Figure1A

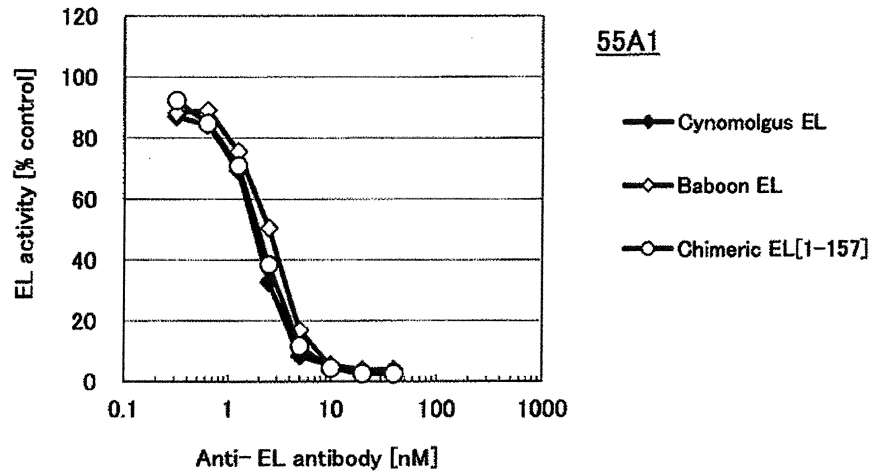


Figure1B

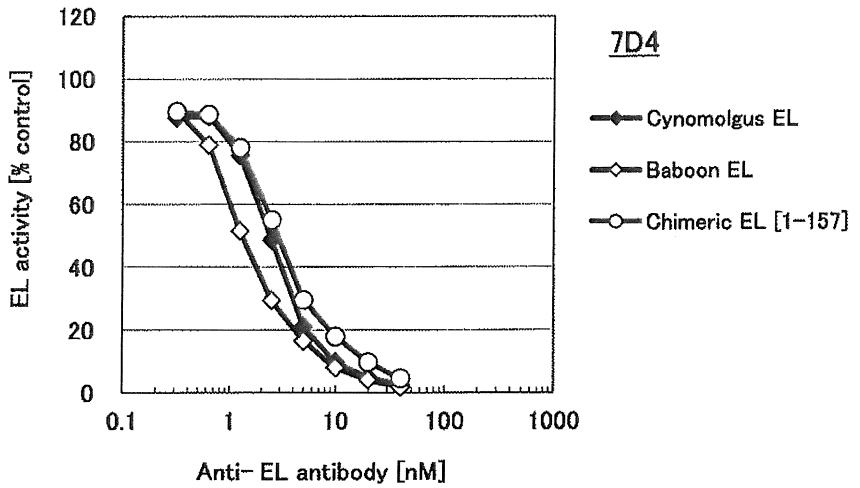


Figure1C

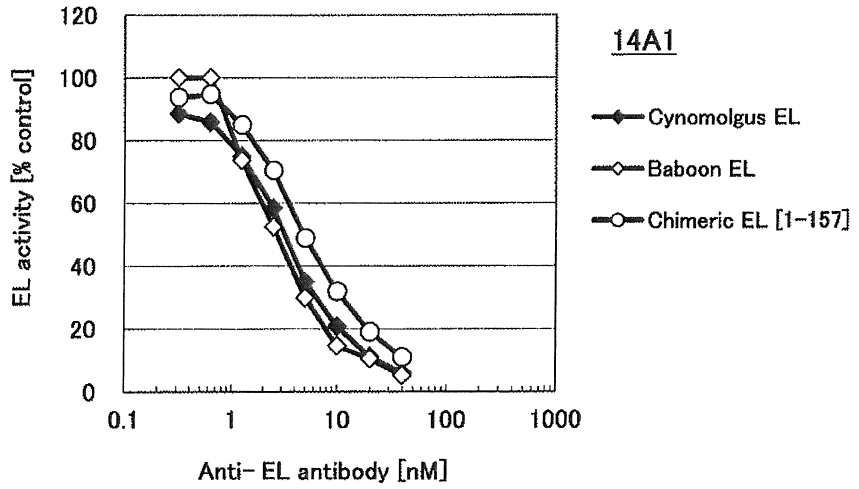


Figure1D

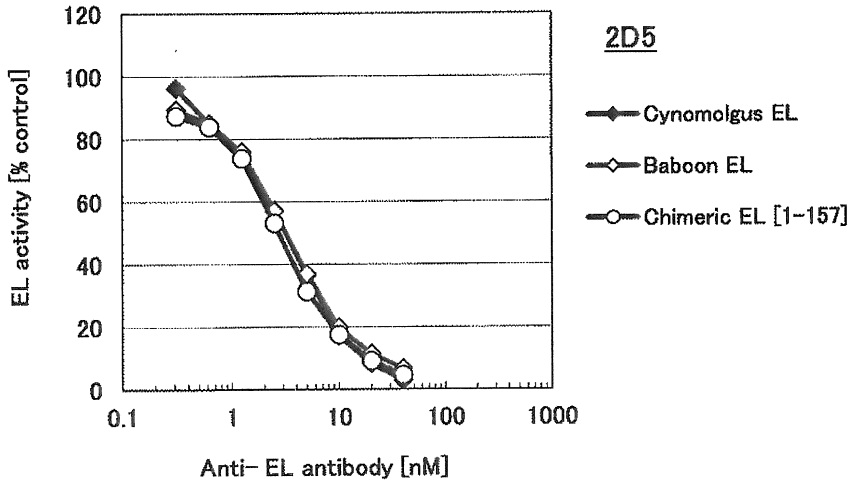


Figure1E

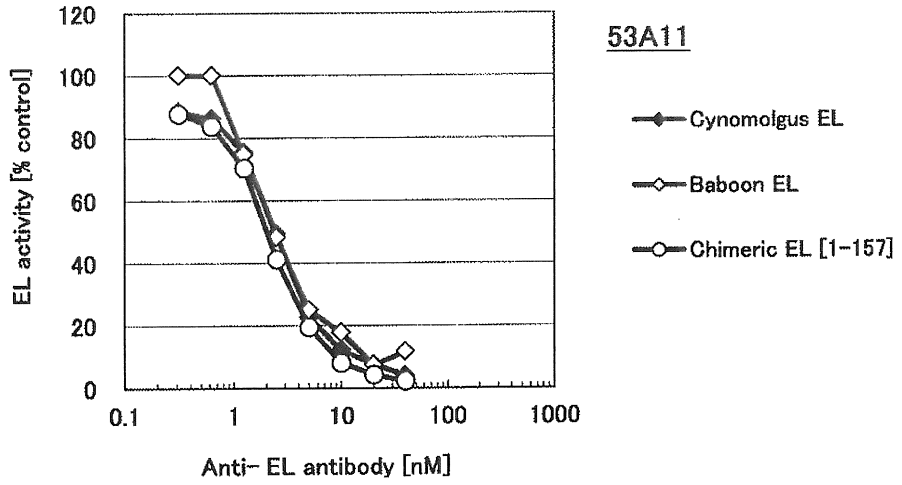


Figure1F

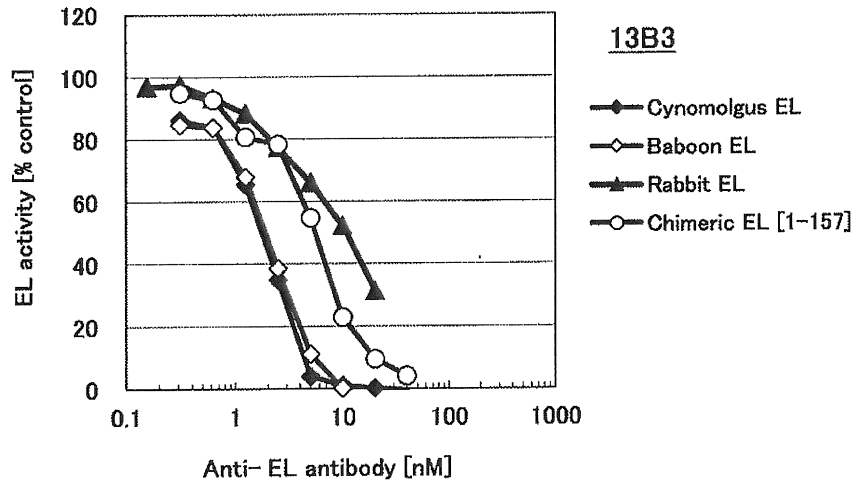


Figure1G

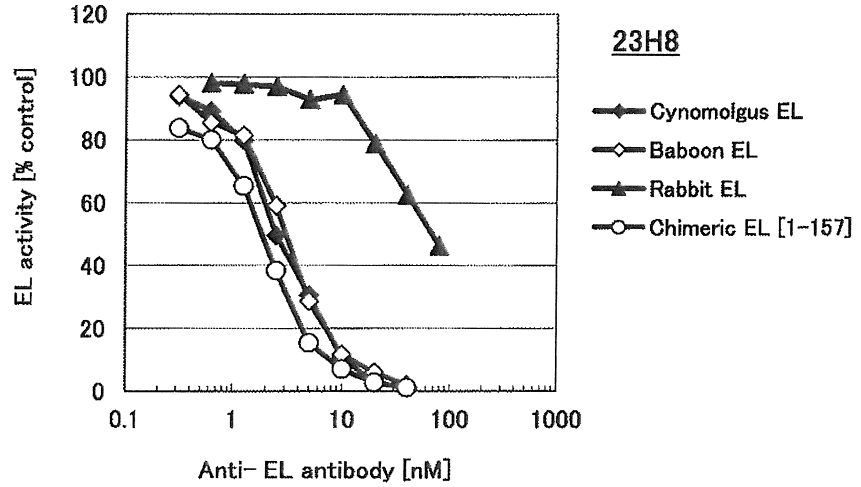


Figure1H

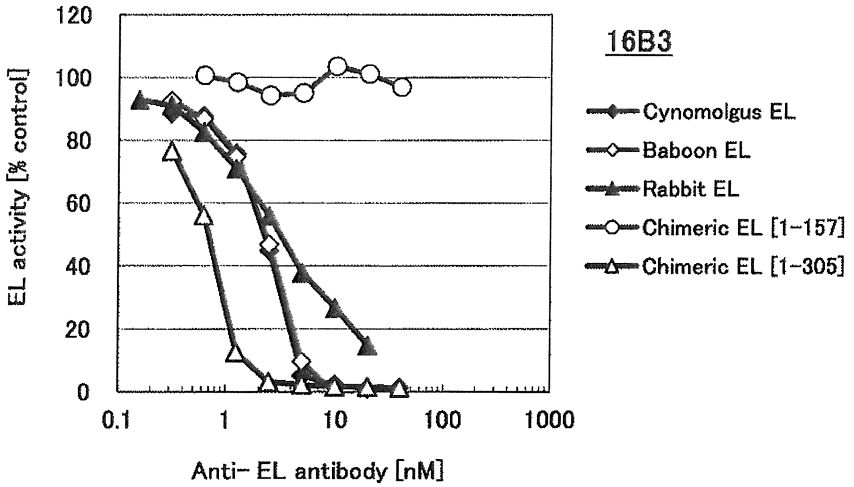


Figure1I

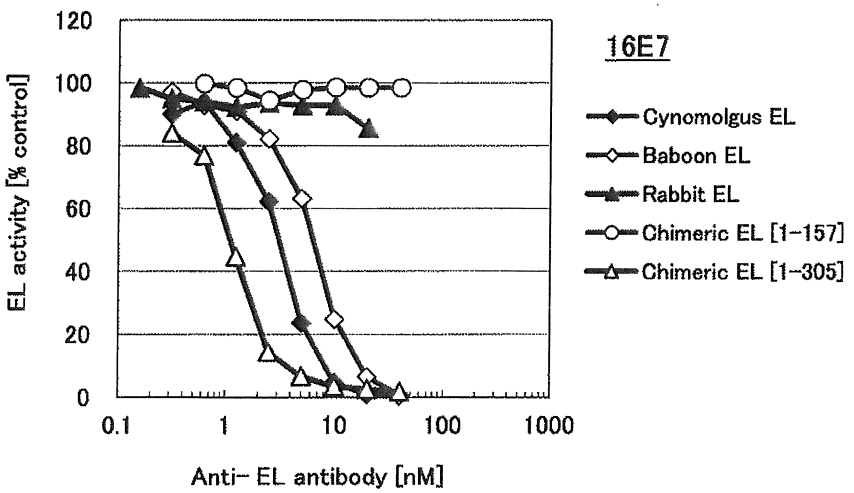


Figure1J

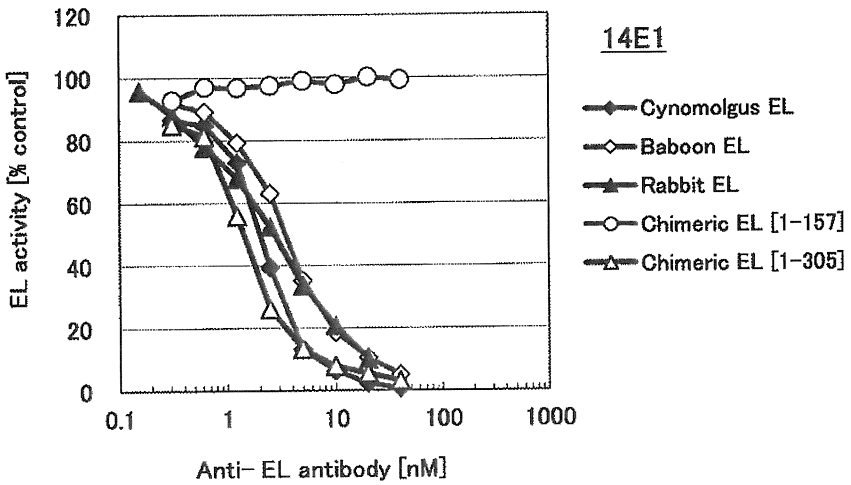


Figure1K

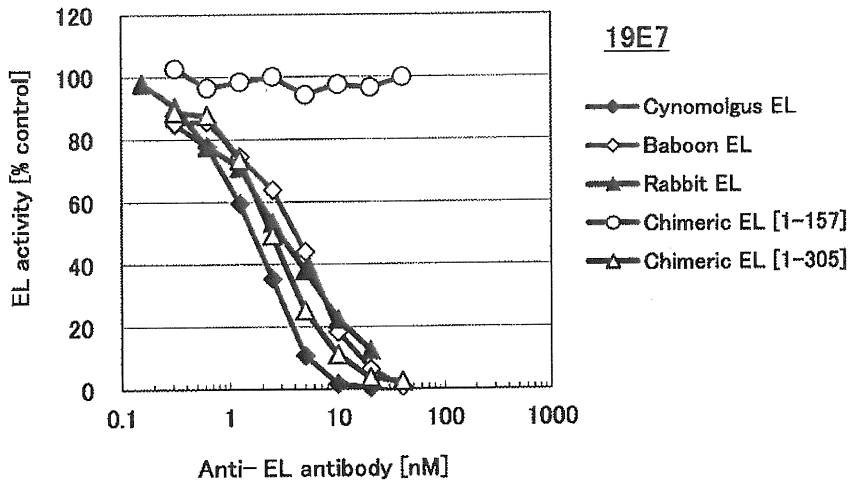


Figure2A

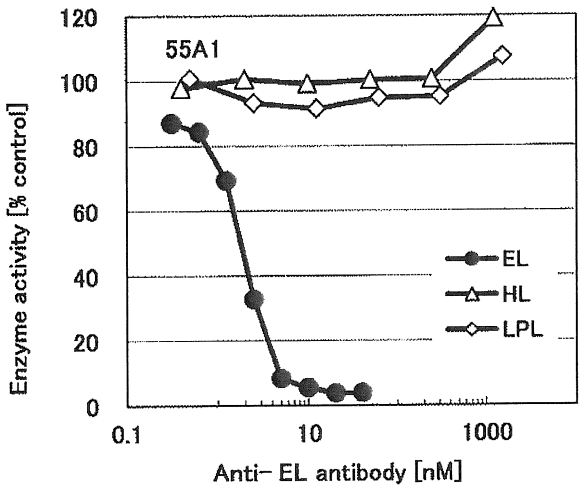


Figure2B

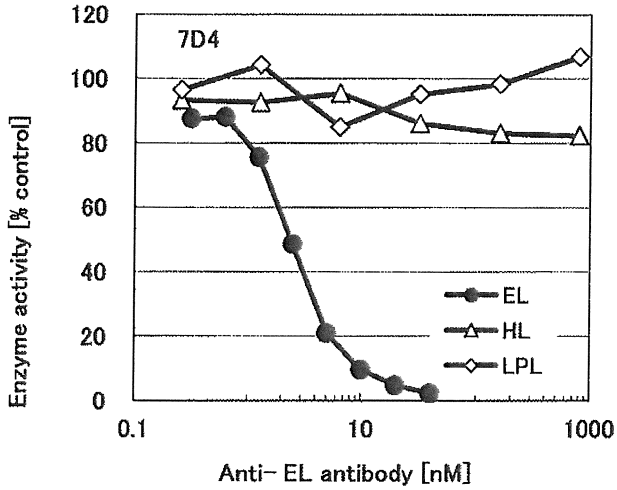


Figure2C

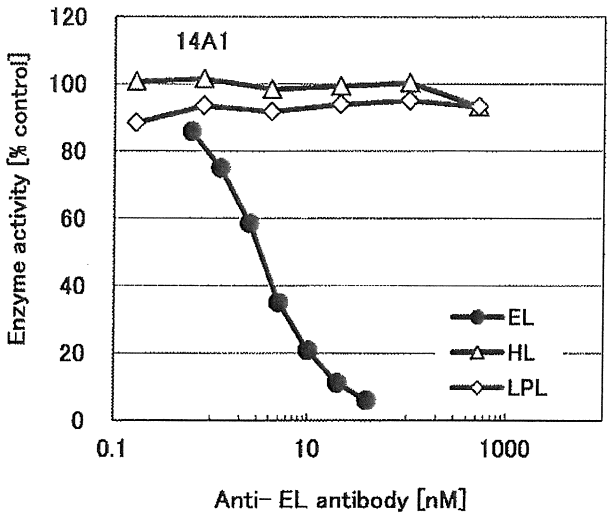


Figure2D

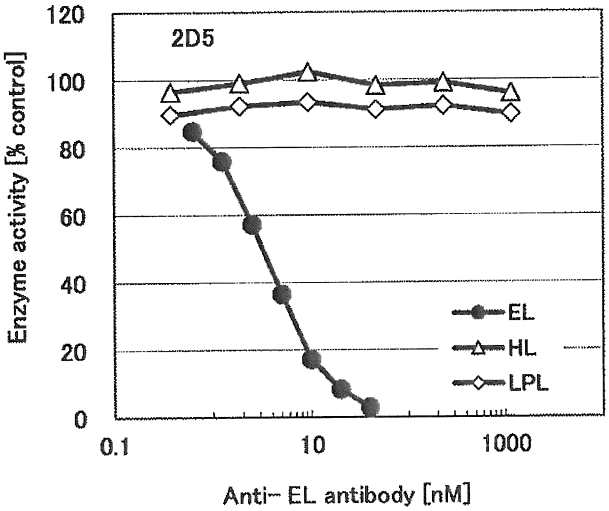


Figure2E

