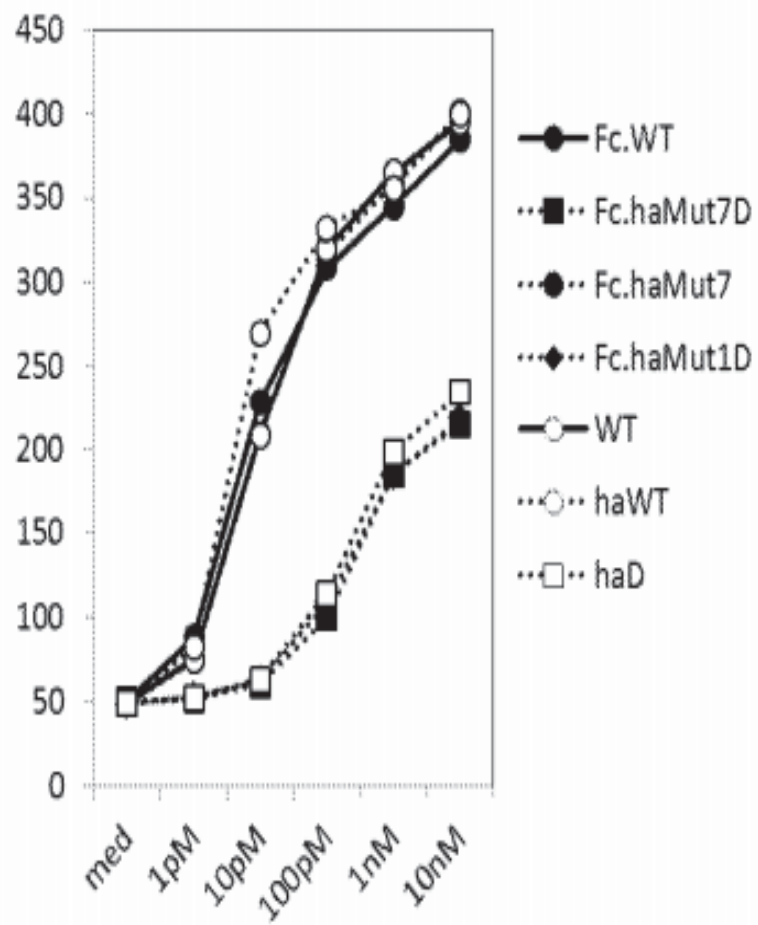


**fosfo-STAT5**  
(MFI)



**FIGURA 1**

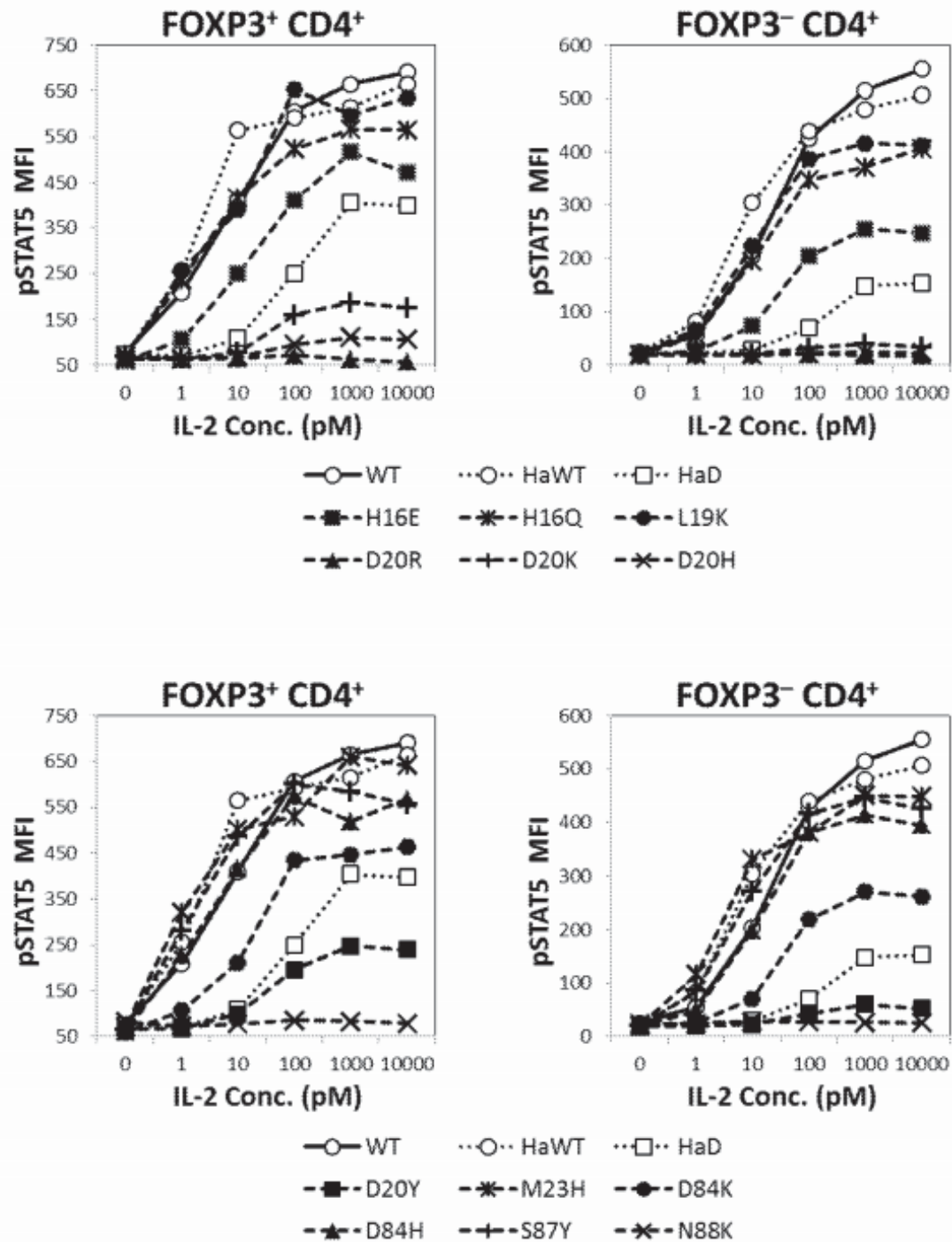


FIGURA 2A

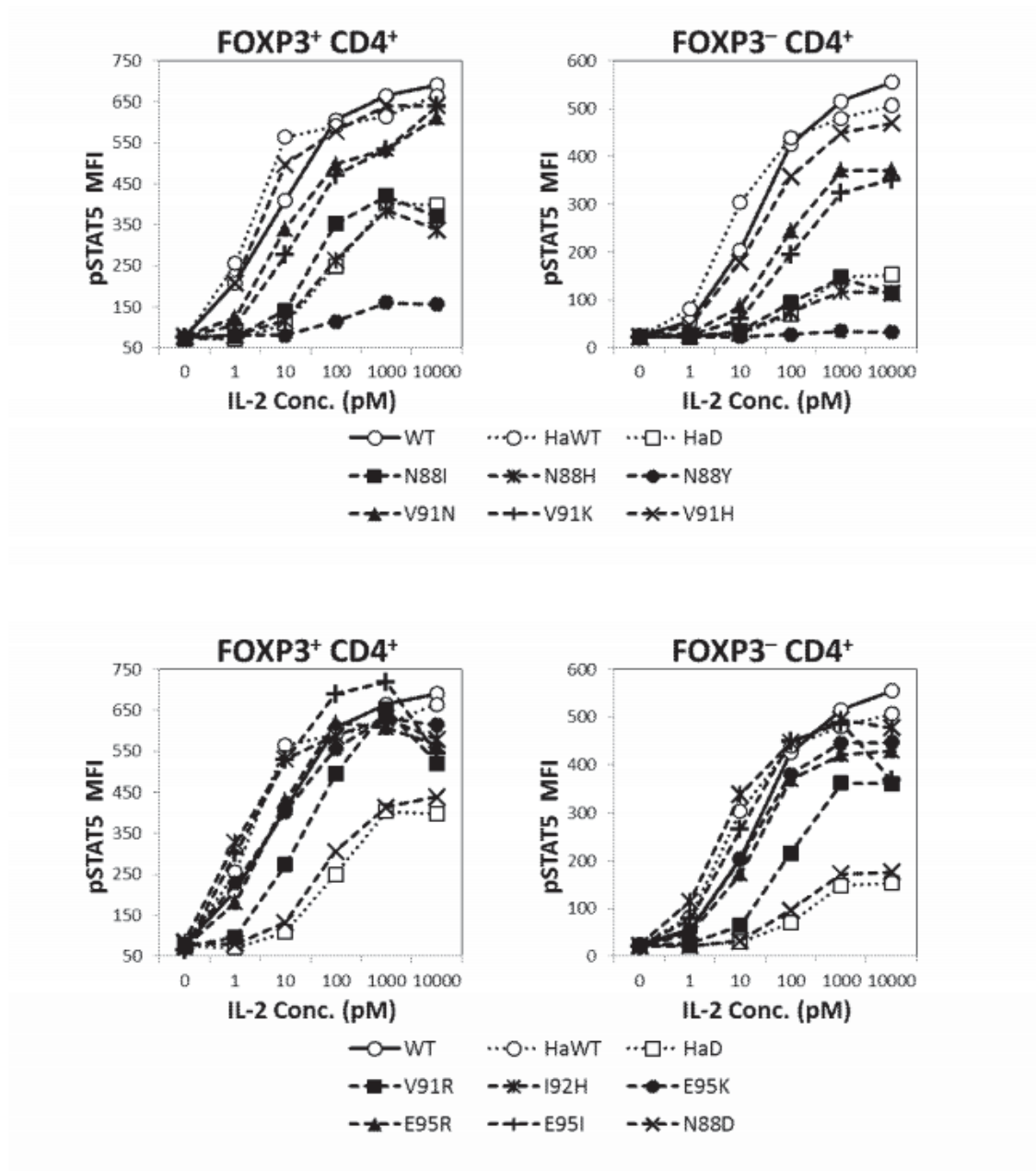


FIGURA 2B

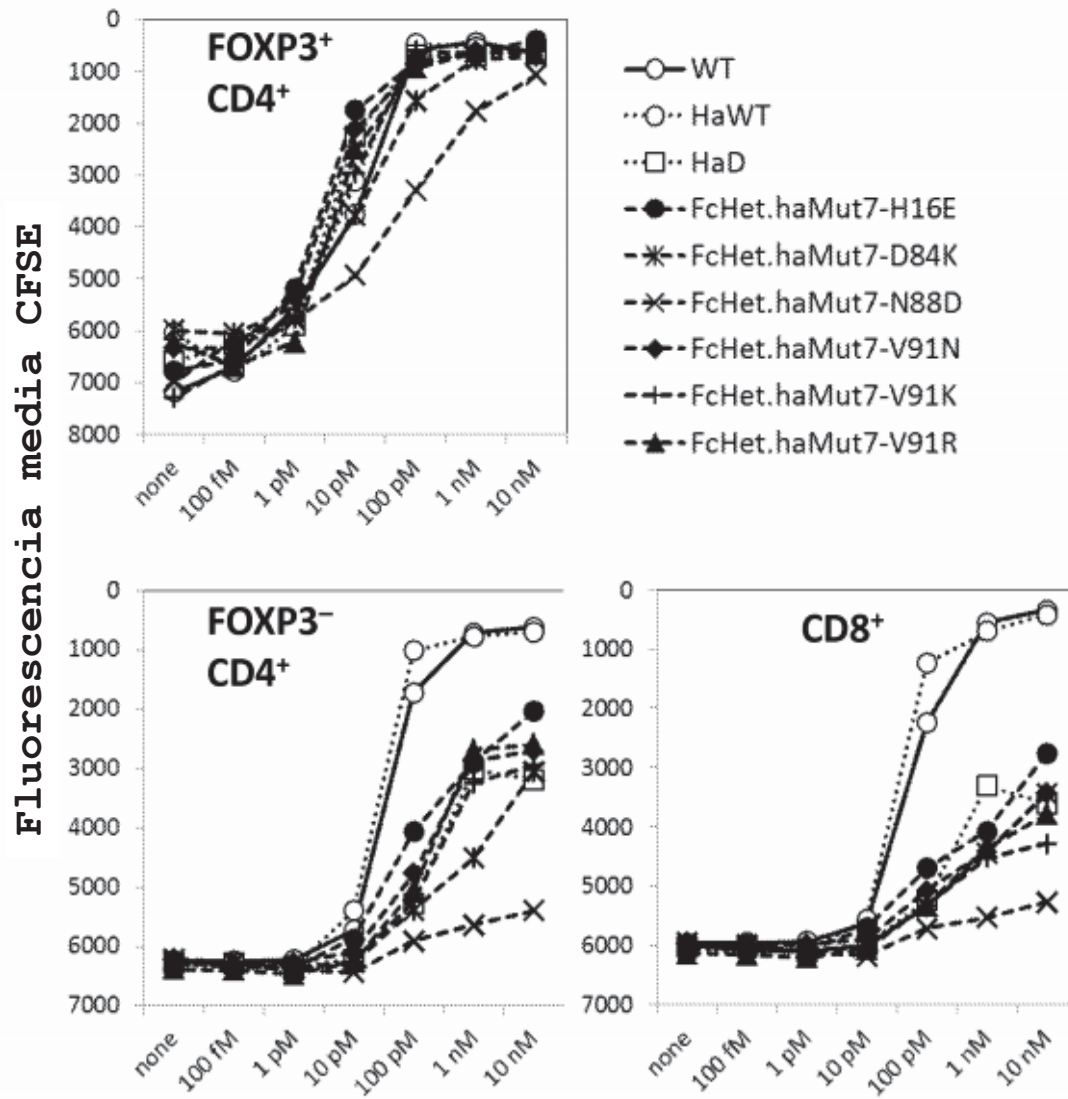
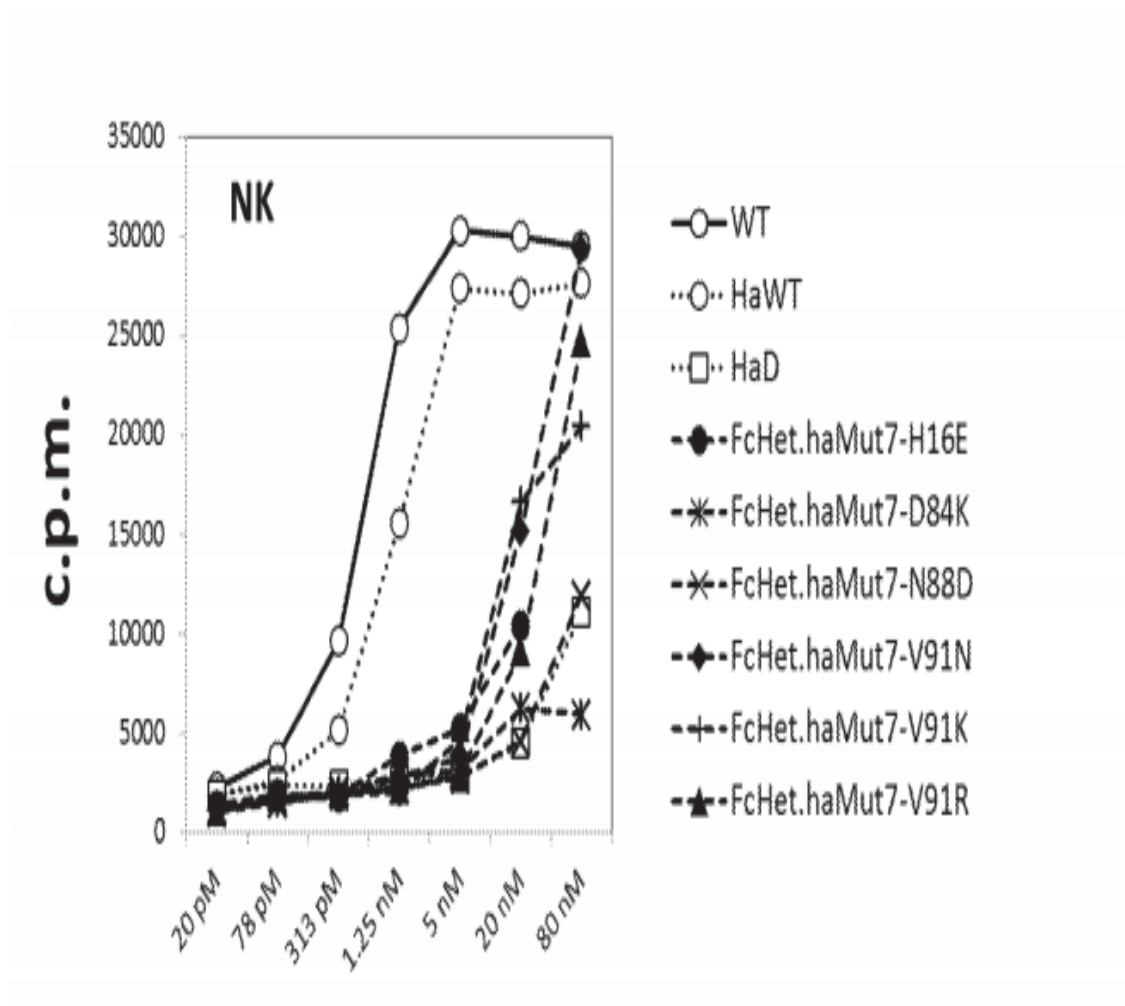


FIGURA 3

**FIGURA 4**

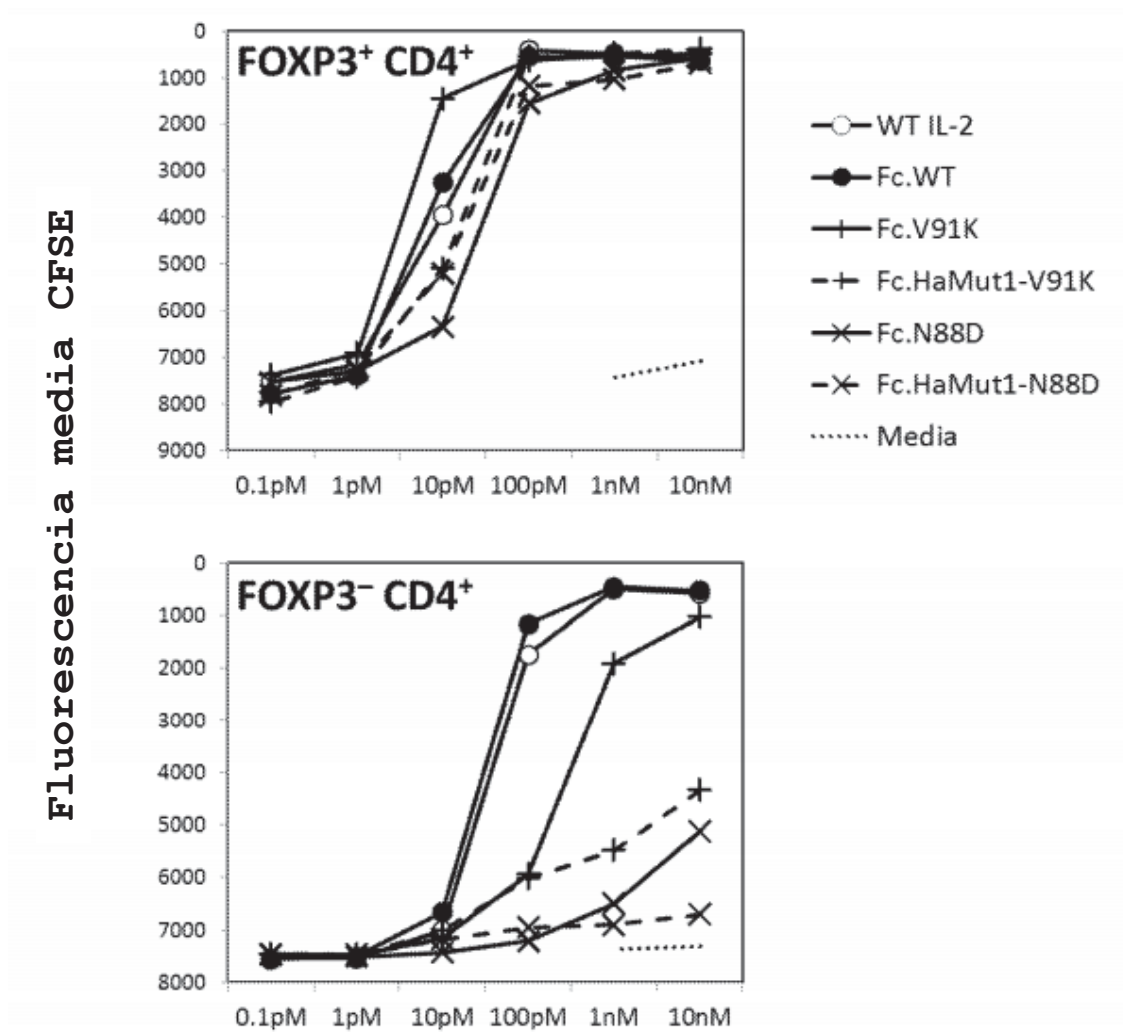
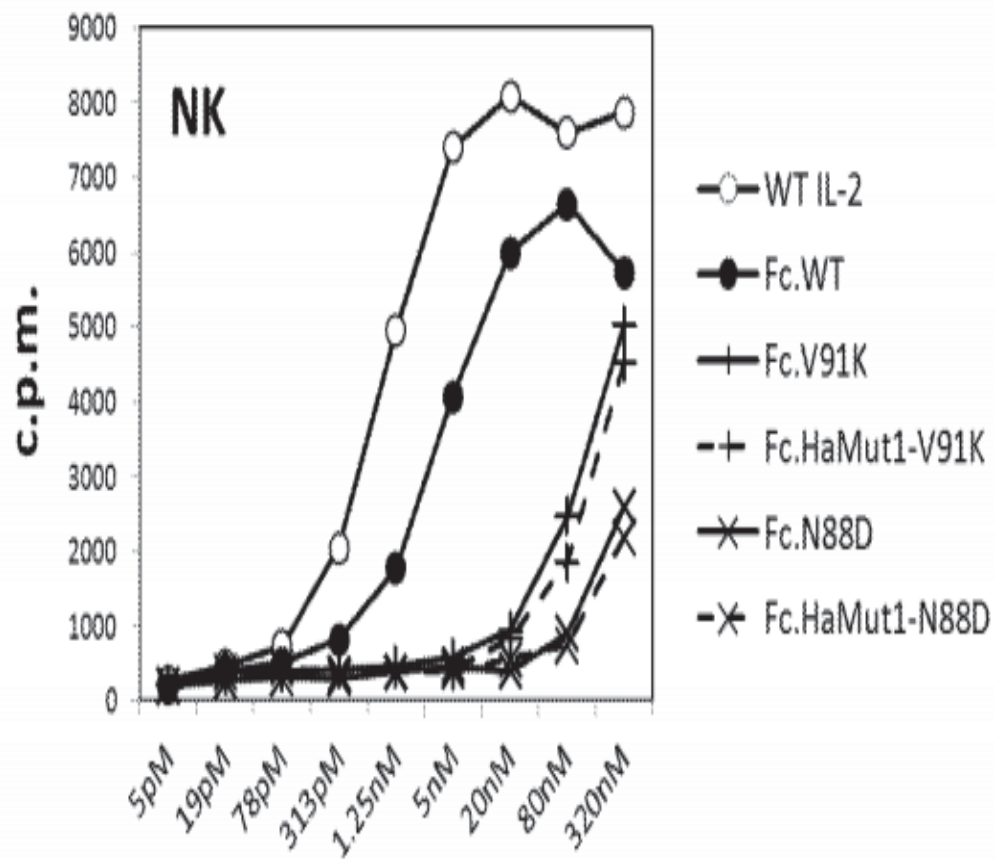


