

# IARC Meeting 53: April 14th 2020: minutes

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

1. The minutes of Meetings 51 and 52 were approved.
2. The committee considered IGLV10-54\*01\_S4180 (A228C) of Genotype A007 VL, Submission S00028. The submitted sequence is as follows:

>IGLV10-54\*01\_S4180

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CAGGCAGGGCTGACTCAGCCACCCTCGGTGTCCAAGGGCTTGAGACAGACCGCCCACTCACC
TGCACTGGGAACAGCAACAATGTTGGCAACCAAGGAGCAGCTTGGCTGCAGCAGCACCAGGGC
CACCTCCCAAACCTATCCTACAGGAATAACAACCGGCCCTCAGGGATCTCAGAGAGATTCT
CTGCATCCAGGTCAGGAAACACAGCCTCCCTGACCATTACTGGACTCCAGCCTGAGGACGAGG
CTGACTATTACTGCTCAGCATGGGACAGCAGCCTCAGTGCTCA
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The sequence was seen in 1.79% of all unmutated rearrangements, with 11279 sequences including 2138 perfect matches to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. The IGKV10-54\*01 allele was also present in the genotype, at a similar frequency (1.77% of all unmutated sequences; 7826 sequences; 2117 unmutated sequences). Haplotype data is unavailable. Plots of the final 3' nucleotides showed a high level of variability, making it impossible to determine the final three nucleotides with certainty. The sequence, up to and including nucleotide 339, was affirmed as a Level 1 sequence. 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:

>IGHV10-54\*i01

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CAGGCAGGGCTGACTCAGCCACCCTCGGTGTCCAAGGGCTTGAGACAGACCGCCCACTCACC
TGCACTGGGAACAGCAACAATGTTGGCAACCAAGGAGCAGCTTGGCTGCAGCAGCACCAGGGC
CACCTCCCAAACCTATCCTACAGGAATAACAACCGGCCCTCAGGGATCTCAGAGAGATTCT
CTGCATCCAGGTCAGGAAACACAGCCTCCCTGACCATTACTGGACTCCAGCCTGAGGACGAGG
CTGACTATTACTGCTCAGCATGGGACAGCAGCCTCAGTGCT**
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3. Discussion continued to try to establish principles by which other submitted lambda sequences could be judged by the IARC. It was suggested that the committee work back from the 3' end of the sequence until there is no doubt. It was suggested that a nucleotide should be present in 80% of sequences, if it is to be confirmed. Higher levels of variation at positions well before the gene end were then highlighted, pointing to the challenges we face with light chain sequences. Once again, the need for software developers to have an awareness of the existence of truncated sequences, and to modify programs to ensure that such sequences are properly considered in any analysis. Awareness of these issues may best be promoted by a manuscript from the IARC and Germline Working Group.
4. The next meeting (Meeting 54) will be held on April 27th at 10:30 UTC.

The meeting ended at 11:30 UTC.