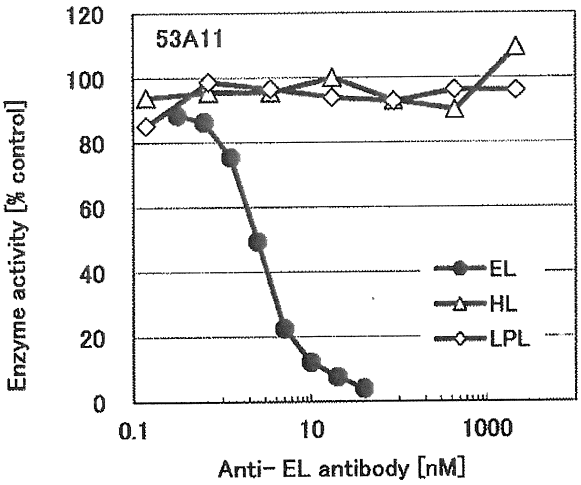


Figure2F

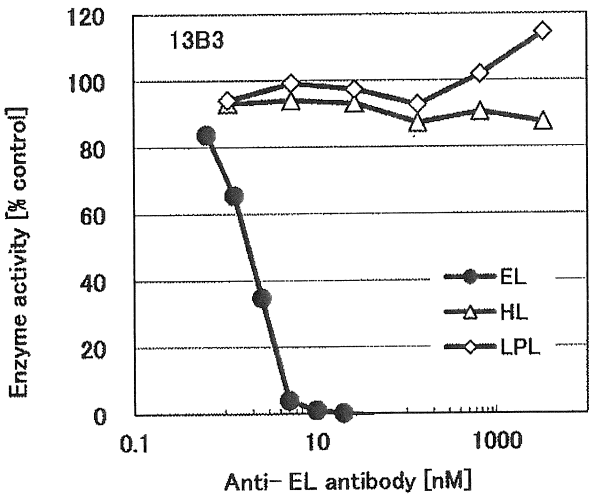


Figure2G

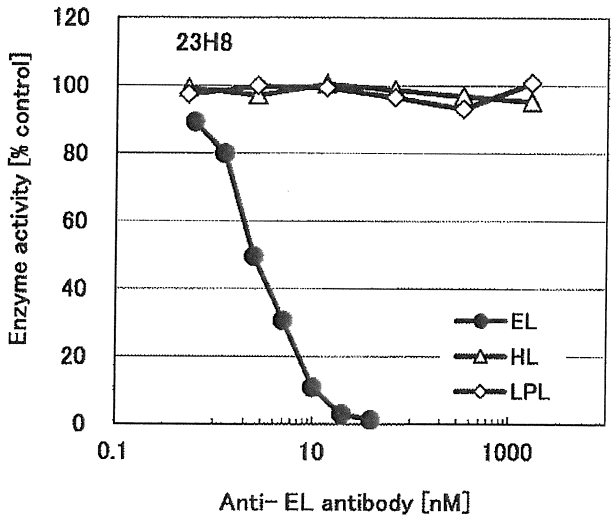


Figure2H

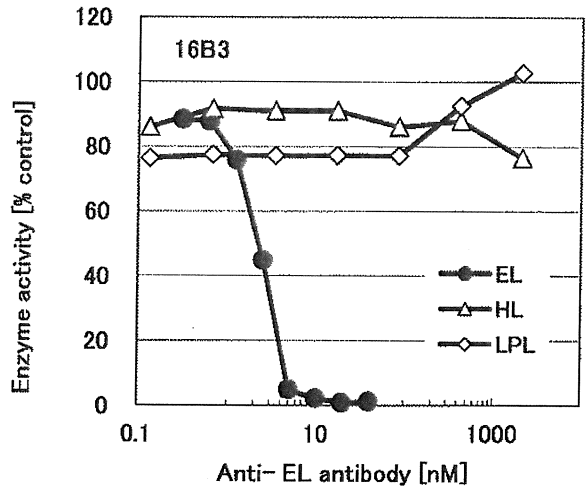


Figure2I

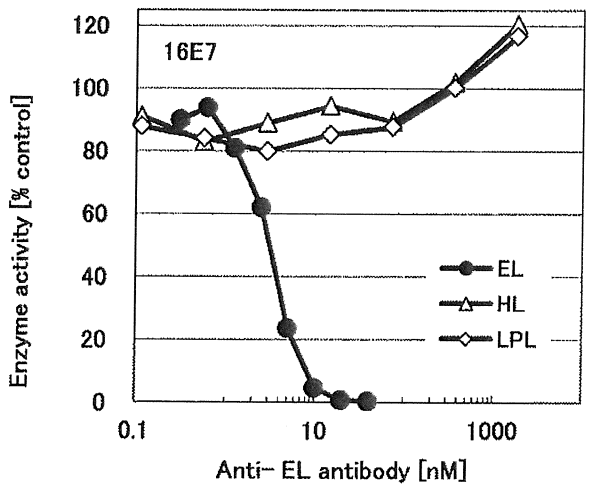


Figure2J

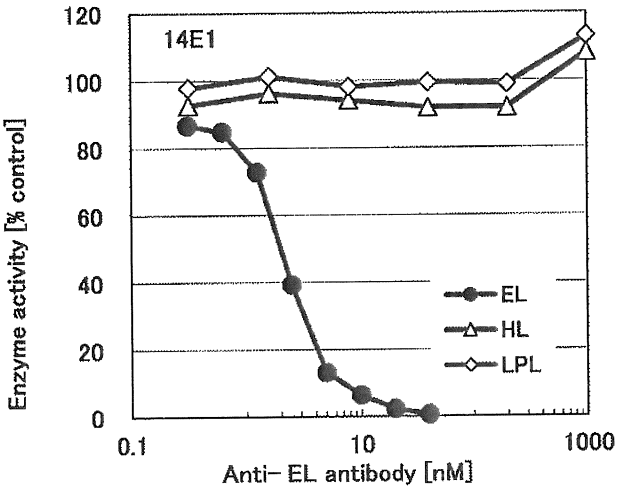


Figure2K

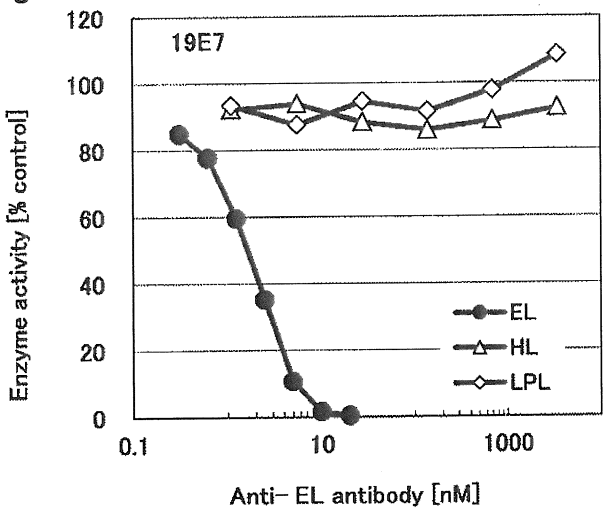


Figure2L

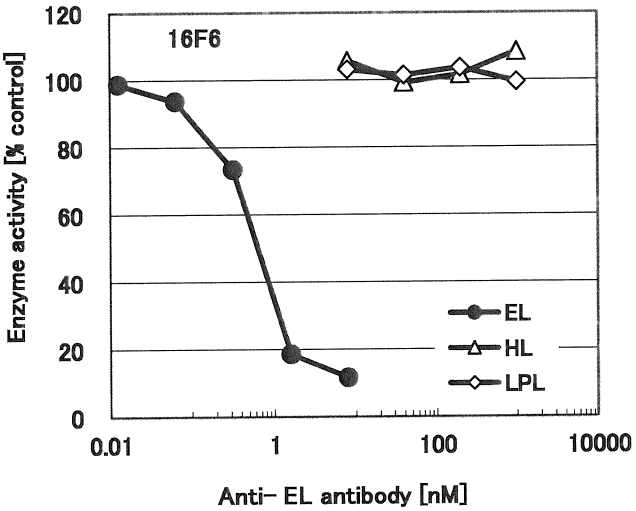


Figure3A

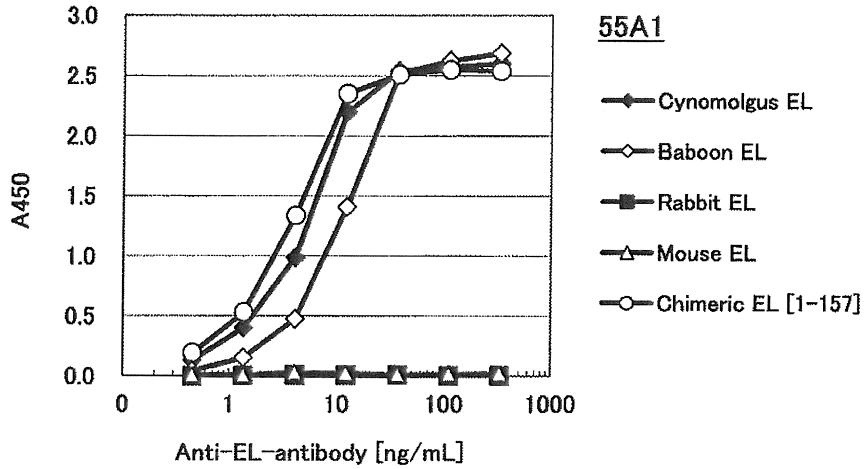


Figure3B

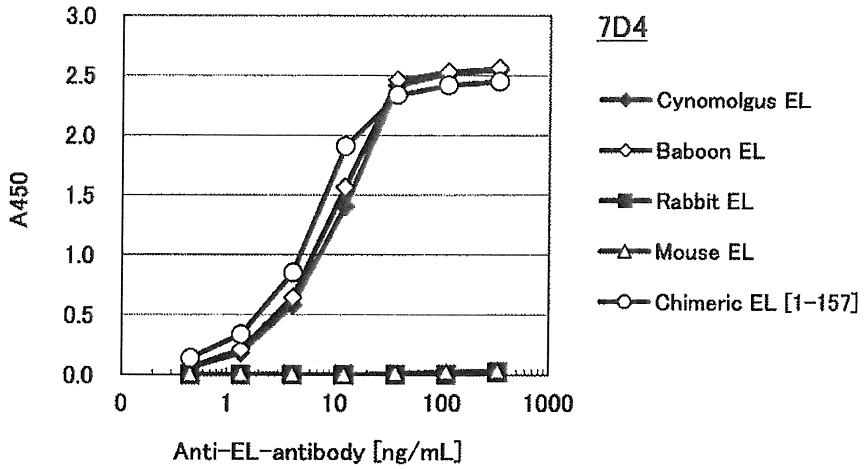


Figure3C

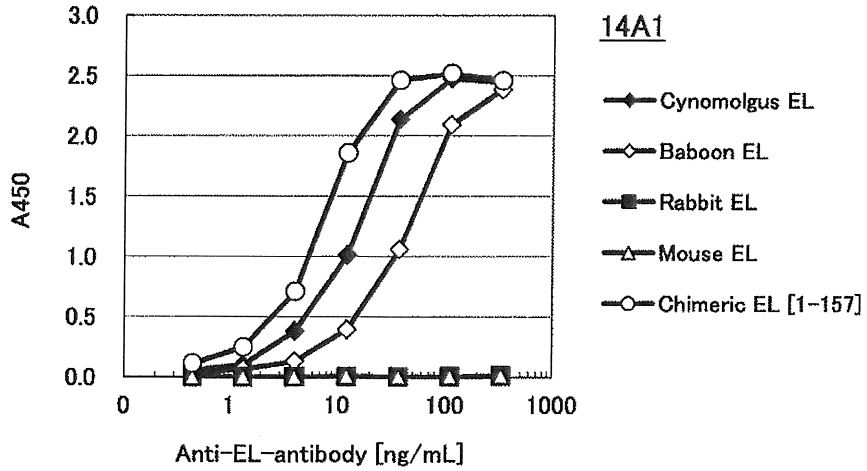


Figure3D

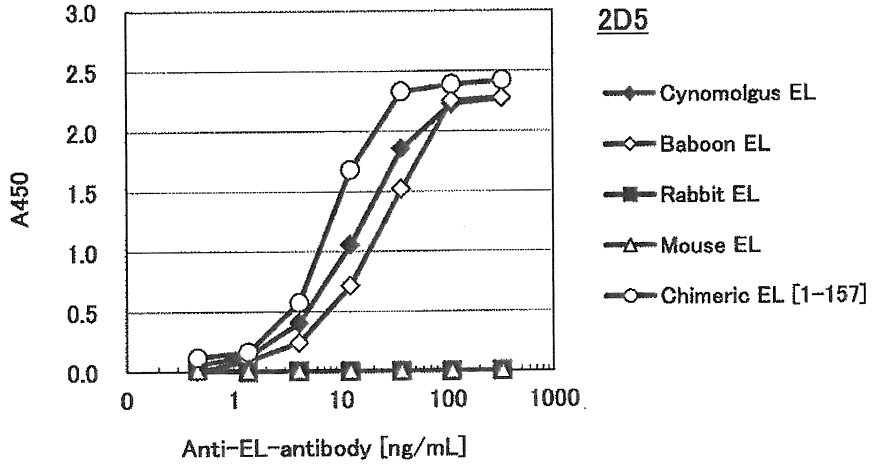


Figure3E

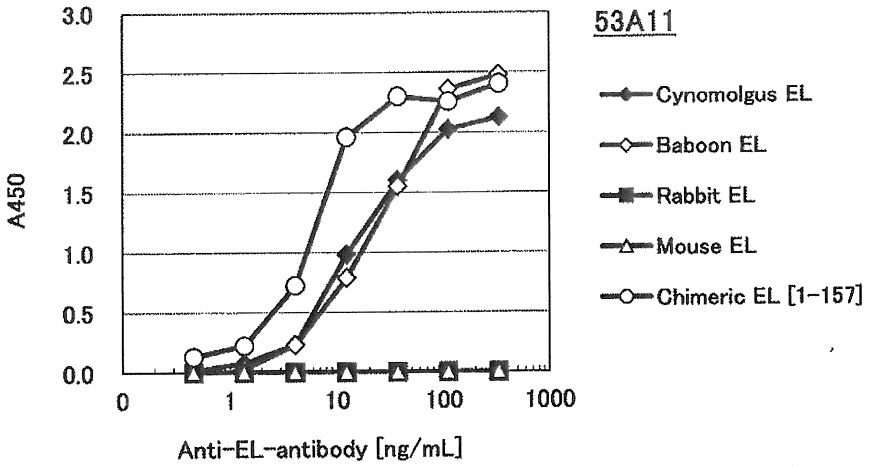


Figure3F

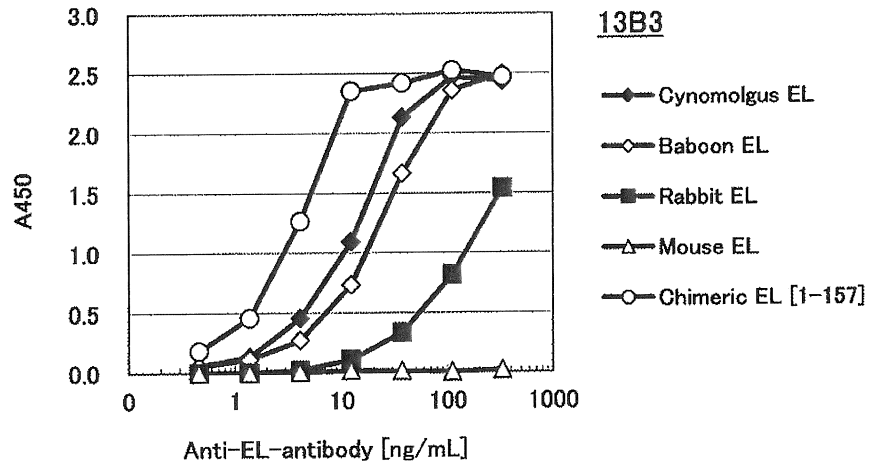


Figure3G

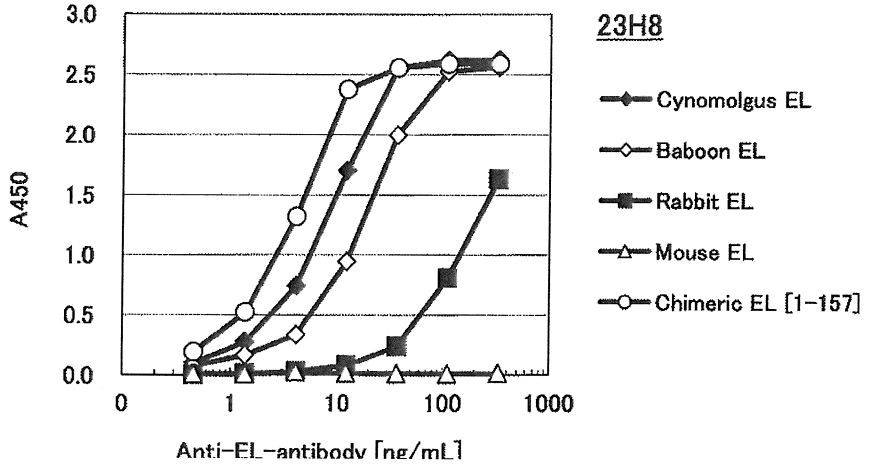


Figure3H

