‘Name’, ‘Length’, ‘Type’, ‘V gene’, ‘ V gene 2nd choice’, ‘V gene 3rd choice’, ‘D gene’, ‘ D gene 2nd choice’, ‘D gene 3rd choice’, ‘J gene’, ‘ J gene 2nd choice’, ‘J gene 3rd choice’, ‘Stop codons?’, ‘Reading frame’, ‘Productive?’, ‘Strand’, ‘End of V gene’, ‘V to D Junction’, ‘D region’, ‘D to J junction’, ‘Beginning of J’, ‘V to J junction’, ‘FWR1 first base’, ‘FWR1 last base’, ‘FWR1 length’, ‘FWR1 matches’, ‘FWR1 mismatches’, ‘FWR1 gaps’, ‘FWR1 percent identity’, ‘CDR1 first base’, ‘CDR1 last base’, ‘CDR1 length’, ‘CDR1 matches’, ‘CDR1 mismatches’, ‘CDR1 gaps’, ‘CDR1 percent identity’, ‘FWR2 first base’, ‘FWR2 last base’, ‘FWR2 length’, ‘FWR2 matches’, ‘FWR2 mismatches’, ‘FWR2 gaps’, ‘FWR2 percent identity’, ‘CDR2 first base’, ‘CDR2 last base’, ‘CDR2 length’, ‘CDR2 matches’, ‘CDR2 mismatches’, ‘CDR2 gaps’, ‘CDR2 percent identity’, ‘FWR3 first base’, ‘FWR3 last base’, ‘FWR3 length’, ‘FWR3 matches’, ‘FWR3 mismatches’, ‘FWR3 gaps’, ‘FWR3 percent identity’, ‘IgBLAST mutation count’, ‘IgBLAST Sequence Alignment’, ‘Germline V begin’, ‘Germline V end’, ‘Germline D1 begin’, ‘Germline D1 end’, ‘Germline D2 begin’, ‘Germline D2 end’, ‘Germline J begin’, ‘Germline J end’, ‘ V begin’, ‘ V end’, ‘ D1 begin’, ‘ D1 end’, ‘ D2 begin’, ‘ D2 end’, ‘ J begin’, ‘ J end’, ‘Project’, ‘Grouping’, ‘Subgroup’, ‘Species’, ‘Sequence’, ‘ Germline sequence’, ‘CDR3 DNA’, ‘CDR3 peptide’, ‘CDR3 length’, ‘CDR3 first base’, ‘CDR3 last base’, ‘Specificity’, ‘Subspecificity’, ‘Clonal Pool’, ‘Clonal Rank’, ‘V locus’, ‘J locus’, ‘D locus’, ‘Date and time entered’, ‘Comments’, ‘ Quality’, ‘Total Mutations’, ‘Mutation list’, ‘Insertions & deletions’, ‘CDR3 molecular weight’, ‘CDR3 isoelectric point’, ‘Blank3’, ‘Blank4’, ‘Blank5’, ‘Blank6’, ‘Blank7’, ‘Blank8’, ‘Blank9’, ‘Blank10’, ‘Blank11’, ‘Blank12’, ‘Blank13’, ‘Blank14’, ‘Blank15’, ‘Blank16’, ‘Blank17’, ‘Blank18’, ‘Blank19’, ‘Blank20’, ‘ID’