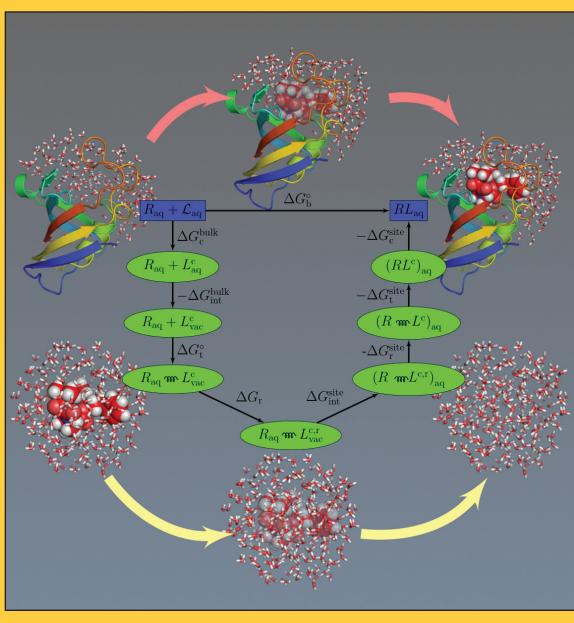
FEBRUARY 26, 2009 VOLUME 113 NUMBER 8 pubs.acs.org/JPCB

THE JOURNAL OF PHYSICAL CHEMISTRY

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Computation of the Binding Free Energy of a Ligand to a Protein Using the Double Decoupling Method (see page XA)

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