STRUCTURAL BIOLOGY COMMUNICATIONS

Volume 71 (2015)

Supporting information for article:

The structure of C290A,C393A Aurora A provides structural insights into kinase regulation

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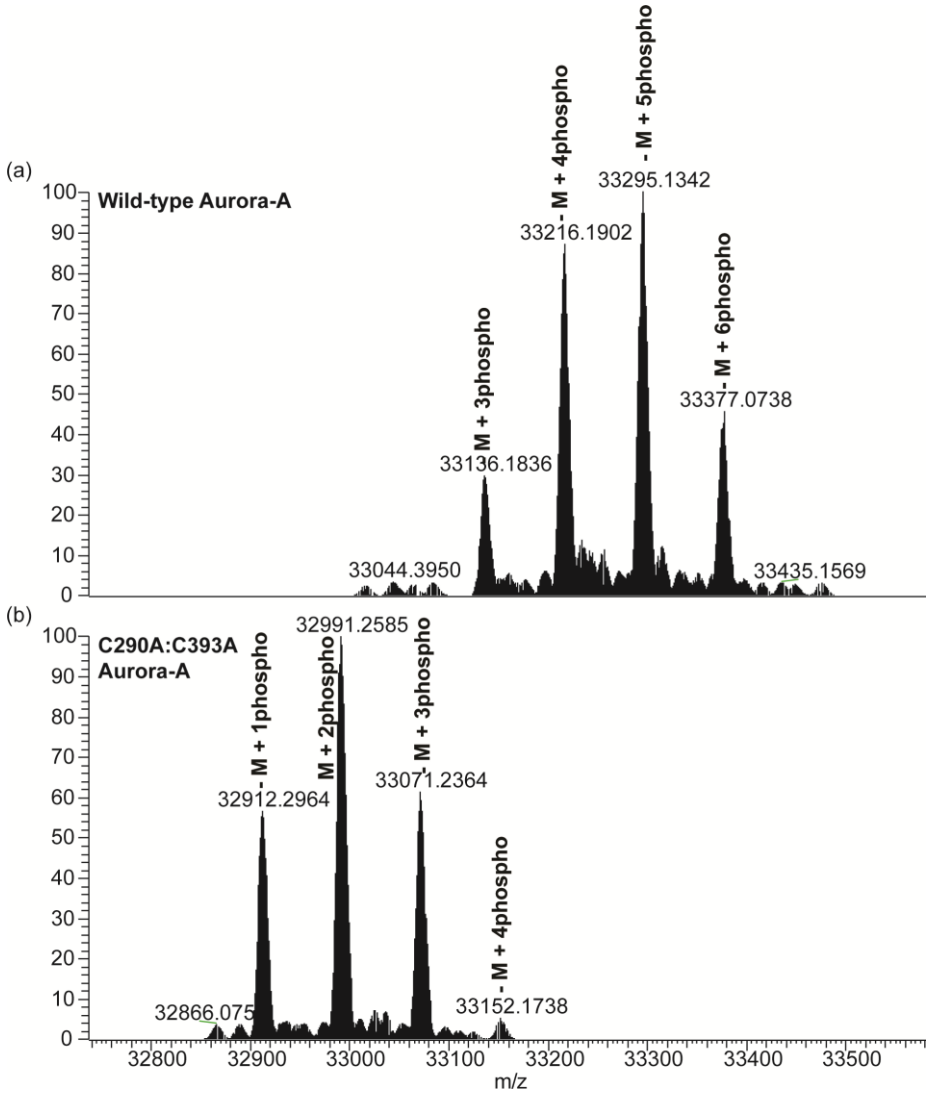
(a)
Wild-type Aurora-A
M + 3phospho
M + 4phospho
M + 5phospho
M + 6phospho
33044.3950
33136.1836
33216.1902
33295.1342
33377.0738
33435.1569
(b)
C290A:C393A
Aurora-A
M + 1phospho
M + 2phospho
M + 3phospho
M + 4phospho
32866.075
32912.2964
32991.2585
33071.2364
33152.1738
m/z

