



Supplement of

Imatinib disassembles the regulatory core of Abelson kinase by binding to its ATP site and not by binding to its myristoyl pocket

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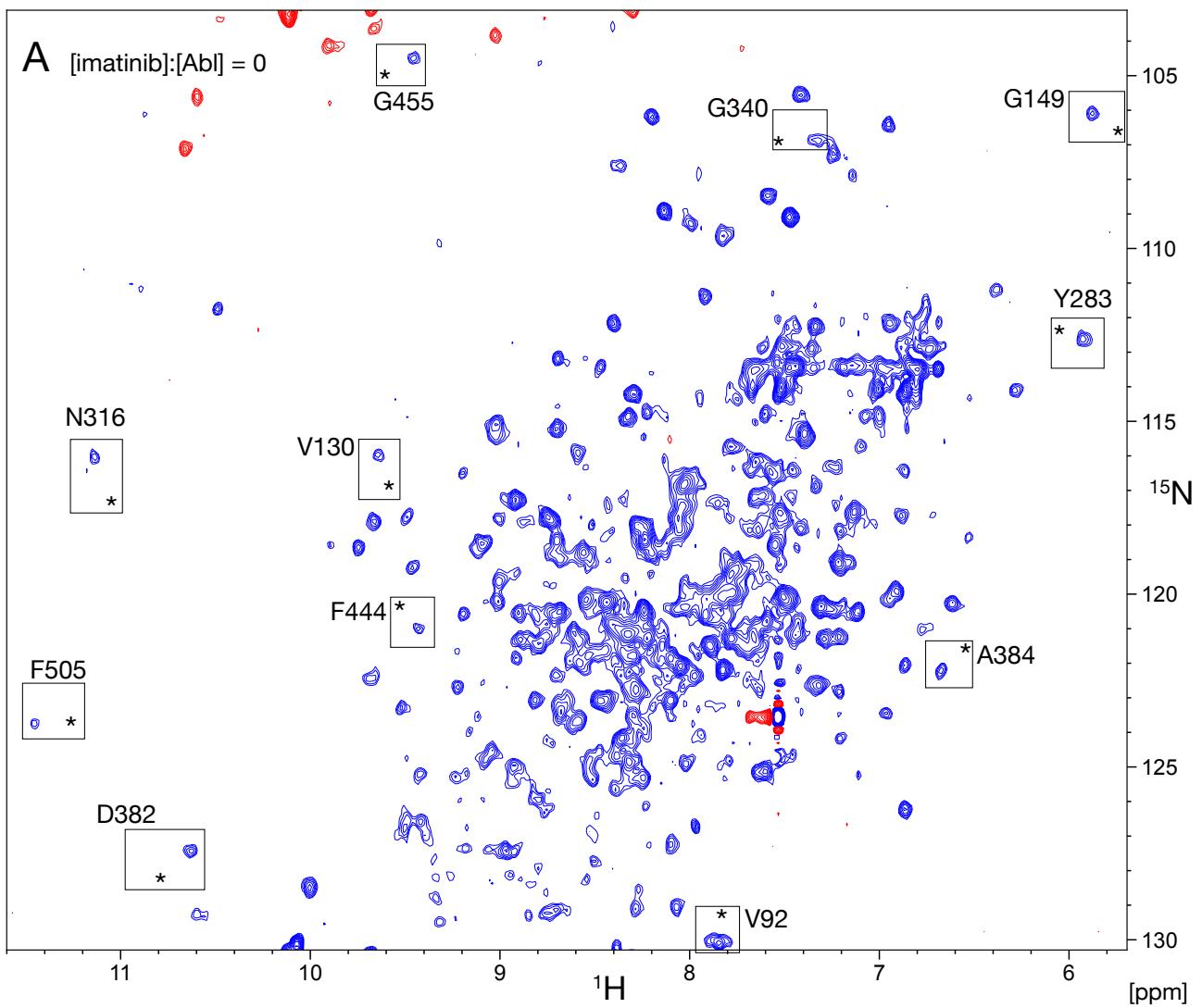
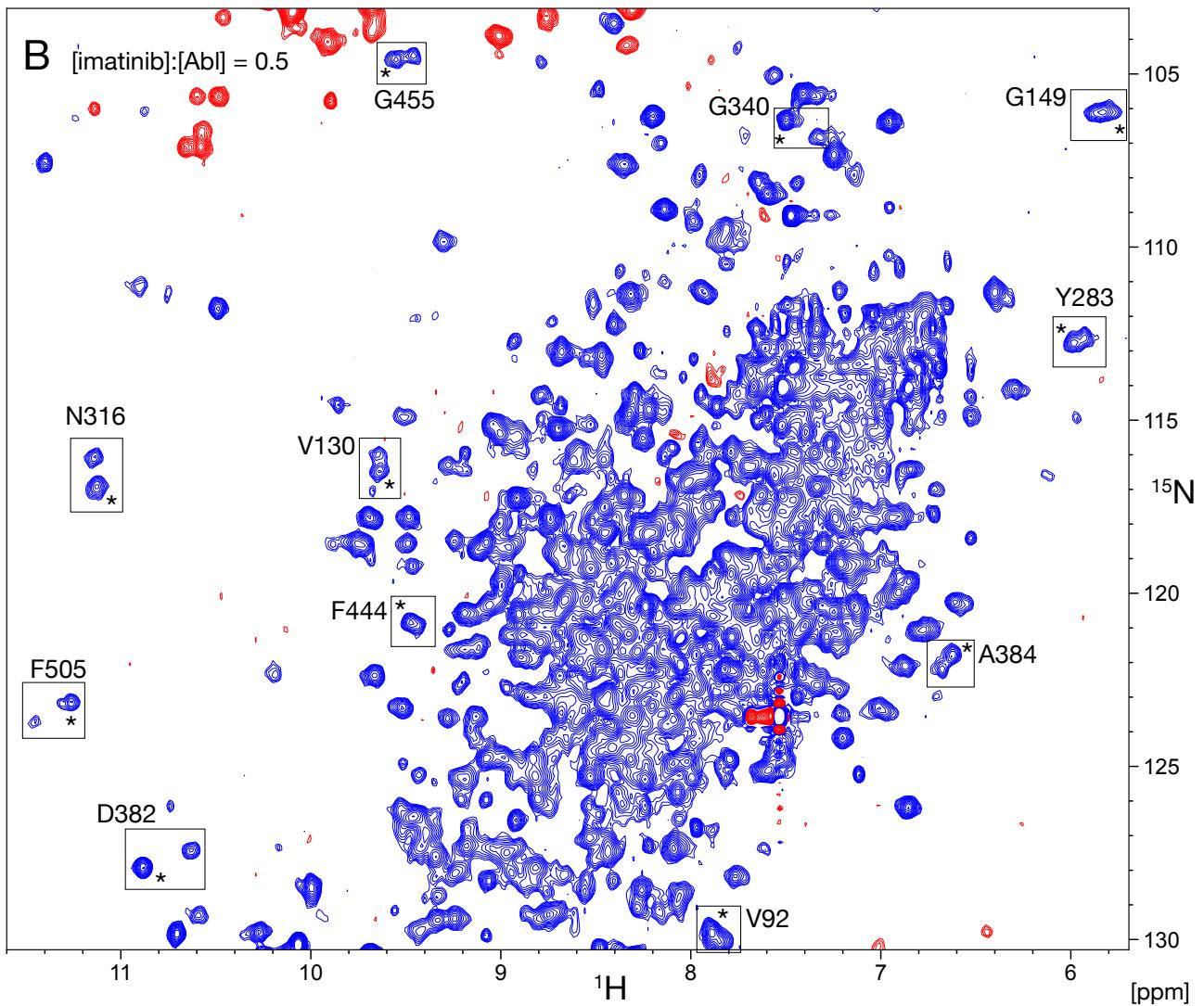


