATYFCQQ
YYSGWAFGQG
TKVEIKRTVA
APSVFIFPPS
120
DEOLKSGTAS
VVCLLNNFYP
REAKVQWKVD
NALQSGNSQE
SVTEQDSKDS
TYSLSSTLTL
180
SKADYEKHKV
YACEVTHQGL
SSPVTKSFNR
GEC
213

Sequence 45: "Amino acid sequence of heavy chain variable region of anti-CDH6 antibody (mutated anti-CDH6 antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 122    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..122           | mol_type = protein<br>organism = Homo sapiens |

Residues

EVQLVQSGAE
VKKPGASVKV
SCKASGYTFT
RNFMHWVRQA
PGQGLEWMGW
IYPGDGETEY
60
AOKFQGRVTI
TADTSTSTAY
MELSSLRSED
TAVYYCARGV
YGGFAGGYFD
FWGQGTLVTV
120
SS
122

Sequence 46: "Amino acid sequence of heavy chain of anti-CDH6 antibody LALA-DG variant (mutated anti-CDH6 antibody 1)"

| Length | Molecule Type | Organism     | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------|--------------------------------|------------------|
| 452    | AA            | Homo sapiens | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                    |
|-------------|------------------|-----------------------------------------------|
| source      | 1..452           | mol_type = protein<br>organism = Homo sapiens |

Residues

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| EVOLVOSGAE | VKKPGASVKV | SCKASGYTFT | RNFMHWVROA | PGOGLEWMGW | IYPGDGETEY | 60  |
| AQKFQGRVTI | TADTSTSTAY | MELSSLRSED | TAVYYCARGV | YGGFAGGYFD | FWGQGTLLTV | 120 |
| SSASTKGPSV | FPLAPSSKST | SGGTAALGCL | VKDYFPEPVT | VSWNSGALTS | GVHTFPAVLQ | 180 |
| SSGLYSLSSV | VTVPSSSLGT | QTYICNVNHK | PSNTKVDDKV | EPKSCDKTHT | CPPCPAPEAA | 240 |
| GGPSVFLFPP | KPKDTLMISR | TPEVTCVVVG | VSHEDPEVKF | NWYVDGVEVH | NAKTKPREEQ | 300 |
| YNSTYRVVSV | LTVLHQDWLN | GKEYKCKVSN | KALPAPIEKT | ISKAKGQPRE | PQVYTLPPSR | 360 |
| EEMTKNQVSL | TCLVKGFYPS | DIAEWESNG  | QPENNYKTTT | PVLDSGGSFF | LYSKLTVDKS | 420 |
| RWQQGNVFSC | SVMHEALHNN | YTQKSLSLSP | GK         |            |            | 452 |

Sequence 47: "Endo-S WT"

| Length | Molecule Type | Organism               | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|------------------------|--------------------------------|------------------|
| 995    | AA            | Streptococcus pyogenes | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                              |
|-------------|------------------|---------------------------------------------------------|
| source      | 1..995           | mol_type = protein<br>organism = Streptococcus pyogenes |