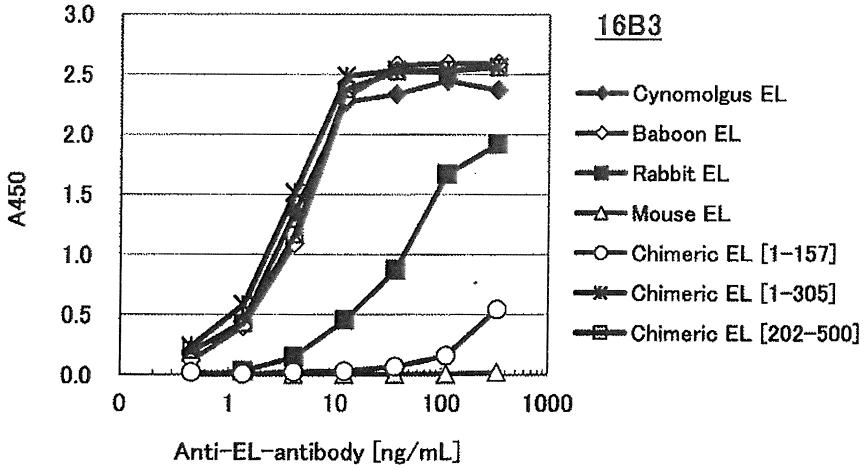


Figure3I

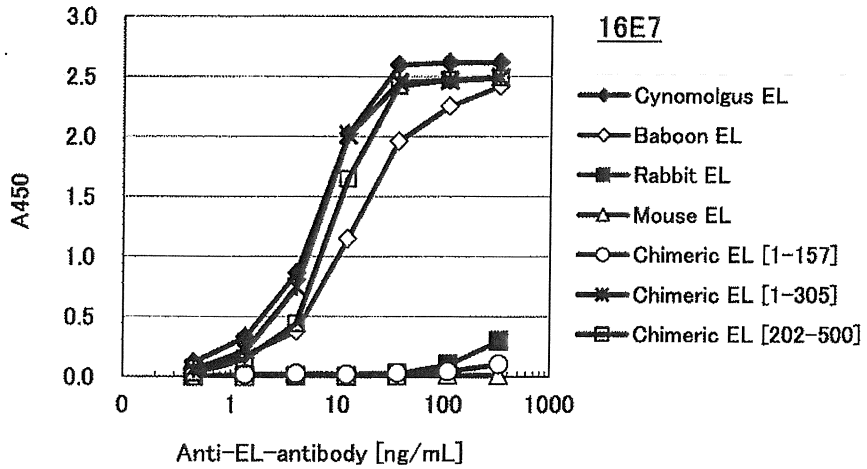


Figure3J

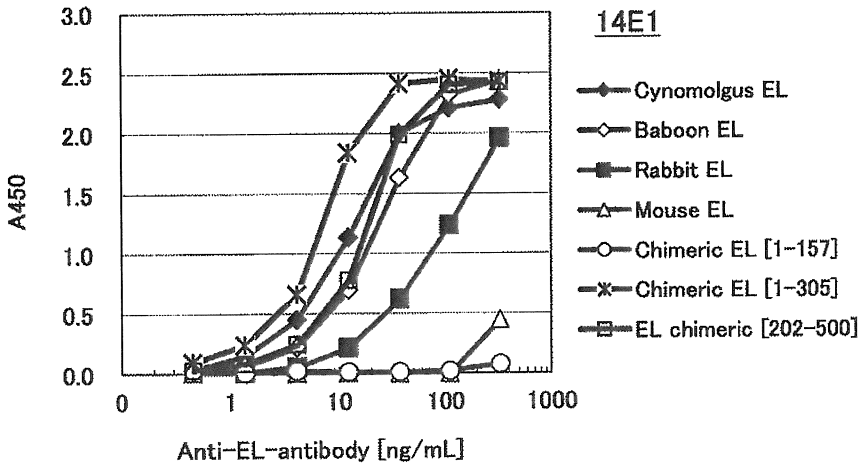


Figure3K

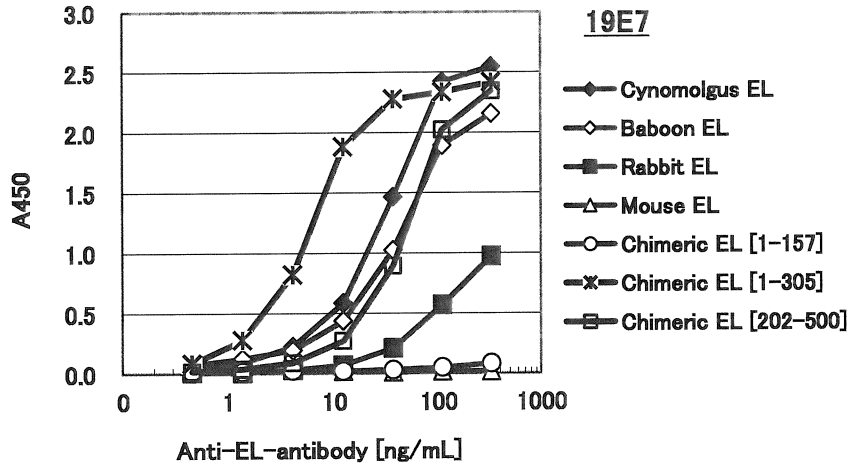


Figure3L

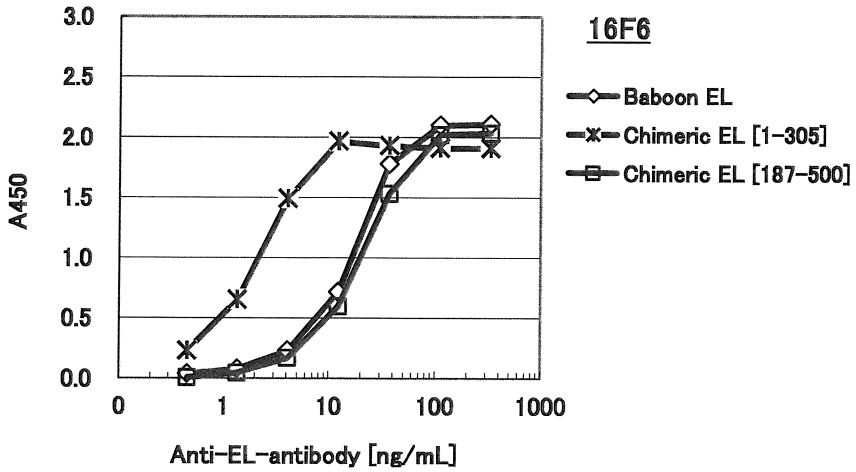


Figure4A

Heavy chain of 55A1

CDR1 CDR2

QIHLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYSGVPTYAGDF

KGRFAFSLETSASTAYLQINNLKNEDTATYFCARRGYYGRRYFDVWGTGTTVTVSS

CDR3

Light chain of 55A1

CDR1 CDR2

DIVLTQSPASLAVSLGQRATISCKASQSVDYDVDSYMHWYQQKPGQPPKLLIYAASNLASGI

PARFSGGGSGTDFTLNIHPVEEEDVATYYCQQTIEDPPTFGGGTKLEIK

CDR3

Figure4B

Heavy chain of 7D4

CDR1 CDR2

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKDLKWMGWINTYSGVPTYADDF

KGRFAFSLETSASTAYLQINNLKNEDTATYFCARFSYYGRHYFDYWGQGTTLTVSS

CDR3

Light chain of 7D4

CDR1 CDR2

DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPQLLIYAASNLGSGI

PARFSGSGSGTDFTLNIHPVEEEDAATYYCHQSTDDPPWTFGGGTKLEIK

CDR3

Figure4C

Heavy chain of 14A1

CDR1 CDR2

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYSGVPTYADDF
KGRFAFSLETSASTAYLQINNFKNEDTATYFCARFSYYGRHYFDYWGQGTALTASS

CDR3

Light chain of 14A1

CDR1 CDR2

DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLKSGI
PARFSGSGSGTDFTLNIHPVEEEDAATYYCQQTTDDPPWTFGGGTKLEIK

CDR3

Figure4D

Heavy chain of 2D5

CDR1 CDR2

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYSGVPTYTDDF
KGRFAFSLETSASTAFLQINNLKNEDTATYFCARFSYYGRHYFDYWGQGTTLTVSS

CDR3

Light chain of 2D5

CDR1 CDR2

DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMHWYQQKPGQPPKLLIYAASNLESGI
PARFSGSGSGTDFTLNIHPVEEEDAATYYCQQTNDDPPWTFGGGTKLEIK

CDR3

Figure4E

Heavy chain of 53A11

CDR1 CDR2

EVQLQQSGPELLKPGASVKISCKASGYTFTDYTMHWVKQSHGKSLEWIGGINPYYGGTTYNEKF
KDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAKGDYYGGSYNYWGQGTTLTVSS

CDR3

Light chain of 53A11

CDR1 CDR2

DIVLTQSLATLSVTPGDSVSLSCRASQDISNSLHWYQQKSHESPRLLIKYASQSISGIPSRF
SGSGSGTDFTLSINSVETEDFGMYFCQQSNSWPYTFGGGTKLEIK

CDR3

Figure4F

Heavy chain of 13B3

CDR1 CDR2

EVQLQQSGPELLKPGASVKISCKASGYTFTEYTMHWVKQSHGKSLEWIGSINPYYGGTSYNEKF
KDKATLTVDKSSNTAYMEFRSLTSEDCAVYYCARYGNYVGYFDYWGQGTTLTVSS

CDR3

Light chain of 13B3

CDR1 CDR2

ENVLTQSPAIMSASLGEKVTMSCRASSSVHYMYWYQQKSDASPKLWIYYTSNLAPGVPDRFS
GSGSGNSYSLTISSMEGEDAATYYCQQFTSSPYTFGGGTKLEIK

CDR3

Figure4G

Heavy chain of 23H8

CDR1 CDR2

EVQLQQSGPELLKPGASVKISCKASGYTFTDNTIHWVKQSHGKSLEWIGHINPYYGGTNNNEKF
KDKATLTVDKSSSTAYMELRSLTSEDSAIYYCARKGIYYSSPFDYWGQGTTLTVSS