FIGURA 5

**FIGURA 6**

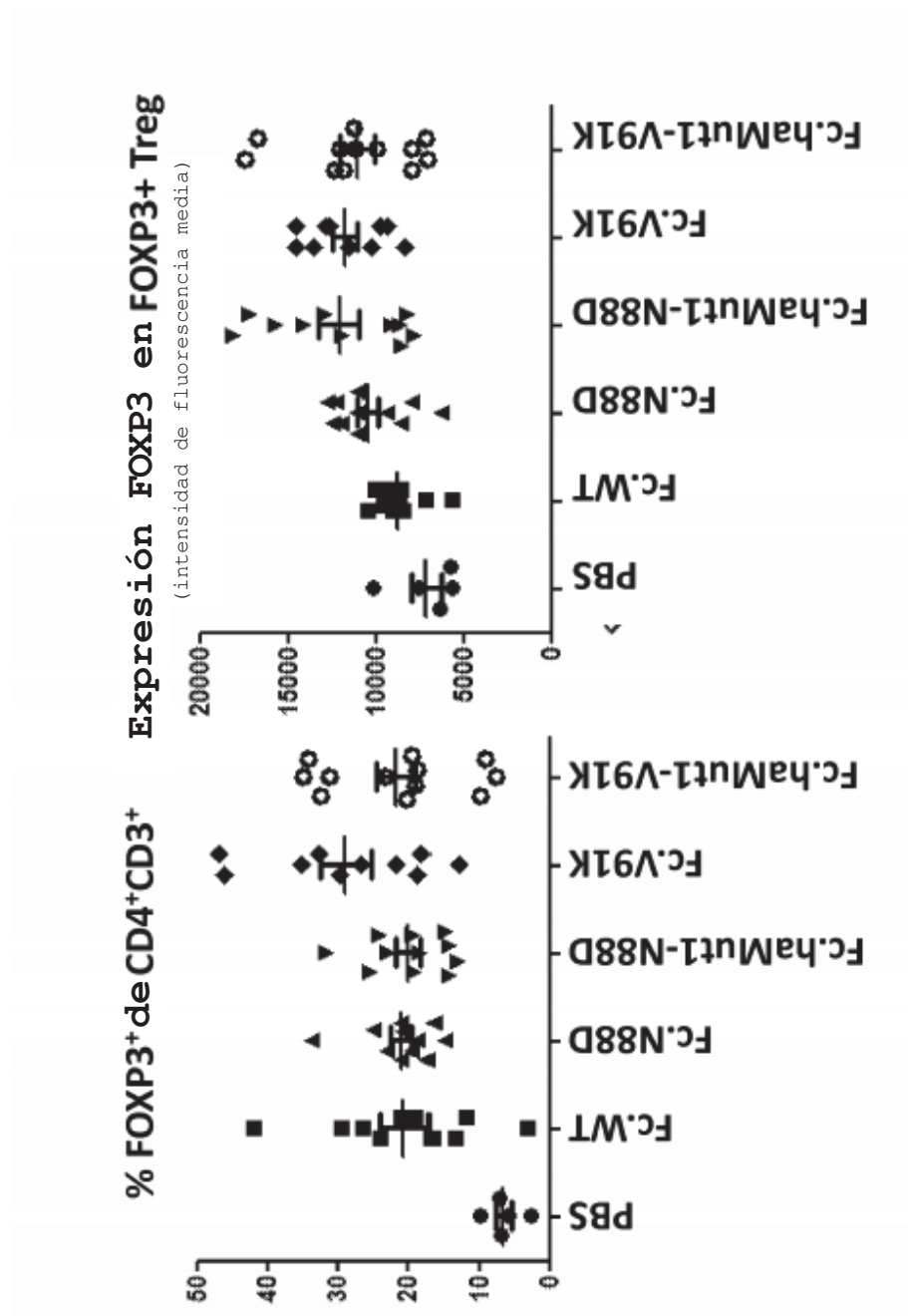


FIGURA 7A

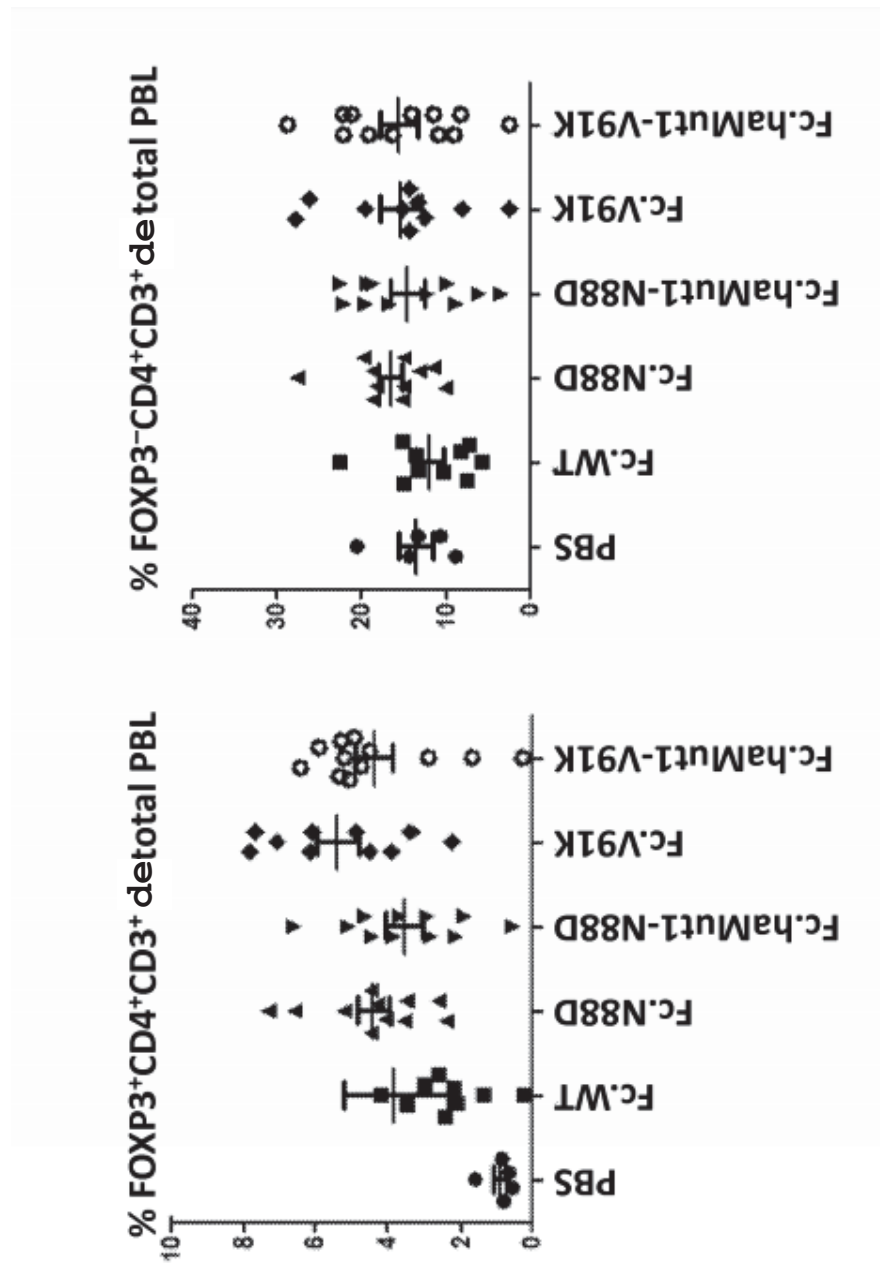


FIGURA 7B

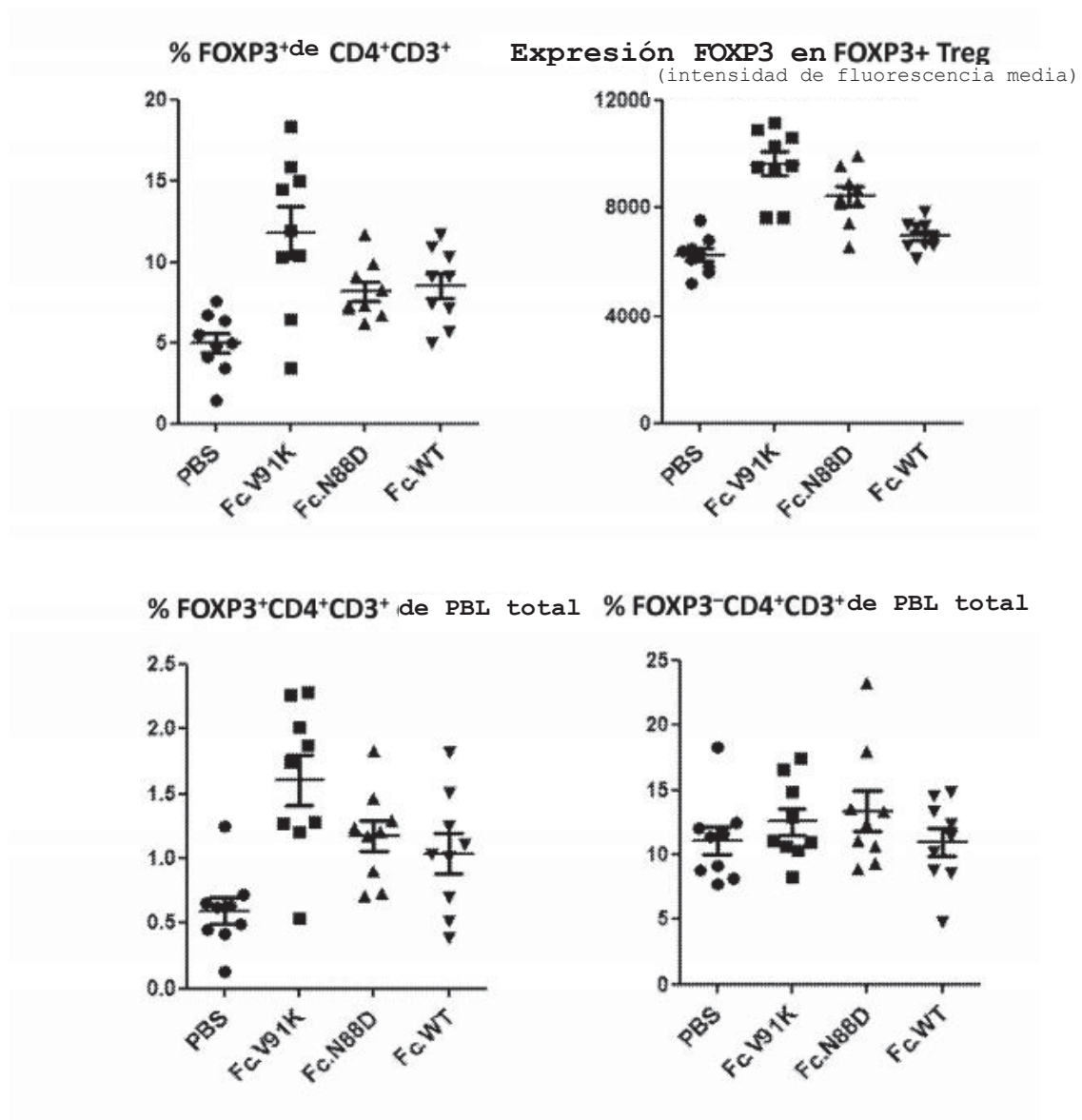


FIGURA 8

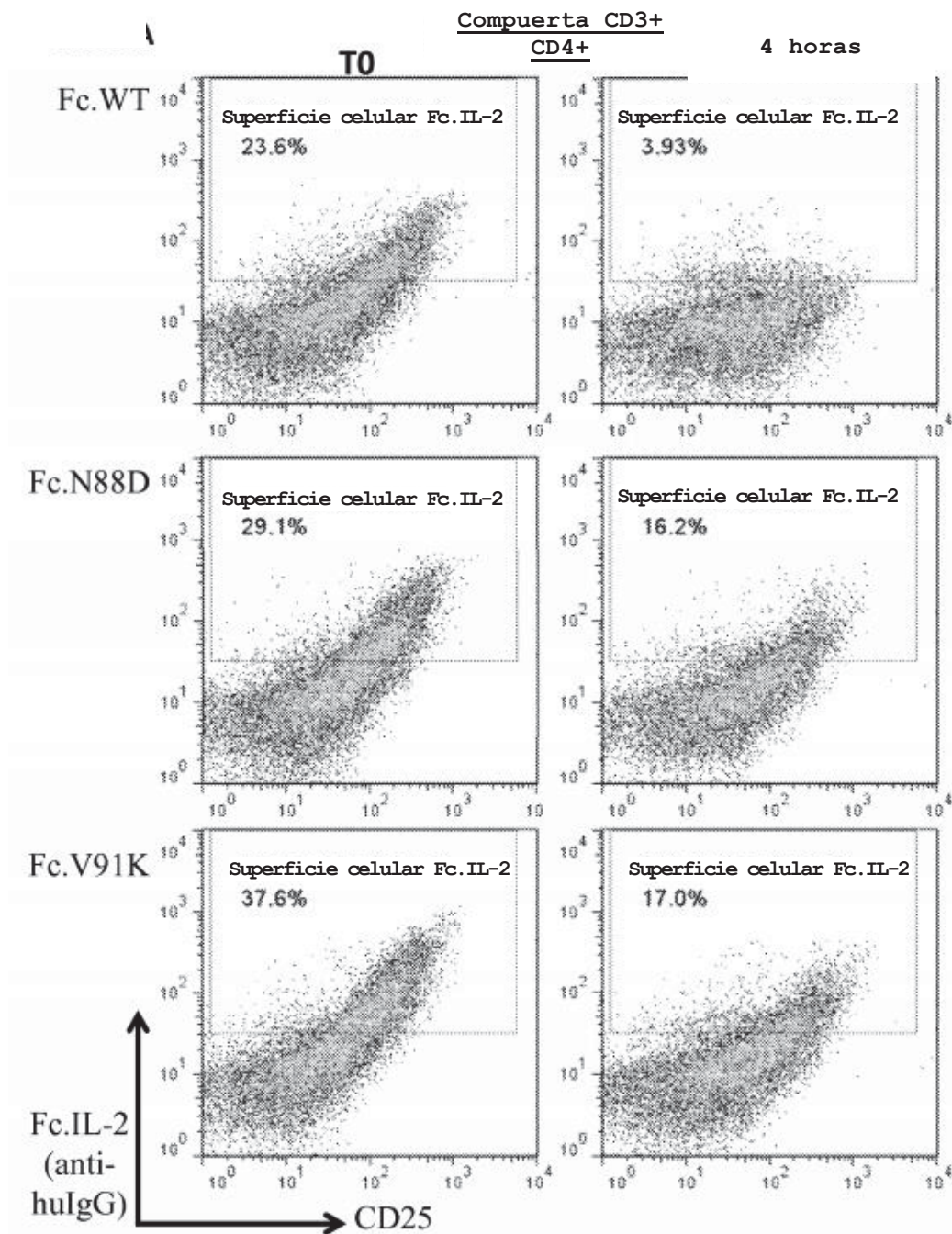


FIGURA 9A

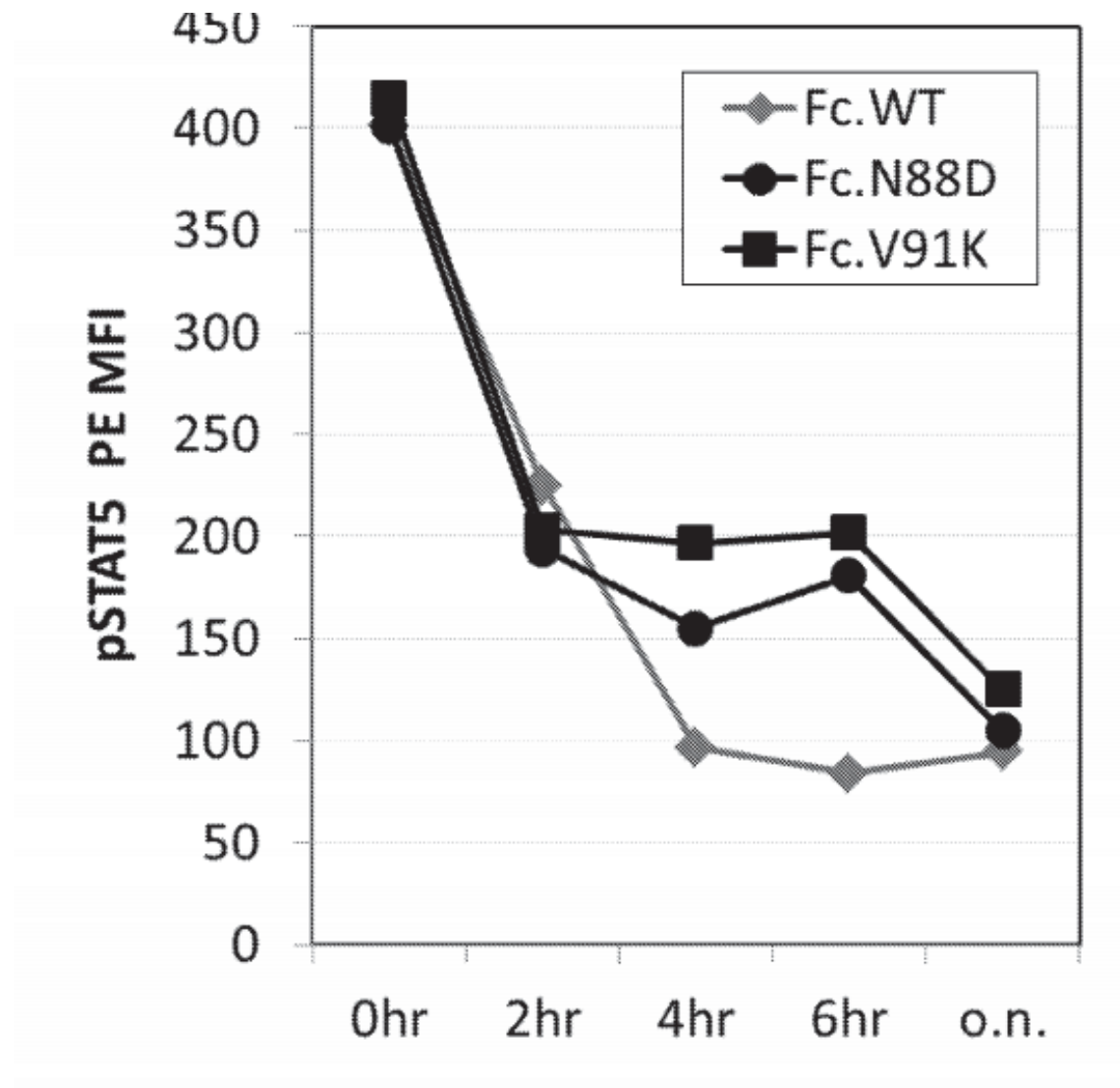


FIGURA 9B

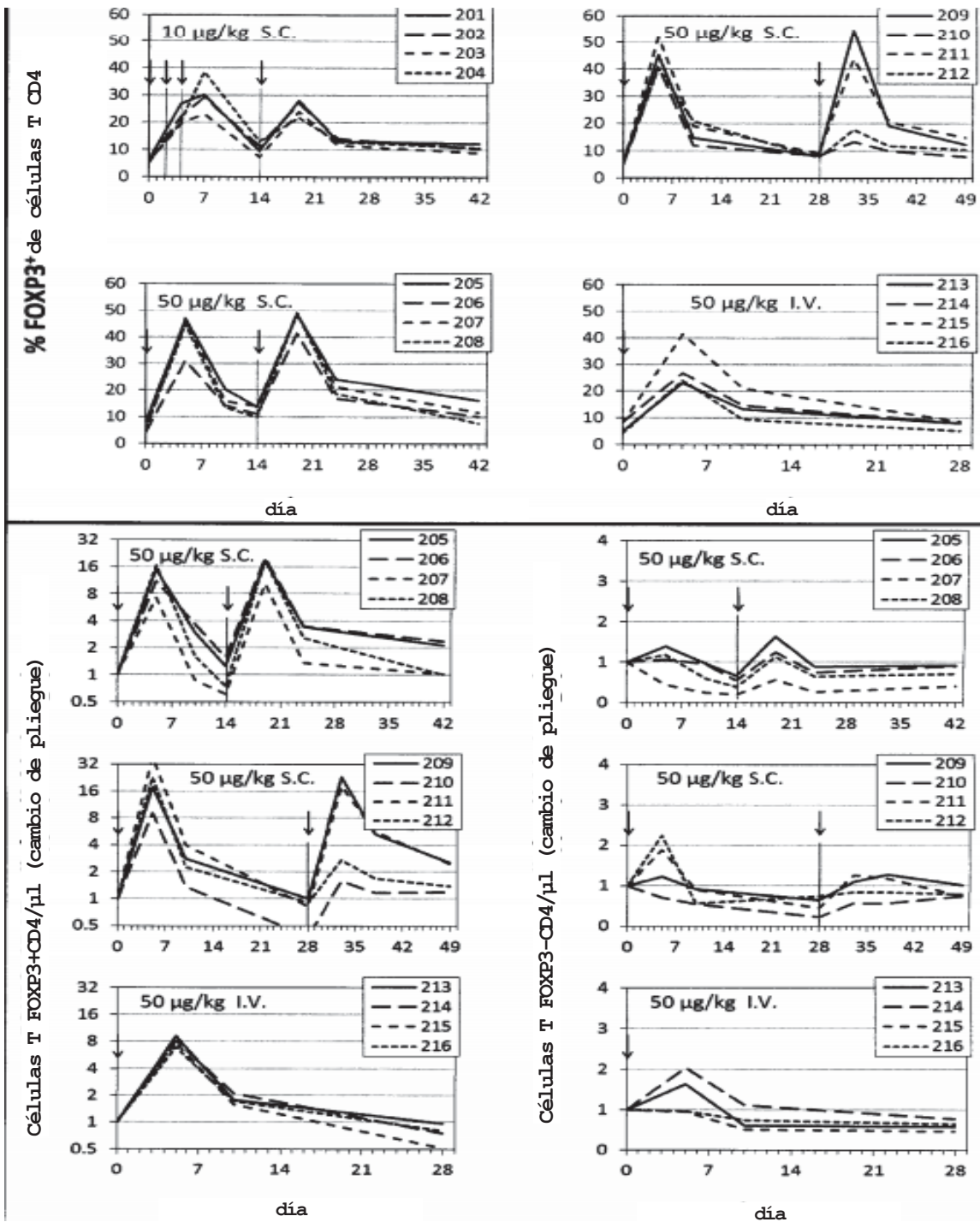
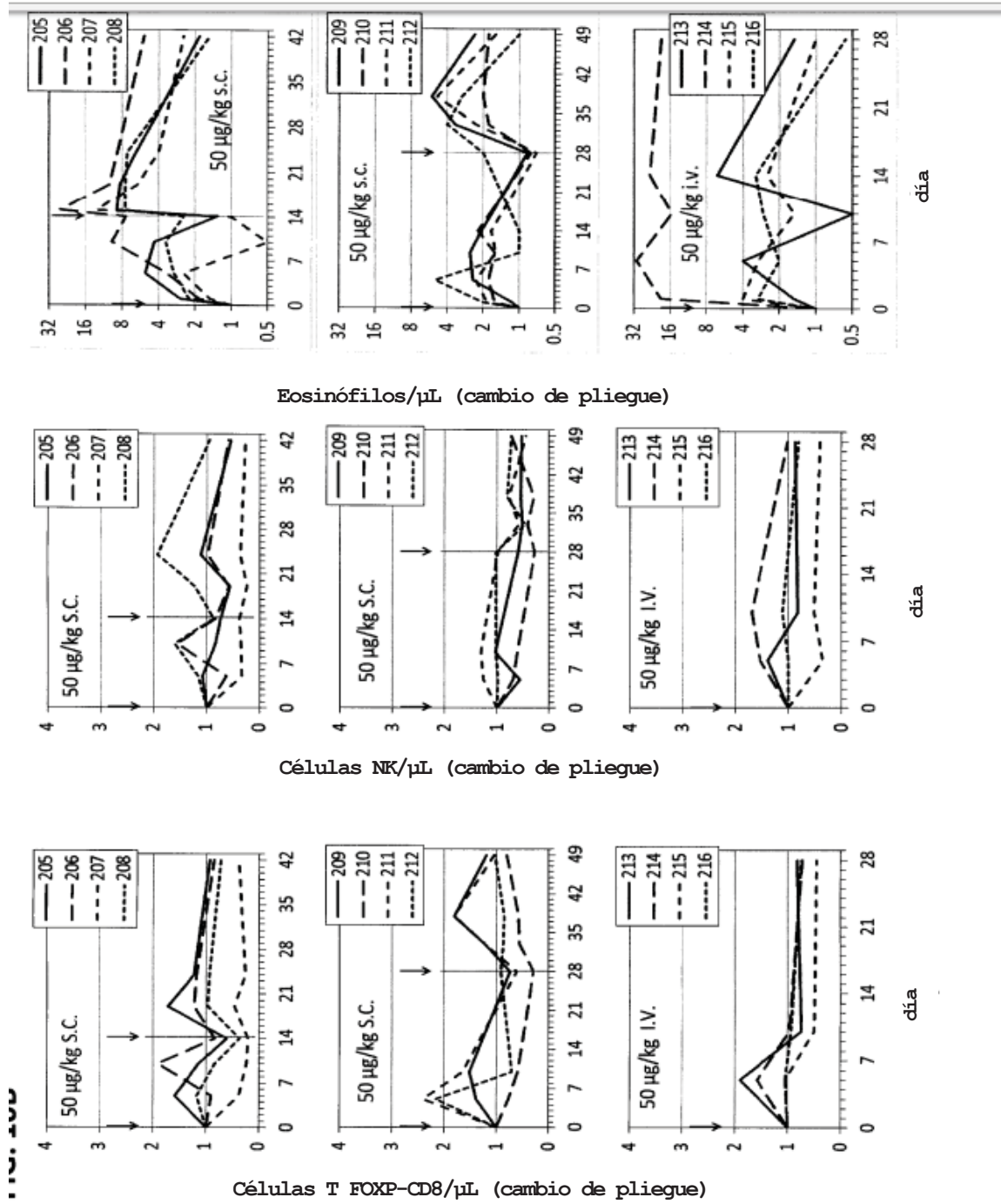


