

# IARC Meeting 57: July 7th 2020: minutes

The meeting commenced at 10:30 UTC. AC, MO, CS and WL were in attendance. Corey Watson and Gur Yaari also attended.

1. The minutes of Meeting 56 were approved by the meeting attendees.
2. The meeting considered the inference of the variant IGLV2-14\*03x sequence in Genotype A007 VL, Submission S00028. The sequence appears to be an extension of the presently truncated IGLV2-14\*03 sequence. The submitted sequence is as follows:

>IGLV2-14\*03x

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cagtctgcctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgtt
gggtgtataactatgtctcctggtaccaacaacacccaggcaagcccccaactcatgattatgatgtcagtaatcggccctc
aggggtttctaatacgtctctctggctccaagtctggcaacacggcctcctgacctctctgggctccaggctgaggacgaggctg
attattactgcagctcatatacaagcagcagcactctc
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The sequence was seen in 6.08% of all unmutated rearrangements, with 71,826 sequences including 7262 perfect alignments to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. A second inferred IGLV2-14 allele, a likely extension of the truncated sequence IGLV2-14\*04, was also present in the genotype, at a similar frequency. Haplotype data is unavailable. Plots of the final 3' nucleotides were considered, but the variability seen made it impossible to consider the final two nucleotides of the sequence. The sequence has previously been reported as IGLV2-14\*p05. The sequence, up to and including nucleotide 337, was affirmed as the Level 1 sequence, IGLV2-14\*i01. Uncertainty regarding nucleotides 338-339 will be indicated in IARC and OGRDB publications by two dots at the end of the affirmed sequence. The accepted sequence is as follows:

>IGLV2-14\*i01

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cagtctgcctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgtt
gggtgtataactatgtctcctggtaccaacaacacccaggcaagcccccaactcatgattatgatgtcagtaatcggccctc
aggggtttctaatacgtctctctggctccaagtctggcaacacggcctcctgacctctctgggctccaggctgaggacgaggctg
attattactgcagctcatatacaagcagcagcactc..
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3. The meeting considered the inference of the variant IGLV2-14\*04x sequence in Genotype A007 VL, Submission S00028. The sequence appears to be an extension of the presently truncated IGLV2-14\*04 sequence. The submitted sequence is as follows:

>IGLV2-14\*04x

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cagtctgcctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgtt
gggtgtataactatgtctcctggtaccaacagcaccaggcaagcccccaactcatgattatgatgtcagtaatcggccctc
aggggtttctaatacgtctctctggctccaagtctggcaacacggcctcctgacctctctgggctccaggctgaggacgaggctg
attattactgcagctcatatacaagcagcagcactctc
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The sequence was seen in 6.88% of all unmutated rearrangements, with 21,083 sequences including 8224 perfect alignments to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. A second inferred IGLV2-14 allele, IGLV2-14\*i01, was also present in the genotype, at a similar frequency. Haplotype data is unavailable.

Plots of the final 3' nucleotides were considered, but the variability seen made it impossible to consider the final two nucleotides of the sequence. These were not part of the Genbank submission. The sequence has previously been reported as IGLV2-14\*p07. The sequence, up to and including nucleotide 337, was affirmed as the Level 1 sequence, IGLV2-14\*i02, pending submission of sequence data to GenBank and supporting sequence reads to SRA/ENA. Uncertainty regarding nucleotides 338-339 will be indicated in IARC and OGRDB publications by two dots at the end of the affirmed sequence. The accepted sequence is as follows:

>IGLV2-14\*i02

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cagtctgccctgactcagcctgcctccgtgtctgggtctcctggacagtcgatcaccatctcctgcactggaaccagcagtgacgtt
gggtgtataactatgtctcctggtagcaacagcaccaggcaaaagccccaaactcatgattatgatgtcagtaatcggccctc
aggggtttctaatacgcttctctggctccaagtctggcaacacggcctcctgacctctctgggctccaggctgaggacgaggctg
attattactgcagctcatatacaagcagcagcactctc..
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4. The meeting considered the inference of a variant of the IGLV3-21 sequence in Genotype A007 VL, Submission S00028. The submitted sequence is as follows:

