

S2 Table. The top 20 scoring peptides from each of the four prediction algorithms were shortlisted and synthesised for antigenicity screening with Sudanese visceral leishmaniasis (VL) serum samples. ‘C.reported’ was calculated by dividing the reported amount by the volume of the solvent mixture in which the peptides were dissolved, while ‘C.280’ and ‘C.205’ were calculated based on the molar absorbances at 280 and 205 nm, respectively. All concentrations are given in mg/ml. MW is given in g/mol

| ID | Sequence | Peptide length | MW | Purity | C.reported | C.280 | C.205 |
|-------------|------------------|----------------|---------|--------|------------|-------|-------|
| abc_01_CVTQ | CVTQEHFREAMAKTNP | 16 | 2287.63 | 0.58 | 2 | NA | 3.27 |
| abc_02_KEAP | KEAPGATEKDRAKATP | 16 | 2095.38 | 0.57 | 2 | NA | 3.14 |
| abc_03_TAYI | TAYIMRPLDHGADVTL | 16 | 2198.57 | 0.69 | 2 | 2.75 | NA |
| abc_04_MITN | MITNDDAPVRDVSFLT | 16 | 2187.45 | 0.45 | 1.23 | NA | NA |
| abc_05_MPTV | MPTVDERQTFMFSATF | 16 | 2333.71 | 0.4 | 2.31 | NA | NA |
| abc_06_TRTG | TRTGDYAFSYDKMLDM | 16 | 2339.67 | 0.55 | 1.13 | NA | NA |
| abc_07_KSTI | KSTISGHLLMEKGLVD | 16 | 2153.57 | 0.53 | 2 | NA | 2.65 |
| abc_08_KEAI | KEAITTFREEDPKVTD | 16 | 2304.58 | 0.48 | 2 | NA | NA |
| abc_09_HVYS | HVYSELGKKFGAAADP | 16 | 2115.41 | 0.51 | 2 | 3.42 | 4.23 |
| abc_10_LGMG | LGMISGGGEEGARKGP | 16 | 1941.23 | 0.56 | 2 | NA | 2.52 |
| abc_11_VAYQ | VAYQETPESERAELPP | 16 | 2241.48 | 0.52 | 2 | 2.22 | 2.13 |
| abc_12_AGTG | AGTGFPYREMPMNAP | 16 | 2195.61 | 0.72 | 2 | 3.95 | NA |
| abc_13_TDSW | TDSWGFFGVFDGHVND | 16 | 2225.4 | 0.57 | 1.33 | NA | NA |
| abc_14_HKKS | HKKSTEDNDDDAFCAP | 16 | 2218.37 | 0.54 | 1 | NA | NA |
| abc_15_YGLA | YGLAFDPYGGTAGLYD | 16 | 2105.33 | 0.54 | 1.33 | 0.74 | 0.76 |
| abc_16_WEEW | WEEWGNPNYKYDYDM | 16 | 2612.86 | 0.49 | 1.73 | 1.68 | 1.43 |
| abc_17_HSTI | HSTIGVHPTSAEELCS | 16 | 2093.33 | 0.65 | 2 | NA | 2.68 |
| abc_18_EKCI | EKCIELKPDFVKGYAR | 16 | 2321.76 | 0.53 | 0.87 | 3.85 | 1.08 |
| abc_19_PAGI | PAGINIPNYDDIRQTV | 16 | 2211.5 | 0.57 | 0.77 | 1.69 | 0 |
| abc_20_TGTI | TGTIDNGVVKMEKAE | 16 | 2146.44 | 0.55 | 2 | NA | NA |
| BP_01_CSPP | CSPPPPSPSPHPRPPS | 16 | 2062.38 | 0.7 | 2 | NA | 1.98 |
| BP_02_GEGS | GEGSPTSPTSPPKQGS | 16 | 1939.11 | 0.65 | 2 | NA | 2.08 |
| BP_03_AEAG | AEAGAPAGSGAPPPAD | 16 | 1760.92 | 0.56 | 2 | NA | NA |
| BP_04_KPAP | KPAPPKPKESKEPENA | 16 | 2172.55 | 0.59 | 2 | NA | 1.88 |