FIGURA 10A



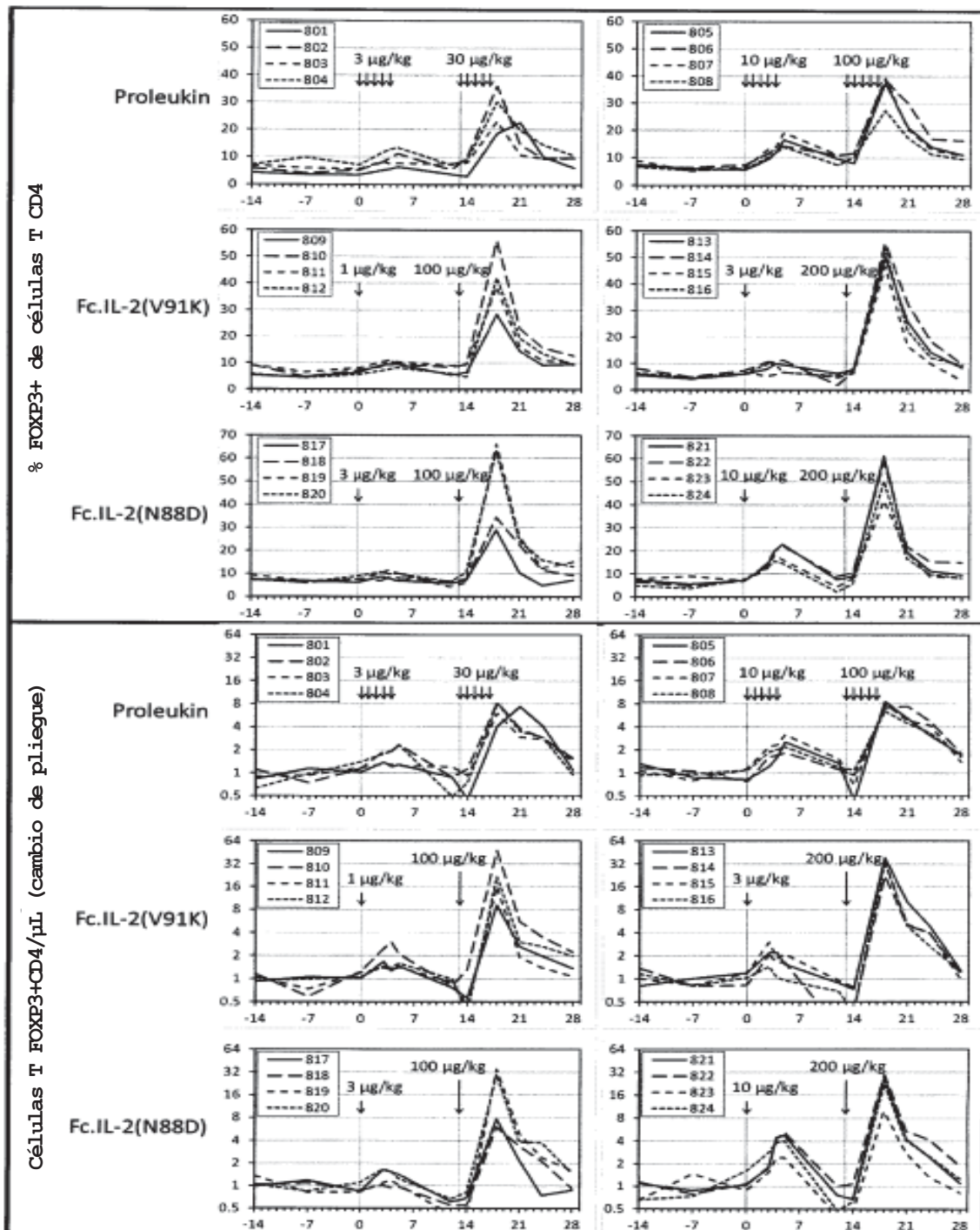


FIGURA 11A

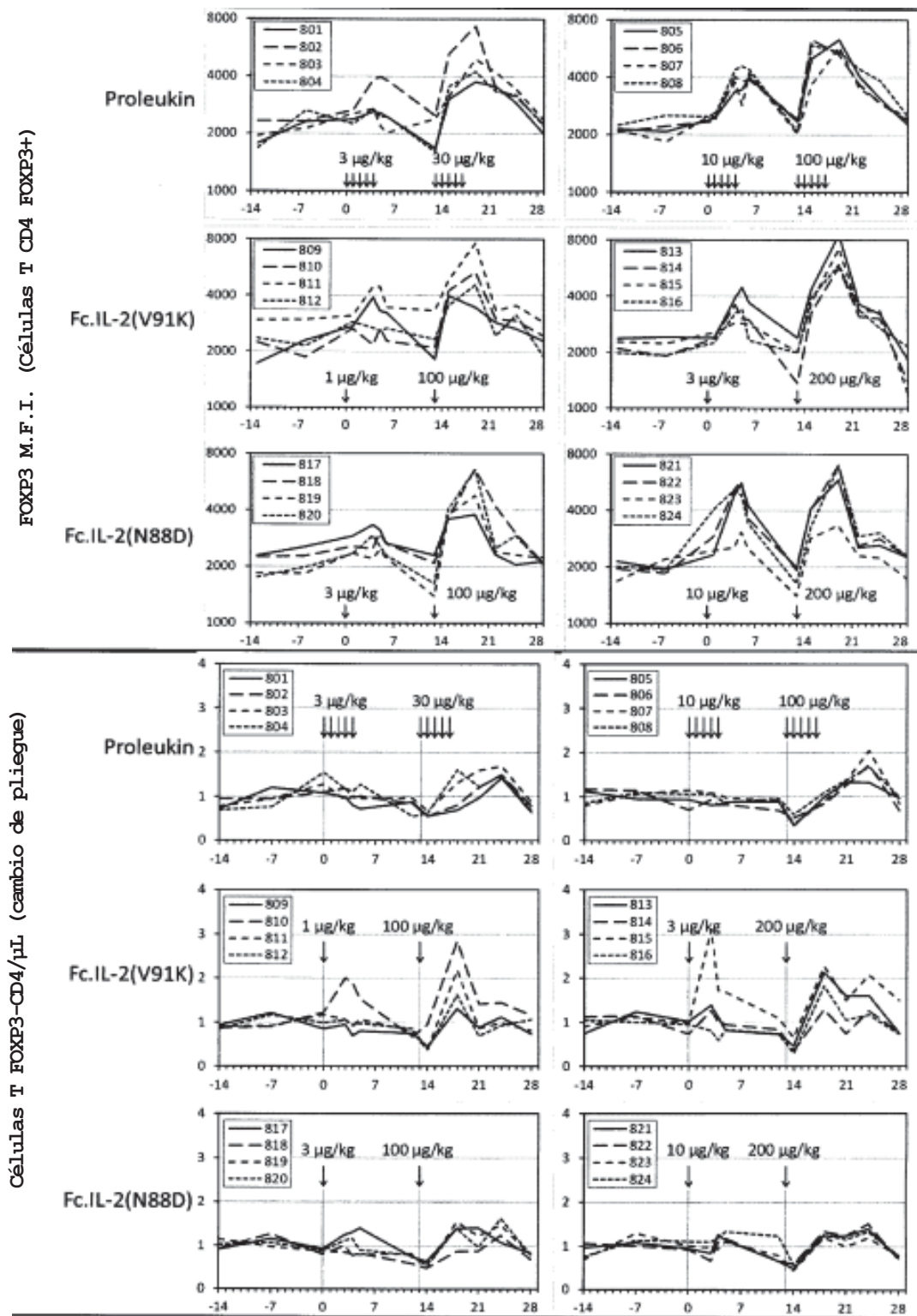


FIGURA 11B

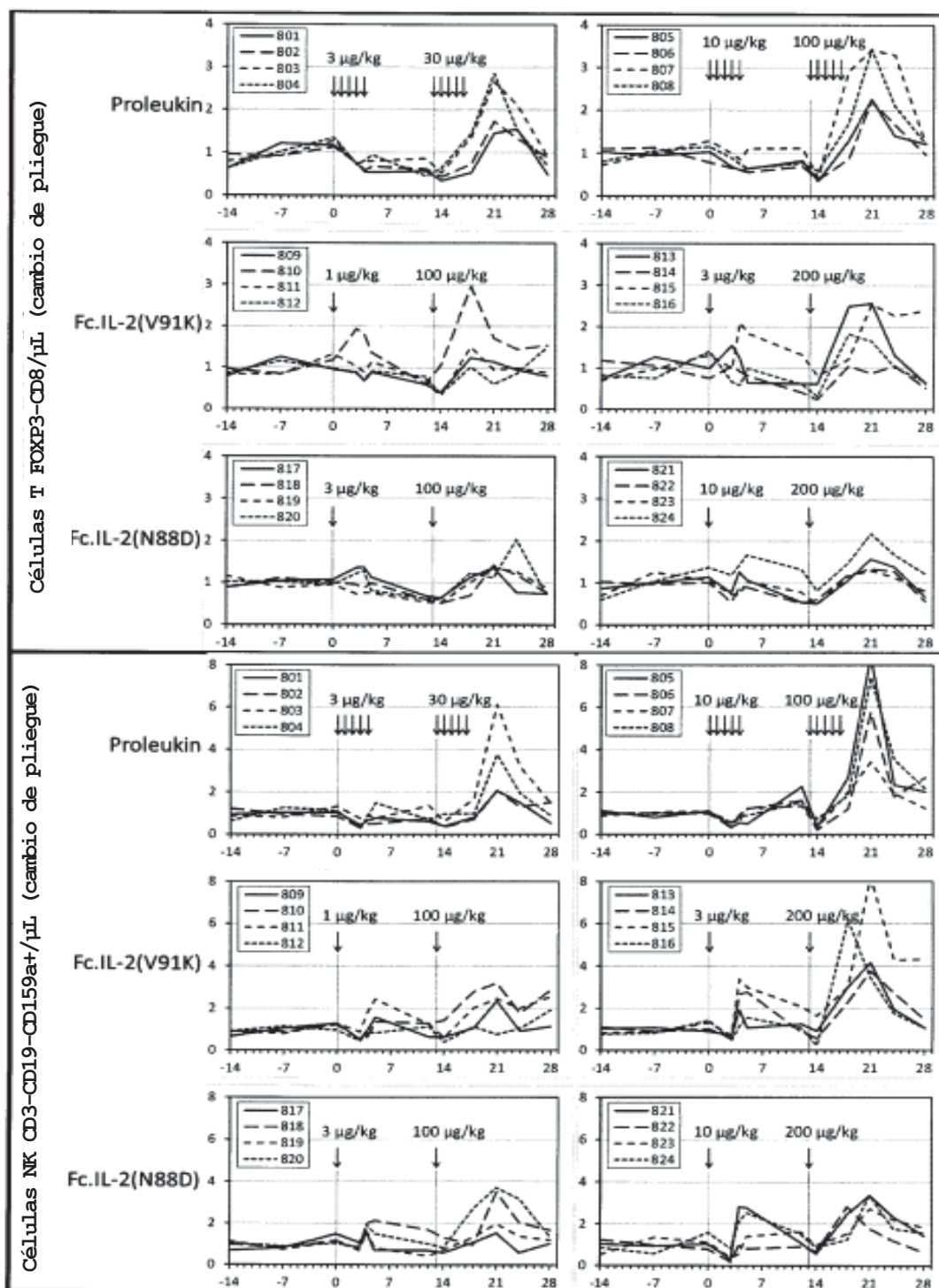


FIGURA 11C

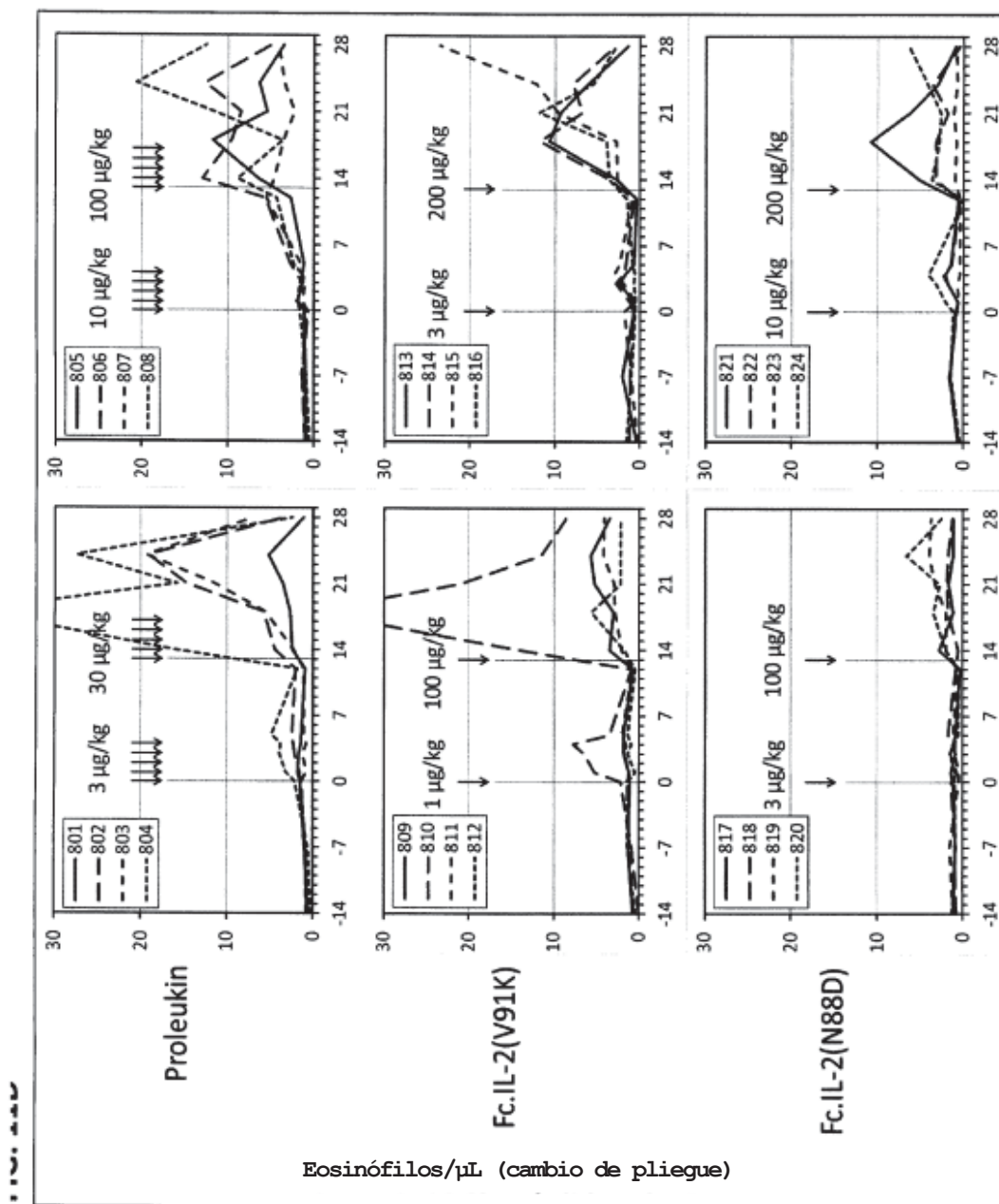


FIGURA 11D

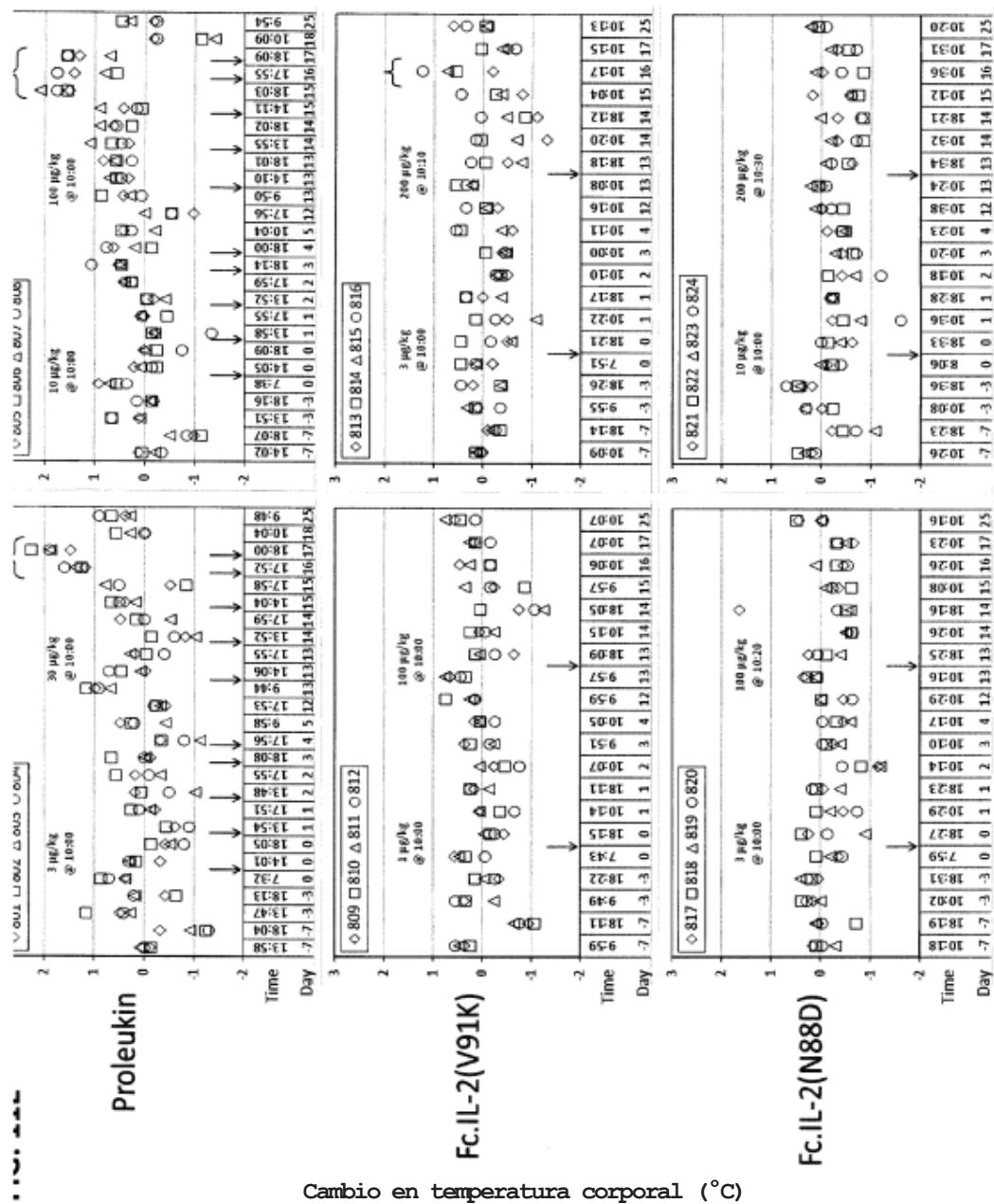


FIGURA 11E

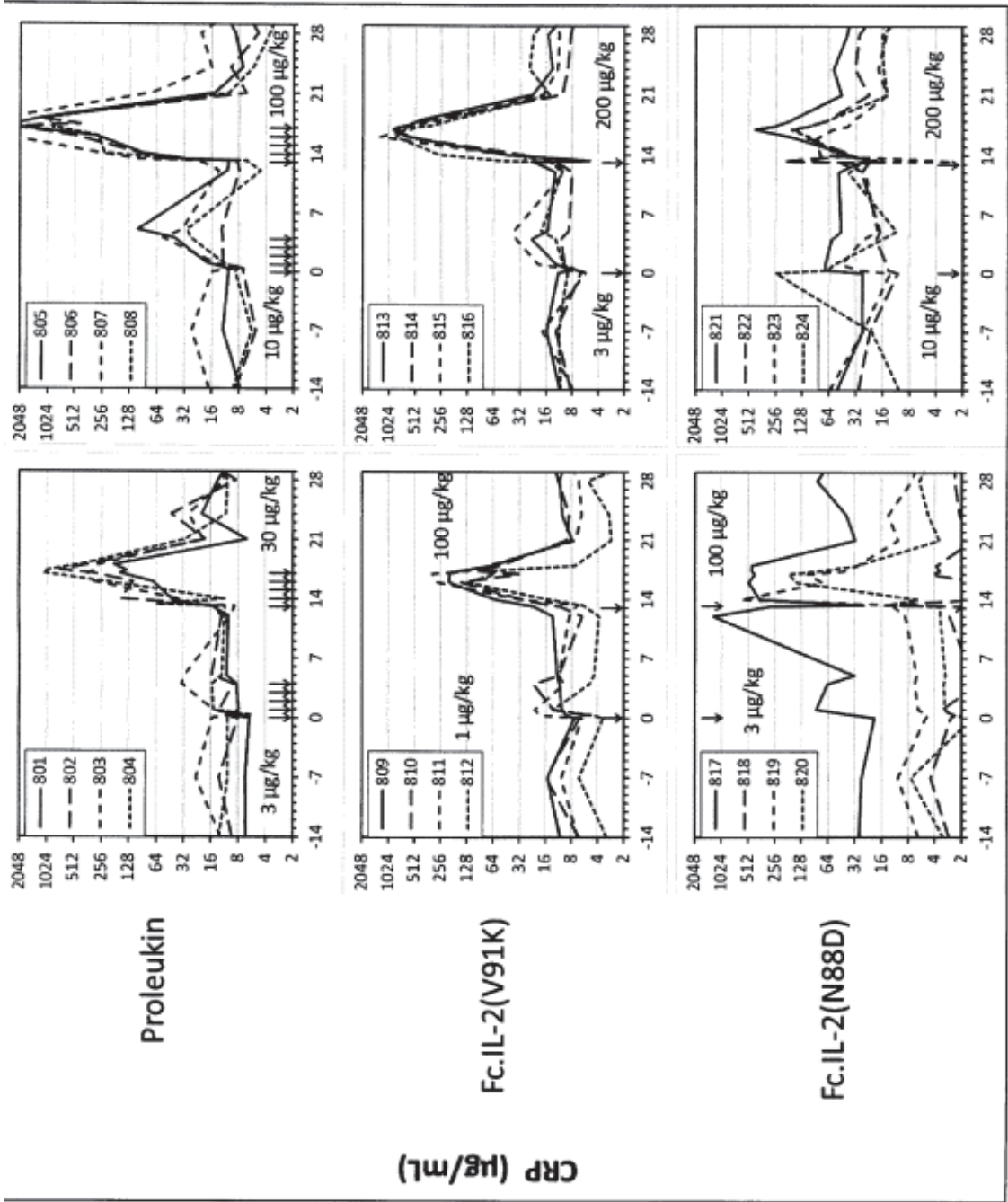


FIGURA 11F

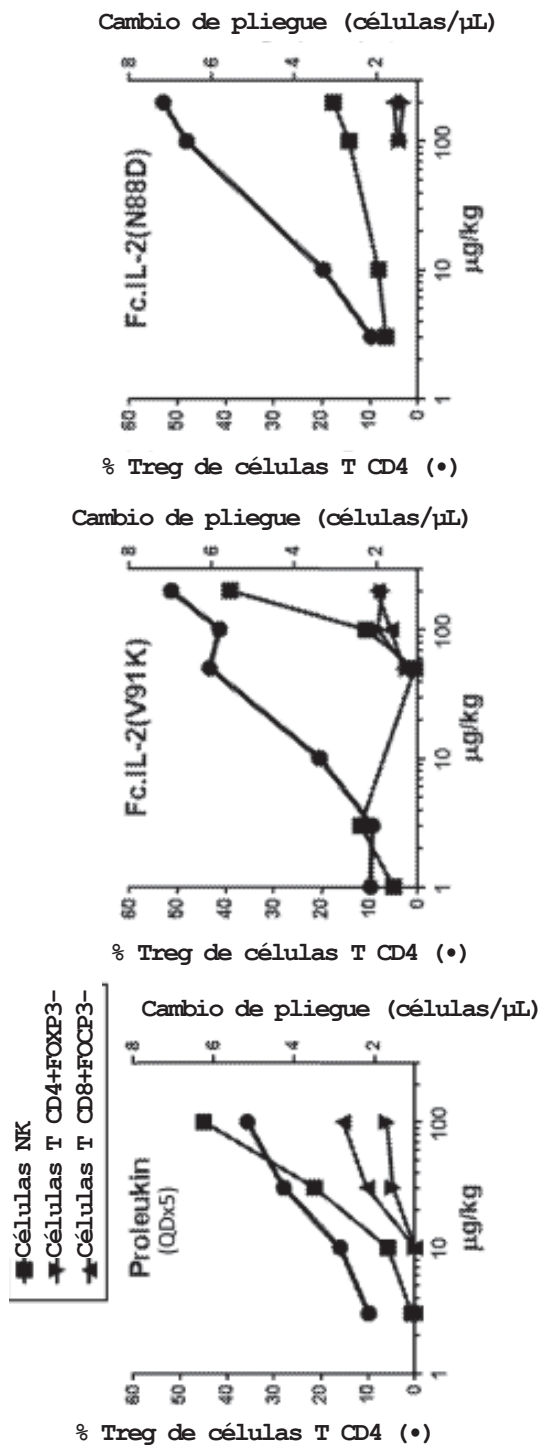


FIGURA 12A

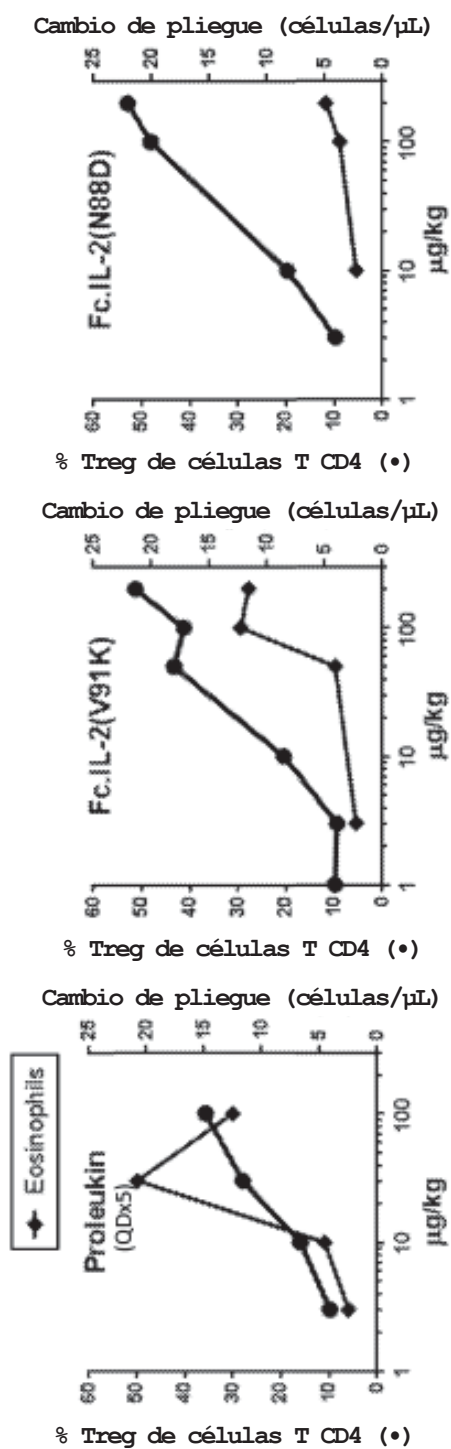


FIGURA 12B

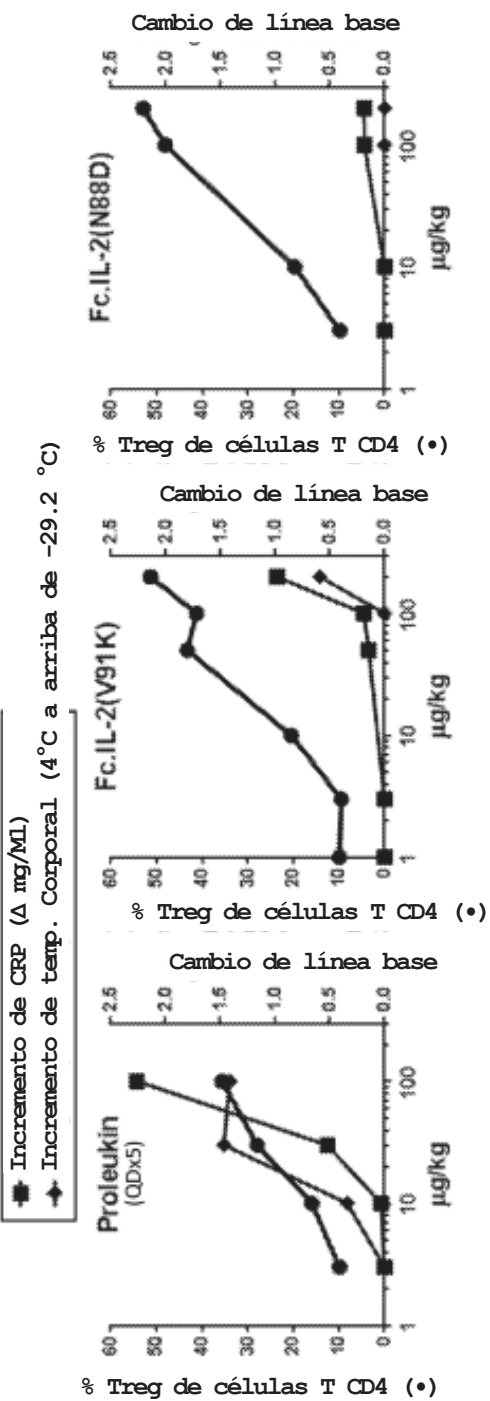


FIGURA 12C

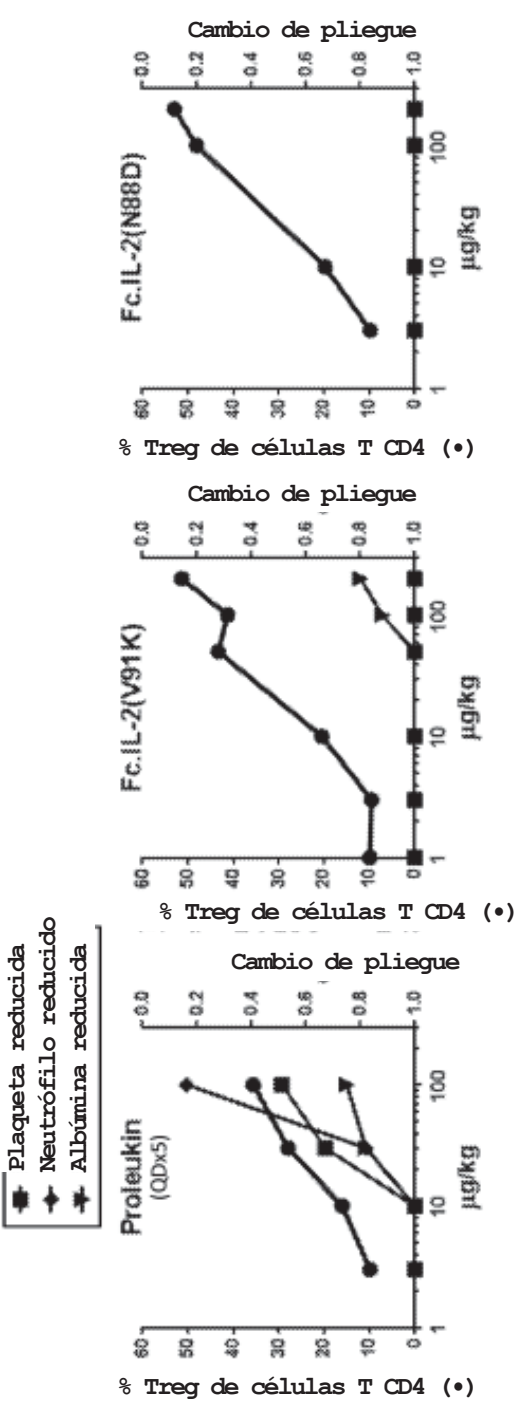


FIGURA 12D

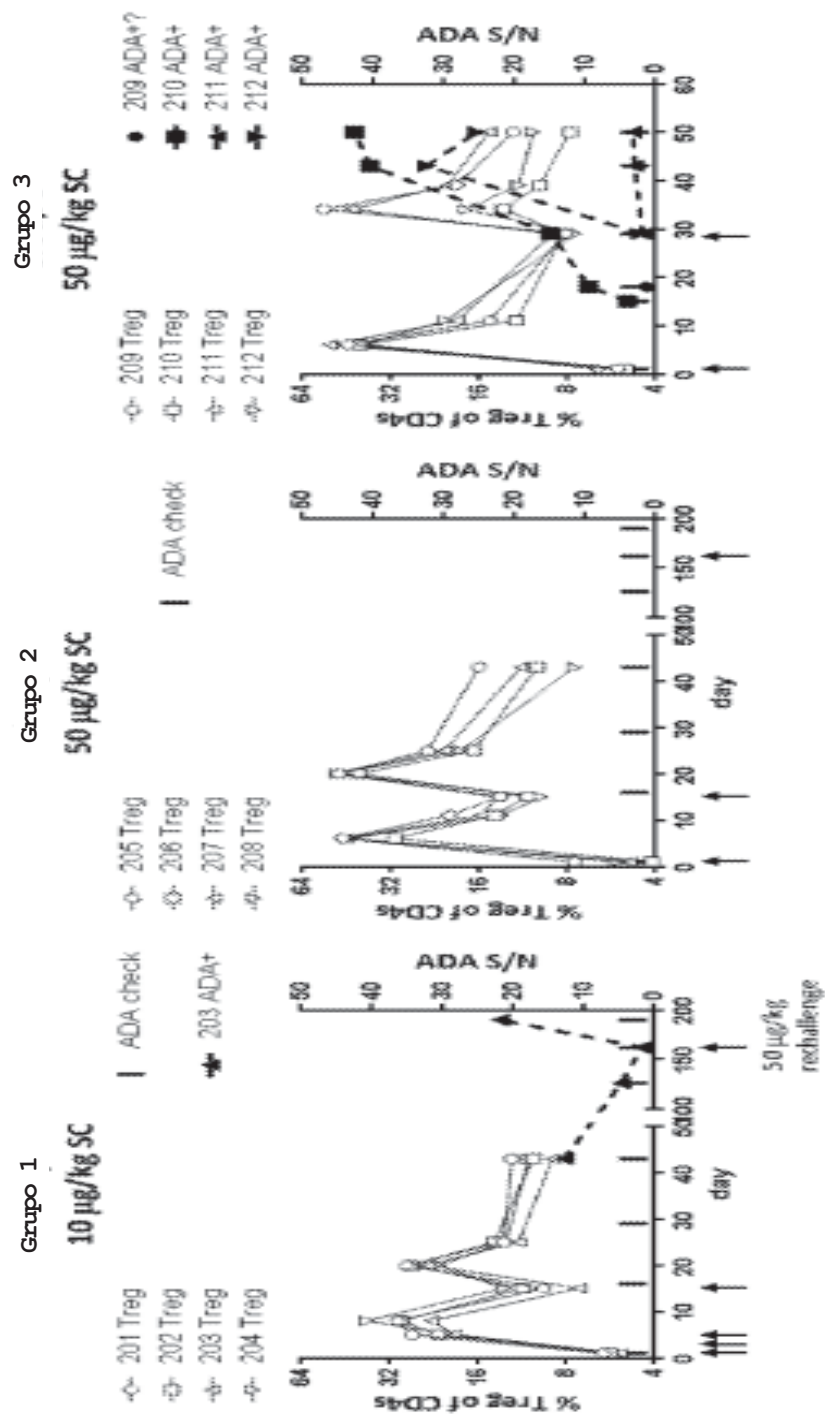


FIGURA 13

|   | L12  | Q13  | E15  | H16  | L19  | D20  | M23  | R81  | D84  | S87  | N88  | V91  | I92  | L94  | E95  |
|---|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| A | 1.18 | 0.82 | 1.26 | 2.51 | 2.05 | 1.61 | 0.68 | 1.61 | 1.53 | -0.1 | 2.13 | 1.22 | 1.04 | 0.21 | 0.68 |
| D | 0.49 | 0.81 | 0.99 | 2.39 | 1.7  | 0    | 0.41 | 1.19 | 0    | -0.4 | 1.1  | 0.52 | 0.29 | -0.2 | 0.15 |
| E | 0.93 | -0.1 | 0    | 1.01 | 1.58 | 0.49 | 0.01 | 0.93 | 2.4  | -0.4 | 2.15 | 1.89 | 0.75 | -0.9 | -0   |
| F | 0.1  | 0.86 | -0.5 | 0.97 | -0.9 | 1.6  | 0.2  | -0   | 0.98 | -1.5 | 1.3  | -0.6 | 0.18 | -0   | -0.5 |
| G | 1.36 | 1.08 | 1.51 | 3.06 | 2.73 | 1.83 | 0.82 | 1.62 | 2.11 | 0.19 | 2.78 | 1.88 | 1.29 | 0.32 | 1.11 |
| H | -0.1 | -0   | 0.29 | 0.42 | 0.18 | 0.55 | 0.39 | 0.52 | 1.64 | -0.3 | 1.69 | 0.5  | -0.1 | 0.04 | 0.84 |
| I | -0.1 | 0.45 | 0.06 | 0.91 | 0.73 | 0.74 | -0.1 | 1.01 | 1.76 | -0.9 | 0.25 | 0.98 | 0    | -0.6 | 0.48 |
| K | 1.19 | 0.25 | 0.85 | 3.98 | -0.3 | 1.56 | 0.22 | 1.04 | 2.66 | 0.01 | 3.72 | 2.7  | 1.57 | 0.59 | 0.73 |
| L | 0    | 0.33 | -0.1 | 1.47 | 0    | 0.57 | 0.14 | 1.11 | 1.16 | -0.8 | 0.29 | 0.74 | -0.3 | 0    | 0.12 |
| M | 1.09 | -0.1 | 0.41 | 1.86 | 1.2  | 0.96 | 0    | 0.9  | 2.04 | -1   | 2.17 | 1.09 | 0.72 | 0.09 | 0.64 |
| N | 0.26 | 0.66 | 0.68 | 1.59 | 1.31 | 0.16 | 0.26 | 1.38 | 0.66 | -0.5 | 0    | 0.32 | 0.89 | -0.3 | 0.5  |
| P | 0.89 | 0.24 | 1.01 | 2.18 | 0.97 | 0.86 | 0.34 | 1.36 | 1.18 | -0.5 | 0.89 | 0.28 | 0.33 | -0.1 | 0.08 |
| Q | 1.27 | -0   | 0.21 | 0.94 | 0.98 | 0.61 | -0.2 | 1.11 | 2.41 | -0.2 | 1.46 | 0.73 | -0.3 | 0.08 | 0.51 |
| R | 1.04 | -0.2 | 0.48 | 2.69 | 1.17 | 1.33 | 1.19 | 0    | 1.69 | 1.15 | 2.19 | 1.23 | 1.8  | 0.47 | 1.03 |
| S | 1.35 | 0.85 | 1.3  | 2.73 | 2.33 | 1.25 | 0.89 | 1.71 | 2.06 | 0    | 2.19 | 1.54 | 0.8  | 0.24 | 0.68 |
| T | 1.11 | 0.6  | 0.88 | 1.91 | 1.58 | 1.16 | 0.67 | 1.69 | 2.3  | -0.2 | 1.17 | 0.72 | 0.53 | 0.07 | 0.6  |
| V | 0.77 | 0.75 | 0.45 | 1.76 | 1.64 | 1.22 | 0.28 | 1.34 | 0.69 | -0.3 | 2.2  | -0   | 0.54 | -0.1 | 0.31 |