CDR3

Light chain of 23H8

CDR1 CDR2

DIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGTVKLLISYTSKLHSGVPS

RFSGSGSGTDYSLTISNLEREDFATYFCQQGNTLPFTFGSGTNLEIK

CDR3

Figure4H

Heavy chain of 16B3

CDR1 CDR2

DVKLVESGGGLVQPGGSLKLSCTASGFTFSGYTMSWVRQTPEKRLELVAEISFARDRAFYPDTV
KGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRLGGRNHDYWYFDVWGTGTTVTVSS

CDR3

Light chain of 16B3

CDR1 CDR2

DIVLTQSPTSLAVSPGQRATISCRASESVEYYGTSLMQWYQQKPGQRPQLLIYAASNVESGV
PARFSGSGSGTDFSLNIHPVEEDDIAVYFCQQSWKVPFTFGSGTKLEIK

CDR3

Figure4I

Heavy chain of 16E7

CDR1 CDR2

EVKLVESGGGLVQPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLELVAEISFTRSRAFYPDTV
KGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARLGGNNYDYWYFDVWGTGTTVTVSS

CDR3

Light chain of 16E7

CDR1 CDR2

DIVLTQSPTSLAVSLGQRATISCRASESVEYYGTSLMQWYQQKPGQRPKLLIYAASNVESGV
PARFSGSGSGTDFSLNIHPVEEDDIAMYFCQQSWKVPFTFGSGTKLEIK

CDR3

Figure4J

Heavy chain of 14E1

CDR1 CDR2

QVQLQQSGAELVKPGASVRLSCKASGYTFTKYTIHWVKQRSGQGLEWIGWFYPGSDSIKYNEKF
KDKATLTADKSSRTVYMELSRLTSEDSAVYFCARHEEYTNSLAYWGQGTLVTVSA

CDR3

Light chain of 14E1

CDR1 CDR2

DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQQPDGTVKLLIYYTSRLHSGVPSRF
SGSGSGTDYSLTISNLEQEDIATYFCQQGYTLPWTFGGGTNLEIK

CDR3

Figure4K

Heavy chain of 19E7

CDR1 CDR2

QVQLQQPGSVLVRPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIHPYSGNNNNNEKF
KGKATLTVDTSSSTAYVDLSRLTSEDSAVYYCARYDSNYVFAYWGQGTLVTVSA

CDR3

Light chain of 19E7

CDR1 CDR2

QIVLTQSPAIMSASPGEGVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFS
GSGSGTSYSLTISRMEAEDAATYYCQQRDSYLTFGSGTKLEVK

CDR3

Figure4L

Heavy chain of 16F6

CDR1 CDR2

QVQLQQSGAELMKPGASVKISCKATGYTFSTYWIAWVKQRPGHGLEWIGEILPGSAKTKYNKKF
KGKATFTADTSSNTAYMQLSSLTSEDSAVYYCAVYDYGADYWGQGTSVTVSS

CDR3

Light chain of 16F6

CDR1 CDR2

DIVMTQSHKFMSTSVGDRVSITCKASQDVYTAVAWYQQKPGQSPKLLIYSASYRFTGVPDRF
TGSGAGTEFTFTINSVQAEDLAVYYCQQHYSIPRTFGGGTKLEIK

CDR3

Figure5A

```
55A1    1:QIHLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYSGVPTY 60
7D4     1:QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKDLKWMGWINTYSGVPTY 60
14A1    1:QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYSGVPTY 60
2D5     1:QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYSGVPTY 60

55A1   61:AGDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARRGYYGRRYFDVWGTGTTVTVSS 120
7D4    61:ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARFSYYGRHYFDYWGQGTTLTVSS 120
14A1   61:ADDFKGRFAFSLETSASTAYLQINNFKNEDTATYFCARFSYYGRHYFDYWGQGTALTASS 120
2D5    61:TDDFKGRFAFSLETSASTAFLQINNLKNEDTATYFCARFSYYGRHYFDYWGQGTTLTVSS 120
```

Figure5B

```
55A1    1:DIVLTQSPASLAVSLGQRATISCKASQSVDYDVDSYMHWYQQKPGQPPKLLIYAASNLAS 60
7D4     1:DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPQLLIYAASNLGS 60
14A1    1:DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLKS 60
2D5     1:DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMHWYQQKPGQPPKLLIYAASNLES 60

55A1   61:GIPARFSGGGSGTDFTLNIHPVEEEDVATYYCQQTIEDPP-TFGGGTKLEIK        111
7D4    61:GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCHQSTDDPPWTFGGGTKLEIK        112
14A1   61:GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQTTDDPPWTFGGGTKLEIK        112
2D5    61:GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQTNDDPPWTFGGGTKLEIK        112
```

Figure5C

```
53A11    1:EVQLQQSGPELLKPGASVKISCKASGYTFTDYTMHWVKQSHGKSLEWIGGINPYYGGTTY 60
13B3     1:EVQLQQSGPELLKPGASVKISCKASGYTFTEYTMHWVKQSHGKSLEWIGSINPYYGGTSY 60
23H8     1:EVQLQQSGPELLKPGASVKISCKASGYTFTDNTIHWVKQSHGKSLEWIGHINPYYGGTNN 60

53A11   61:NEKFKDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAKGD-YYGGSYNYWGQGTTLTVSS 119
13B3    61:NEKFKDKATLTVDKSSNTAYMEFRSLTSEDCAVYYCARYG-NYVGYFDYWGQGTTLTVSS 119
23H8    61:NEKFKDKATLTVDKSSSTAYMELRSLTSEDSAIYYCARKGIYYSSPFDYWGQGTTLTVSS 120
```

Figure5D

```
53A11    1:DIVLTQSLATLSVTPGDSVSLSCRASQDISNSLHWYQQKSHESPRLLIKYASQSISGIPS 60
13B3     1:ENVLTQSPAIMSASLGEKVTMSCRASSSV-HYMYWYQQKSDASPKLWIYYTSNLAPGVPD 59
23H8     1:DIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGTVKLLISYTSKLHSGVPS 60

53A11   61:RFSGSGSGTDFTLSINSVETEDFGMYFCQQSNSWPYTFGGGTKLEIK              107
13B3    60:RFSGSGSGNSYSLTISSMEGEDAATYYCQQFTSSPYTFGGGTKLEIK              106
23H8    61:RFSGSGSGTDYSLTISNLEREDFATYFCQQGNTLPFTFGSGTNLEIK              107
```

Figure6A

```
16B3     1:DVKLVESGGGLVQPGGSLKLSCTASGFTFSGYTMSWVRQTPEKRLELVAEISFARDRAFY 60
16E7     1:EVKLVESGGGLVQPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLELVAEISFTRSRAFY 60

16B3    61:PDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRLGGRNHDYWYFDVWGTGTTVTV 120
16E7    61:PDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARLGGNNYDYWYFDVWGTGTTVTV 120

16B3   121:SS                                                          122
16E7   121:SS                                                          122
```

Figure6B

```
16B3    1:DIVLTQSPTSLAVSPGQRATISCRASESVEYYGTSLMQWYQQKPGQRPQLLIYAASNVES 60
16E7    1:DIVLTQSPTSLAVSLGQRATISCRASESVEYYGTSLMQWYQQKPGQRPKLLIYAASNVES 60

16B3   61:GVPARFSGSGSGTDFSLNIHPVEEDDIAVYFCQQSWKVPFTFGSGTKLEIK         111
16E7   61:GVPARFSGSGSGTDFSLNIHPVEEDDIAMYFCQQSWKVPFTFGSGTKLEIK         111
```

Figure6C

```
14E1    1:QVQLQQSGAELVKPGASVRLSCKASGYTFTKYTIHWVKQRSGQGLEWIGWFYPGSDSIKY 60
19E7    1:QVQLQQPGSVLVRPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIHPYSGNNNN 60

14E1   61:NEKFKDKATLTADKSSRTVYMELSRLTSEDSAVYFCARHEEYTNSLAYWGQGTLVTVSA 119
19E7   61:NEKFKGKATLTVDTSSSTAYVDLSRLTSEDSAVYYCARYDS-NYVFAYWGQGTLVTVSA 118
```

Figure6D

```
14E1    1:DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQQPDGTVKLLIYYTSRLHSGVPS 60
19E7    1:QIVLTQSPAIMSASPGEGVTITCSASSSVS-YMHWFQQKPGTSPKLWIYSTSNLASGVPA 59

14E1   61:RFSGSGSGTDYSLTISNLEQEDIATYFCQQGYTLPWTFGGGTNLEIK             107
19E7   60:RFSGSGSGTSYSLTISRMEAEDAATYYCQQRDSY-LTFGSGTKLEVK             105
```

Figure7A

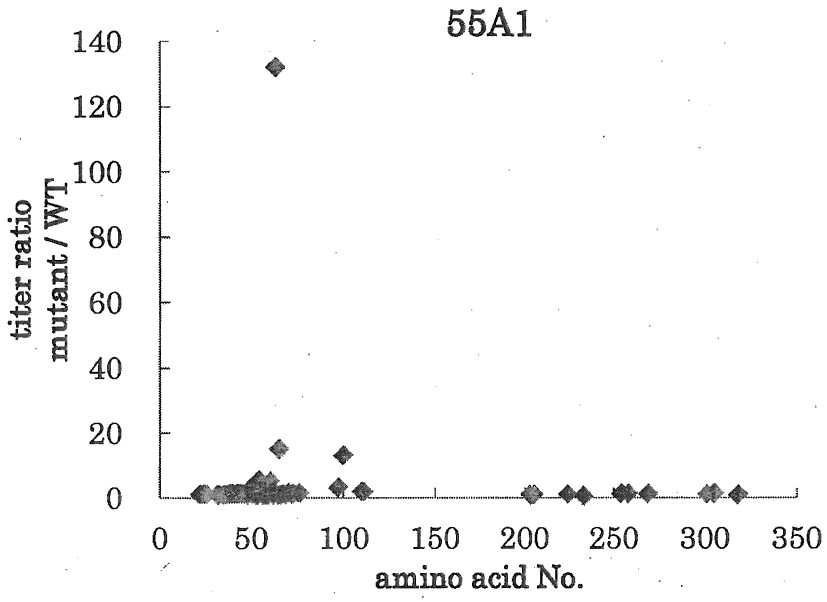

55A1
140
120
100
80
60
40
20
0
titer ratio
mutant / WT
0
50
100
150
200
250
300
350
amino acid No.