Residues

|             |            |             |            |             |             |     |
|-------------|------------|-------------|------------|-------------|-------------|-----|
| MDKHLLVKRT  | LGCVCAATLM | GAALATHHDS  | LNTVKAEECT | VOVOKGLPST  | DSLHYLSENS  | 60  |
| KKEFKEELSK  | AGQESQKVKE | TLAKAQOQADK | QAQELAKMKI | PEKTPMKPLH  | GPLYGGYFRT  | 120 |
| WHDKTSDPTE  | KDKVNSMGEL | PKEVDLAFIF  | HDWTKDYSLE | WKELATKHVP  | KLNKQGTRVI  | 180 |
| RTIPWRFLAG  | GDNSGIAEDT | SKYPNTPPEGN | KALAKAIVDE | YVYKYNLDGL  | DVDVEHDSIP  | 240 |
| KVDKKEDTAG  | VERSIQVFEE | IGKLIGPKGV  | DKSRLFIMDS | TYMADKNPLI  | ERGAPYINLL  | 300 |
| LVQVYGSQGE  | KGGWEPVSNR | PEKTMEERWQ  | GYSKYIRPEQ | YMIGFSFYEE  | NAQEGNLWYD  | 360 |
| INSRKDEDKA  | NGINTDITGT | RAERYARWQP  | KTGGVKGGIF | SYAIDRDGVA  | HQPKKYAKQK  | 420 |
| EFKDATDNIF  | HSDYSVSKAL | KTMVKDKDSY  | DLIDEKDFPD | KALREAVMAQ  | VGTRKGDLER  | 480 |
| FNGTLRLDNP  | AIOSLEGLNK | FKKLAQLDLI  | GLSRITKLDR | SVLPANMKPG  | KDTLETVLET  | 540 |
| YKKDNKEEPA  | TIPPVSLKVS | GLTGLKELDL  | SGFDRETLAG | LDAATLTSLE  | KVDISGNKLD  | 600 |
| LAPGTENROI  | FDTMLSTISN | HVGSNEQTVK  | FDKQKPTGHI | PDTYGKTSLE  | LPVANEKVDL  | 660 |
| QSOLLFGTGT  | NOGTLINSEA | DYKAYQNHKI  | AGRSFVDSNY | HYNNFKVSYE  | NYTVKVTGST  | 720 |
| LGTTTDPKTLA | TDKEETYKVD | FFSPADKTKA  | VHTAKVIVGD | EKTMMVNLAE  | GATVIGGSAD  | 780 |
| PVNARKVFDG  | QLGSETDNIS | LGWDSKQSII  | FKLKEDGLIK | HWREFFNDSAR | NPETTINKPIQ | 840 |
| EASLQIFNIK  | DYNLDNLEN  | PNKFDDEKYW  | ITVDTYSAQG | ERATAFSNTL  | NNITSKYWRV  | 900 |
| VFDTKGDRYS  | SPVVPQLQIL | GYPLPNADTI  | MKTVTTAKEL | SQQKDKFSQK  | MLDELKIKEM  | 960 |
| ALETSLNSKI  | FDVTAINANA | GVLKDCIEKR  | QLLKK      |             |             | 995 |

Sequence 48: "Endo-S2 WT"

| Length | Molecule Type | Organism               | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|------------------------|--------------------------------|------------------|
| 843    | AA            | Streptococcus pyogenes | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                              |
|-------------|------------------|---------------------------------------------------------|
| source      | 1..843           | mol_type = protein<br>organism = Streptococcus pyogenes |

Residues

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| MDKHLLVKRT | LGCVCAATLM  | GAALATHHDS | LNTVKAEECT | VOTGKTDQOV | GAKLVQEIREE | 60  |
| GKRGPLYAGY | FRTWHDRAST  | GIDGKQOHPE | NTMAEVPKEV | DILFVFHDHT | ASDSPFWSEL  | 120 |
| KDSYVHKLHQ | QGTALVQITIG | VNELNGRTGL | SKDYPDTPEG | NKALAAAIK  | AFVTDGRVDG  | 180 |

LDIDIEHEFT NKRTPEEDAR ALNVFKEIAO LIGKNGSDKS KLLIMDTTIS VENNPIFKGI 240  
AEDLDYLLRO YYGSOGGEAE VDTINSDWNO YONYIDASQF MIGFSFFEEES ASKGNLWFDV 300  
NEYDPNNPEK GKDIIEGTRAK KYAEWQPSTG GLKAGIFSIA IDRDGVAHVP STYKNRTSTN 360  
LORHEVDNIS HTDYTVSRKL KTLMTEDKRY DVIDQKDIPD PALREQIIQQ VGQYKGDLER 420  
YNKTLVLTDG KIONLKGLEK LSKLOKLELR QLSNVKEITP ELLPESMKKD AELVMVGMTG 480  
LEKLNLSGLN ROTLDGIDVN SITHLTSFDI SHNSLDLSEK SEDRKLLMTL MEQVSNHQKI 540  
TVKNTAFENO KPKGYYPTY DTKEGHYDVD NAEHDILTDF VFGTVTKRNT FIGDEEAFAI 600  
YKEGAVDGRQ YVSKDYTYEA FRKDYKGYKV HLTASNLGET VTSKVTATTD ETYLVDSVDG 660  
EKVVHHMKLN IGSGAIMMEN LAKGAKVIGT SGDFEQAKKI FDGEKSDRFF TWGOTNWIAP 720  
DLGEINLAKE WRLFNAETNT EIKTDSSLNV AKGRLQILKD TTIDLEKMDI KNRKEYLSND 780  
ENWTDVAQMD DAKAIFNSKL SNVLSRYWRF CVDGGASSYY PQYTELQILG QRLSNDVANT 840  
LKD 843