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| ID | Sequence | Peptide length | MW | Purity | C.reported | C.280 | C.205 |
|-------------|-------------------|----------------|---------|--------|------------|-------|-------|
| BP_05_TAKP | TAKPKQQDEDPDGAAE | 16 | 2125.28 | 0.63 | 2 | NA | NA |
| BP_06_GGDR | GGDRGGGTGNEDDDYE | 16 | 2039.02 | 0.79 | 2 | 2.95 | 2.05 |
| BP_07_MQQP | MQQPPTQPQKQKQQ | 16 | 2345.71 | 0.53 | 2 | NA | 3.13 |
| BP_08_EEEE | EEEEEEEEEEEPQATR | 16 | 2417.44 | 0.61 | 1.62 | NA | NA |
| BP_09_RSDP | RSDPSGGGGGNRDDNE | 16 | 2015.04 | 0.6 | 2 | NA | NA |
| BP_10_APAS | APASAPAPAPAAATP | 16 | 1783.06 | 0.67 | 2 | NA | 2.61 |
| BP_11_KRGG | KRGGDKDGGGESGEAA | 16 | 1916.04 | 0.62 | 2 | NA | NA |
| BP_12_RSQQ | RSQQGEQEPEEDEEEV | 16 | 2343.41 | 0.63 | 2 | NA | NA |
| BP_13_QQLS | QQLSSPPPPRERAED | 16 | 2219.45 | 0.57 | 2 | NA | NA |
| BP_14_EPEV | EPEVGEEEPQPEEEEDA | 16 | 2238.31 | 0.72 | 2 | NA | NA |
| BP_15_AAPS | AAPSGGPGSGNSDEEDL | 16 | 1928 | 0.68 | 2 | NA | NA |
| BP_16_SDVT | SDVTGGGGGGSGGGG | 16 | 1560.6 | 0.64 | 1 | NA | NA |
| BP_17_GQQQ | GQQQQQDDPPAGQQGV | 16 | 2119.28 | 0.82 | 2 | NA | NA |
| BP_18_AETP | AETPADDAGQPHEPEK | 16 | 2117.26 | 0.71 | 2 | NA | NA |
| BP_19_PPSA | PPSAGSKDGA PSDGVP | 16 | 1864.05 | 0.51 | 2 | NA | NA |
| BP_20_DATP | DATPAAANGEGPGKEN | 16 | 1924.06 | 0.65 | 2 | NA | NA |
| EpQ_01_AYAT | AYATMLKDVQWKVRKS | 16 | 2349.82 | 0.58 | 2 | 6.79 | 6.25 |
| EpQ_02_HEKL | HEKLVQDIWKKLEAKG | 16 | 2347.79 | 0.58 | 2 | 4.28 | 4.01 |
| EpQ_03_SCSV | SCSVKLGWKNAVNNC | 16 | 2161.55 | 0.57 | 2 | 6.56 | 6.9 |
| EpQ_04_MAYV | MAYVCELGPNQGWK | 14 | 2021.38 | 0.58 | 0.88 | 6.49 | NA |
| EpQ_05_LKDP | LKDPKQYQSIVDAEWK | 16 | 2373.73 | 0.31 | 2 | 1.88 | NA |
| EpQ_06_ERCE | ERCEDPNAWKGPTNGG | 16 | 2156.35 | 0.62 | 1.33 | 1.92 | NA |
| EpQ_07_DNPA | DNPAGPTTWKSDEPAL | 16 | 2124.33 | 0.62 | 1.73 | 1.8 | 1.88 |
| EpQ_08_YGIS | YGISFPKNPMLTEWKT | 16 | 2337.77 | 0.43 | 2 | 2.69 | 2.79 |
| EpQ_09_GMSS | GMSSDQLLQFLQQQQ | 16 | 2289.63 | 0.48 | 1.86 | NA | NA |
| EpQ_10_AAKK | AAKKKRVGCWK | 11 | 1700.11 | 0.56 | 2 | 2.29 | 2.22 |
| EpQ_11_NIRI | NIRHLGDTIRIAPCK | 16 | 2245.71 | 0.51 | 1.1 | NA | 2.33 |