>IGLV3-21\*01\_S5562

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tcctatgtgctgactcagccaccctcagtgctcagtggtggcccaggaaagacggccaggattacctgtgggggaaacaacattgg
aagtaaaagtgtgactggtaccagcagaagccaggccaggccccctgtgctggtcatctattatgatagcgaccggccctcag
ggatccctgagcgattctctggctccaactctgggaacacggccaccctgacctcagcaggggtcgaagccgggggatgaggc
cgactattactgcaggtgtgggatagtagtagtagatcatcc
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The sequence was seen in 1.61% of all unmutated rearrangements, with 9,680 sequences including 1925 perfect alignments to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. A second IGLV3-21 allele, IGLV3-21\*03, was also present in the genotype, at a higher frequency, but the inferred allele still accounted for 35% of all IGLV3-21 alignments. Haplotype data is unavailable. Plots of the final 3' nucleotides were considered, but the variability seen made it impossible to consider the final two nucleotides of the sequence. The sequence, up to and including nucleotide 339, was affirmed as the Level 1 sequence, IGLV3-21\*i01. Uncertainty regarding nucleotides 340-341 will be indicated in IARC and OGRDB publications by two dots at the end of the affirmed sequence. The accepted sequence is as follows:

>IGLV3-21\*i01

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Tcctatgtgctgactcagccaccctcagtgctcagtggtggcccaggaaagacggccaggattacctgtgggggaaacaacattgg
aagtaaaagtgtgactggtaccagcagaagccaggccaggccccctgtgctggtcatctattatgatagcgaccggccctcag
ggatccctgagcgattctctggctccaactctgggaacacggccaccctgacctcagcaggggtcgaagccgggggatgaggc
cgactattactgcaggtgtgggatagtagtagtagatcat..
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Since submission of this sequence to IARC, it has been incorporated into the IMGT database as IGLV3-21\*04.

5. The meeting considered the inference of a variant of the IGLV3-25 sequence in Genotype A007 VL, Submission S00028. The submitted sequence is as follows:

>IGLV3-25\*02\_S7225

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tcctatgagctgacacagccaccctcggtgtcagtggtccccaggacagacggccaggatcacctgctctggagatgcattgcca
aagcaatatgcttattggtaccagcagaagccaggccaggccccctgtgctggtgatataaagacagtgagaggccctcagg
gatccctgagcgattctctggctccagctcagggacaacagtcacgttgacctcagtggtgagtgccaggcagaagacgaggctg
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actattactgtcaatcagcagacagcagtggtacttatcc

The sequence was seen in 4.53% of all unmutated rearrangements, with 16,227 sequences including 5410 perfect alignments to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. A second IGLV3-25 allele, IGLV3-25\*02, was also present in the genotype, at a lower frequency, and the inferred allele accounted for 73% of all IGLV3-25 alignments. Haplotype data is unavailable. Plots of the final 3' nucleotides were considered, but the variability seen made it impossible to consider the final two nucleotides of the sequence. These were not part of the Genbank submission. The sequence has previously been reported as IGLV3-25\*p04. The sequence, up to and including nucleotide 339, was affirmed as the Level 1 sequence, IGLV3-25\*i01. It appears to represent the full length version of the previously truncated IGLV3-25\*03 sequence. It was subsequently noted that since the submission of this sequence, an identical genomic sequence has been accepted by IMGT as the full length sequence IGLV3-25\*03. The sequence, up to and including nucleotide 339 will be submitted to IMGT as IGLV3-25\*i01 as a record of the rearrangability (and therefore likely functionality) of the sequence.

Since submission of this sequence to IARC, it has been incorporated into the IMGT database as IGLV3-25\*03.

6. The meeting considered the inference of a variant of the IGLV7-46 sequence in Genotype A007 VL, Submission S00028. The variant was present at a relatively low frequency, being seen in just 0.03% of all unmutated rearrangements, with a total of 656 alignments including 31 perfect alignments to the inferred allele. The submitted sequence was rejected by the committee as supporting inference data was insufficient.
7. The meeting briefly considered the inference of a variant of the IGLV6-57 sequence in Genotype A007 VL, Submission S00028. Consideration of this sequence will be concluded at the next IARC meeting.
8. The next meeting (Meeting 58) will be held on Monday July 20th at 10:30 UTC. MC will be asked to attend the meeting when consideration of Submission S00028 has been completed.

The meeting ended at 11:37 UTC.