

The T cell receptor from an influenza-A specific murine CTL clone

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Recognition of virus infected cells by cytotoxic T lymphocytes, (CTLs), is dependent upon the specific association of viral antigen, class I MHC molecules and T cell receptor. An understanding of the molecular details of this tripartite interaction requires a detailed study of cloned CTLs of known antigen specificity. We report here the sequences of the alpha and beta chains from the T cell receptor of a murine CTL (F5), whose antigenic specificity has been well characterised (1). The clone F5 recognises a peptide consisting of amino acids 365-379 from the 1968 influenza-A nucleoprotein (2) in association with H-2D<sup>b</sup> (3). The alpha chain is derived from a member of the variable region gene family, V<sub>4</sub> (4), joined to a unique J region JF5. The beta chain is derived from the gene segments V<sub>β</sub>11, D<sub>β</sub>2.1 J<sub>β</sub>2.1 C<sub>β</sub>2 (5).

TCR-F5-ALPHA 27 54 81 108
ATG AAC TAT TCT CCA GCT TTA GTG ACT GTG ATG CTG TTT GTG TTT GGG AGG ACC CAT GGA GAC TCA GTA ACC CAG ATG CAA GGT CAA GTG ACC CTC TCA GAA GAC GAC
MET Aen Tyr Ser Fro Ala Leu Val Thr Val MET Leu Phe Val Phe Gly Arg Thr His Gly Asp Ser Val Thr Gln MET Gln Gly Gln Val Thr Leu Ser Gln Asp Asp
135 162 189 216
TTC CTA TTT ATA AAT TCT ACT TAT TCA ACC ACA TGG TAC CCG ACT CTT TTC TGG TTC CTA TTT ATA AAC TGT ACT TAT TCA ACC ACA TGG TAC CCG ACT CTT TTC
Phe Leu Phe Ile Aen Cys Thr Tyr Ser Thr Thr Trp Tyr Fro Thr Leu Phe Trp Tyr Val Gln Tyr Fro Gly Gln Tyr Fro Gly Gln Tyr Fro Gln Val Thr Thr
243 270 297 324
AAC AAC AAG AGA ATC AGC ACA GGT TTT GAA GCT ACA TAT GAT AAA GGA ACA ACG TCC TTC CAG TTG CAG AAA GGC TCA GTG CAG CAG TCA GAC TGT GCT GTG TAC
Aen Aen Lys Gly Ile Ser Arg Gly Phe Gln Ala Thr Tyr Asp Lys Gly Thr Thr Ser Phe His Leu Gln Lys Ala Ser Val Gln Gln Leu Ser Ser Ala Val Tyr Tyr
351 378 405 432
TGT GTG CTG GGT GAT CGA CAG GGA GGC AGA GCT CTG ATA TTT GGA ACA ACG ACC AGC GTA TCA GTC ACC CCG AAC ATC CAG AAC CCA GAA CPT GCT GTG TAC CAG TTA
Cys Val Leu Gly Asp Arg Gln Gln Gly Arg Ala Leu Ile Phe Gly Thr Gly Thr Thr Val Ser Val Ser Fro Aen Ile Gln Aen Fro Gln Fro Ala Val Tyr Gln Leu
459 486 513 540
AAA GAT CCG TCT CAG GAC AGC ACC CTC TCG CTG TTC ACC GAC TTT GAC TCC CAA ATC AAT GTG CCG AAA ACC ATG GAA ACT TTT CCA ACC TTC ATC ACT GAC AAA ACT
Lys Asp Fro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Aen Val Fro Lys Thr MET Gln Ser Gly Thr Phe Ile Thr Asp Lys Thr
567 594 621 648
GTG CTG GAC ATG AAA GCT AAT GAT TCC AAG ACC AAT GGG GGC ATT GCC TGG ACC AAC CAG ACA ACC TTC ACC TGC CAA GAT ATC TTT AAA GAG ACC AAC GCC ACC
Val Leu Asp MET Lys Ala MET Asp Ser Lys Ser Aen Gly Ala Ile Ala Trp Ser Aen Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Gln Thr Aen Ala Thr Tyr
675 702 729 756
CCC AGT TCA GAC GTF CCC TGT GAT GGC ACG TGT ACT GAG AAA ACC TTT GAA ACA GAT ATG AAC CTA AAC TTT CAA AAC CTG TCA GTT ATG GGA CTC CGA ATC CTC CTG