| W | -1.4 | 0.47 | -0.7 | -0.6 | -2.4 | 3.88 | 0.08 | -0.7 | 0.33 | -0   | 2.88 | -0.5 | -0.3 | -0.2 | -0.4 |
| Y | 0.25 | 0.62 | -0.2 | 1.55 | -1.8 | 0.96 | 0.06 | -0.3 | 0.82 | -0.6 | 1.07 | -0.4 | -0.3 | -0   | 0.63 |

FIGURA 14

|   | L12   | Q13  | E15  | H16  | L19  | D20  | M23 | R81  | D84  | S87   | N88  | V91  | I92  | L94  | E95  |
|---|-------|------|------|------|------|------|-----|------|------|-------|------|------|------|------|------|
| A | 2.9   | 3.4  | 4.8  | 12.1 | 7.0  | 6.0  | 3.5 | 5.4  | 8.1  | 1.4   | 11.7 | 8.4  | 5.6  | -0.3 | 6.5  |
| D | 5.9   | 8.2  | 8.6  | 21.0 | 17.8 |      | 5.6 | 6.9  |      | -3.4  | 14.4 | 13.5 | 9.8  | 0.1  | 3.6  |
| E | 6.9   | 2.5  |      | 13.7 | 12.1 | 19.0 | 4.1 | 4.3  | 1.6  | -0.4  | 20.4 | 4.4  | 8.6  | -1.2 |      |
| F | -3.0  | -1.5 | 0.0  | -3.9 | -0.2 | 13.4 | 2.0 | 3.3  | 2.3  | -7.7  | 26.4 | 0.3  | 4.1  | -0.2 | 3.4  |
| G | 3.2   | 4.8  | 6.4  | 15.1 | 9.8  | 6.8  | 3.8 | 5.5  | 9.8  | 2.1   | 13.5 | 12.8 | 7.5  | -0.1 | 8.6  |
| H | 4.4   | 1.1  | -2.2 |      | 5.9  | 12.3 | 3.2 | 3.3  | 4.9  | -5.9  | 21.3 | 4.2  | 12.0 | -0.2 | 2.8  |
| I | 1.2   | 3.9  | 2.2  | 2.9  | 1.9  | 4.6  | 0.9 | 2.5  | 6.0  | -1.8  | 12.7 | 1.2  |      | -0.2 | 4.1  |
| K |       | 2.0  | 7.9  | 8.1  |      | 25.8 | 1.6 | 3.7  | 14.4 | 4.7   | 24.1 | 9.3  | -3.0 | 1.3  | 8.6  |
| L | -4.2  | -1.1 | -3.5 | 3.1  | -1.7 | 5.1  | 1.4 | 2.2  | 2.8  | -2.3  | 1.9  | 0.5  | -1.9 |      | 3.4  |
| M | -1.5  | -0.6 | -4.7 | -4.0 | -3.2 | 4.0  |     | -2.2 | 7.0  | -6.0  | -0.9 | -4.6 | -7.4 | 0.0  | -2.4 |
| N | -1.0  | 2.8  | 6.4  | 7.7  | 5.9  | -0.4 | 2.3 | 5.3  | 4.7  | -1.9  |      | 4.2  | -1.8 | -0.3 | 6.9  |
| P | 2.4   | 2.6  | 3.9  | 7.1  | 7.0  | 7.5  | 3.1 | 4.7  | 6.9  | 0.2   | 13.1 | 4.0  | 2.1  | -0.2 | 5.9  |
| Q | 1.9   | 0.2  | -2.2 | 1.1  | 4.4  | 3.1  | 0.5 | 0.8  | 8.7  | -2.7  | 3.0  | -0.5 | -5.7 | 0.1  | 1.4  |
| R | -14.9 | 2.2  | -0.8 | 6.6  | -7.4 | 16.6 | 3.4 |      | 10.9 | 3.4   | 5.4  | 4.0  | -4.5 | 1.3  | 4.7  |
| S | 2.1   | 0.3  | 4.5  | 10.6 | 6.1  | 2.4  | 3.2 | 5.6  | 6.2  |       | 9.0  | 6.7  | 5.2  | -0.3 | 6.5  |
| T | 0.9   | 0.1  | 2.3  | 5.1  | 7.3  | 5.0  | 2.3 | 4.6  | 4.9  | 0.1   | 8.2  | 4.3  | 3.9  | -0.5 | 4.2  |
| V | 1.3   | -2.1 | 2.1  | 7.8  | 3.9  | 4.2  | 2.0 | 4.8  | 5.9  | 0.4   | 5.6  |      | 1.4  | -0.3 | 5.7  |
| W | -0.5  | -1.9 | -7.8 | 8.9  | 3.6  | 39.6 | 2.9 | 3.6  | -0.5 | -13.1 | 36.8 | -0.9 | 2.9  | -4.7 | -1.2 |
| Y | -6.0  |      | 1.0  | -3.2 | 4.9  | 37.4 | 1.7 | 2.0  | 4.4  | -13.2 | 27.0 | -0.6 | -5.4 | -0.2 | 3.7  |

