**Supplementary Tables.**

**Table. S1**

PspA MHC-I binding peptides determined by two different servers.

|  |  |  |  |
| --- | --- | --- | --- |
| Server | Start position | End position | Best ranked epitope in the region |
| Propred I |  |  | Log score |
|  | 400 | 423 | 7.96 |
|  | 454 | 462 | 7.96 |
|  | 494 | 508 | 7.96 |
| IEDB |  |  | Percentile rank |
|  | 400 | 430 | 0.2 |
|  | 454 | 469 | 0.3 |
|  | 495 | 509 | 0.3 |
|  |  |  |  |

**Table. S2**

CbpA MHC-I binding peptides determined by two different servers.

|  |  |  |  |
| --- | --- | --- | --- |
| Server | Start position | End position | Best ranked epitope in the regions |
| Propred I |  |  | Predicted IC50 value |
|  | 55 | 78 | 8.5 |
|  | 90 | 107 | 5.39 |
|  | 123 | 141 | 7.78 |
|  | 284 | 296 | 7.78 |
|  | 316 | 324 | 6.57 |
|  | 459 | 487 | 6.39 |
|  | 494 | 507 | 6.39 |
|  | 514 | 527 | 6.39 |
|  | 559 | 596 | 7.96 |
| IEDB |  |  | Percentile |
|  | 2 | 43 | 0.3 |
|  | 63 | 78 | 0.7 |
|  | 83 | 108 | 0.4 |
|  | 113 | 137 | 1.8 |
|  | 182 | 228 | 1.2 |
|  | 236 | 292 | 3.8 |
|  | 300 | 326 | 2.4 |

**Table. S3**

PhtD MHC-II binding peptides evaluated by two different servers

|  |  |  |  |
| --- | --- | --- | --- |
| Server | Start position | End position | Best ranked epitope in the regions |
| MHCPred |  |  | Predicted IC50 value |
|  | 9 | 55 | 7.9 |
|  | 91 | 109 | 8.41 |
|  | 150 | 190 | 8.38 |
|  | 214 | 231 | 8.54 |
|  | 343 | 377 | 7.79 |
|  | 402 | 435 | 8.33 |
|  | 507 | 557 | 8.44 |
|  | 567 | 593 | 7.87 |
|  | 652 | 675 | 8.68 |
|  | 792 | 828 | 8.6 |
| RANKPEP |  |  | Best Rank |
|  | 65 | 102 | 29.96 |
|  | 169 | 253 | 30.23 |
|  | 372 | 433 | 38.74 |
|  | 552 | 590 | 57.2 |
|  | 606 | 634 | 16.90 |
|  | 644 | 696 | 32.25 |

**Table. S4**

PiuA MHC-II binding peptides determined by two different servers.

|  |  |  |  |
| --- | --- | --- | --- |
| Servers | Start position | End position | Best ranked epitope in the region |
| MHCpred |  |  |  |
|  | 2 | 19 | 8.07 |
|  | 31 | 62 | 8.46 |
|  | 70 | 91 | 8.27 |
|  | 99 | 107 | 7.45 |
|  | 139 | 157 | 7.93 |
|  | 179 | 190 | 7.94 |
|  | 253 | 284 | 7.67 |
| RANKPEP |  |  |  |
|  | 28 | 42 | 8.45 |
|  | 72 | 171 | 31.8 |
|  | 192 | 216 | 11.58 |
|  | 223 | 233 | 20.11 |
|  | 245 | 262 | 16.49 |

**Table. S5**

Predicted PspA CTL epitopes by CTLpred and PAComplex.

|  |  |  |  |
| --- | --- | --- | --- |
| **Servers** | **Start position** | **End position** | **Score** |
| CTLpred |  |  | **Score (ANN)** |
|  | 403 | 411 | 0.98 |
|  | 426 | 434 | 0.92 |
|  | 463 | 471 | 0.93 |
|  | 485 | 493 | 0.96 |
|  | 487 | 495 | 0.95 |
| PAComplex |  |  | **Best joint Z-value in the region** |
|  | 107 | 113 | 3.74 |
|  | 204 | 216 | 3.47 |
|  | 343 | 353 | 4.64 |
|  | 375 | 384 | 4.25 |

**Table. S6**

Predicted CbpA CTL epitopes by CTLpred and PAComplex.