Fro Ser Ser Asp Val Fro Cys Asp Ala Thr Leu Thr Gln Lys Ser Phe Gln Thr Asp MET Aen Leu Aen Phe Gln Aen Leu Ser Val MET Gly Leu Arg Ile Leu Cys
783 810 837 864
CTG AAA GTA GCC GGA TTT AAG CTG CTC ATG ACC CTG AGG CTG TGG TCC AGT TGA
Leu Lys Val Ala Gly Phe Aen Leu Leu MET Thr Leu Arg Leu Trp Ser Ser .
TCR-F5-BETA 27 54 81 108
ATG GCC ACC AGG CTC CTT TTC TGT CTG GTT CTT TGC TTC TTG AGA GCA GAA CCA ACA AAT GCT GGT GTC CTC CAA ACA CCA CTT AGC CAG AAC GTG ACA GGG AAG GGA CAA
MET Ala Fro Arg Leu Leu Phe Cys Leu Val Leu Cys Phe Leu Arg Ala Gln Fro Thr Aen Ala Gly Val Ile Gln Thr Fro Arg His Lys Val Thr Gly Lys Gly Gln
135 162 189 216
GAA GCA ACT CTC TGG TOT GAG CCA ATT TCA GGA CAT AGT GCT GTF TTC TGG TAC AGA CAG ACC ATT GTG CAG GGC CTG GAG CTC ATC TAC TTT GGA AAT CAA GCT
Glu Ala Thr Leu Trp Cys Glu Fro Ile Ser Gly His Ser Ala Val Phe Thr Tyr Arg Gln Thr Ile Val Gln Gly Lys Gln Gln Phe Leu Ile Tyr Phe Arg Aen Gln Ala
243 270 297 324
CCT ATA GAT GAT TCA GGG ATG CCC AAG GAA CGA TTC TCA GCT CAG ATG CCC AAT CAG TGG CAC TCA ACT GTG AAG ATC CAG ACC ACC CAA CCC CAG CAG TCA GCG GTG
Fro Ile Asp Asp Ser Gly MET Fro Lys Glu Arg Phe Ser Ala Gln MET Fro Aen Gln Ser His Ser Thr Leu Lys Ile Gln Ser Thr Gln Fro Gln Asp Ser Ala Val
351 378 405 432
TAT CTT TOT GCA ACC AGC TCC GGC ACT GGG GGG CAT GCT GAG CAG TTC TTC GGA CGA GGG AGA CGA CTC ACC GTT CTG AAG GAT GTG AGA AAT GTG ACT CCA CCC AAG
Tyr Leu Cys Ala Ser Ser Ser Arg Thr Gly Gly His Ala Gln Phe Phe Gly Fro Gly Thr Arg Leu Thr Val Leu Gln Asp Leu Arg Aen Val Thr Fro Fro Lys
459 486 513 540
GTC TCC TTG TTT GAG CCA TCA AAA CGA GAG ATT GCA AAC AAA CAA AAG GCT ACC CTC GTC TGC TTG GGC AGG GGC TTC CTT GAC CAG CTG GAG CTG ACC TGG
Val Ser Leu Phe Gln Fro Ser Lys Ala Gln Ile Ala Aen Lys Gln Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Fro Asp His Val Gln Leu Ser Trp
567 594 621 648
GTG AAT GGC AAG GAG GTC CAG AGT GGG GCT AGC ACG GAC OCT CAG GCC TAC AAG GAG AGC AAT TAT AGC TAC TCC CTG AGC AGC CCG CTC AGG GTC TCT GCT ACC TTC
Val Aen Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Fro Gln Ala Tyr Lys Glu Ser Aen Tyr Ser Tyr Cys Leu Ser Ser Ser Arg Leu Arg Val Ser Ala Thr Phe
675 702 729 756
TGG CAG AAT COT CGA AAC CAC TTC CCC TCC CAA GAG TTC CAT GGG CTT TCA GAG GAG GAC AAG TGG CCA GAG GGC TCA CCC AAA COT GTC ACA CAG AAC ATC AGT
Trp His Aen Fro Arg Aen His Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Gln Gln Asp Lys Trp Fro Gln Gly Ser Fro Lys Fro Val Thr Gln Aen Ile Ser
783 810 837 864
CGA GAG GGC TGG GGC CGA GCA ACC TGT GGA ATC ACT TCA GCA TCC TAT CAT CAG GGG GTF CTG TCT GCA ACC ATC CTC TAT GAG ATC CTA CTG GGG AAG GCC ACA
Ala Gln Ala Trp Gly Arg Ala Asp Cys Gly Ile Thr Gln Ala Ser Tyr His Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Gln Ile Leu Leu Gly Lys Ala Thr Leu
891 918 945 972
TAT GCT GTG CTG GTC ACT GGC CTG GTG CTG ATG GGC ATG AAA AAA AAT TCC TGA
Tyr Ala Val Leu Val Ser Gly Leu Val Leu MET Ala MET Val Lys Lys Lys Aen Ser .

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