Sequence 49: "Endo-Si WT"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 928    | AA            | Streptococcus iniae | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                           |
|-------------|------------------|------------------------------------------------------|
| source      | 1..928           | mol_type = protein<br>organism = Streptococcus iniae |

Residues

MNKRLLVKRT FGCVCAAAAIL GVAPLSHPTI VEAREELKMP NGLEQSIADV EAKIDALTYL 60  
SKNSKDEFKH SMYEIPSNRE HKPVSPKQAL QNAKKADAQA ERLAKMTIPK KEELKALEGP 120  
LYGGYFRTWQ DKTSDDPTETN KVNSFGELPK EVDLAFVFHD YTKDYSLFEW ELATKQVPKL 180  
NKQGTNRVIR IPWRFLSGAD HSDISADKEK FPNTEAGNKA LAKAIVDEYV YKYNLDGLDI 240  
DIERDSVPKV NDKEDEPEALA RTVEVFKEIG KLIGANGADK SRLIMDDTTY TAEENPLIKE 300  
TAQYLNLLLV QVYGFSGENG NYLHHKNILD ETSSMEGRWQ GYSKYIRPEQ YMVGFSFYEE 360  
KDFNNRWKDI NEEDPSDPHI GEKIQGTAE RYAKWQPKTG GLKGGLFSYA IDRDGVAQPK 420  
OKTEHPELDQ IVKSEYKYSK ALKKLMMTDD QYQPIDQSDP PDKALRESII KQVGTTRGD 480  
ERFKGTLRLD NPEIKDLTGL NKLLRVAKLE LINLPKITKI DKDDLQNLK PLTDNQKSNL 540  
EIKGTYDDSK LYKDIPAFDL VISGLSGLES LDISGHQDRT LSGIDASTLP SLKAINISDN 600  
HFDLAQGTEN RHILDTILAT LAKNGASTAS FDKQKPKGLY PESYSTAPLH LOVGQKINV 660  
IDDLIFGTRT NONTLINTEN DFEAYKEQTI QGKPFIAPDY LYDNFKVSYK EYSASIVDST 720  
LAETTDKTIID TAKAETYQVT VSNKDGGKTVH SVKVIYVDEK PMMVNLAODA KIIGTDNMTQ 780  
SAKVFDGOKD QFLLSWNKDS SVIFELKTPG TAKHWRFFDD GKNDSVTLVS FKGDASNFT 840  
EKDKAENWVE ITKDSRKND DVFSSPLEVD NAKYLKVTIK KEAKYIYFNE LQILGYPGVV 900  
AKKTADDLRP TEADKSDDKS DKNDTEAK 928

Sequence 50: "Endo-M WT"

| Length | Molecule Type | Organism       | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|----------------|--------------------------------|------------------|
| 744    | AA            | Mucor hiemalis | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                      |
|-------------|------------------|-------------------------------------------------|
| source      | 1..744           | mol_type = protein<br>organism = Mucor hiemalis |