FIGURA 15

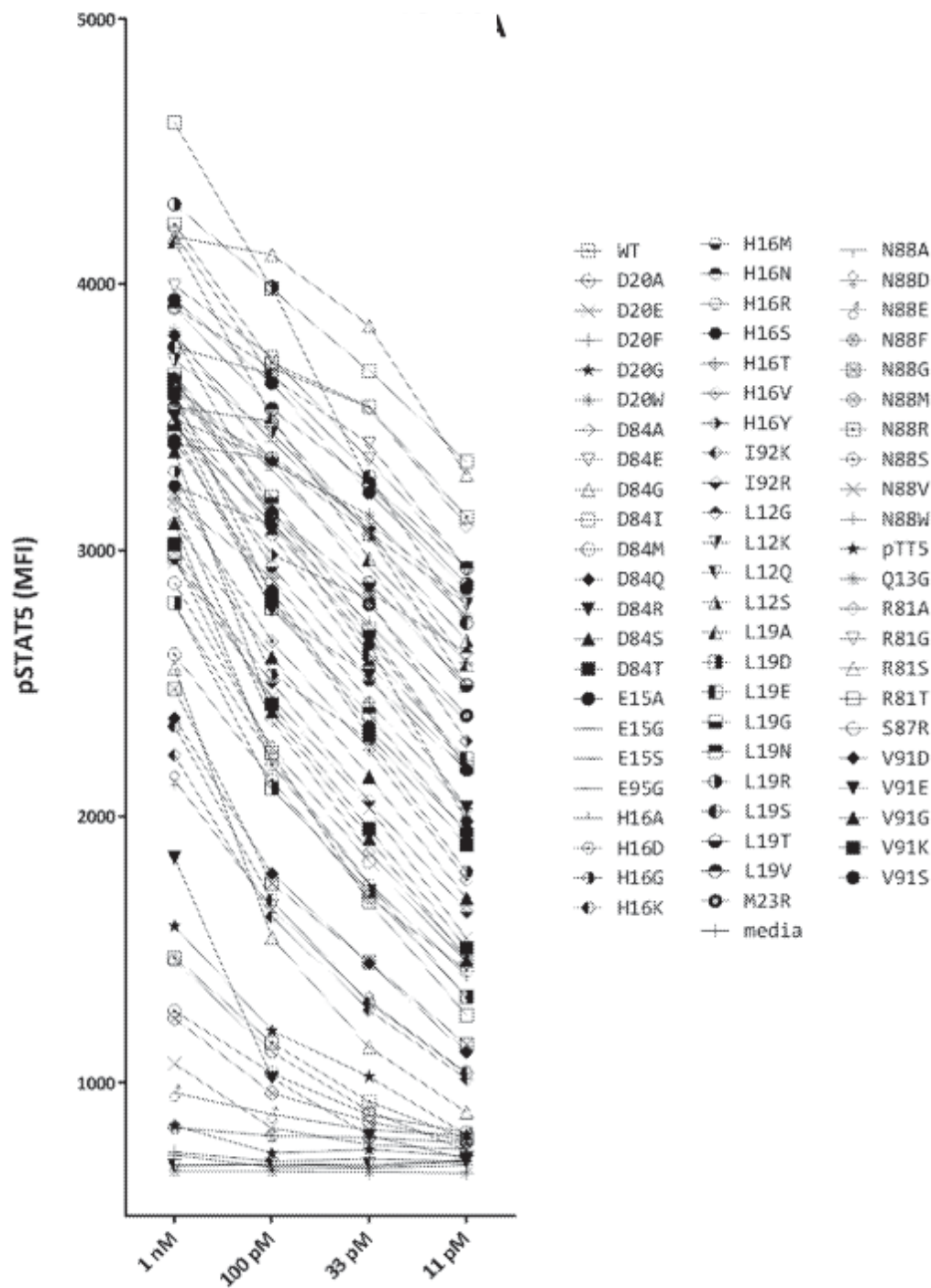


FIGURA 16A

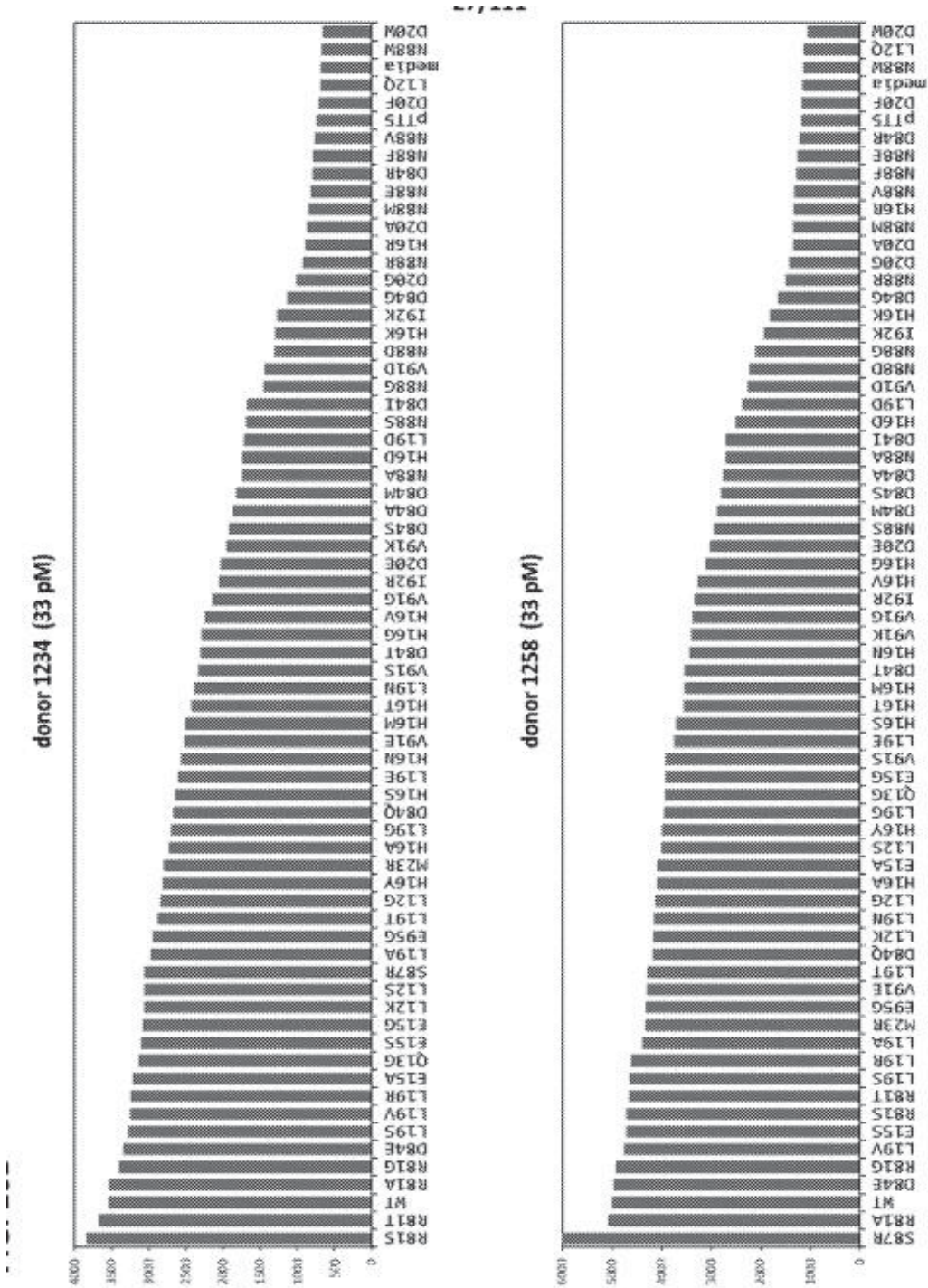


FIGURA 16B

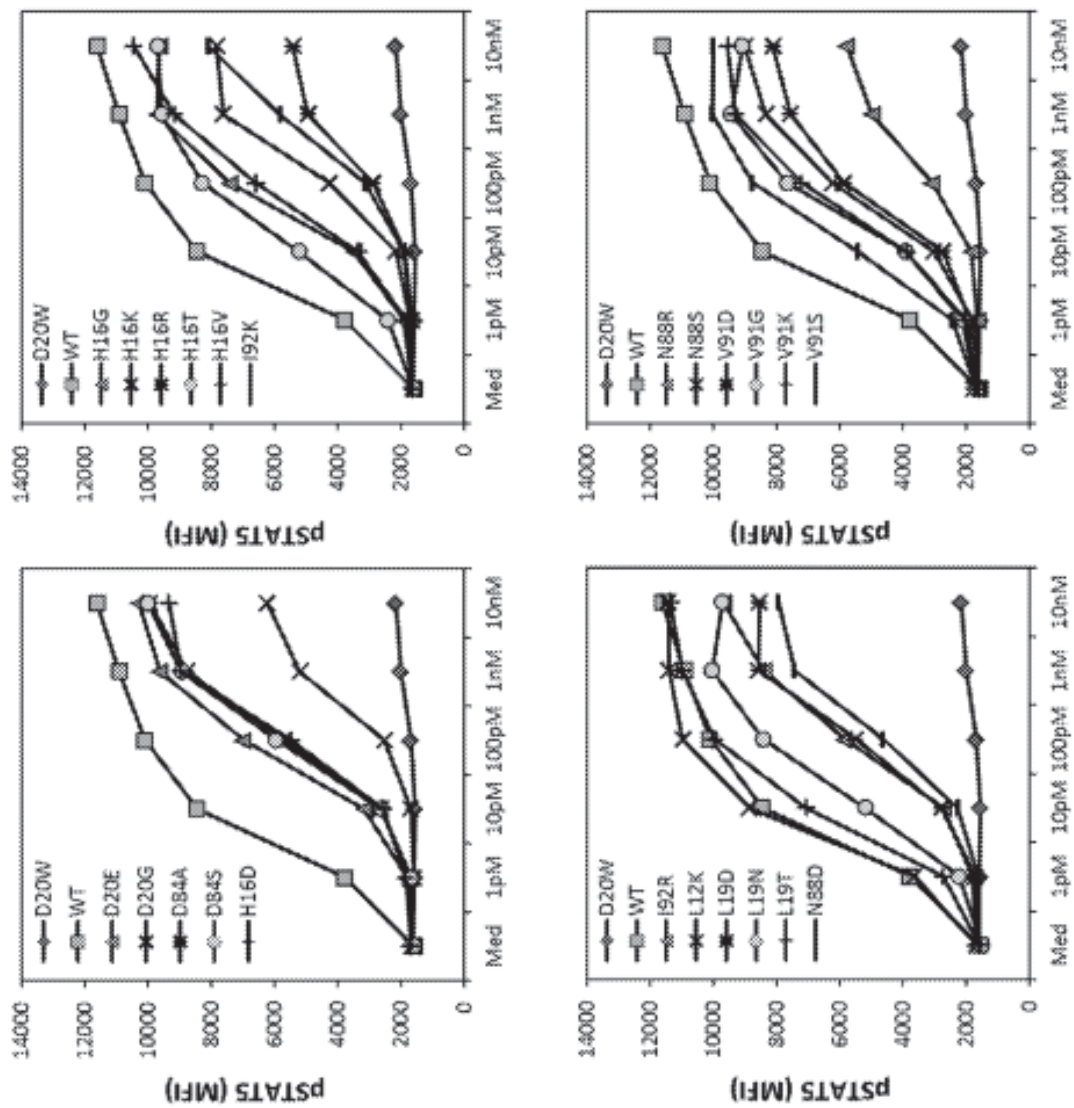


FIGURA 17

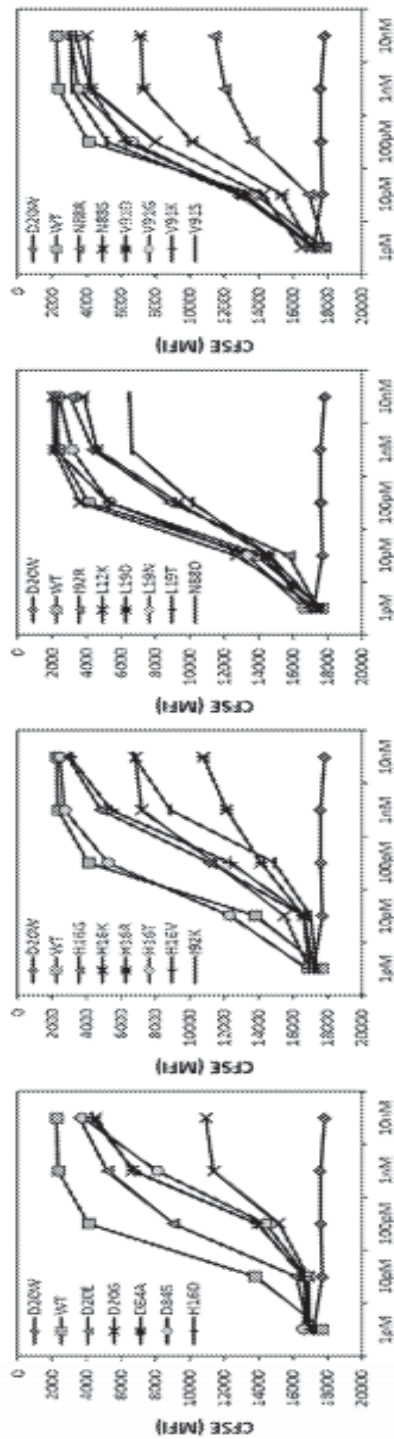
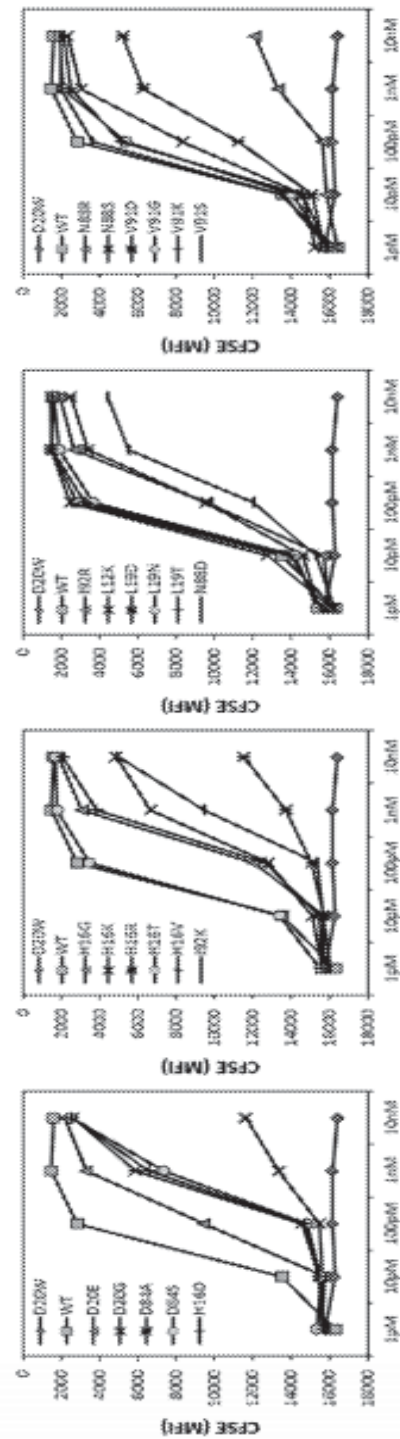