Figure S1 continued overleaf



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Figure S1 continued overleaf

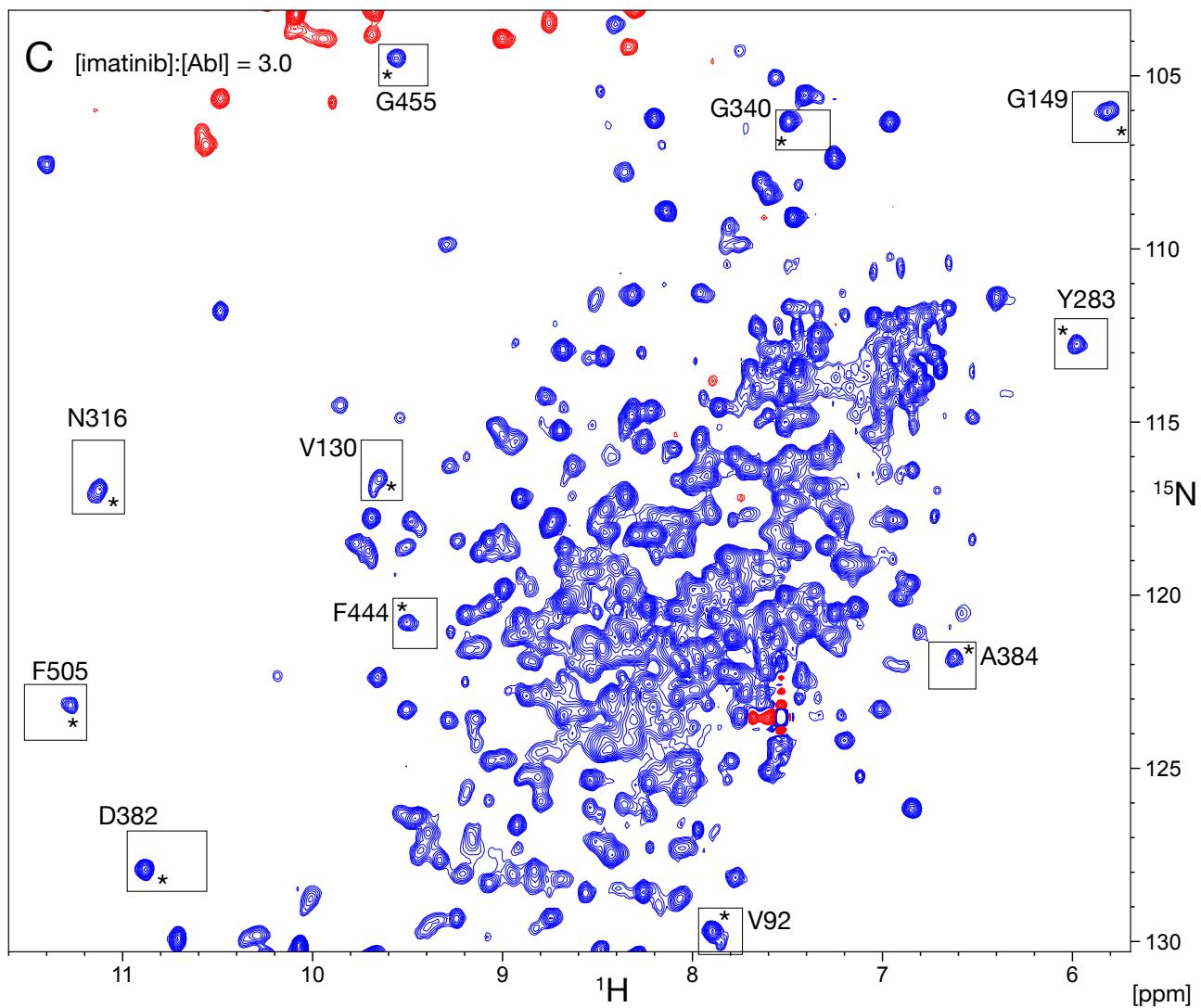


Figure S1. Full ^1H - ^{15}N TROSY spectra of the Abl^{83-534} core at various molar imatinib: Abl^{83-534} ratios. The panels 20 depict the full spectral range, from which the regions in Figure 2A were selected. [imatinib]:[Abl^{83-534}] = 0 (panel A), 0.5 (panel B), 3.0 (panel C). Selected resonances from residues in the SH3 (V92, V130), SH2 (G149), and kinase domain (Y283, N316, G340, D382, A384, F444, G455, F505), which clearly differ in their apo and imatinib-bound states, are marked by rectangles and assignment information. The resonances of the imatinib-bound state are marked by an asterisk.