Residues

MPSLQLOPDD KLAPVSFALK SMNELRDWTP DEKIKFNVSS VALQPRVKNA LKPQLLLTHD 60  
MAGGYKEDKN IOGNKYKDIY NIOYWHLADT FVYFSHERVS IPPVNWNTAC HRNGVKCLGT 120  
FLVEGNMQMH EMEALLHGPP LLNNTDDPMR LWSPYYADQL VAIKHYGFD GWLFNIECEF 180  
FPFPTNPKFK AEELAKFLHY FKEKLHNEIP GSOLIWYDSM TNEGEIHWON QLTWKNELFF 240  
KNTDGIFLNY WKKKEYPEMA RRVAEGIGRS GLEVYFGTDV WGRHTYGGGG FKSYPKGVKTA 300  
YSAMTSSALF GMAWTYEHFE KSEFEKMDRL FWCQGGKYSYD PPPPPKPNPD EKEVESDDSE 360  
DELMYGHKKG IADTVESIPV PSTDWFVTNF DRGFGNRFY RGRLLSOPW SHLSHOAILP 420  
NKSYPNPEII PTDONIKITS SLDCDHGAFL GGTSLIIGKO RFNHRESHDV ETEISIPLYK 480  
LSLDASKGCS LRYTYRTLMM KDVKLTVACH FSLKTNDSDN FFKVWOPDEN FSEFYDDGMR 540  
ATVTTENSTE SRCFLRLTTE EDTGENDWIT KTINVPAPVE GSOLYITRLE VSVLDTAGL 600  
VGLVNOVIAC LGYISITPTE NSGIKTDSSR TIQDLFWKQ KYTKIGKESL DDIAQEEVHR 660  
YYGTLNWEIT ANVVNAWEEI DYNNVFKES DDSATRIFLG TAFCNQFRVS GLDIILSKLP 720  
KIVIEAVNKE GYISSSGSID LSLN 744

Sequence 51: "Endo-Rp WT"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 696    | AA            | Rhizomucor pusillus | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                           |
|-------------|------------------|------------------------------------------------------|
| source      | 1..696           | mol_type = protein<br>organism = Rhizomucor pusillus |

Residues

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| MPSLELQOAA | DTRLFESMPL | QTMNELGSWE | PSNASRANIA | TIPLHORSNL | DPAEPLIVT  | 60  |
| HDMAGGYKED | SNIQNTYDT  | IYSCQYWOYV | DTFIYFSHHR | VTIPPVNWIN | ACHRNGVKTL | 120 |
| GTFIVEGAAG | MFALERFVYG | PEPGORNSWS | PYYADKLVDI | AEFYGFDGWL | LNIESDFFFL | 180 |
| YRNPSLKAIH | LAKLLRYLKN | AMHARVPGSE | IIWYDSMTTN | GSVQWQNNIT | PKNSIFFEAA | 240 |
| DGIFLNYWMN | ATVPPLALQV | AHRLGRQGS  | VYFGTDVWGR | GTFGGGGFDS | YLAVGTARAF | 300 |
| KTSSALFGTA | WIYEHFGKKD | FELMDRLWL  | GGDQSEYPAQ | EGEQNRTVKV | TSHLGRHPGI | 360 |
| ADVSPVRSAP | GKTWFATWFD | RGYGTGFYYO | GKKLLSOPWS | HLSHQSIPP  | LIARLOREEN | 420 |
| HGLSYFLADD | DAYIGGTSLL | IAAEITQERO | LPLYOLEYDV | TEGCEVOFIY | KSPEPDMOGK | 480 |
| IDIYLNLOVT | DILPDELAFY | WODVTDASSO | ADATTAMRLY | LNENTVIYIK | PSRKOELAEG | 540 |
| WLLCSVRVPP | TYPLGIATIK | ELGIHVDGKE | TVLFRLGLLT | TIPLGDAPSA | LSRITOVOLQ | 600 |
| RDEDIHSKCP | SSSCELWATL | SWMMEHNSKE | DWDQVDHYMI | FFKNVDSKAE | PIFLGTSFST | 660 |
| EYRISGLEIK | KHGNSIEIWA | VNRLGTVIAR | QDIDIQ     |            |            | 696 |