FIGURA 18B



Proliferación de FOXP3+HELIOS+CD4+

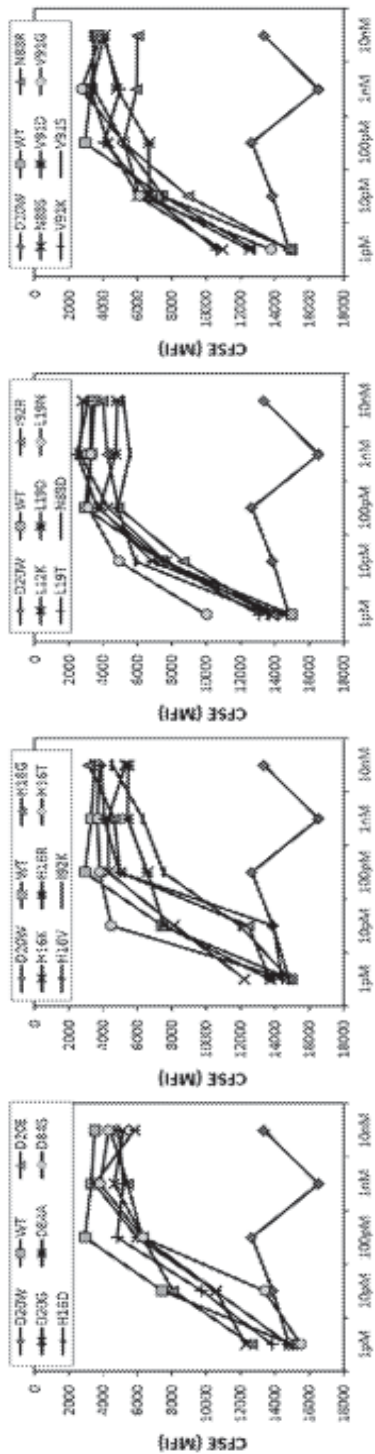


FIGURA 18C

FOXP3 MFI en FOXP3+HELIOS+CD4+

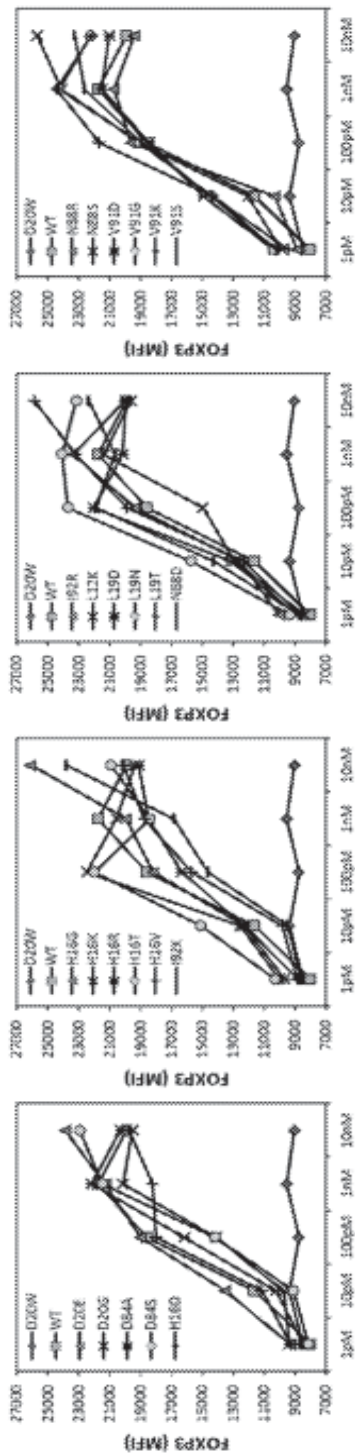


FIGURA 18D

Proliferación de Nk

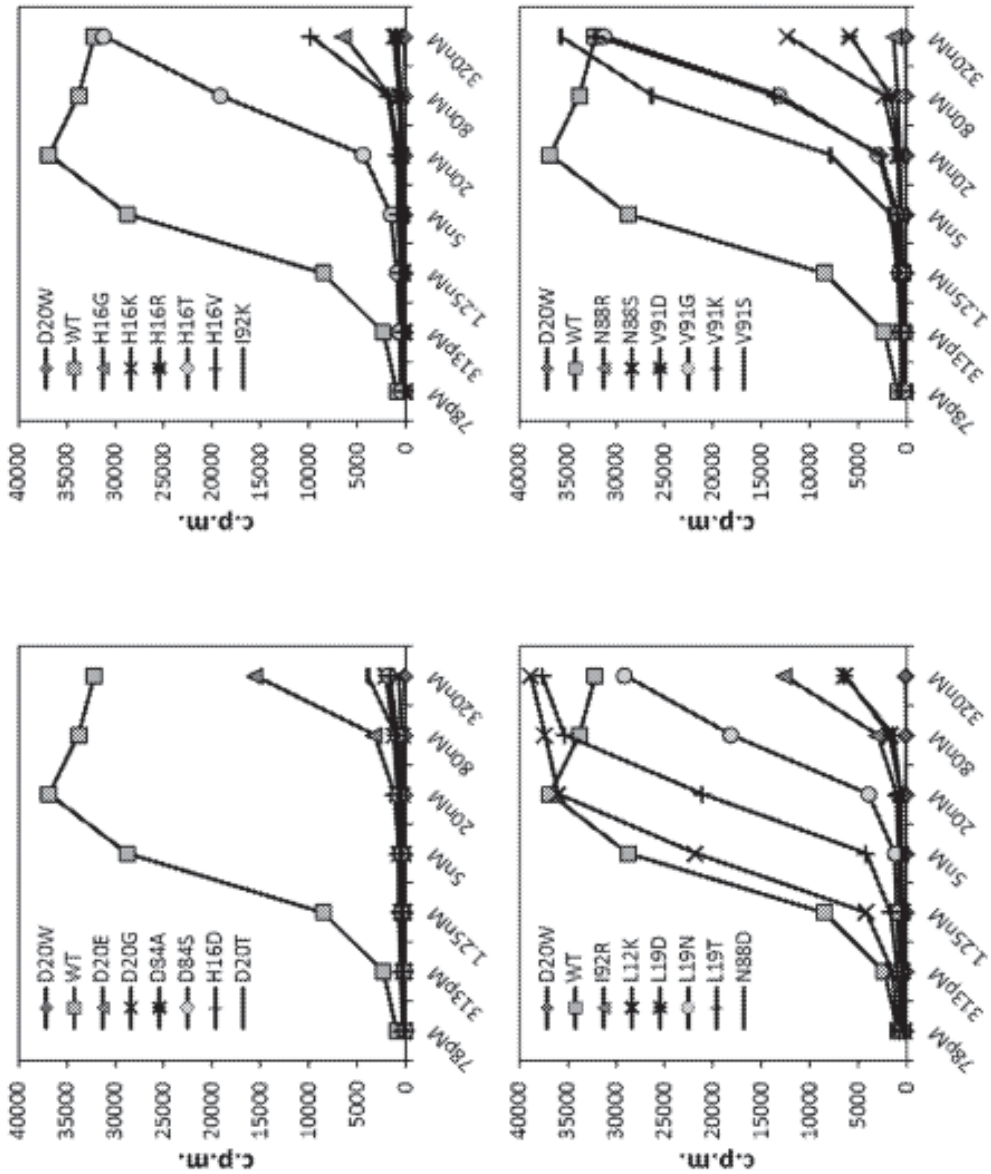


FIGURA 19

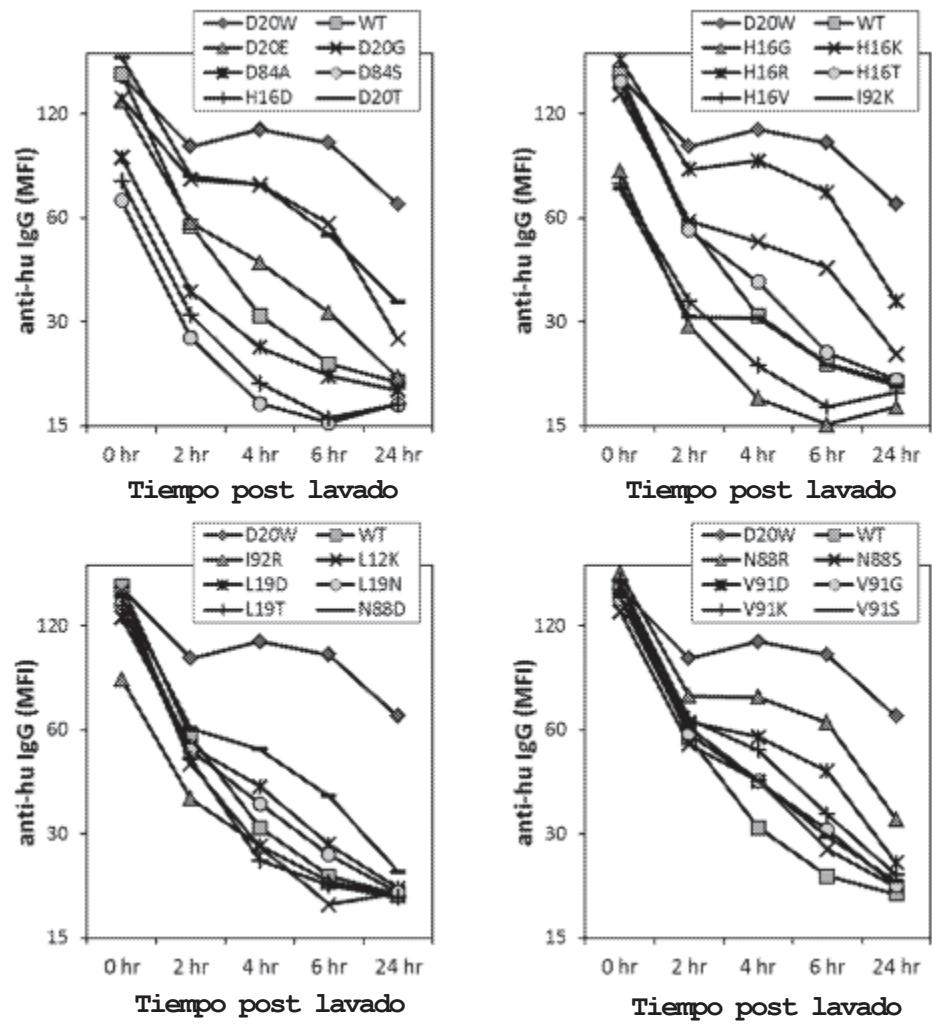


FIGURA 20A

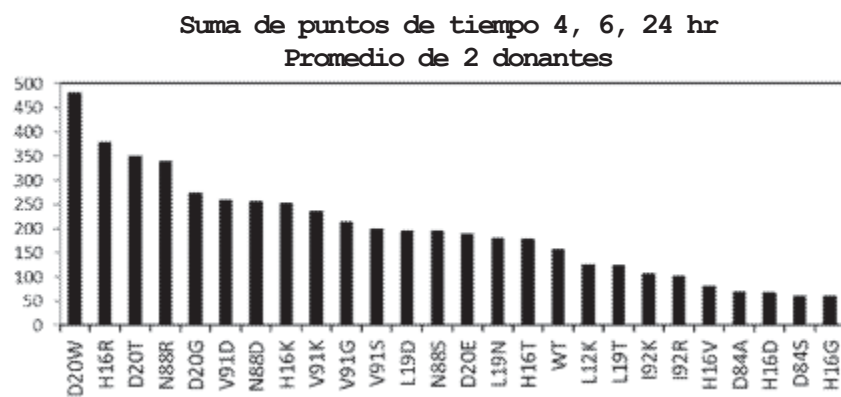


FIGURA 20B

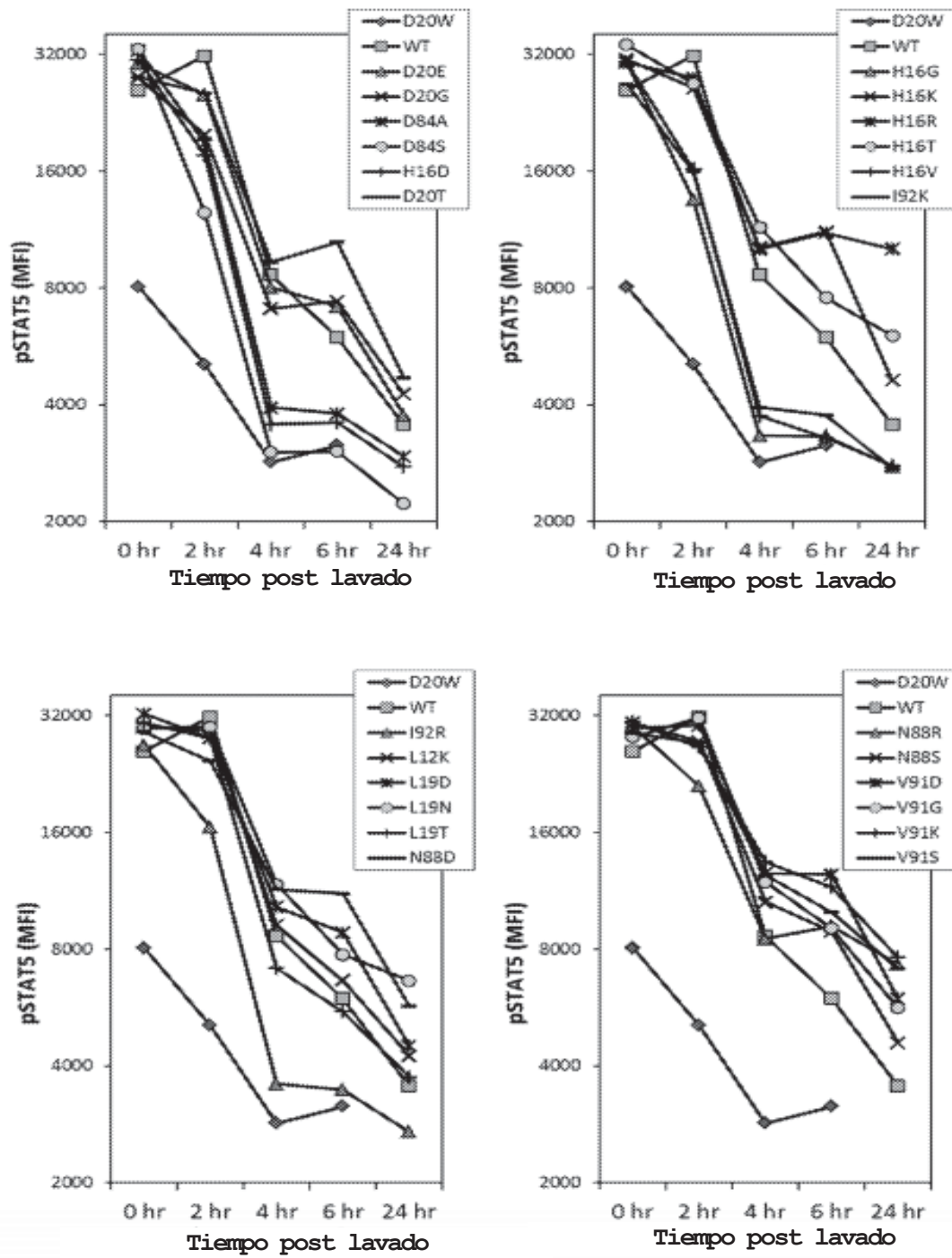


FIGURA 21

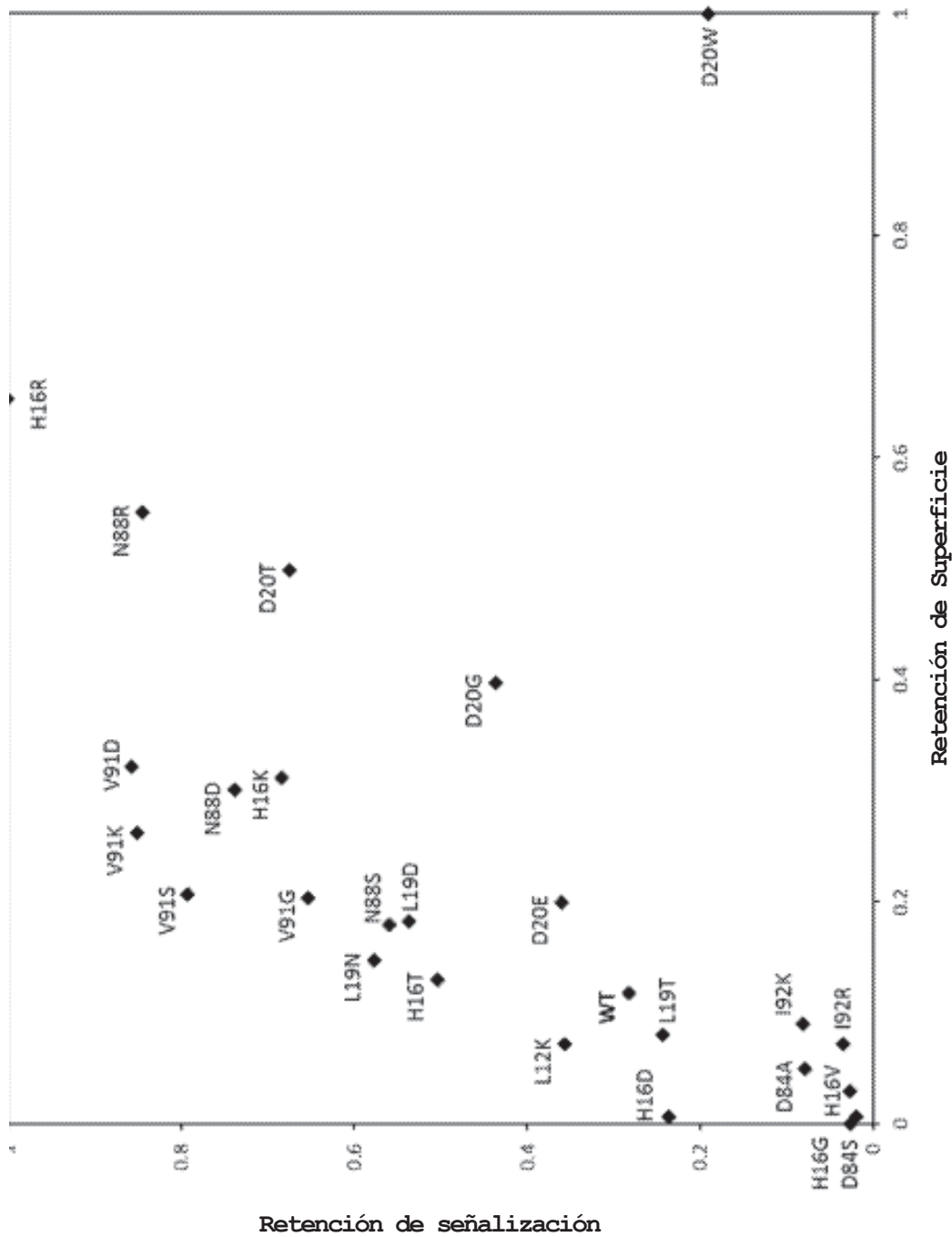
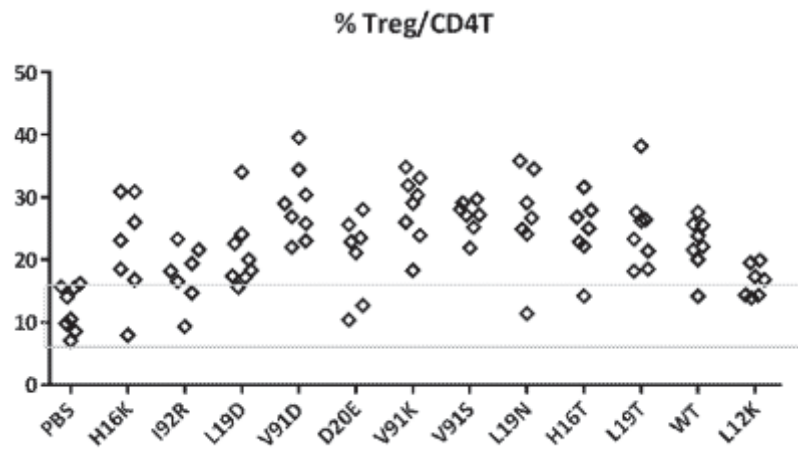
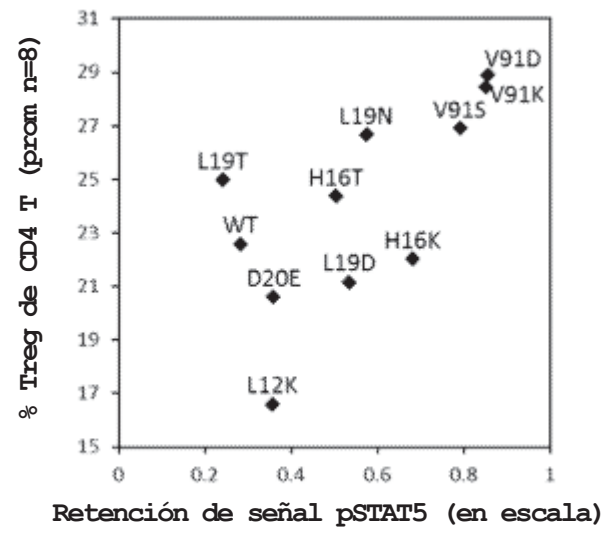


FIGURA 22

**FIGURA 23A**

**FIGURA 23B**

Fc(N297G\_delK)::G4S::IL-2(L12G, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQGGQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(L12K, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQKQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(L12Q, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQQQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(L12S, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQSQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24A**

IgG1Fc(N297G\_delK)::G4S::huIL-2(Q13G, C125A)

**MDMRVPAQLLGLLLLWLRGARC** DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLGLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(E15A, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG GG  
GGSAPTSSSTKKTQLQLAHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(E15G, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLGHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(E15S, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLSHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24B**

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16A, C125A)

**MDMRVPAQLLGLLLLWLRGARC** DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEALLDLQMLNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16D, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG GG  
GGSAPTSSSTKKTQLQLEDLLDLQMLNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16G, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEGLLLDLQMLNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16K, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEKLLDLQMLNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24C**

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16M, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
*DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS*  
*TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV*  
*YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL*  
*DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG*  
**GG***SAPTSSTKKTQLQLEMLLLDLQMILNGINNYKNPKLTRMLTFKFYMP*  
*KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINIVIVLELK*  
*GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT*

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16N, C125A)

**MDMRVPAQLLGLLLLWLRGARC DKTHTCPPCPAPELLGGPSVFLFPPKPK**  
*DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS*  
*TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV*  
*YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL*  
*DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG*  
**GG***SAPTSSTKKTQLQLENLLLDLQMILNGINNYKNPKLTRMLTFKFYMP*  
*KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINIVIVLELK*  
*GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT*

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16R, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
*DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS*  
*TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV*  
*YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL*  
*DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG*  
**GG***SAPTSSTKKTQLQLERLLLDLQMILNGINNYKNPKLTRMLTFKFYMP*  
*KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINIVIVLELK*  
*GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT*

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16S, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
*DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS*  
*TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV*  
*YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL*  
*DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG*  
**GG***SAPTSSTKKTQLQLESLLLDLQMILNGINNYKNPKLTRMLTFKFYMP*  
*KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINIVIVLELK*  
*GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT*

**FIGURA 24D**

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16T, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLETLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16V, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEVLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(H16Y, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEYLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(L19A, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLADLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24E**

IgG1Fc(N297G\_delK)::G4S::huIL-2(L19D, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
**DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS**  
**TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV**  
**YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV**  
**DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGG**  
**GG**SAPTSSSTKKTQLQLEHLLDLQMLNGINNYKNPKLTRMLTFKFYMP  
**KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK**  
**GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT**

IgG1Fc(N297G\_delK)::G4S::huIL-2(L19E, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
**DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS**  
**TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV**  
**YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV**  
**DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGG**  
**GG**SAPTSSSTKKTQLQLEHLLDLQMLNGINNYKNPKLTRMLTFKFYMP  
**KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK**  
**GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT**

IgG1Fc(N297G\_delK)::G4S::huIL-2(L19G, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
**DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS**  
**TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV**  
**YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV**  
**DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGG**  
**GG**SAPTSSSTKKTQLQLEHLLGDLQMLNGINNYKNPKLTRMLTFKFYMP  
**KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK**  
**GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT**

IgG1Fc(N297G\_delK)::G4S::huIL-2(L19N, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
**DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS**  
**TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV**  
**YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV**  
**DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGG**  
**GG**SAPTSSSTKKTQLQLEHLLNDLQMLNGINNYKNPKLTRMLTFKFYMP  
**KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK**  
**GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT**

**FIGURA 24F**

IgG1Fc(N297G\_delK)::G4S::huIL-2(L19R, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLRDQLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(L19S, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLSDQLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(L19T, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLTDQLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(L19V, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLVDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24G**

G1Fc(N297G\_delK)::G4S::hulL-2(D20A, C125A)

**IDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 /RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 FLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVL  
 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GSAPTSSSTKKTQLQLEHLLALQMLNGINNYKNPKLTRMLTFKFYMP  
 <ATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 SETTFMCEYADETATIVEFLNRWITFAQSIISTLT

G1Fc(N297G\_delK)::G4S::hulL-2(D20E, C125A)

**IDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 /RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 FLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVL  
 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GSAPTSSSTKKTQLQLEHLLLELQMLNGINNYKNPKLTRMLTFKFYMP  
 <ATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 SETTFMCEYADETATIVEFLNRWITFAQSIISTLT

G1Fc(N297G\_delK)::G4S::hulL-2(D20F, C125A)

**IDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 /RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 FLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVL  
 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GSAPTSSSTKKTQLQLEHLLFLQMLNGINNYKNPKLTRMLTFKFYMP  
 <ATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 SETTFMCEYADETATIVEFLNRWITFAQSIISTLT

G1Fc(N297G\_delK)::G4S::hulL-2(D20G, C125A)

**IDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
 TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 /RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 FLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVL  
 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GSAPTSSSTKKTQLQLEHLLGLQMLNGINNYKNPKLTRMLTFKFYMP  
 <ATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
 SETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24H**

IgG1Fc(N297G\_delK)::G4S::huIL-2(D20W, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLWLQMI LNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(M23R, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLDLQRI LNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(R81A, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLCLEEEELKPLEEVLNLAQSKNFHLAPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(R81G, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLCLEEEELKPLEEVLNLAQSKNFHLGPRDLISNINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24I**

IgG1Fc(N297G\_delK)::G4S::huIL-2(R81S, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
*DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYG*  
*TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV*  
*YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV*  
*DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG*  
GGSAPTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEELKPLEEVLNLAQSKNFHLSPRDLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(R81T, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
*DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYG*  
*TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV*  
*YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV*  
*DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG*  
GGSAPTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEELKPLEEVLNLAQSKNFHLTPRDLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(D84A, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
*DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYG*  
*TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV*  
*YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV*  
*DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG* GG  
GGSAPTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEELKPLEEVLNLAQSKNFHLRPRALISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(D84E, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
*DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYG*  
*TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV*  
*YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV*  
*DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG*  
GGSAPTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEELKPLEEVLNLAQSKNFHLRPRELISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24J**

IgG1Fc(N297G\_delK)::G4S::huIL-2(D84G, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRGLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(D84I, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRILISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(D84M, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRMLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(D84Q, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRQLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24K**

IgG1Fc(N297G\_delK)::G4S::huIL-2(D84R, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVL  
 DSDGSAFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRRLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(D84S, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVL  
 DSDGSAFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRSLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(D84T, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVL  
 DSDGSAFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRTLISNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(S87R, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVL  
 DSDGSAFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLIRNINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24L**

IgG1Fc(N297G\_delK)::G4S::hulL-2(N88A, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISAINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::hulL-2(N88E, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISEINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::hulL-2(N88F, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISFINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::hulL-2(N88G, C125A)

**MDMRVPAQLLGLLLLWLRGARC**DKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
KKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISGINVIVLELK  
GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24M**

IgG1Fc(N297G\_delK)::G4S::huIL-2(N88M, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISMINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(N88S, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISSINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(N88V, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISVINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::huIL-2(N88W, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLCLEELKPLEEVLNLAQSKNFHLRPRDLISWINVIVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 24N**

gG1Fc(N297G\_delK)::G4S::huIL-2(V91D, C125A)

**1DMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 'TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 'SDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
 'GSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINDIVLELK  
 'SETTFMCEYADETATIVEFLNRWITFAQSIISTLT

gG1Fc(N297G\_delK)::G4S::huIL-2(V91E, C125A)

**1DMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 'TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 'SDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
 'GSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINEIVLELK  
 'SETTFMCEYADETATIVEFLNRWITFAQSIISTLT

gG1Fc(N297G\_delK)::G4S::huIL-2(V91G, C125A)

**1DMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 'TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 'SDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
 'GSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINGIVLELK  
 'SETTFMCEYADETATIVEFLNRWITFAQSIISTLT

gG1Fc(N297G\_delK)::G4S::huIL-2(V91S, C125A)

**1DMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 'TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 'SDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGGG  
 'GSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINSIVLELK  
 'SETTFMCEYADETATIVEFLNRWITFAQSIISTLT

**FIGURA 240**

IgG1Fc(N297G\_delK)::G4S::hulL-2(I92K, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVKVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::hulL-2(I92R, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVRVLELK  
 GSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

IgG1Fc(N297G\_delK)::G4S::hulL-2(E95G, C125A)

**MDMRVPAQLLGLLLLWLRGARCDKTHTCPPCPAPELLGGPSVFLFPPKPK**  
 DTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGS  
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 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  
 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGG  
GGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMP  
 KKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLGLK  
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**FIGURA 24P**

### Fc(N297G\_delK)::G4S::IL-2(L12G, C125A)

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cgttgagtttttgaatcggtggatcacttttgcctcaatccatcatctcca  
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### IgG1Fc(N297G\_delK)::G4S::hulL-2(L12K, C125A)

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**FIGURA 25A**

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(L12Q, C125A)**

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(L12S, C125A)**

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 gacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtgga  
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**FIGURA 25B**

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IgG1Fc(N297G\_delK)::G4S::hulL-2(Q13G, C125A)

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FIGURA 25C

IgG1Fc(N297G\_delK)::G4S::hulL-2(E15A, C125A)

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IgG1Fc(N297G\_delK)::G4S::hulL-2(E15G, C125A)

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**FIGURA 25D**

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**IgG1Fc(N297G\_delK)::G4S::hull-2(E15S, C125A)**

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**IgG1Fc(N297G\_delK)::G4S::hull-2(H16A, C125A)**

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**FIGURA 25E**

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(H16D, C125A)**

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**FIGURA 25F**

I  
IgG1Fc(N297G\_delK)::G4S::hulL-2(H16G, C125A)

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IgG1Fc(N297G\_delK)::G4S::hulL-2(H16K, C125A)

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FIGURA 25G

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IgG1Fc(N297G\_delK)::G4S::hulL-2(H16M, C125A)

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IgG1Fc(N297G\_delK)::G4S::hulL-2(H16N, C125A)

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FIGURA 25H

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IgG1Fc(N297G\_delK)::G4S::hulL-2(H16R, C125A)

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**FIGURA 25I**

## IgG1Fc(N297G\_delK)::G4S::hulL-2(H16S, C125A)

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## IgG1Fc(N297G\_delK)::G4S::hulL-2(H16T, C125A)

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FIGURA 25J

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IgG1Fc(N297G\_delK)::G4S::hulL-2(H16V, C125A)

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IgG1Fc(N297G\_delK)::G4S::hulL-2(H16Y, C125A)

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**FIGURA 25K**

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IgG1Fc(N297G\_delK)::G4S::hull-2(L19A, C125A)

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**FIGURA 25L**

**IgG1Fc(N297G\_delK)::G4S::hulL-2(L19D, C125A)**

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(L19E, C125A)**

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**FIGURA 25M**

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(L19G, C125A)**

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(L19N, C125A)**

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**FIGURA 25N**

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 aagaaggctactgagttgaagcacttgcaatggttgaggaggaggttgaa  
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IgG1Fc(N297G\_delK)::G4S::hulL-2(L19R, C125A)

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FIGURA 250

## IgG1Fc(N297G\_delK)::G4S::hull-2(L19S, C125A)

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## IgG1Fc(N297G\_delK)::G4S::hull-2(L19T, C125A)

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FIGURA 25P

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IgG1Fc(N297G\_delK)::G4S::hulL-2(L19V, C125A)

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IgG1Fc(N297G\_delK)::G4S::hulL-2(D20A, C125A)

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FIGURA 25Q

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IgG1Fc(N297G\_delK)::G4S::hulL-2(D20E, C125A)

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**FIGURA 25R**

## IgG1Fc(N297G\_delK)::G4S::hulL-2(D20F, C125A)

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## IgG1Fc(N297G\_delK)::G4S::hulL-2(D20G, C125A)

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FIGURA 25S

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IgG1Fc(N297G\_delK)::G4S::hulL-2(D20W, C125A)

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IgG1Fc(N297G\_delK)::G4S::hulL-2(M23R, C125A)

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**FIGURA 25T**

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IgG1Fc(N297G\_delK)::G4S::hulL-2(R81A, C125A)

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FIGURA 25U

**IgG1Fc(N297G\_delK)::G4S::hulL-2(R81G, C125A)**

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(R81S, C125A)**

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**FIGURA 25V**

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(R81T, C125A)**

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(D84A, C125A)**

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**FIGURA 25W**

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IgG1Fc(N297G\_delK)::G4S::hull-2(D84E, C125A)

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FIGURA 25X

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## IgG1Fc(N297G\_delK)::G4S::hulL-2(D84I, C125A)

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FIGURA 25Y

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(D84M, C125A)**

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(D84Q, C125A)**

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**FIGURA 25Z**

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IgG1Fc(N297G\_delK)::G4S::hulL-2(D84R, C125A)

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FIGURA 25AA

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IgG1Fc(N297G\_delK)::G4S::hulL-2(D84S, C125A)

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**FIGURA 25DD**

II

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IgG1Fc(N297G\_delK)::G4S::hulL-2(N88G, C125A)

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FIGURA 25EE

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**FIGURA 25FF**

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IgG1Fc(N297G\_delK)::G4S::hulL-2(N88V, C125A)