|  |  |  |  |
| --- | --- | --- | --- |
| **Servers** | **Start position** | **End position** | **Score** |
| CTLpred |  |  | **Score (ANN)** |
|  | 60 | 68 | 0.99 |
|  | 273 | 281 | 0.99 |
|  | 313 | 321 | 0.98 |
| PAComplex |  |  | **Best joint Z-value in the region** |
|  | 12 | 21 | 4.06 |
|  | 66 | 82 | 3.94 |
|  | 189 | 194 | 3.63 |
|  | 232 | 237 | 3.42 |
|  | 293 | 310 | 3.97 |
|  | 318 | 326 | 3.58 |

**Table. S7**

Predicted linear B-cell epitopes in final construct by BCPRED server.

|  |  |  |
| --- | --- | --- |
| Start Position | Epitopes | Score |
| 203 | PGNGKVPYDAIISEELLMKD | 0.91 |
| 280 | RAAAQAYAKEKGLTPPSTAA | 0.90 |
| 4 | AKYKNGGFFVQYGGAYKRHH | 0.89 |
| 109 | AAKVTFDLGAADTIRALGFE | 0.89 |
| 155 | LIIASPRTQKFVDKFKEIAP | 0.87 |
| 23 | HQVQEGLNIEKYQIHRLVSG | 0.86 |
| 211 | DAIISEELLMKDPNGPGPGE | 0.85 |
| 186 | ELAKLDKSIQEVATGPGPGN | 0.84 |
| 99 | VDDADIGNEAAAKVTFDLGA | 0.83 |
| 374 | EEKIAAYWYYLNSNGAMATG | 0.82 |
| 313 | SKKEELTSKTKKEIDAAFEQ | 0.82 |
| 235 | RYIPAKDLSAETAAGIDSKL | 0.82 |
| 218 | LLMKDPNGPGPGENGVPRYI | 0.82 |
| 73 | EVAATLAYRFGNVTPRVSYA | 0.81 |
| 31 | IEKYQIHRLVSGYDNDALYA | 0.80 |
| 267 | PGPGKKDSLSEAERAAAQAY | 0.80 |
| 247 | AAGIDSKLAKQESLSHKLGG | 0.80 |

**Table. S8**

Predicted linear B-cell epitopes in final construct by APCPred server.

|  |  |  |
| --- | --- | --- |
| Start position | End position | Epitopes |
| 9 | 20 | GGFFVQYGGAYK |
| 28 | 351 | GLNIEKYQIHRLVSGYDNDALYASVAVQQQDAK  LTDASNSHNSQTEVAATLAYRFGNVTPRVSYAH  GFKGLVDDADIGNEAAAKVTFDLGAADTIRALG  FEKNGPGPGNVGSMKEPDLEAIAALEPDLIIASPR  TQKFVDKFKEIAPGPGPGTQKAKEELAKLDKSIQ  EVATGPGPGNGKVPYDAIISEELLMKDPNGPGPG  ENGVPRYIPAKDLSAETAAGIDSKLAKQESLSHK  LGGPGPGKKDSLSEAERAAAQAYAKEKGLTPPS  TAAYKYLRELNVLEEKSKKEELTSKTKKEIDAA  FEQFNKDTLKPGEKVEEAQAAY |
| 362 | 385 | ELEIAAYKEPQNEEKIAAYWYYLN |
| 390 | 425 | MATGWLQYNGSWYYLNANGAMAAAYLQYNGSWYYLN |
| 436 | 447 | QYNGSWYYLNAN |

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  |  |

**Table. S9**

Conformational B-cell epitopes determined from 3D model of protein vaccine using DiscoTope 2.0 server.

