

# Real-time Recognition of *Mycobacterium tuberculosis* and Lipoarabinomannan using the Quartz Crystal Microbalance

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## Equations used to calculate equilibrium association and rate constants

$\theta$	degree of surface coverage	$\Delta m$	change in mass
$\alpha_0$	correlation factor	$\Delta m_{\max}$	maximum change in mass
$\mu$	rate at which atoms strike the surface per unit area	$k_a$	associate rate constant
$v_1$	rate of evaporation from a completely covered surface	$k_d$	disassociation rate constant
$K_a$	equilibrium association constant	$t$	time
$C$	liquid concentration	$\tau$	tau

$$(S-1) \quad \theta = \alpha_0 \mu / (v_1 + \alpha_0 \mu)$$

$$(S-8) \quad v_a = k_a C (1 - \theta)$$

$$(S-2) \quad \theta = C / (K_a^{-1} + C)$$

$$(S-9) \quad v_d = k_d \theta$$

$$(S-3) \quad \theta = \Delta m / \Delta m_{\max}$$

$$(S-10) \quad k_a C (1 - \theta) = k_d \theta$$

$$(S-4) \quad \Delta m = \Delta m_{\max} K_a C / (1 + K_a C)$$

$$(S-11) \quad \theta(t) = k_a C / (k_a C + k_d) \{1 - \exp [-(k_a C + k_d)t]\}$$

$$(S-5) \quad C / \Delta m = C / \Delta m_{\max} + 1 / \Delta m_{\max} K_a$$

$$(S-12) \quad \theta(t) = \theta [1 - \exp (-t/\tau)]$$

$$(S-6) \quad \Delta m = -\Delta m / K_a C + \Delta m_{\max}$$

$$(S-13) \quad \ln(1 - \Delta m / \Delta m_{\max}) = -t/\tau$$

$$(S-7) \quad 1/\Delta m = 1/K_a \Delta m_{\max} C + 1/\Delta m_{\max}$$

$$(S-14) \quad -1/\tau = k_a C + k_d$$

The equation used to define Langmuir adsorption isotherms in gaseous environments (Eq. S-1), has also been used to describe isotherms occurring in liquid (Eq. S-2).[1] In liquid environments the degree of surface coverage can be represented by the change in mass at a given time over the maximum change in mass for the given concentration (Eq. S-3). Incorporating this equation into the mathematical equation for Langmuir adsorption isotherms (Eq. S-4), and rearranging allows for graphical determination of binding constants by varying the concentration of protein in solution (Eqs. S-5 through S-7).[2-4] These equations allow direct calculation of equilibrium constants which would not be as definitive if  $\Delta m_{\max}$  were instead approached asymptotically as is traditionally done.

At equilibrium, the velocities of adsorption and desorption at the surface of the crystal can be described in terms of respective rate constants and degree of surface coverage (Eqs. S-8 and S-9).[5, 6] The

association and dissociation velocities can be assumed to be equal at equilibrium, and can be algebraically rearranged to form the general Langmuir isotherm (Eq. S-10).

Monolayer formation with time is equal to the velocity of association minus the velocity of dissociation. Integrating this differential equation using a Laplace transform (boundary condition:  $\theta = 0$  at  $t = 0$ ) results in Eq. S-11.[7] Substituting the Langmuir isotherm using the principle of microscopic reversibility and allowing  $k_a C + k_d$  to be represented by  $\tau^{-1}$  presents a more simplified equation (Eq. S-12).[7, 8] Using the assumption that the maximum degree of surface coverage is one and  $\theta(t) = \Delta m / \Delta m_{\max}$ ,  $\tau$  can be calculated at various concentrations (Eq. S-13) and then graphed as  $C$  versus  $\tau^{-1}$  to extrapolate  $k_a$  and  $k_d$  which can be used for comparison with isotherm methods (Eq. S-14).[3, 9]