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**FIGURA 25GG**

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IgG1Fc(N297G\_delK)::G4S::hulL-2(V91D, C125A)

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FIGURA 25HH

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**IgG1Fc(N297G\_delK)::G4S::hulL-2(V91E, C125A)**

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**FIGURA 25II**

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 ggtggaagcgctccaacttcctcctccactaagaagactcaattgcaatt  
 ggagcacttggtgttggtgacttgcaaatgatcttgatgggtatcaataatt  
 acaagaatccaaagttgactcggatggtgacttttaagttttacatgccaa  
 aagaaggctactgagttgaagcacttgcaatggttgaggaggaggtgaa  
 gccattggaggagggttttgaatttggctcaatccaagaattttcacttgc  
 ggccacgggacttgatctccaatatcaatGGGatcggttttggagttgaag  
 ggttccgagactacttttatgtgtgagtacgctgacgagactgctactat  
 cgttgagtttttgaatcgggtggatcacttttgcctcaatccatcatctcca  
 ctttgact

**IgG1Fc(N297G\_delK)::G4S::hulL-2(V91S, C125A)**

atggacatgagagtgacctgcacagctgctgggcctgctgctgctgtggct  
 gagaggcgccagatgcgacaaaactcacacatgccaccgtgcccagcac  
 ctgaactcctgggggggaccgtcagtccttctcttccccccaaaacccaag  
 gacacctcatgatctcccggaaccttgaggtcacatgcgtgggtgggtgga  
 cgtgagccacgaagacctgaggtcaagttcaactggtacgtggacggcg  
 tggaggtgcataatgccaaagacaaagccgcgggaggagcagtacggcagc  
 acgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaa  
 tggcaaggagtacaagtgaagggtctccaacaaagccctcccagcccca  
 tcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtg  
 tacaccctgcccccatcccgggaggagatgaccaagaaccaggtcagcct  
 gacctgcctgggtcaaaggcttctatcccagcgcacatcgccgtggagtggg  
 agagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctg  
 gactccgacgggtccttcttctctatagcaagctcaccgtggacaagag  
 caggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctc  
 tgcacaaccactacacgcagaagagcctctccctgtctccgggtggaggt  
 ggtggaagcgctccaacttcctcctccactaagaagactcaattgcaatt  
 ggagcacttggtgttggtgacttgcaaatgatcttgatgggtatcaataatt  
 acaagaatccaaagttgactcggatggtgacttttaagttttacatgccaa  
 aagaaggctactgagttgaagcacttgcaatggttgaggaggaggtgaa  
 gccattggaggagggttttgaatttggctcaatccaagaattttcacttgc  
 ggccacgggacttgatctccaatatcaatTCGatcggttttggagttgaag  
 ggttccgagactacttttatgtgtgagtacgctgacgagactgctactat

**FIGURA 25JJ**

cgttgagtttttgaatcgggtggatcacttttgetcaatccatcatctcca  
ctttgact

IgG1Fc(N297G\_delK)::G4S::hulL-2(I92K, C125A)

atggacatgagagtgccctgcacagctgctgggcctgctgctgctgtggct  
gagaggcgccagatgcgacaaaactcacacatgccaccgtgccagcac  
ctgaactcctggggggaccgtcagttcttctcttccccccaaaacccaag  
gacaccctcatgatctcccggaccctgaggtcacatgcgtgggtggga  
cgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcg  
tggaggtgcataatgccaaagacaaagccgcgggaggagcagtacggcagc  
acgtaccgtgtgggtcagcgtcctcaccgtcctgcaccaggactggctgaa  
tggcaaggaggtacaagtgcaaggtctccaacaaagccctcccagcccca  
tcgagaaaaccatctccaaagccaaagggcagcccccagagaaccacaggtg  
tacaccctgcccccatcccgggaggagatgaccaagaaccagggtcagcct  
gacctgcctgggtcaaaggcttctatcccagcgacatcgccgtggagtgagg  
agagcaatgggcagccggagagaacaactacaagaccacgcctcccgtgctg  
gactccgacggctccttcttctctatagcaagctcaccgtggacaagag  
caggtggcagcaggggaacgtcttctcatgctccgtgatgcagtgaggctc  
tgcacaaccactacacgcagaagagcctctccctgtctccgggtggaggt  
ggtggaagcgctccaacttctctcctccactaagaagactcaattgcaatt  
ggagcacttggttggttgacttgcaaatgatcttgaatggtatcaataatt  
acaagaatccaaagttgactcggatggttgacttttaagttttacatgcc  
aagaaggctactgagttgaagcacttgcaatggttgaggaggaggttgaa  
gccattggaggaggttttgaatttggtcgaatccaagaattttcacttgc  
ggccacgggacttgatctccaatatcaatgtgAAGgttttgaggttgaa  
ggttccgagactacttttatgtgtgagtacgctgacgagactgctactat  
cgttgagtttttgaatcgggtggatcacttttgetcaatccatcatctcca  
ctttgact

IgG1Fc(N297G\_delK)::G4S::hulL-2(I92R, C125A)

atggacatgagagtgccctgcacagctgctgggcctgctgctgctgtggct  
gagaggcgccagatgcgacaaaactcacacatgccaccgtgccagcac  
ctgaactcctggggggaccgtcagttcttctcttccccccaaaacccaag  
gacaccctcatgatctcccggaccctgaggtcacatgcgtgggtggga  
cgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcg  
tggaggtgcataatgccaaagacaaagccgcgggaggagcagtacggcagc  
acgtaccgtgtgggtcagcgtcctcaccgtcctgcaccaggactggctgaa  
tggcaaggaggtacaagtgcaaggtctccaacaaagccctcccagcccca  
tcgagaaaaccatctccaaagccaaagggcagcccccagagaaccacaggtg  
tacaccctgcccccatcccgggaggagatgaccaagaaccagggtcagcct  
gacctgcctgggtcaaaggcttctatcccagcgacatcgccgtggagtgagg  
agagcaatgggcagccggagagaacaactacaagaccacgcctcccgtgctg

**FIGURA 25KK**

gactcogacgggtccttcttctctctatagcaagctcacogtggacaagag  
caggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctc  
tgcacaaccactacaogcagaagagcctctccctgtctccgggtggaggt  
ggtggaagcgctccaacttctctctccactaagaagactcaattgcaatt  
ggagcacttggttggttgacttgcaaatgatcttgaatggtatcaataatt  
acaagaatccaaagttgactcggatggtgacttttaagttttacatgcc  
aagaaggctactgagttgaagcacttgcaatggttgaggaggaggtgaa  
gccattggaggaggttttgaatttggtcaatccaagaattttcacttgc  
ggccacgggacttgatctccaatatcaatgtgAGAgttttggagttgaag  
ggttcogagactacttttatgtgtgagtacgctgacgagactgctactat  
cgttgagtttttgaatcgggtggatcacttttgctcaatccatcatctcca  
ctttgact

IgG1Fc(N297G\_delK)::G4S::hull-2(E95G, C125A)

atggacatgagagtgcctgcacagctgctgggcctgctgctgctgtggct  
gagaggcgccagatgcgacaaaactcacacatgccaccgtgccacagcac  
ctgaactcctggggggacogtcagtcttctcttccccccaaaacccaag  
gacacctcatgatctcccgaccctgaggtcacatgcgtgggtggtgga  
cgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcg  
tggaggtgcataatgccaaagacaaagccgcgggaggagcagtacggcagc  
acgtaccgtgtggtcagcgtctctcaccgtctctgcaccaggactggctgaa  
tggcaaggagtacaagtgaaggtctccaacaaagccctcccagcccca  
tcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtg  
tacacctgcccccatcccgggaggagatgaccaagaaccaggtcagcct  
gaactgcctgggtcaaaggcttctatcccagcgacatcgccgtggagtggg  
agagcaatgggcagccggagaaactacaagaccacgcctcccgtgctg  
gactcogacgggtccttcttctctatagcaagctcacogtggacaagag  
caggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctc  
tgcacaaccactacaogcagaagagcctctccctgtctccgggtggaggt  
ggtggaagcgctccaacttctctctccactaagaagactcaattgcaatt  
ggagcacttggttggttgacttgcaaatgatcttgaatggtatcaataatt  
acaagaatccaaagttgactcggatggtgacttttaagttttacatgcc  
aagaaggctactgagttgaagcacttgcaatggttgaggaggaggtgaa  
gccattggaggaggttttgaatttggtcaatccaagaattttcacttgc  
ggccacgggacttgatctccaatatcaatgtgatcgttttgGGGttgaag  
ggttcogagactacttttatgtgtgagtacgctgacgagactgctactat  
cgttgagtttttgaatcgggtggatcacttttgctcaatccatcatctcca  
ctttgact

**FIGURA 25LL**

# Secuencias de Aminoácidos de Dominio Variable de Cadena Ligera

|       | FR1                                                                                                                        | CDR1 | FR2 | CDR2 | FR3 | CDR3 | FR4 |
|-------|----------------------------------------------------------------------------------------------------------------------------|------|-----|------|-----|------|-----|
| 9D6   | DI VMTQ TPLSLPVTTFGEPA SISC RSQS LLS DSGNTYL DWY LQKPGQSPOLLIVITLSYRASGVDPDRFSGSGTSDFTLKISRVEAEDVGYVYCMORIEPPLTFGGGTVKEIKR |      |     |      |     |      |     |
| 2C3   | EIVLTQSPGTL SLSPGERATLS CRASQSFSSSYLVAYVQKPGQAPRLIYGA SSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYVYCYQGSSPLTFGGGTVKEIKR             |      |     |      |     |      |     |
| 14C9  | DI VLTQ TPLSLPVTTLGQPASISCRSSHLLIHS DGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR         |      |     |      |     |      |     |
| 8B12  | DI VMTQ TPLSLPVTTLGQPASISCRSSQNLVQSDGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR          |      |     |      |     |      |     |
| 16A4  | DI VMTQ TPLSLPVTTLGQPASISCRSSQNLVQSDGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR          |      |     |      |     |      |     |
| 16E1  | DI VMTQ TPLSLPVTTLGQPASISCRSSQNLVQSDGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR          |      |     |      |     |      |     |
| 13A1  | DI VMTQ TPLSLPVTTLGQPASISCRSSHLSLVHSDGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR         |      |     |      |     |      |     |
| 8F10  | DI AMSQPLSLPVTTFGEPA SISC RSQS LLS DSGNTYL DWY LQKPGQSPOLLIVITLSYRASGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR        |      |     |      |     |      |     |
| 12C4  | DI VMTQ TPLSLPVTTFGEPA SISC RSQS LLS DSGNTYL DWY LQKPGQSPOLLIVITLSYRASGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR      |      |     |      |     |      |     |
| 9B12  | DI VMTQ TPLSLPVTTFGEPA SISC RSQS LLS DSGNTYL DWY LQKPGQSPOLLIVITLSYRASGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR      |      |     |      |     |      |     |
| 3H5   | DI VMTQ TPLSLPVTTLGQPASISCRSSQNLVQSDGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR          |      |     |      |     |      |     |
| 18A6  | DI VMTQ TPLSLPVTTLGQPASISCRSSQNLVQSDGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR          |      |     |      |     |      |     |
| 10A6  | DI VMTQ TPLSLPVTTLGQPASISCRSSQNLVQSDGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR          |      |     |      |     |      |     |
| 10H7  | DI VMTQ TPLSLPVTTLGQPASISCRSSHNLVRS DGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR         |      |     |      |     |      |     |
| 15A10 | DI VMTQ TPLSLPVTTLGQPASISCRSSQNLVQSDGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR          |      |     |      |     |      |     |
| 12D2  | DI VMTQ TPLSLPVTTLGQPASISCRSSHLLIHS DGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR         |      |     |      |     |      |     |
| 9B10  | DI VMTQ TPLSLPVTTLGQPASISCRSSHLLIHS DGN TYLSW LQRP GPQPRLLIYKISNRFSGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMQTTFPTFGGTVKEIKR         |      |     |      |     |      |     |
| 17D3  | EIVLTQSPGTL SLSPGERATLS CRASQSFSSSYLVAYVQKPGQAPRLIYGA SSRATGIPDRFSGSGTDFTLTISRLEPEDFAVYVYCYQGSSPLTFGGGTVKEIKR              |      |     |      |     |      |     |
| 15G11 | EIVLTQSPGTL SLSPGERATLS CRASQSFSSSYLVAYVQKPGQAPRLIYGA SSRATGIPDRFSGSGTDFTLTISRLEPEDFAVYVYCYQGSSPLTFGGGTVKEIKR              |      |     |      |     |      |     |
| 14D7  | DI QMTQSPSSLSASVGDRTVITCRASQTISSYLVAYVQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR               |      |     |      |     |      |     |
| 18F3  | SYELTQPPSVSVSPGQTARIACSGDALPRKFAYWYQKSGQAPVLVIVSDSRPSGIPERFSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                    |      |     |      |     |      |     |
| 17D9  | DI QMTQSPSSLSASVGDRTVITCRASQDIDRLG WYQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                |      |     |      |     |      |     |
| 21F8  | DI QMTQSPSSLSASVGDRTVITCRASQDIDRLG WYQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                |      |     |      |     |      |     |
| 22B9  | DI QMTQSPSSLSASVGDRTVITCRASQDIDRLG WYQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                |      |     |      |     |      |     |
| 21D10 | DI QMTQSPSSLSASVGDRTVITCRASQDIDRLG WYQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                |      |     |      |     |      |     |
| 14A6  | DI QMTQSPSSLSASVGDRTVITCRASQDIDRLG WYQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                |      |     |      |     |      |     |
| 11D6  | DI QMTQSPSSLSASVGDRTVITCRASQDIDRLG WYQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                |      |     |      |     |      |     |
| 10A9  | DI VMTQ TPLSLPVTTFGEPA SISC RSQS LLS DSGNTYL DWY LQKPGQSPOLLIVITLSYRASGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMORIEPPLTFGGGTVKEIKR   |      |     |      |     |      |     |
| 16E3  | DI VMTQ TPLSLPVTTFGEPA SISC RSQS LLS DSGNTYL DWY LQKPGQSPOLLIVITLSYRASGVDPDRFSGSGTDFTLKISRVAEDVGYVYCMORIEPPLTFGGGTVKEIKR   |      |     |      |     |      |     |
| 14G7  | DI QMTQSPSSLSASVGDRTVITCRASQDIDRLG WYQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                |      |     |      |     |      |     |
| 5H3   | SYELTQPPSVSVSPGQTARIACSGDALPRKFAYWYQKSGQAPVLVIVSDSRPSGIPERFSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                    |      |     |      |     |      |     |
| 2B12  | SYELTQPPSVSVSPGQTARIACSGDALPRKFAYWYQKSGQAPVLVIVSDSRPSGIPERFSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                    |      |     |      |     |      |     |
| 26H7  | DI QMTQSPSSLSASVGDRTVITCRASQDIDRLG WYQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                |      |     |      |     |      |     |
| 26C12 | DI QMTQSPSSLSASVGDRTVITCRASQDIDRLG WYQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                |      |     |      |     |      |     |
| 2H11  | SYELTQPPSVSVSPGQTARIACSGDALPRKFAYWYQKSGQAPVLVIVSDSRPSGIPERFSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                    |      |     |      |     |      |     |
| 18H9  | DI QMTQSPSSLSASVGDRTVITCRASQDIDRLG WYQKPGKAPKRLIYAS SFGSGVPSRFGSGSGTDFTLTISRLEPEDFAVYVYCYQSHYIPRTFGGTVKEIKR                |      |     |      |     |      |     |

FIGURA 26

**Secuencias de Ácido Nucleico de Cadena Ligera**

9D6

GATATTGTGATGACCCAGACTCCACTCTCCTTGCCCCTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAG  
 TCAGAGCCTCTTAGATAGTGATGAGGGAAACACCTATTTGGACTGGTACCTGCAGAAGCCAGGGCAGTCTCCACA  
 GCTCCTGATCTATACGCTTTCCTATCGGGCCTCTGGAGTCCCAGACAGGTTCA GTGGCACTGGGTGAGACTGAT  
 TTCACACTGAAAATCAGCAGGGTGGAGGCTGAGGATGTTGGAGTTTATTACTGCATGCAACGTATAGAGTTTCCTC  
 TCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA

2C3

GAAATTGTATTGACGCAGTCTCCAGGCACCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCA  
 GTCAGAGTTTTAGCAGCAGCTACTTAGTCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGG  
 TGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCCGGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCAT  
 CAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCTCTCACTTTCGGCGGA  
 GGGACCAAGGTGGAGATCAAACGA

14C9

GATATTGTGCTGACCCAGACTCCACTCTCCTCACCTGTACCCTTGGACAGCCGGCCTCCATCTCCTGCAGGTCTAG  
 TCATCACCTCATACAGTGATGGAAACACCTACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTC  
 CTAATTTATAAGATTTCTAACCGGTTCTCTGGGGTCCCAGACAGATTCACTGGCAGTGGGACAGGGACAGATTTCA  
 CACTGAAAATCAGCAGGGTGGAGCTGGGGATGTCGGGGTTTATTACTGCATGCAAACTACACAATTTCCGACGT  
 TCGGCCAAGGGACCAAGGTGGAAATCAAACGA

8B12

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTACCCTTGGACAGCCGGCCTCCATCTCCTGCAGGTCCAG  
 TCAAAACCTCGTTCAAAGTGATGGAAACACCTACTTGAGTTGGCTTCACCAGAGGCCAGGCCAGCCTCCAAGACTC  
 CTAATTTATAAGATTTCTAACCGGTTCTCTGGGGTCCCAGACAGATTCACTGGCAGTGGGGCAGGGACAGATTTCA  
 CACTGAAAATCAGCAGGGTGGAGCTGAGGATGTCGGGGTTTATTCTGCATGCAAACTACACAATTTCCGACGTT  
 CGGCCAAGGGACCAAGGTGGAAATCAAACGA

**FIGURA 27A**

16A4

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTACCCCTTGGACAGCCGGCCTCCATTCCTGCAGGTCTAG  
TCAAATCCTCGTAAACAGTGATGGAAACACCTACTTGAGTTGGCTTCACCAGAGGCCAGGCCAGCCTCCAAGACTC  
CTAATTTATAAGATTCTAACC GGTTCTCTGGGGTCCCAGACAGATTCA GTGGCAGTGGGGCAGGGACAGATTTC  
CACTGAAAATCAGCAGGGTGGAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAACCTACACAATTTCCGACGT  
TCGGCCAAGGGACCAAGGTGGAAATCAAACGA

16E1

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTACCCCTTGGACAGCCGGCCTCCATCTCCTGCAGGTCTAG  
TCAAAGCCTCGTACGCAGTGATGGAAACACCTACTTGAGTTGGCTTCACCAGAGGCCAGGCCAGCCTCCAAGACT  
CCTAATTTATAAGATTCTAACC GGTTCTCTGGGGTCCCAGACAGATTCA GTGGCAGTGGGGCAGGGACAGATTTC  
AACTGAAAATCAGCAGGGTGGAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAACCTACACAATTTCCGACG  
TTCGGCCAAGGGACCAAGGTGGAAATCAAACGA

13A1

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTACCCCTTGGACAGCCGGCCTCCATCTCCTGCAGGTCTAG  
TCACAGCCTCGTACACAGTGATGGACACACCTACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTC  
CTACTTTATAAGATTCTAACC GGTTCTCTGGGGTCCCAGACAGATTCA GTGGCAGTGGGGCAGGGACAGATTTC  
CACTGAAAATCAGCAGGGTGGAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAACCTACACAATTTCCACTTT  
CGGCGGAGGGACCAAGGTGGAGATCAAACGA

8F10

GATATTGCGATGAGTCAGTCTCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATGTCATGCAGGTCTA  
GTCAGAGCCTCCTGCATAGTAATGGATTCAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGGT  
CCTGATCCATTTGGGTTCTGATCGGGCCTCCGGGGTCCCTGACAGGTTCA GTGGCAGTGGATCAGGCACAGATTTT  
ACATTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGAATTTATTACTGCATGCAAGCTCTACAAACTCCTCTCA  
CTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA

**FIGURA 27B**

12C4

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAG  
TCAGAGCCTCCTACATAGTAATGGATTCAACTATTTGGATTGGTTCTGCAGAAGCCAGGACAGTCTCCACAGCCC  
CTGATCTATTTGGGTTCTGATCGGGCCTCCGGGGTCCCTGACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTA  
CACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAACTCCGCTCA  
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA

9B12

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAG  
TCAGAGCCTCCTGCATAGTAATGGATTCAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC  
CTGATCTATTTGGGTTCTGATCGGGCCTCCGGGGTCCCTGACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTA  
CACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAACTCCGCTCA  
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA

3H5

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTCACCCCTGGACAGCCGGCCTCCATATCCTGCAGGTCCAG  
TCAAAGCCTCGTAAACATTGATGGAAGTACCCACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACT  
CCTAATTTATAAGATTCTAACCGTTCTCTGGGGTCCCAGACAGATTCAGTGGCAGTGGGGCAGGGACAGATTTTC  
AACTGAAGATCAGCAGGGTGGAAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAACTACACAATTTCCACAC  
TTCGGCCAAGGGACACGACTGGAGATTAAACGA

18A6

GAAATTGTGATGACCCAGACTCCACTCTCCTCACCTGTCACCCCTGGACAGCCGGCCTCCATTTCTGCAGGTCTAG  
TCAAAGCCTCGTTCAGAGTGATGGAATCACCTACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTC  
CTAATTTATAAGATTTCTAACCGTTCTCTGGGGTCCCAGACAGATTCAGTGGCAGTGGGGCAGGGACAGATTTCA  
CACTGAAAATCAGCAGGGTGGAAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAACTACACAATTTCCGACGT  
TCGGCCAAGGGACCAAGGTGGAAATCAAACGA

**FIGURA 27C**

10A6

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTCACCCTTGGACAGCCGGCCTCCATCTCCTGCAGGTCTAG  
TCAAAGCCTCGTAAACAGTGATGGAAACACCTACTTGAATTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACT  
CCTAATTTATAAGATTTCTAACCGGTTCTCTGGGGTCCCAGACAGATTCAGTGGCAGTGGGGCAGGGACAGATTT  
ACACTGAAAATCAGCAGGGTGGAAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAGCTACACAATTTCCGACG  
TTCGGCCAAGGGACCAAGGTGGAAATCAAACGA

10H7

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTCACCCTTGGACAGCCGGCCTCCATCTCCTGCAGGTCCAG  
TCACAACCTCGTACGCAGTGATGGAAACACCTACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACT  
CCTAATTTATAAGATTTCTAACCGGTTCTCTGGGGTCCCAGACAGATTCAGTGGCAGTGGGGCAGGGACAGATTT  
ACACTGAAAATCAGCAGGGTGGGAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAGCTACACAATTTCCACC  
TTCGGCCAAGGGACGCGACTGGAGATTAAACGA

15A10

AATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTCACCCTTGGACAGCCGGCCTCCATCTCCTGCAGGTCTAG  
TCAAAGCCTCGTACAACTGATGGAAACACATATTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACC  
CCTAATTTATAAGATTTCTAACCGGTTTTCTGGGGTCCCAGACAGATTCAGTGGCAGTGGGGCAGGGACAGATTT  
ACACTGAAAATCAGCAGGGTGGGAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAGTAACACAATTTCCACC  
TTCGGCCAAGGGACACGACTGGAGATTAAACGA

12D2

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTCACCCTTGGACAGCCGGCCTCCATCTCCTGTAGGTCTAG  
TCATAACCTCATACACAGTGATGGAAACACCTACTTGAGTTGGCTTCACCAGAGGCCAGGCCAGCCTCCAAGACTC  
CTAATTTATAAGATTTCTAACCGGTTCTCTGGGGTCCCGACAGATTCAGTGGCAGTGGGGCAGGGACAGATTTCA  
CACTGAAAATCAGCAGGGTGGGAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAACTTCACAGTTTCCCACTTT  
CGGCGGAGGGACCAAGGTGGAGATCAAACGA