Sequence 52: "Endo-CC WT"

| Length | Molecule Type | Organism            | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------|--------------------------------|------------------|
| 787    | AA            | Coprinopsis cinerea | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                           |
|-------------|------------------|------------------------------------------------------|
| source      | 1..787           | mol_type = protein<br>organism = Coprinopsis cinerea |

Residues

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| MPIAGKKFHP | RALPEFWRTF | REMDEWRATO  | TGPOARPAEG | ILKYVPRKIR | PADIAGKGRL | 60  |
| LVSHDYKGGY | VEDPFSKSYS | FNWFESTDSE  | NYFAHHRITI | PPPEWINAHA | ROGVPILGTI | 120 |
| TFEGGSDEDI | LRMVIKTPG  | STSNFHAERN  | AEYTVPVSSY | YAELEADLAV | ERGFDGWLLN | 180 |
| VEIGLOGGSE | QARGLAAWVA | LLQOEVLKKV  | GPHGLVIWYD | SVTVRGDLWM | QDRLNAFNLP | 240 |
| FFLNSSGIFT | NYWVYNDAPQ | KOIDFLSRVD  | PNLTGOTAEP | HOYNLQKTIQ | DIYIGVDVWG | 300 |
| RGSHGGGGFG | AYKAIEHADP | KGLGFSVALF  | AQGWTEWTEE | EKPGWNWAQF | WDYDSKLWVG | 360 |
| PPGVVEAPDH | TVKPGGYPCV | HGPFQPTISSF | FLTYPPPDPL | DLPEYTNFCP | GIGDAWFEVG | 420 |
| KEVFRSETGW | TDMDKQTTVG | DLVWPRPKIY  | DLPSQNASQA | TLNAAFNFND | AWNNGNSLQI | 480 |
| NLTVPGGATT | YGAYWPIQV  | FTFSSRRQYE  | ASIVYKPGLS | GKTRFDAKYE | VGIRTITGED | 540 |
| QGKIISNTTT | EVGNWRIQTH | ILFEIETPVE  | GGSIIVPSSI | GLVIAVSNVS | TTEQFEFFPL | 600 |
| VGQITIHPHL | PDRYKEFKPA | LLWLLFTPSA  | GTNSLDGTLT | WDVVAAIERP | PPVEINNPDD | 660 |
| AQIPWNLQPT | KQEWFPDFLY | FNVYVLELLD  | GGGQGPPOWT | GTTGYDGEKK | RFFIYDESLP | 720 |
| PTSGLRRFTF | QIEGVLETGE | STHWYDAPAA  | PSATAGGEQK | RTRRTSLKSV | LSPLRRKKSK | 780 |
| GDISVAK    |            |             |            |            |            | 787 |

Sequence 53: "Endo-Om WT"

| Length | Molecule Type | Organism       | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|----------------|--------------------------------|------------------|
| 772    | AA            | Ogataea minuta | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers         |
|-------------|------------------|--------------------|
| source      | 1..772           | mol_type = protein |

| Feature Key | Feature Location | Qualifiers                       |
|-------------|------------------|----------------------------------|
|             |                  | organism = <i>Ogataea minuta</i> |