Figure7B

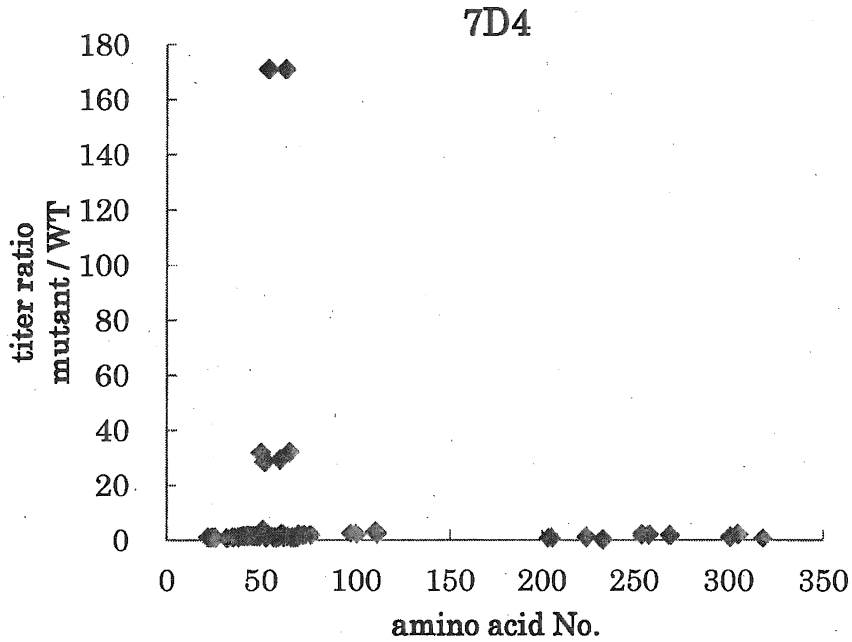

7D4
180
160
140
120
100
80
60
40
20
0
titer ratio
mutant / WT
0
50
100
150
200
250
300
350
amino acid No.