**FIGURA 27D**

9B10

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTACCCTTGGACAGCCGGCCTCCATCTCCTGCAGGTCTAG  
TCATAACCTCCTACACAGTGATGGAAACACCTACTTGAGTTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTC  
CTAATTTATGAGATTTCTAACCGGTTCTCTGGGGTCCCAGACAGATTCAGTGGCAGTGGGGCAGGGACAGATTTCA  
CACTGAAAATCAGCAGGGTGGAAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAGTTACACAATTTCCCACTTT  
CGGCGGCGGGACCAAGGTGGAGATCAAACGA

17D3

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCA  
GTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGG  
TGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCAT  
CAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGCTCACTTTCGGCGGA  
GGGACCAAGGTGGAGATCAAACGA

15G11

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGTAGGGCCA  
GTCAGAGTGTTAGCAGCAGGTAAGCTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCCATG  
GTCCATTAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGACAGATTTCACTCTCACCAT  
CAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAATTCATCGATCACCTTCGGCCAA  
GGGACACGACTGGAGATTAAACGA

14D7

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAA  
GTCAGACCATTAGCAGTTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGGTCCTGATCTATGCTGC  
ATCCAGTTTCAAAGTGGGGTCCCATCAAGGTTCAAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC  
AGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTCACTATATCCCTCGGACGTTTCGGCCAAGGGA  
CCAAGGTGGAAATCAAACGA

**FIGURA 27E**

18F3

TCCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCCAGGACAAACGGCCAGGATCGCCTGCTCTGGAGAT  
GCATTGCCAAGAAAATTTGCTTATTGGTACCAGCAGAAGTCAGGCCAGGCCCTGTGCTGGTCATCTCTGAGGACA  
GCAGACGACCCTCCGGGATCCCTGAGAGATTCTCTGGCTCCAGCTCAGGGACAATGGCCACCTTGACTATCAGTG  
GGGCCAGGTGGAGGATGAAGCTGACTACTACTGTTTCTCAACAGACAGCAGTGCTAATCATAGGGTATTCGGCG  
GAGGGACCAAGCTGACCGTCCTAGGT

17D9

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAA  
GTCAGGACATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTG  
CATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTAGCGGCAGTGGATCTGGGACAGAATTCACCTCTACAATCG  
GCAGCCTGCAGCCTGAAGATTTACAACCTTATTACTGTCTACAGCATAATAGTTACCCGCTCACTTCGGCGGAGG  
GACCAAGGTGGAGATCAAACGA

21F8

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAA  
GTCAGGGCATTAGAGATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATATTG  
CAACCAGTTTGCAAAGTGGGGTCCCATCAAGGTTAGCGGCAGTGGATCTGGGACAGAATTCACCTCTACAATCA  
GCAGCCTGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATATTAGTTACCCGTGGACGTTGCGCCAAGG  
GACCAAGGTGGAAATCAAACGA

22B9

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAA  
GTCAGGACATCAGAGATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGTTG  
CATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTAGCGGCAGTGGATCTGGGACAGAATTCACCTCTACAATCA  
GCAGCCTGCAGCCTGAAGATTTGCAACTTATTACTGTCTACAGCATATTAGTTACCCGTGGACGTTGCGCCAAGG  
GACCAAGGTGGAAATCAAACGA

**FIGURA 27F**

21D10

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAA  
 GTCAGGACATTAGAGATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGTTG  
 TATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACAATCA  
 GCAGCCTGCAGCCTGAAGATTTTGAACCTATTACTGTCTACAGCATAATGGTTACCCGTGGACGTTTCGGCCAAGG  
 GACCAAGGTGGAAATCAAACGA

14A6

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAA  
 GTCAGGGCATTGGAGATGATTTAGGCTGGTATCAGCAGAAAGCCAGGAAAAGCCCCTCAGCGCCTGATCTATTCTG  
 CATCCAGTTTGCCAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCCTCTCACAATCA  
 GCAGCCTGCAGCCTGAAGATTTTGAACCTATTACTGTCTACAGCATAATAGTTACCCCTCGCAGTTTTGGCCAGGG  
 GACCAAGCTGGAGATCAGACGA

11D6

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAA  
 GTCAGGACATTGAACATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTG  
 CATCCACTTTGCCAAGTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCCTCTCACAATCAG  
 CAGCCTGCAGCCTGAAGATTTTGAACCTATTACTGTCTACAGCATAATAGTTTCCCTCGCAGTTTTGGCCAGGGGA  
 CCCAGCTGGAGATCAAACGA

10A9

GATATTGTGATGACCCAGACTCCACTCTCCCTGCCCCTGACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAC  
 TCAGAGCCTCTTGATGGTGATGATGGAAACACCCTTTTGGACTGGTACCTGCAGAAGCCAGGGCAGTCTCCACA  
 GCTCCTGATCTATACGCTTTCCTATCGGGCCTCTGGAGTCCAGACAGGTTTCAGTGGCAGTGGGTTCAGGCACTGAT  
 TTCACACTGAAAATCAGCAGGGTGGAGGCTGAGGATGTTGGAGTTTATTACTGCATGCAACGTTTAGAGTTTCCTC  
 TCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA

**FIGURA 27G**

16E3

GACATTGTGATGACCCAGACTCCACTCTCCTTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAG  
TCAGAGCCTCTTGGATAGTGATGAAGGAAACACCTTTTTGGATTGGTACCTGCAGAAGCCAGGGCAGCCTCCACA  
GCTCCTGATCTATACGCTTTCCTATCGGGCCTCTGGAGTCCCAGACAGGTTCA GTGGCAGTGGGTCAGGCACTGAT  
TTCACACTGAAAATCAGCAGGGTGGAGGCTGAGGATGTTGGAGTTTATTACTGCATGCAACGTATAGAGTTTCCTC  
TCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA

14G7

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGA  
GTCAGGACATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTACGATGC  
ATCCAATTTGGAAACAGGGTCCCATCAAGGTTCA GTGGAAGTGGATCTGAGACAGATTTTACTTTCACCATCAGC  
AGCCTGCAGCCTGAAGATATTGCAACATATTACTGTCAACAGTATGAAAATCTCCATTCACTTTCGGCCCTGGGAC  
CAAAGTGGATATCAAACGA

5H3

TCCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACCTGCTCTGGAGAT  
GCATTGCCAAGGCAATATGCTTATTGGTACCAGCAGAAGCCAGGCCAGGCCCTATGCTGGTGATATATAAAGAC  
AGTGAGAGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAGCTCAGGGACAACAGTCACGTTGACCATCAGT  
GGAGTCCAGGCAGAAAGACGAGGCTGACTATTACTGTCAATCAGCAGACAGCAGTGGTACTTATGTGGTATTCGGC  
GGAGGGACCAAGCTGACCGTCCTAGGT

2B12

TCCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCCCAGGACAAACGGCCAGGATCACCTGCTCTGGAGAT  
GCATTGCCAAGAAAATATGCTTATTGGTACCAGCAGAAGTCAGGCCAGGCCCTGTGCTGGTCATCTATGAGGAC  
AGCAAACGACCCTCCGGGATCCCTGAGAGATTCTCTGGCTCCAGCTCAGGGACAATGGCCACCTTGACTATCAGTG  
GGGCCCAGGTGGAGGACGAAGCTGACTACTACTGTTACTCAACAGACAGCAGTGGTAATCATTATGTCTTCGGAA  
CTGGGACCAAGGTCACCGTCCTAGGT

**FIGURA 27H**

26H7

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGA  
 GTCAGGACATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGTTCCTGATCTACGATGC  
 ATCCAATTTGGAAACAGGGGTCCCATCAAGGTTCAGTGGAAGTGGATCTGGGACAGATTTTTTTTACCATCAGC  
 AACCTGCAGCCTGAAGATATTGCAACATATTTCTGTCAACAGGATGATAATCTCCCATTCACTTTCGGCCCTGGGAC  
 CAAAGTGGATATCAAACGA

26C12

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGA  
 GTCAGGACATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTACGATGC  
 ATCCAATTTGGAAACAGGGGTCCCATCAAGGTTCAGTGGAAGTGGATCTGGGACAGATTTTACTTTCACCATCAGC  
 AGCCTGCAGCCTGAAGATATTGCAACATTTTACTGTCAACAGTATGATAATCTCCCATTCACTTTCGGCCCTGGGAC  
 CAAAGTGGATATCAAACGA

2H11

TCCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCCAGGACAAACGGCCAGGATCACCTGCTCTGGAGAT  
 GCATTGCCAAGAAAATTTGCTTATTGGTACCAGCAGAAGTCAGGCCAGGCCCTGTGCTGGTCATCTATGAGGAC  
 AGGAAACGACCCTCCGGGATCCCTGAGAGATTCTTGCTCCAGCTCAGGGACAATGGCCACCTTGACTATCAGT  
 GGGGCCCAGGTGGAGGATGAAGCTGACTACTACTGTTACTCAACAGACCGCAGTGGTGATCATGTGGTATTCGGC  
 GGAGGGACCAAGCTGACCGTCCTAGGT

18H9

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGGGCGA  
 GTCAGGGTATTAGCAACTGGTTAGTCTGGTATCAGCAGAAACCAGGGAAACCCCTAAACTCCTGATCTATGCTGC  
 ATCCAGTTTGCAAAATGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC  
 AGCCTGCAGACTGAAGATTTTGCAACTTACTATTGTCAACAGGCTCTCAGTTTCCCGTGGACGTTTCGGCCAGGGA  
 CCAAGGTGGAAGTCAAACGA

FIGURA 27I



**Secuencias de Ácido Nucleico de Cadena Pesada**

9D6

GAGGTGCAGTTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTC  
TGGATACAGGTTTACCAGCTACTGGATCGGCTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGA  
TCATCCATCCTGGTGA CTCTGATACCAGATACAGCCCGTCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCC  
ATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACTGCCATATATTACTGTACGAGACAGGGT  
AGAAGCTTCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

2C3

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTC  
TGGATACAGGTTTACCAGCTACTGGATCGGCTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGA  
TCATCTATCCTGGTGA CTCTGATACCAGATACAGCCCGTCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCC  
ATCAGCGCCGCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGACAACAA  
GTGGCTGGTATGTTGGA CTACTGGGGCCAAGGGAACCTGGTCACCGTCTCCTCA

14C9

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
TGGATTACCTTCAGTATTTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACAGT  
TATATGGTATGATGGAAGTAATGAATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAGGA  
CTTCGACTCCCACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

8B12

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
TGGATTACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAG  
TTATATGGTATGATGGAAGTAATGAATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
CAAGAACACGCTGTATCTACAAATGCACAGCCTGAGAGCCGAGGACACGGCTGTGTATTATTGTGCGAGAGAAGA  
ATGGTTCGGGGAGGCGGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

**FIGURA 29A**

16A4

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCAGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAG  
 TTATATGGTATGATGGAAGTAATGAATATTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTC  
 CAAGAACACGCTGTTTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGA  
 TTGGTTCGGGGAGGCGGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

16E1

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACAGT  
 TATATGGAATGATGGAAGTAATGAATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTC  
 AAGAACACGCTGTTTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAGAT  
 TGGCTCGGGGAGGCGGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

13A1

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAG  
 TTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTC  
 CAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAG  
 AGTGGGAGCTAGAGGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

8F10

CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTCACCTTCAGTAGTTATGGCATGTACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGT  
 TATATGGTATGATGGAAGTAATAAATACTATGTAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTC  
 AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGC  
 AGTGGCTGGTACGGGACGGGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT  
 CCTCA

**FIGURA 29B**

12C4

CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTCACGTTTCACTAGTTATGGCATGTACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAG  
 TTATATGGTATGATGGAAGTAATAAATACCATGGAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
 CAAGAATACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAAAGGAGC  
 AGTGGCTGGTACGGGACGGGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT  
 CCTCA

9B12

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCAGAGACTCTCCTGTGCAGCGTC  
 TGGATTCACCTTAGTAGTTATGGCATGTACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGT  
 TATATGGTATGATGGAAGTAATAAAAACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
 AAGAATACGTTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATCACTGTGCGAAAGGAACA  
 GTGGCTGGTACGGGACGGGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCT  
 TCA

3H5

CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTCACCTTCAGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGT  
 TATTTGGTTTGATGGAAGTAATAAATACTATGTAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
 AAGAATACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGCGGGACGAT  
 TTTTGGAGTGATTATCCTTTTACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

18A6

CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCT  
 GGATTCACCTTCAGGAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGT  
 TATATCAGATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
 AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGACCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCTC  
 TATAGCAGTGCCTGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

**FIGURA 29C**

10A6

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTACCTTCAGTAGCTATGACATACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGT  
 TATATGGAATGATGGAAGTATTAATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
 AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGG  
 GGAGCAGTGGCGGGGCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

10H7

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTACCTTCAGTAGCTATGACATACTGGGTCCGTCAAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGT  
 TATATGGTATGATGGAAGTATTAATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
 AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCAG  
 GAGCAGTGGCTGGCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

15A10

CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTACCTTCAGTACCTATGGCATGCACTGGGTCCGCCAGGCTCCAGACATGGGGCTGGAGTGGGTGGCAGT  
 TATATGGTATGATGGAAGTAATAAATACTATGCAGACTCTGTGAAGGGCCGATTACCATCTCCAGAGACATTCC  
 AAGAACACGCTGTATCTGGAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACAA  
 CTGGGGATCCGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA

12D2

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTACCTTCAGTACCTATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGT  
 TATATGGTATGATGGAATTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
 AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGAG  
 TTAATATGATAGTAGTGGTTATTACTACGGGGAGGACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC  
 TCA

FIGURA 29D

9B10

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTACCTTCAGTAGCTATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGT  
 TATCTGGTATGATGGAATTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
 AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGAG  
 TTAATATGATAGTAGTGGTTATTACTTCGGGGAGGACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC  
 TCA

17D3

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCT  
 GGATTCACCTTCAGTGACTACTACATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTCATAC  
 ATTAGTAGTAGTGGTAGTATCATTTTTACGCAGACTCTGTGAAGGGCCGATTACCATGTCCAGGGACAACGCCA  
 AGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTATTGTGTGAGAAGGATTA  
 GTATAACCCCTTTTACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

15G11

CAGGTACCTTGAAGGAGTCTGGTCCTGTGCTGGTGAACCCACAGAGACCCTCACGCTGACCTGCACCGTCTCTG  
 GGTCTCACTCAGCAATGCTAGAATGGGTGTGAGCTGGATCCGTGAGCCCCAGGGAAGGCCCTGGAGTGGCTTG  
 CACACATTTTTTCGAATGACGAAAAATCCTACAGCACATCTCTGAAGAGCAGGCTCACCATCTCAAGGACACCTCC  
 AAAAGCCAGGTGGTCCTTACCATGACCAACATGGACCTGTGGACACAGCCACATATTACTGTGTACGGATACCGA  
 GATGGCTACAACCCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

14D7

CAGGTGCAGCTGCAGGAGTCGGGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT  
 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAAGTGGATCCGCCAGCACCAGGGAAGGGCCTGGAGTGGAT  
 TGGGTACATCTATTACAGTGGGAACACCCACTACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACG  
 TCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGATTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGACT  
 GGGGACGTGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA

**FIGURA 29E**

18F3

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCG  
 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGAT  
 TGGGTACATCTATTATAGTGGGAGCACCGACTACAACCCGTCCCTCAAGAGTCGAGGTATCATATCAGGAGACAC  
 GTCTAAGAACCAGTTCTCCCTGAAGCTGAACTCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGA  
 GGGGAGGTTGCGGGAGTTAGGCTCCTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

17D9

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCT  
 GGTGGCTCCGTACAGCAGTGGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCAGGGAAGGGACTGGAGTGGAT  
 TGGGAATACCTATTACAGTGGGAGCACCAACTACAAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACG  
 TCCAAGAACCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGGGAGAGAC  
 CGGGGTAGAGCAGTGGTCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

21F8

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTC  
 TGGATACACCTTCACCAATTATGATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATG  
 GATGAACCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTC  
 CATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAAGTA  
 GGCAGTGGCTGGTACTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

22B9

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTC  
 TGGATACACCTTCACCAATTATGATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATG  
 GATGAACCCTAACAGTGGTAACACAGGCTATGTACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTC  
 CATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAAGTA  
 GGCAGTGGCTGGTACTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

**FIGURA 29F**

21D10

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTC  
TGGATACAGGTTACCAAGTTATGATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGAT  
GGATGAACCCAAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACC  
TCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAAGT  
AGGCAGTGGCTGGTACTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

14A6

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTC  
TGGATACACCTTCACCACTTATGATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATG  
GATGAACCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTC  
CATAAGCACAGCCTACATGGAGCTGAGCAGCCTAAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGCC  
GGCAGTGGCTGGGCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

11D6

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTC  
TGGATACACCTTCACCAATTATGATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGGATG  
GATGAACCCTAATAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTC  
CATAAACACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGCC  
GGCAGTGGCTGGGCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

10A9

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTC  
TGGATACAGCTTTACCAGCCAGTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAGGCCTGGAGTGGATGGGGA  
TCATCTTTCCTGGTGA CTCTGATACCAGATACAGCCCCTCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCC  
ATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGCGACAGGGT  
AGAAGTTACCACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

**FIGURA 29G**

16E3

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTC  
 TGGATACGGCTTTACCACTACTGGATCGGCTGGGTGCGCCAGATGCCCGGAAAAGGCCTGGAGTGGATGGGGA  
 CCATCTATCCTGGTGA CTCTGATACCAGATACAGTCCGTCCTTCCAAGGCCAGGTACCTTCTCAGCCGACAAGTCC  
 ATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGACAGGGT  
 AGAAGTTACTACTACTTCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

14G7

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTC  
 TGGATACAGCTTTACCGACTACTGGATCGGCTGGGTGCGCCAGATGCCCGGAAAAGGCCTGGAATGGATGGGGA  
 TCATCTATCCTTATGACTCTGATACCAGATACAGCCGTCCTTCCAAGGCCAGGTACCTTCTCAGCCGACAAGTCC  
 ATCAGCACCGCCTACCTGCGGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGACATCGG  
 GGGGGGAGGTCCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

5H3

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTC  
 TGGATACAGCTTTACCAGCTACTGGATCGGCTGGGTGCGCCAGATGCCCGGAAAAGGCCTAGAATGGATGGGGA  
 TCATCTATCCTGGTGA CTCTGATACCACATACAGCCGTCCTTCCAAGGCCAAGTCACCATCTCAGCCGACAAGTCC  
 ATCAACACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAGAGGGT  
 TTCGGGGAGTCTATTCACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

2B12

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTC  
 TGGATACAATTTTACCACTACTGGATCGGCTGGGTGCGCCAGATGTCCGGGAAAAGGCCTGGAGTGGATGGGAA  
 TCATCTATCCTGGTGA CTCTGAAACCAGATACAGCCGTCCTTCCAAGGCCAGGTACCATCTCAGCCGACAAGTC  
 CATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGG  
 AGGGGGATGGAGTGGTTGGGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

**FIGURA 29H**

26H7

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTC  
 TGGATACAGGTTTACCACTACTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGA  
 TCATCTATCCTGGTGA CTCTGATACCAAATACAGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCC  
 ATCAGTACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGT  
 GGATATAGTGGCCGTTCTACTACTACGGTATGGACGTCTGGGGCCAGGGGACCGCGGTACCGTCTCCTCA

26C12

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTC  
 TGGATACAGGTTTACCAGCTACTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGA  
 TCATCTTTCCTGGTGA CTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCC  
 ATCACCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATCTATTACTGTGCGGACATGGG  
 CATGGCAGCTCGTCCGGGCGGACCTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCC  
 TCA

2H11

GAGGTGCAGCTGGTGAATCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTC  
 TGGATACAAC TTTACCACCTACTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGA  
 TCATCTATCCTGGTGA CTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGTCACCATTTAGCCGACAAGTCC  
 ATCAACACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACAGCCATTTATTACTGTGCGAGAGACACA  
 GGATACTTTGACTACTGGGGCCAGGGCACCTGGTCACCGTCTCCTCA

18H9

CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTC  
 TGGATTACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCCTGGAGTGGGTGGCAGT  
 TATCTGGTATGATGGAAGTAATAAATTCTATGTAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCC  
 AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGACCCGG  
 GTCCGATTACTACTTCTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

**FIGURA 29I**

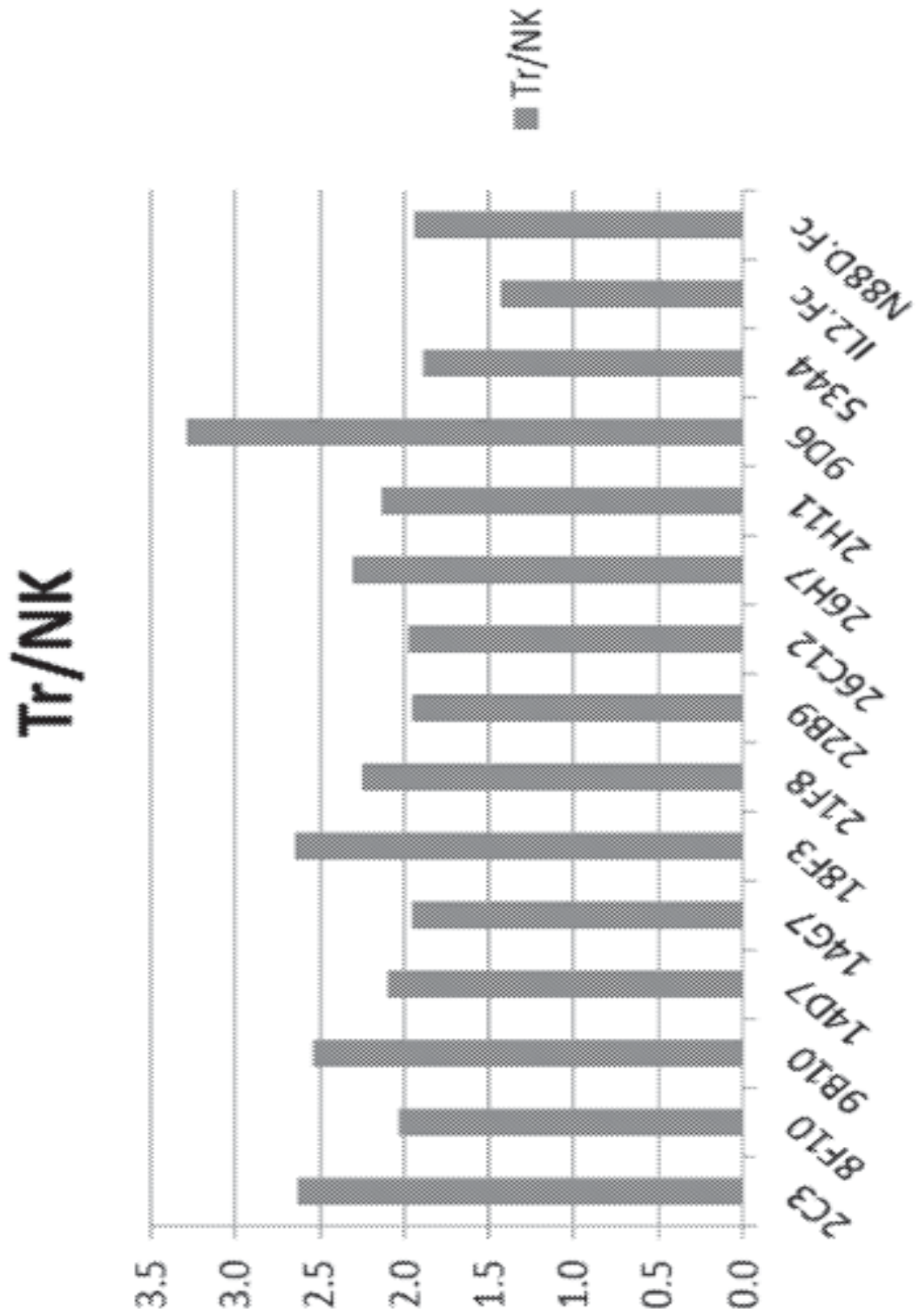


FIGURA 30