Supplementary table S1: Primers used in RT-qPCR studies.

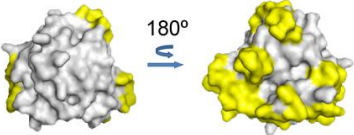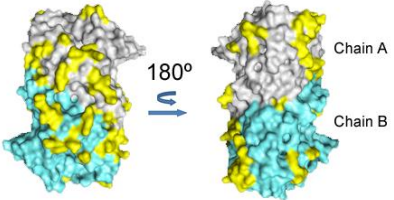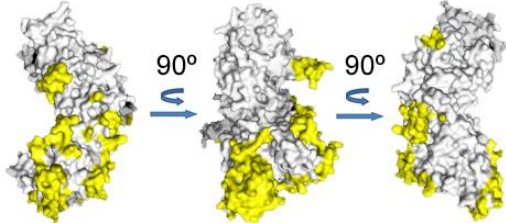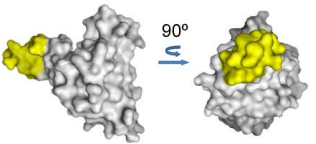| Gene	Forward primer (5´–3´)	Nt position[1]	Reverse primer (5´–3´)	Nt position[2]
Rv2624	agccgacgatgaaaacaatc	16	atgtgtcggcttgatcactg	150
Rv0382c	cgactgggactattcggttg	176	ccttcgataagtcgctgcat	323
Rv0009	gacatcaagatcgccctgtt	72	atgcgttttgggtcgaatag	172
Rv1144	catcaacctagtcggcacct	323	aggcggtgttaatgatgacg	427
Rv0407	ccgtcgaaaaggtaggtcaa	877	cgactggaagagctccagaa	978
Rv1223	cgatcaaccacggtaactcc	1141	gccaccaatttcatctcgtt	1283
Rv2241	gagcgtggatcagatggaat	241	gtggttgaaaccgacctcat	366

[1] refers to the position in the gene of the 5´ base of the forward primer

[2] refers to the position in the gene of the 5´ base of the reverse primer

Supplementary table S2: Primers used to amplify the validated genes.

Gene	Forward primer (5´–3´)	Reverse primer (5´–3´)
Rv2624c	caccatgtctgggagaggagagcc	tcagcggcgaacgacaagca
Rv0009	caccatggcagactgtgattccgt	tcaggagatggtgatcgact
Rv0407	caccgtggctgaactgaagctagg	tcagccaagtcgccgcaacc
Rv2241	ttaggccccgggaccgggatccgtg	caccgtggcgtcgtatttgcccgacattg
Rv1223	caccgtggatactagggtggacac	ctaggtgctatcggggtccg

Supplementary table S3: B-cell epitope prediction

Protein	Crystal Structure	3D Model Template[1]	DP[2]	Figure[3]	Predicted Epitope density[4] (pmol/cm^2)
Rv0009 Iron-regulated peptidyl-prolyl cis-trans isomerase A **PpiA**	PDB id: 1W74 Chain: A BU: Monomer		**38** (171)		**35±13**
Rv0407 f420-dependent glucose-6-phosphate dehydrogenase	PDB id: 3B4Y Chains: A-B BU: Homodimer		**28** (333)		**19±7**
Rv2241 Pyruvate dehydrogenase E1 component **AceE**	NA	PDB id: 1L8A Chain: A BU: Homodimer	**173** (895)		**58±22**
Rv2624c Hypothetical stress protein	NA	PDB id: 1MJH Chain: A BU: Homodimer	**21** (279)		**16±6**

[1]For those proteins with no published 3D structures (NA), we performed structure homology modeling using the SWISS-MODEL server, an on-line free-access tool (http://swissmodel.expasy.org/workspace). The Protein Data Bank identification (PDB id) of template structure used is indicated.

[2]Discotope prediction (DP) were residues with scores >-3,7 determined by DiscoTope 2.0 algorithm. Total # residues on protein 3D structure were indicated between brackets. DiscoTope 2.0 server is a free access prediction tool (http://www.cbs.dtu.dk/services/DiscoTope-2.0/).

[3]Predicted discontinuous B cell epitopes were highlighted in yellow on the published or modeled 3D structures. Molecules were depicted using the PyMOL software.

[4]To estimate the predicted surface density of binding sites per ELISA microplate wells, we considered the following parameters: (1) Number of Discotope predicted aminoacidic residues per molecule; (2) Mw of Rv protein+ Mw of GST/HIS-tag; (3) Maximal protein binding capacity of Microplate (Corning High Binding Polystyrene)=500 ng/cm^2 ; (4) Based on published data, one conformational epitope involve between 8-22 aminoacids (95% CI= 8.6-19). The table informed value is Median±Range. Min and Max range values were calculated by considering 19 and 8.6 aminoacids /epitope, respectively.