Figure7C

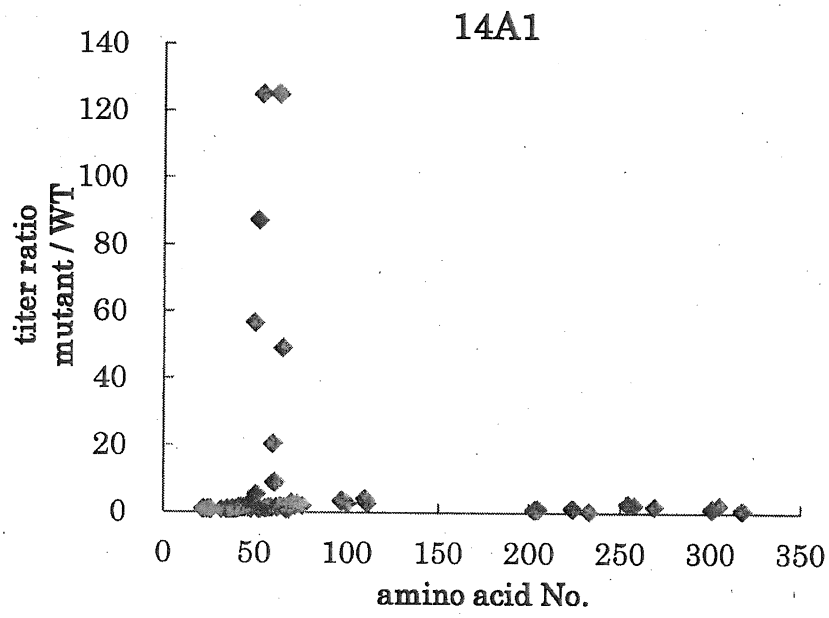


Figure7D

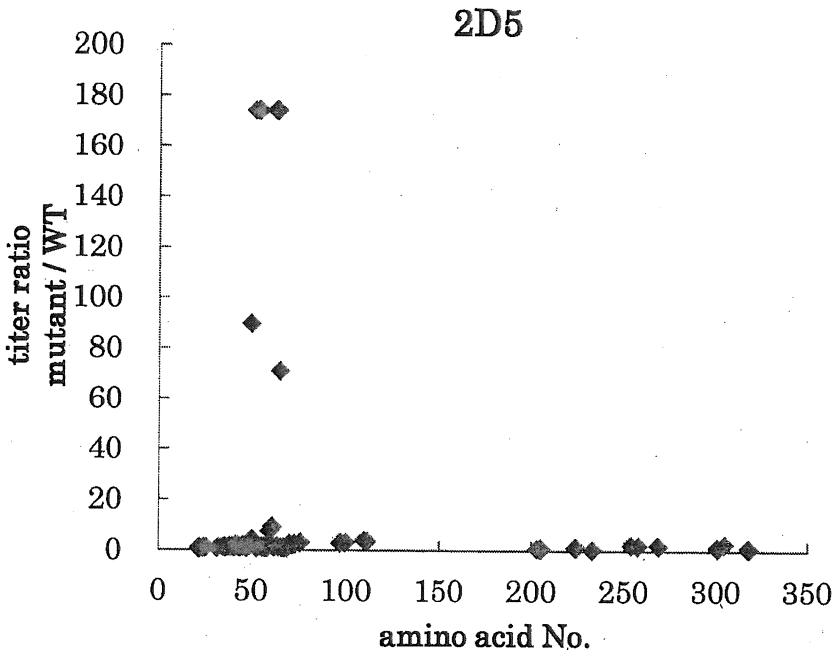


Figure7E

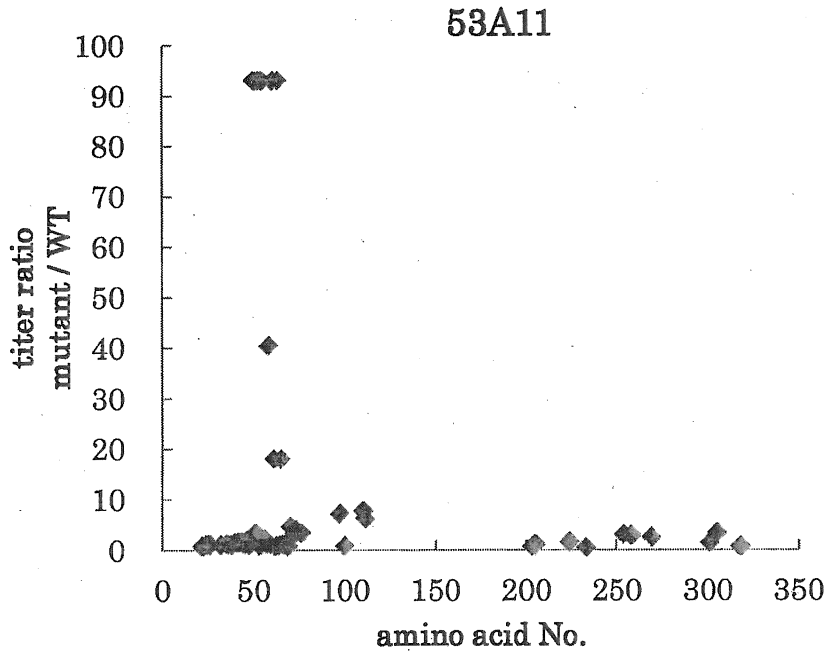


Figure7F

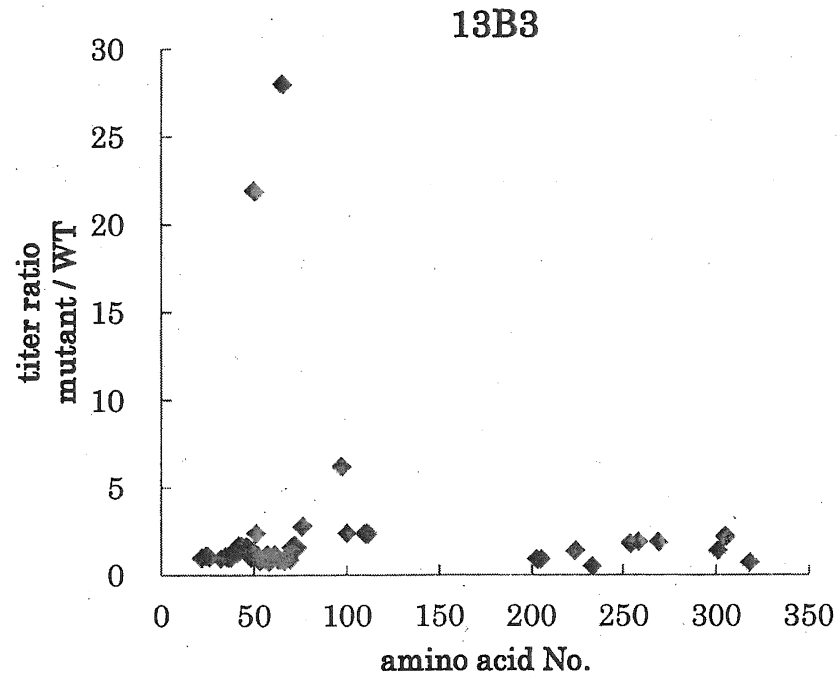


Figure7G

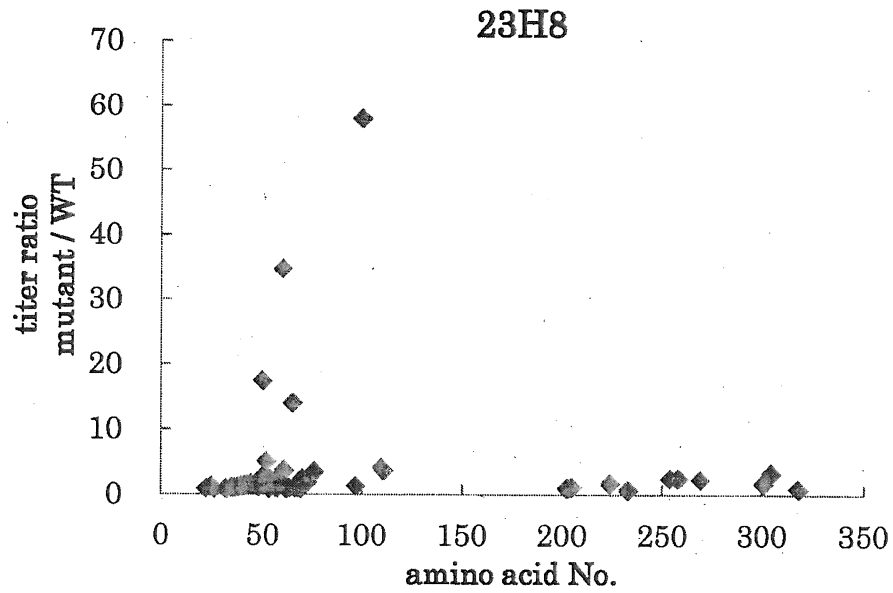


Figure7H

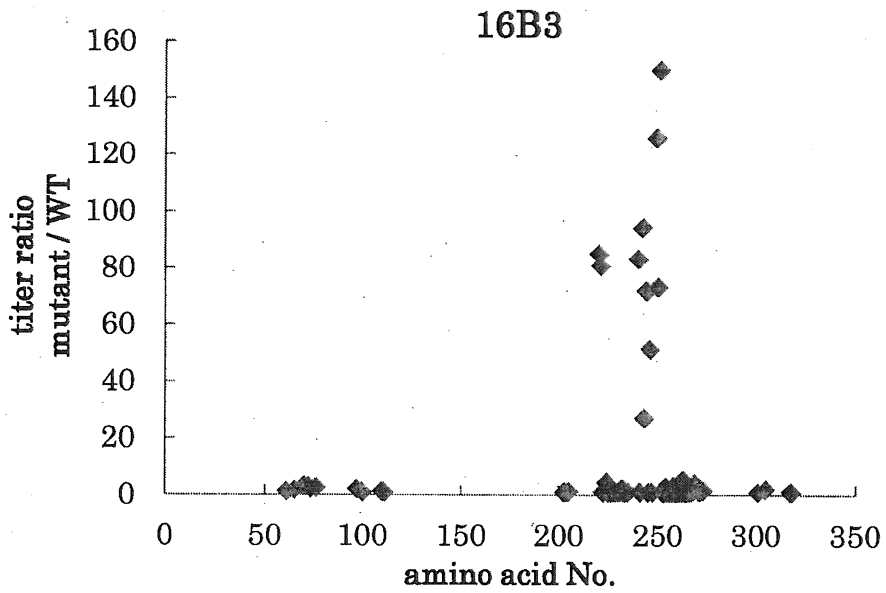


Figure7I

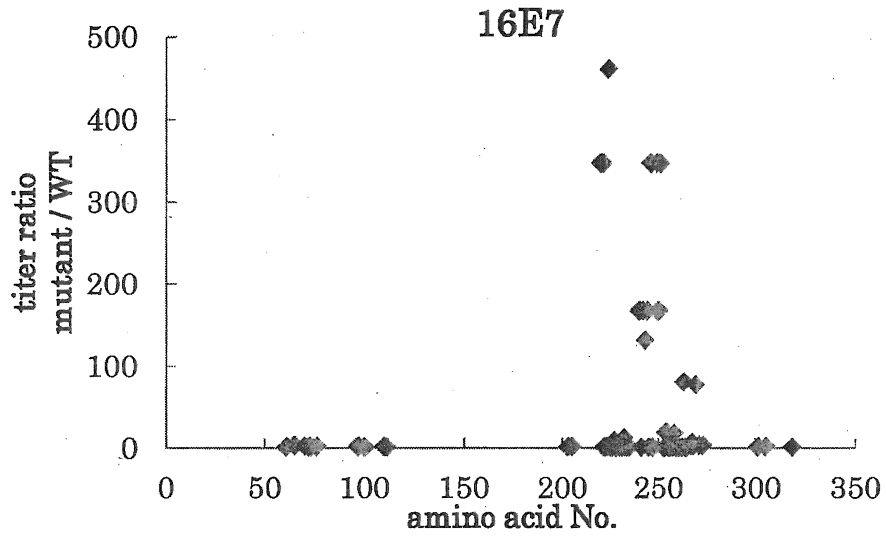


Figure7J

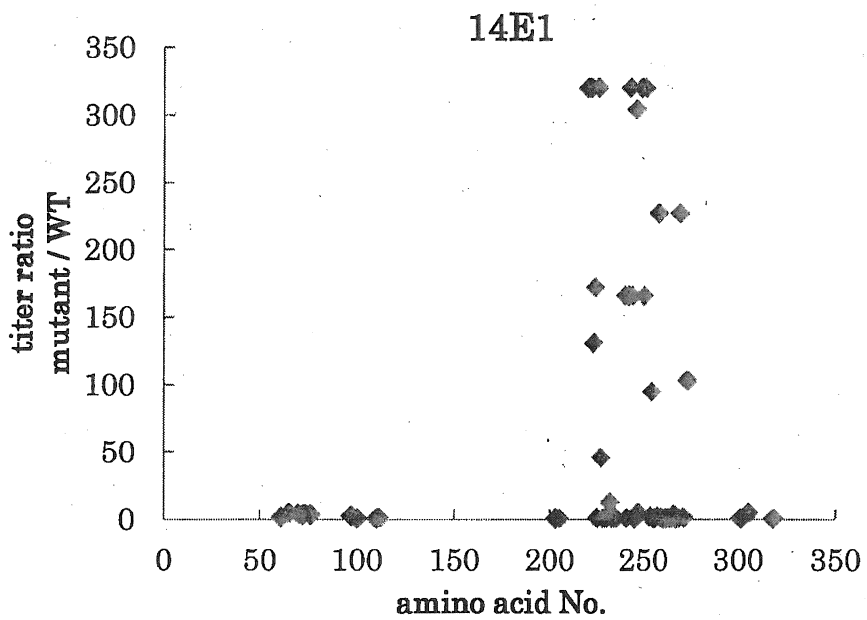
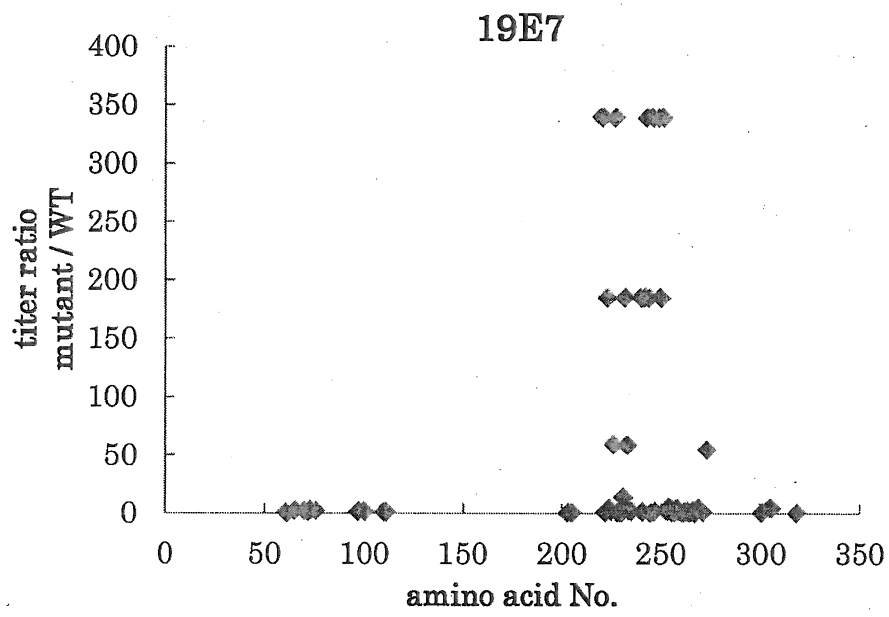


Figure7K


19E7
400
350
300
250
200
150
100
50
0
titer ratio
mutant / WT
0
50
100
150
200
250
300
350
amino acid No.