### Residues

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| MAQSOLLGGA | VRPVFFDKLE | ELRRWHTOSA  | NLSRESELDS | LNVATEPFSS | YERAOTGSGS | 60  |
| RSSEPVPGDK | EDPPIKLMVC | HDFKGGYODY  | EDAQPLGYFP | HPTGSRYFLO | YPOLIDQFVY | 120 |
| FSHHRVTVP  | VNWINFCHRN | GIKCFGTVIF  | EGNASKDFEE | LDRLVSRDEK | GDFVFDAL   | 180 |
| KLAAHYGF   | YLLNIETTF  | NTKIAADLEP  | FAEQLKSLH  | CLDSKNELIW | YDSYVFPANK | 240 |
| VSYTNGVTES | NYNFFSLSDA | FFSNYWVWNIK | NLOENIKNVG | VLGVQKKIYV | GYDVWGRGTL | 300 |
| VGKGGFDSSL | ACKMIAKFKS | NVALFAPAWT  | YESLGPKDFN | ONDARFWIGL | FENESSISST | 360 |
| VPPHSSAVYK | INESSFIFYT | NFSSGEGNRF  | FSKGSEVYRK | NWVNGSLQFD | LPIDLHRKDK | 420 |
| NGLOWALDKS | DAFHGGACLE | IKYSEIKDEN  | GYQIFNNQMV | SDFTLFNFTK | ECHFTVNVK  | 480 |
| VTYKLNHKTK | STFKIKIKYI | IERRFRSVQT  | VRTGYLTIPL | LSTSGKWFTV | EESFQINLOT | 540 |
| SHEYIVLESA | HVTYDEDRSA | DSFFRSYIVE  | DSAITSVIDN | EEYEKLINSE | IYNDDDEDW  | 600 |
| ILVPSDVSIS | SSESQSNDSK | TOYLGRLKLF  | NKSTPKTRTL | EGTAPLLRIG | EFAIISANNY | 660 |
| PSSNFLAVTS | VKSIESRLE  | GDSLVLNMQ   | VGEGHQKGV  | YYIIYVNGAV | VGLSVAPKFI | 720 |
| YQDTELASEN | SASARSNYKK | SGLGSSSDRK  | SKVRVDSVDK | LGNVFTGSEV | WV         | 772 |

### Sequence 54: "Endo-Sd WT"

| Length | Molecule Type | Organism                          | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|-----------------------------------|--------------------------------|------------------|
| 1067   | AA            | <i>Streptococcus dysgalactiae</i> | No                             | No               |

### Features

| Feature Key | Feature Location | Qualifiers                                                         |
|-------------|------------------|--------------------------------------------------------------------|
| source      | 1..1067          | mol_type = protein<br>organism = <i>Streptococcus dysgalactiae</i> |

### Residues

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| MDKRLLVKRT  | LGCVCSATLM  | GTILGTHHDS | LISVKAEEKI | TOVSOTSTST | DDLHYLSENS | 60   |
| KKEFKEELSK  | EKVPEKVKEI  | LSKAQOANKQ | AQELAEMKVP | DKIPMKPLNG | PLYGGYFRTW | 120  |
| HDKTSDPLEK  | DKVNSMGELP  | KEVDLAFVFH | DWTKDYSLFW | KELATKHVPK | LNKQGTVRIR | 180  |
| TIPWRFLAGG  | DNSGIAEDAS  | KYPNTPEGNK | ALAKAIVDEY | VYKYNLDGLD | VDIEHDSIPK | 240  |
| VNGEASDENL  | KRSIDVFEET  | GKLIGPKGAD | KSRLFIMDST | YMADKNPLIE | RGAPYIDL   | 300  |
| VQVYGSQGEQ  | GEFONDTKSV  | TKTPEERWOG | YSKYIRPEQY | MIGFSFYEEK | AGSGNLWYDI | 360  |
| NARKDEDTAN  | GINDDITGTR  | AERYARWQPK | TGGVKGGFIS | YAIRDRGVAH | QPKQIAEKDK | 420  |
| QSVKNNRPLI  | SEITDNIFHS  | NYSVSKTLKT | VMLKDKAYDL | IDEKDFPDKA | LREAVMAQVG | 480  |
| TRKGDLERFN  | GTLRLDNPAI  | QSLEGLNKF  | KLAQLDLIGL | SRIIKLDQSV | LPANMKPGKD | 540  |
| PLETVLETYK  | KNGKEEPAII  | PPVSLTVSGL | TGLKELDL   | FDRETLAGID | AATLTSLEKV | 600  |
| DISDNKLDLA  | PKTENROI    | VMLSTVNNNA | GISEOSIKFD | NOKPAGNYP  | TYGATNLQLP | 660  |
| VRQEKIDLQH  | QLLFGTITNQ  | GTLINEADY  | KTYRNOKIAG | RNFVDPDYPY | NNFKVSHDNY | 720  |
| TVKVTDSITLG | TTTTDKMLATD | KEETYKVDF  | SPTDKTKAVH | TAKVIVGDEK | TMMVNLAEGA | 780  |
| TVIKSENDEN  | AOKVFN      | YNPLSFNNKS | SIIFEIKDPS | LAKYWRLFND | SSKDKKDYIK | 840  |
| EAKLEVFTGO  | LNAEADV     | LEKPDNVVTV | STYSGEEKVF | SHSLDNISAK | YWRVTVDNKK | 900  |
| DQYGYVSLPE  | LQILGYPLPN  | ADTIMKTVTV | AKELSQKDK  | FPOQLLDEST | AKEAVVEASL | 960  |
| NSKLFDTGVI  | NTNVEALKNV  | VDECLAYEKN | KETAFKATED | YRAAVNGVKA | ESVTVEEMAQ | 1020 |
| LKDLIGKAAH  | LNSKIDAKLA  | DREYDKDLLG | LIGELTNITR | TVKSFVK    |            | 1067 |

