

# IARC Meeting 61: October 13th 2020: minutes

The meeting commenced at 10:00 UTC. AC, MC, MO, CS and WL were in attendance. Corey Watson and Gur Yaari were also present.

1. A number of edits to the minutes of meeting 60 were discussed, and it was agreed to accept the amended minutes, unless other concerns are raised via email in the coming week.
2. It was noted that the scheduled meeting on 22/9/20 did not proceed as a formal meeting, as two members of the IARC were unable to attend.
3. The meeting considered the inference of the variant IGHV3-21\*01\_a184g\_t190a\_a191c in the VDJbase dataset of sample P1\_I80\_S1. The sequence was seen in 2.73% of all unmutated rearrangements, with 1207 sequences including 1054 perfect matches to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. IGHV3-21\*01 was also present in the genotype, at a similar frequency (2.37% of all unmutated sequences, 1066 sequences, 917 unmutated sequences). Plots of the final 3' nucleotides were unavailable, and no haplotyping data was available. The sequence was tentatively affirmed as a Level 1 sequence, and the final 3' nucleotides will be considered at a later date, when terminal nucleotide plots become available, at which time the affirmed sequence will be noted in the IARC minutes.
4. The meeting considered the inference of the variant IGHV3-30\*19\_t189c, in the VDJbase dataset of sample P1\_I49\_S1. The sequence was seen in 2.35% of all unmutated rearrangements, with 313 sequences including 113 perfect matches to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. IGHV3-30\*18 also present in the genotype. Plots of the final 3' nucleotides of the inference were unavailable. Discussion particularly focused upon haplotype data relating to IGHV3-30, IGHV3-33 and IGHV3-30-3. These data raise the possibility that the inference is an allele of IGHV3-30-3, though it is most similar to IGHV3-30\*19. IARC policy has been that sequences are given an IMGT gene name based upon the sequence to which they are most similar. Consideration of this particular inference led this policy to be reconsidered, and it was agreed that further discussion is required before the policy can be confirmed or modified. Because of the uncertainty regarding the most suitable name for the inferred sequence, it was affirmed as a Level 0 sequence. The final 3' nucleotides will be considered at a later date, at which time the affirmed sequence will be noted in the IARC minutes. It was noted that the P1\_I49\_S1 dataset had a relatively low percentage of unmutated sequences for all genes in the dataset. GY agreed to investigate why this P1 dataset does not share the high percentage of unmutated sequences that is seen in other P1\_S1 datasets.
5. The next meeting (Meeting 62) will be held on Tuesday November 3rd at 10:00 UTC.

The meeting ended at 11:05 UTC.