|  |  |  |  |
| --- | --- | --- | --- |
| Position | Residues | Contact number | Discotope score |
| 2-8 | AAAKYKN | 7-8-9-1-15-6-18 | -2.805,-3.104,-1.120,0.082  -0.669,1.173,-0.081 |
| 10 | G | 15 | -3.403 |
| 19-38 | YKRHHQV  QEGLNIEK  YQIHR | 14,9,27,26,10,9,24,11,17  0,0,15,1,0,2,19,3,33,19,10 | -2.505,-1.850,-2.756,  -2.235,-0.079,-0.317  -0.495,1.069,0.835  2.673,2.332,1.327  3.481,3.978,3.353,  1.639,2.556,-3.149  -3.265,-2.913 |
| 56-57 | QQ | 8,16 | -3.657,-2.890 |
| 59-68 | AKLTDAS  NSH | 14,11,24,26,8,15,29,6,33,8 | -3.053,0.111,-1.612,  -2.425,1.351,0.996  0.249,2.246,-2.487  -1.745 |
| 83-84 | GN | 6,2 | -3.479,-2.528 |
| 86 | T | 6 | -2.769 |
| 101-103 | DAD | 0,4,1 | -2.110,-2.210,-3.189 |
| 159-164 | SPRTQK | 10,6,12,13,0,6 | -3.512,-1.130,-1.074  -1.950,1.081,-0.410 |
| 166-168 | VDK | 12,4,19 | -2.688,-0.107, |
| 170-171 | KE | 10,8 | -0.791,-1.325 |
| 174-247 | PGPGPGT  QKAKEEL  AKLDKSI  QEVATGP  GPGNGK  VPYDAII  SEELLMK  DPNGPGP  GENGVPR  YIPAKDLS  AETA | 10,10,29,5,8,6,22,9,13,8,  7,5,6,5,8,7,7,13,9,2,8,8,3,  17,1,27,3,6,16,0,6,2,18,26,  17,17,13,18,5,8,21,4,8,12,  20,20,19,26,24,14,6,15  ,11,16,35,15,24,5,7,17,24,  31,19,27,14,6,8,  11,10,33,22,10,9,13 | -0.894,-0.714,-3.542,  0.413,0.598,-1.889  -3.116,-0.928,-2.816  -3.655,-1.198,-0.376  -0.505,-1.812,-2.146  -1,707,-2.350,-2.980  -3.575,-2.686,-3.021  -2.433,-0.831,-2.072  0.350,-1.949,2.103  2.208,0.945,2.335  1.498,2.481,-0.166  -1.348,-0.074,-0.359  0.463,0.260,0.400  0.104,-1.479,-0.721  -0.272,-1.137,-1.309  -1.805,-0.881,-1.696  -0.389,0.653,2.120  0.271,0.692,-1.693  -2.327,0.260,-1.145  1.327,0.635,0.269  -0.441,-1.571,-1.525  -2.688,-1.864,-2.721  -1.215,-0.400,-0.349  -2.092,-0.562,1.364  1.176,-0.677, |
| 249 | G | 2 | -.1.688 |
| 252-277 | SKLAKQQ  SLSHKLG  GPGPGKK  DSLSE | 11,29,17,30,21,26,11,2.13,  27,17,38,26,27,14,14,31,4,  16,7,0,19,18,24,24,32 | -3.478,-3.640,-2.019  -2.640,-0.408,-0.978  1.309,2.125,1.027,  -0.530,0.301,-1.870  -0.234,-2.529,-1.400  -0.333,-1.582,2.153  1.100,1.659,3.918  2.660,0.914,-1.224  -2.529,-3.461 |
| 279-280 | ER | 20,19 | -3.577,-3.342 |
| 282 | A | 6 | -3.194 |
| 284-288 | QAYAK | 2,5,27,8,6 | -0.459,0.217,-2.763  -0.596,-0.495 |
| 290-291 | KG | 4,13 | -0.995,-2.477 |
| 293 | T | 8 | -3.249 |
| 295-296 | PS | 5,2 | -3.232,-2.415 |
| 298-299 | AA | 1,2 | -3.101,-2.674 |
| 301 | K | 9 | -3.548 |
| 304-319 | RELNVLE  EKSKKEE  LT | 14,3,0,3,11,10,15,22,25,22  ,27,25,23,32,26,25 | -3.071,-1.095,-2.398  -1.858,-3.310,-2.270  -2.601,-3.155,-2.541  -3.070,-2.811,-3.625  -3.186,-3.086,-3.688  -2.306 |
| 321-323 | KTK | 12,8,14 | 0.228,-0.682,-1.965 |
| 327 | D | 11 | -3.269 |
| 331-347 | EQFNKDT  LKPGEKV  EEA | 30,24,27,14,5,3,10,28,23,  10,4,10,24,5,24,6,1 | -2.856,-1.661,-1.647  1.056,1.349,2.283  1.412,-1.700,-0.045  1.878,1.182,-1.333  -1.711,-1.813,-3.046  -0.597,-0.964 |
| 351-357 | YNYPTNT | 24,24,23,4,15,26,23 | -3.240,-1.710,-1.228  2.581,0.297,-1.224  -2.078 |
| 361-362 | LE | 5,6 | -2.327,-2.262 |
| 364-368 | EIAAY | 14,4,0,7,21 | -3.338,-2.510,-1.551  -3.037,-3.289 |
| 370 | E | 20 | -3.298 |
| 378 | A | 3 | -3.332 |
| 386-387 | SN | 6,10 | 2.742,-2.684 |