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| ID | Sequence | Peptide length | MW | Purity | C.reported | C.280 | C.205 |
|-------------|------------------|----------------|---------|--------|------------|-------|-------|
| EpQ_12.ERRR | ERRRVEYQQFLDVCGQ | 16 | 2451.78 | 0.41 | 1.4 | 6.14 | NA |
| EpQ_13.MDRE | MDRESLCPNWK | 11 | 1804.11 | 0.41 | 2 | 2.06 | NA |
| EpQ_14.SRQM | SRQMTMCKEERIANCK | 16 | 2353.81 | 0.34 | 2 | NA | 1.85 |
| EpQ_15.DWSI | DWSIVERGWK | 10 | 1700.95 | 0.5 | 2.13 | 1.69 | NA |
| EpQ_16.VLVQ | VLVQGAIWGINSYDQW | 16 | 2274.6 | 0.39 | 15 | NA | NA |
| EpQ_17.GRTI | GRTILRNHKWAGNNKV | 16 | 2289.67 | 0.31 | 2 | 2.1 | 1.79 |
| EpQ_18.EKVR | EKVRSGEWKGGTGKSI | 16 | 2215.53 | 0.38 | 2 | 2.13 | 2.11 |
| EpQ_19.PDVA | PDVAHVQQFDLPQEMD | 16 | 2265.57 | 0.52 | 2.31 | NA | NA |
| EpQ_20.ADVT | ADVTATLAWK | 10 | 1500.75 | 0.49 | 1.03 | 1.56 | NA |
| LbT_01.RPGG | RPGGPPGYRTPYTAK | 15 | 2043.35 | 0.45 | 2 | 9.28 | 2.46 |
| LbT_02.TQGD | TQGDRQKIQDAVSAA | 15 | 2013.23 | 0.52 | 1.3 | NA | NA |
| LbT_03.EVKS | EVKSRYNVDVSQNKR | 15 | 2247.54 | 0.53 | 2 | 2.69 | 2.1 |
| LbT_04.VIEM | VIEMTRAFEDDDFDK | 15 | 2256.51 | 0.51 | 2 | NA | NA |
| LbT_05.GSAD | GSADLTPSNLTRPAS | 15 | 1912.12 | 0.47 | 2 | NA | NA |
| LbT_06.VRPI | VRPIPSFDDMPLHQN | 15 | 2191.53 | 0.47 | 2 | NA | NA |
| LbT_07.CELG | CELGNQGWKAVVAD | 15 | 2012.3 | 0.47 | 1.07 | 1.59 | NA |
| LbT_08.APQQ | APQQTQSGIRRVTRA | 15 | 2094.4 | 0.44 | 2 | NA | 2.18 |
| LbT_09.SAEE | SAEEKGTGKRNQITI | 15 | 2057.33 | 0.42 | 2 | NA | 0.7 |
| LbT_10.GEAE | GEAEWLEWESTVLTP | 15 | 2172.42 | 0.54 | 0.96 | 1.08 | 0 |
| LbT_11.EELR | EELRQRHQQPGSPG | 15 | 2129.36 | 0.41 | 0.87 | NA | 0.66 |
| LbT_12.EWAN | EWANKPLDDLDPHPS | 15 | 2159.38 | 0.55 | 2 | 1.57 | 1.56 |
| LbT_13.IKEE | IKEETEMIEGEVVEV | 15 | 2159.48 | 0.5 | 1.62 | NA | NA |
| LbT_14.VSDF | VSDFFGGKELNKSIN | 15 | 2080.36 | 0.74 | 2.92 | NA | 2.12 |
| LbT_15.WEDV | WEDVGGLLDVKRELQ | 15 | 2182.5 | 0.53 | 2 | 1.67 | 0 |
| LbT_16.SGGA | SGGAGPAGGASSGPK | 15 | 1582.72 | 0.53 | 2 | NA | 2.5 |
| LbT_17.KATN | KATNGDTHLGGEDFD | 15 | 2002.12 | 0.57 | 2 | NA | NA |
| LbT_18.EREG | EREGKDITLIGFSRG | 15 | 2103.4 | 0.53 | 1.56 | NA | 2 |

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| ID | Sequence | Peptide length | MW | Purity | C.reported | C.280 | C.205 |
|-------------|-----------------|----------------|---------|--------|------------|-------|-------|
| LbT_19_AWAS | AWASSPAPTERTAP | 15 | 1938.17 | 0.45 | 2 | 4.01 | NA |
| LbT_20_VDRD | VDRDNKKLSSGMVCS | 15 | 2064.4 | 0.51 | 2 | NA | 2.53 |