### Sequence 55: "Endo-Sz WT"

| Length | Molecule Type | Organism                  | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|---------------------------|--------------------------------|------------------|
| 1011   | AA            | <i>Streptococcus equi</i> | No                             | No               |

### Features

| Feature Key | Feature Location | Qualifiers                                                 |
|-------------|------------------|------------------------------------------------------------|
| source      | 1..1011          | mol_type = protein<br>organism = <i>Streptococcus equi</i> |

### Residues

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| MEKQVLVKKT | LKCVCAAALM | VAILAAQHDS | LIRVKAEDKL | VQTSPSVSAI | DALHYLSENS | 60 |
|------------|------------|------------|------------|------------|------------|----|

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| KKEFKEELSK | VEKAQPEKLK | EIVSKAQOAD  | KOAKTLAEMK | VPEKIPMKPL | KGPLYGGYFR | 120  |
| TWHDKTSDBA | EKDKVNSMGE | LPKEVDLAFV  | FHDWTKDYSL | FWQELATKHV | PTLNKQGTRV | 180  |
| IRTIPWRFLA | GGDHSGIAED | AQKYPNTPEG  | NKALAKAIVD | EYVYKYNLDG | LDVDIERDSI | 240  |
| PKVNKESKES | GIERSTQVFE | EIGKLIGPKG  | ADKSRLFIMD | STYMADKNPL | TERGAPYIDL | 300  |
| LLVQVYGTQG | EKGGFDNANH | KAVDTMEERW  | ESYSKYIRPE | QYMGVGSFYE | EKANSGNLWY | 360  |
| DVNVEDDTNP | NIGSEIKGTR | AERYAKWQPK  | TGGVKGGIFS | YGIDRDGVAH | PKKNGPKTPD | 420  |
| LDKIVKSDYK | VSKALKKVM  | NDKSYELIDQ  | KDFDPKALRE | AVIAQVGSRR | GNLERFNGTL | 480  |
| RLDNPDIKSL | EGLNKLKKLA | KLELIGLSQI  | TKLDSSVLPE | NIKPTKDTLV | SVLETYKNDD | 540  |
| RKEEAKAIPQ | VALTISGLTG | LKELNLAGFD  | RDSLAGIDAA | SLTSLEKVDL | SSNKLDLAAG | 600  |
| TENRQILDTM | LATVTKHGGV | SEKTFVFDHQ  | KPTGLYPDTY | GTKSLQLPVA | NDTIDLQAKL | 660  |
| LFGTVTNOGT | LINSEADYKA | YQEQEIAGHR  | FVDSSYDYKA | FAVTYKDYKI | KVTDSTLGV  | 720  |
| DHKDLSTSKE | ETVKVEFFSP | INSTKPVHEA  | KIVVGEEKTM | MVNLAEGATI | IGGDADPTNA | 780  |
| KKVFDGLLNN | DTTTLSTSNK | ASIIIFELKEP | GLVKHWRFFN | DSKISKADYI | KEAKLEAFVG | 840  |
| HLEDSSKVKD | SLEKSTEWVT | VSDYSGEAQE  | FSQPLNNIGA | KYWRITIDNK | KSQYGYVSLP | 900  |
| ELQIIGHRLP | EAATVMTTMA | AAEELSQQKD  | KFSQEQLKEL | EVKVAALKAA | LDNKMFNADT | 960  |
| INASFADVKA | YIDKLLADAA | GKKTLLGKATK | EAQPVATDAK | EKAESENPKA | D          | 1011 |

