Claims

1. Antibody, or antigen-binding fragment thereof, binding to *P. falciparum* sporozoites, wherein the antibody, or the antigen binding fragment thereof, comprises CDRH1, CDRH2, and CDRH3 amino acid sequences and CDRL1, CDRL2, and CDRL3 amino acid sequences (i) according to SEQ ID NOs: 64 – 68 and 70; (ii) according to SEQ ID NOs: 64 – 67 and 69 – 70; (iii) according to SEQ ID NOs: 82 – 86 and 88; (iv) according to SEQ ID NOs: 82 – 85 and 87 – 88; (v) according to SEQ ID NOs: 136 – 140 and 142; (vi) according to SEQ ID NOs: 136 – 139 and 141 – 142; (vii) according to SEQ ID NOs: 206 – 210 and 212; (viii) according to SEQ ID NOs: 206 – 209 and 211 – 212; (ix) according to SEQ ID NOs: 224 – 228 and 230; (x) according to SEQ ID NOs: 224 - 227 and 229 – 230; (xi) according to SEQ ID NOs: 258 – 262 and 264; (xii) according to SEQ ID NOs: 258 – 261 and 263 – 264; (xii) according to SEQ ID NOs: 276 – 280 and 282; (xiv) according to SEQ ID NOs: 276 – 279 and 281 – 282; or (xv) according to SEQ ID NOs: 242 – 247.

2. The antibody, or the antigen binding fragment thereof, according to claim 1, wherein the antibody, or the antigen binding fragment thereof, comprises a heavy chain variable region (VH) and, optionally, a light chain variable region (VL), wherein the heavy chain variable region (VH) comprises or consists of an amino acid sequence according to any of SEQ ID NOs: 71, 89, 143, 213, 231, 248, 265, and 283; or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity.

3. The antibody, or the antigen binding fragment thereof, according to any one of claims 1 – 2, wherein the antibody, or the antigen binding fragment thereof, comprises (i) a heavy chain variable region (VH) amino acid sequence according to SEQ ID NO: 71 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity and/or a light chain variable region (VL) amino acid sequence according to SEQ ID NO: 72 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity; (ii) a heavy chain variable region (VH) amino acid sequence according to SEQ ID

NO: 89 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity and/or a light chain variable region (VL) amino acid sequence according to SEQ ID NO: 90 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity; (iii) a heavy chain variable region (VH) amino acid sequence according to SEQ ID NO: 143 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity and/or a light chain variable region (VL) amino acid sequence according to SEQ ID NO: 144 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity; (iv) a heavy chain variable region (VH) amino acid sequence according to SEQ ID NO: 213 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity and/or a light chain variable region (VL) amino acid sequence according to SEQ ID NO: 214 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity; (v) a heavy chain variable region (VH) amino acid sequence according to SEQ ID NO: 231 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity and/or a light chain variable region (VL) amino acid sequence according to SEQ ID NO: 232 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity; (vi) a heavy chain variable region (VH) amino acid sequence according to SEQ ID NO: 265 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity and/or a light chain variable region (VL) amino acid sequence according to SEQ ID NO: 266 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%,

at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity; (vii) a heavy chain variable region (VH) amino acid sequence according to SEQ ID NO: 283 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity and/or a light chain variable region (VL) amino acid sequence according to SEQ ID NO: 284 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity; or (viii) a heavy chain variable region (VH) amino acid sequence according to SEQ ID NO: 248 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity and/or a light chain variable region (VL) amino acid sequence according to SEQ ID NO: 249 or a functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity.

4. The antibody, or the antigen binding fragment thereof, according to any one of claims 1 – 3, wherein the antibody, or the antigen binding fragment thereof, is a purified antibody, a single chain antibody, Fab, Fab', F(ab')2, Fv or scFv.

5. The antibody, or the antigen binding fragment thereof, according to any one of claims 1 – 4 for use as a medicament.

6. Use of the antibody, or the antigen binding fragment thereof, according to any one of claims 1 – 4 in the manufacture of a medicament for the prevention and/or treatment of malaria.

7. A nucleic acid molecule comprising a polynucleotide encoding the antibody, or the antigen binding fragment thereof, according to any one of claims 1 – 4.

8. The nucleic acid molecule according to claim 7, wherein the polynucleotide sequence comprises or consists of a nucleic acid sequence according to any one of SEQ ID NOs: 73 – 81, 91 – 99, 145 – 153, 215 – 223, 233 – 241, 250 – 257, 267 – 275, 285 – 293; or a

functional sequence variant thereof having at least 70%, at least 75%, at least 80%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity.

9. A vector comprising the nucleic acid molecule according to claim 7 or claim 8.

10. A cell expressing the antibody, or the antigen binding fragment thereof, according to any of claims 1 - 7; or comprising the vector according to claim 12.

11. A pharmaceutical composition comprising the antibody, or the antigen binding fragment thereof, according to any of claims 1 - 4, the nucleic acid according to claim 7 or claim 8, the vector according to claim 9 and/or the cell according to claim 10; optionally further comprising a pharmaceutically acceptable excipient, diluent or carrier.

12. The nucleic acid according to claim 7 or claim 8, the vector according to claim 9, the cell according to claim 10, or the pharmaceutical composition according to claim 11 for use as a medicament.

13. Use of the nucleic acid according to claim 7 or claim 8, the vector according to claim 9, the cell according to claim 10, or the pharmaceutical composition according to claim 11 in the manufacture of a medicament for the prevention or treatment of malaria.

14. Use of the antibody, or the antigen binding fragment thereof, according to any of claims 1 - 4, the cell according to claim 10, or the pharmaceutical composition according to claim 11 for monitoring the quality of an anti-malaria vaccine by checking that the antigen of said vaccine contains the specific epitope in the correct conformation.

15. Use of the antibody, or the antigen binding fragment thereof, according to any of claims 1 - 4, the cell according to claim 10, or the pharmaceutical composition according to claim 11 in *in vitro* diagnosis of malaria.

16. A kit of parts comprising at least one antibody, or the antigen binding fragment thereof, according to any of claims 1 - 4, at least one nucleic acid according to any of claims 7 - 8, at

least one vector according to claim 9, at least one cell according to claim 10, or at least one pharmaceutical composition according to claim 11.