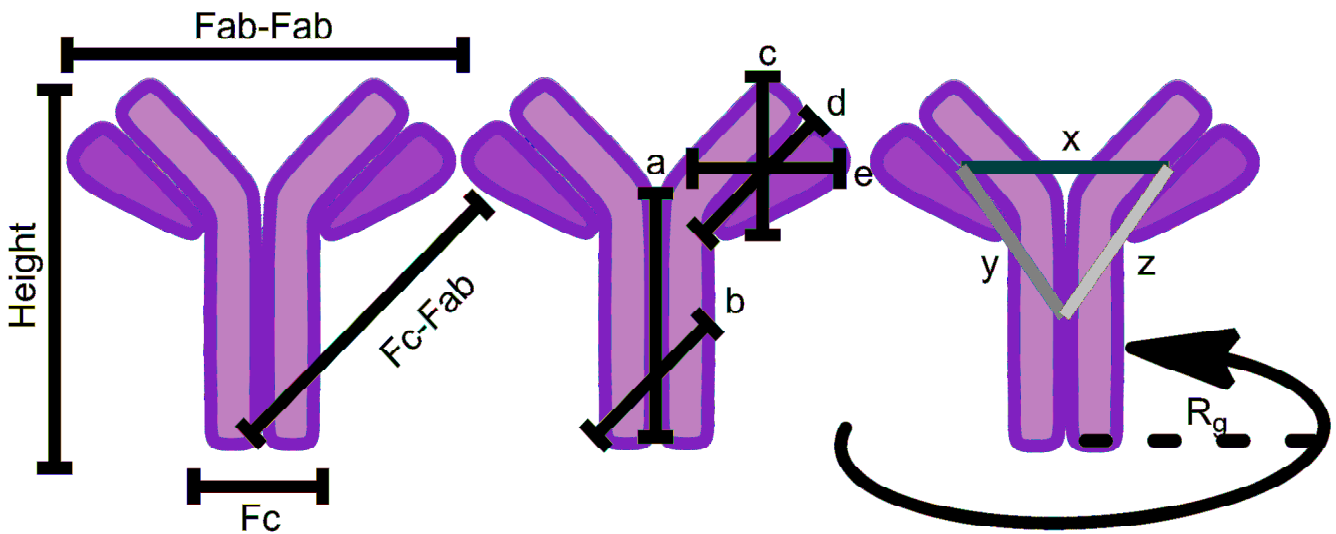


Figure S-1. Literature reports the dimensions of IgG antibodies as follows: Fab-Fab (14.2 nm)[10], height (11.5, 14.0 nm)[11], Fc-Fab (13.6 nm)[12], Fc (0.91[13], 3.8[10] nm),  $R_g$  (6,[14] 5.5[15], 5.6[16] nm),  $a$  (8.5 nm)[10],  $b$  (4.5 nm)[10],  $c*d*e$  (7x5x4 nm)[10],  $x-y-x$  (8.3-7.3-7.9 nm)[17]. These were used to develop spherical (using  $R_g$ ) and elliptical (using  $d$  and  $b$  for the width, Fab-Fab for the length) representations that could be used to examine possible orientations of the IgG molecules immobilized on a QCM crystal through binding of its Fc region to Protein A, thus predicting maximum surface coverage.

