Minutes of IARC meeting 114, Feb 6th, 2023

In attendance: Ayelet Peres, Gur Yaari, Andrew Collins, Martin Corcoran, William Lees, Corey Watson, Mats Ohlin, James Heather

- 1. Approval of minutes of meeting 113 Approved
- **2.** The IUIS Nomenclature subcommittee/IARC/IMGT future interaction Discussion, incl. discussion of the recent update of the IMGT database.

3. Germline reference set manuscript

Discussion. The need for incorporation of IGHD and IGHJ alleles into the manuscript was defined. Focus on trustworthiness of IGHD allele calls, *e.g.* IGHD3-16*01. AC, MC and WL will update the manuscript in this respect.

4. Assessment of inference TRBV5-6*01_T284G in P4_I12_S1 (S00036)

TRBV5-6*01_T284G (substitution: L95W) has been inferred in four genotypes in the VDJbase P4 data set, including in VDJbase P4_I12_S1, a haplotypable data set (based on heterozygocity in TRBJ1-6). The genotype is also implied to carry TRBV5-6*01. No other gene in the IMGT database is highly similar to these alleles of TRBV5-6. The novel allele is the lesser expressed allele in the repertoire (35% allelic frequency; 0.43% of the total error-free population). It is represented by 122 error-free sequences and 118 unique CDR3s in the error-free set. Haplotyping based on allelic diversity in TRBJ1-6 demonstrates perfect separation from TRBV5-6*01.

The discussion of this inference will continue at the next meeting.

Result summary: TRBV5-6*01_T284G	No rearrangement found		
V-GENE and allele	Homsap TRBV5-6*01 F	score = 1356	identity = 99.63% (272/273 nt)
FR-IMGT lengths, CDR-IMGT lengths	[5.6.X]		

1. Alignment for V-GENE and allele identification

Closest V-REGIONs (evaluated from the V-REGION first nucleotide to the 2nd-CYS codon)









Other inferences: *P1_I16*



TRBV5-6*01_T284G- Final 3 nucleotides as a triplet





P4_128:







Position



8 9 10 11 12 13 14 15 16 17 18 52 62 CDR3 AA Length (unmutated)



5. Next meeting Feb 9th, 2023 at 11.00 UTC