Sequence 56: "Endo-Se WT"

| Length | Molecule Type | Organism           | Contains DNA and RNA fragments | Skipped Sequence |
|--------|---------------|--------------------|--------------------------------|------------------|
| 1018   | AA            | Streptococcus equi | No                             | No               |

Features

| Feature Key | Feature Location | Qualifiers                                          |
|-------------|------------------|-----------------------------------------------------|
| source      | 1..1018          | mol_type = protein<br>organism = Streptococcus equi |

Residues

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| MEKQVLVKKT | LKCVCAAAALM | VAILAAQHDS | LIRVKAEDKV | VOTSPSVSAI | DDLHYLSENS  | 60   |
| KKEFKEGLSK | AGEVPEKLKD  | ILSKAQOADK | OAKVLAEMKV | PEKIAMKPLK | GPLYGGYFRT  | 120  |
| WHDKTSDBAE | KDKVNSMGEL  | PKEVDLAFVF | HDWTKDYSFF | WQELATKHVP | TLNKQGTRVI  | 180  |
| RTIPWRFLAG | GGDHSGIAEDT | QKYPNTPEGN | KALAKAIVDE | YVYKYNLDGL | DVDIERDSIP  | 240  |
| KVNGKESNEN | IORSIAVFEE  | IGKLIGPKGA | DKSRLFIMDS | TYMADKNPLI | ERGAQYIDLL  | 300  |
| LVQVYGTQGE | KGDWDPVARK  | PEKTMEERWE | SYSKYIRPEQ | YMGVGSFYEE | NAGSGNLWYD  | 360  |
| INERKDDHNP | LNSEIAGTRA  | ERYAKWQPKT | GGVKGGIFS  | AIDRDGVAHQ | PKKVSDDDEKR | 420  |
| TNKAIKDITD | GIVKSDYKVS  | KALKKVMEND | KSYELIDOKD | FDPKALREAV | IAQVGSRRGD  | 480  |
| LERFNGTLRL | DNPDIKSLEG  | LNKLKKLAKL | ELIGLSQITK | LDSLVLPA   | NKPTKDTLANV | 540  |
| LEAYDSAKKE | ETKAIPOVAL  | TISGLTGLKE | LNLAGFDRDS | LAGIDAASLT | SLEKVDLSSN  | 600  |
| KLDLAAGTEN | ROILDMTLAT  | VTKHGGVSEK | TFVFDHQKPT | GLYPDTYGTG | SLQLPVANDT  | 660  |
| IDLOAKLLFG | TVTNOGTLIN  | SEADYKAYOE | QEIAGHRFVD | SSYDYKAFV  | TYKDYKIKVT  | 720  |
| DSTLGVTDHK | DLSTSKEETY  | KVEFFSPTNS | TKPVHEAKVV | VGAETMMVN  | LAEGATVIGG  | 780  |
| DADPTNAKKV | FDGLLNNDTT  | ILSTSNKASI | IFELKEPGLV | KYWRFFNDSK | TSKADCIEKA  | 840  |
| KLEAFVGHLE | AGSKVKDSLE  | KSSKWTVSD  | YSGEDQEF   | PLNNIGAKYW | RITVDTKGGR  | 900  |
| YNWPSLPELO | TIGYQLPAAD  | LVMAMLATAE | ELSQQKDKFS | QEQKLELEVK | IAALKAALDS  | 960  |
| KMFNADAINA | STADLKAYVD  | KLLADRTDQE | KVARAAKVEQ | PVATDIKENT | EPENPKTD    | 1018 |