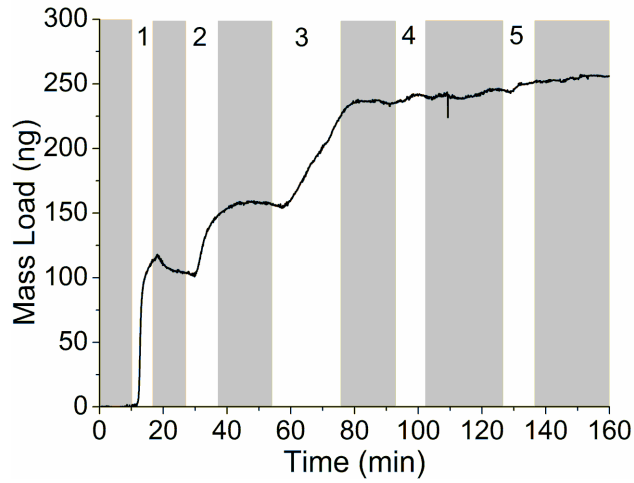


Figure S-2. Reusability of the  $\alpha$ -LAM immunosensor is demonstrated with sequential binding of Mtb and then LAM. The total mass detected in each step is as follows: (1) 101 ng protein A,  $\theta = 17\%$  (2) 53 ng BSA,  $\theta = 106\%$  (3) 83 ng  $\alpha$ -LAM,  $\theta = 18\%$  (4) 4 ng Mtb,  $\theta = 0.3\%$  (5) 6 ng LAM,  $\theta = 13\%$ .

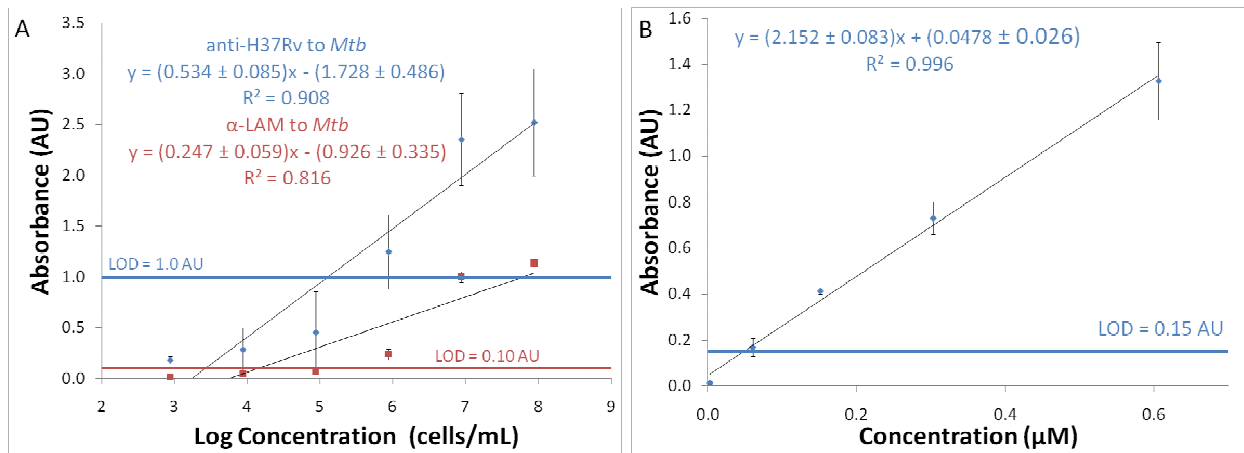


Figure S-3. Detection of *Mtb* using anti-H37Rv and  $\alpha$ -LAM (a) and of LAM using  $\alpha$ -LAM (b) in an ELISA.

## References

- [1] I. Langmuir, Vapor Pressures, Evaporation, Condensation and Adsorption, *J. Am. Chem. Soc.*, 54 (1932) 2798-2832.
- [2] A. Janshoff, H.-J. Galla, C. Steinem, Piezoelectric mass-sensing devices as biosensors-an alternative to optical biosensors?, *Angew. Chem., Int. Ed.*, 39 (2000) 4004-4032.
- [3] A.E. Gerdon, D.W. Wright, D.E. Cliffler, Quartz Crystal Microbalance Detection of Glutathione-Protected Nanoclusters Using Antibody Recognition, *Anal. Chem.*, 77 (2005) 304-310.
- [4] Y. Liu, X. Yu, R. Zhao, D.-H. Shangguan, Z. Bo, G. Liu, Real time kinetic analysis of the interaction between immunoglobulin G and histidine using quartz crystal microbalance biosensor in solution, *Biosens. Bioelectron.*, 18 (2003) 1419-1427.
- [5] K. Saha, F. Bender, E. Gizeli, Comparative Study of IgG Binding to Proteins G and A: Nonequilibrium Kinetic and Binding Constant Determination with the Acoustic Waveguide Device, *Anal. Chem.*, 75 (2003) 835-842.
- [6] Y. Liu, X. Tang, F. Liu, K.a. Li, Selection of Ligands for Affinity Chromatography Using Quartz Crystal Biosensor, *Anal. Chem.*, 77 (2005) 4248-4256.
- [7] D.S. Karpovich, G.J. Blanchard, Direct Measurement of the Adsorption Kinetics of Alkanethiolate Self-Assembled Monolayers on a Microcrystalline Gold Surface, *Langmuir*, 10 (1994) 3315-3322.
- [8] Y. Ebara, K. Itakura, Y. Okahata, Kinetic Studies of Molecular Recognition Based on Hydrogen Bonding at the Air-Water Interface by Using a Highly Sensitive Quartz-Crystal Microbalance, *Langmuir*, 12 (1996) 5165-5170.
- [9] A.E. Gerdon, D.W. Wright, D.E. Cliffler, Quartz Crystal Microbalance Characterization of Nanostructure Assemblies in Biosensing, in: C.S.S.R. Kumar (Ed.) *Nanosystem Characterization Tools in the Life Sciences*, Wiley-VCH Verlag GmbH & Co. KGaA, Weinheim, Germany, 2006, pp. 109-144.
- [10] V.R. Sarma, E.W. Silverton, D.R. Davies, W.D. Terry, The Three-Dimensional Structure at 6 Å Resolution of a Human  $\hat{\text{I}}\text{gG1}$  Immunoglobulin Molecule, *J. Biol. Chem.*, 246 (1971) 3753-3759.
- [11] A.F. Labrijn, P. Poignard, A. Raja, M.B. Zwick, K. Delgado, M. Franti, J. Binley, V. Vivona, C. Grundner, C.-C. Huang, M. Venturi, C.J. Petropoulos, T. Wrin, D.S. Dimitrov, J. Robinson, P.D. Kwong, R.T. Wyatt, J. Sodroski, D.R. Burton, Access of Antibody Molecules to the Conserved Coreceptor Binding Site on Glycoprotein gp120 Is Sterically Restricted on Primary Human Immunodeficiency Virus Type 1, *J. Virol.*, 77 (2003) 10557-10565.
- [12] S. Kimura, W. Laosinchai, T. Itoh, X. Cui, C.R. Linder, R.M. Brown, Jr., Immunogold Labeling of Rosette Terminal Cellulose-Synthesizing Complexes in the Vascular Plant *Vigna angularis*, *Plant Cell*, 11 (1999) 2075-2086.
- [13] L. Yang, M.E. Biswas, P. Chen, Study of Binding between Protein A and Immunoglobulin G Using a Surface Tension Probe, *Biophys. J.*, 84 (2003) 509-522.
- [14] J.N. De Wit, Nutritional and functional characteristics of whey proteins in food products, *J. Dairy Sci.*, 81 (1998) 597-608.
- [15] T. Narita, H. Kitazato, J. Koshimura, K. Suzuki, M. Murata, S. Ito, Effects of protein meals on the urinary excretion of various plasma proteins in healthy subjects, *Nephron*, 81 (1999) 398-405.
- [16] M.O. Mayans, W.J. Coadwell, D. Beale, D.B. Symons, S.J. Perkins, Demonstration by pulsed neutron scattering that the arrangement of the Fab and Fc fragments in the overall structures of bovine IgG1 and IgG2 in solution is similar, *Biochem. J.*, 311 (1995) 283-291.
- [17] M.K. Boehm, J.M. Woof, M.A. Kerr, S.J. Perkins, The fab and fc fragments of IgA1 exhibit a different arrangement from that in IgG: a study by X-ray and neutron solution scattering and homology modelling, *J. Mol. Recognit.*, 286 (1999) 1421-1447.