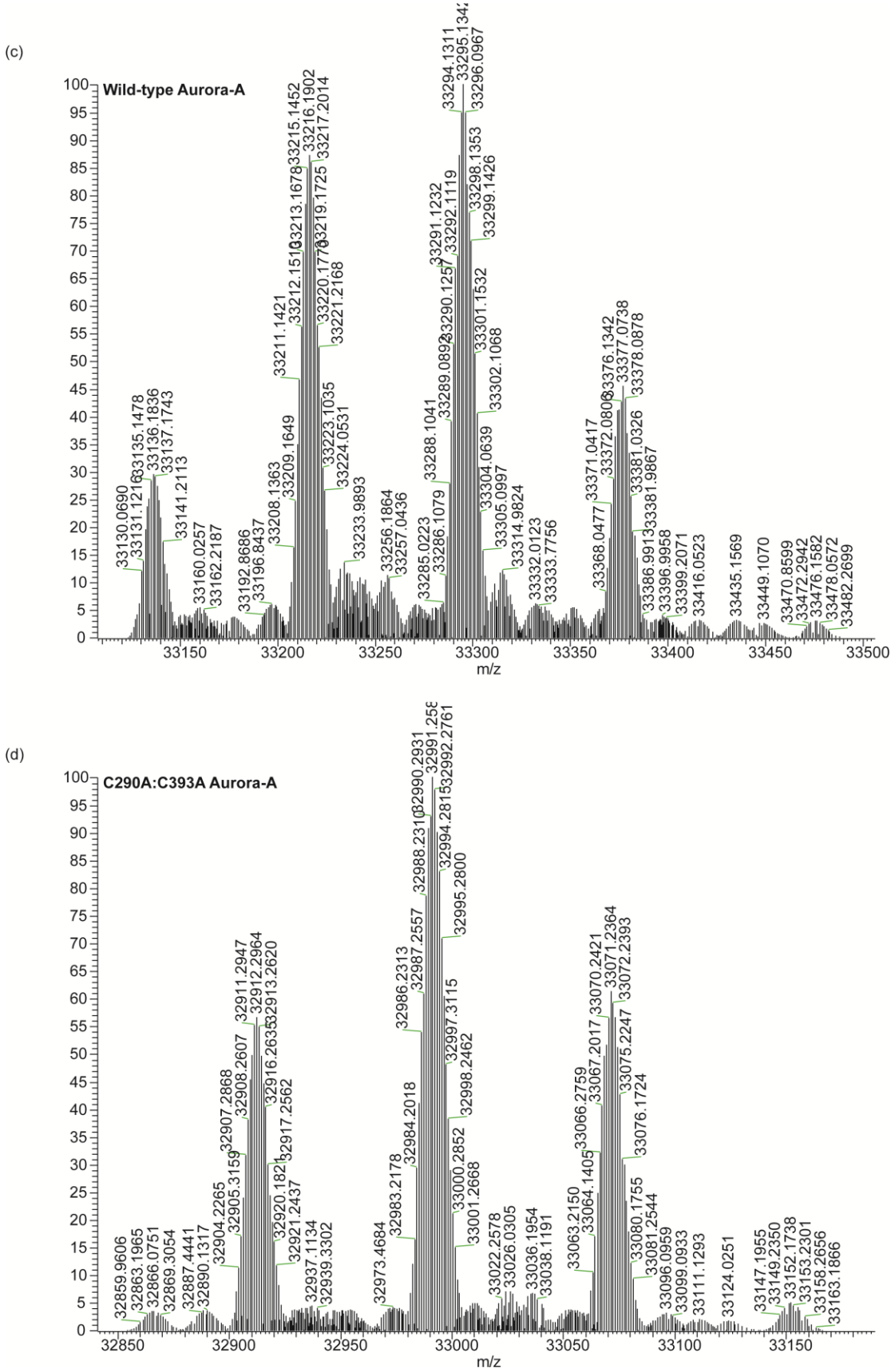

Figure S1 Mass spectrometry of intact Aurora-A. (a) LC-MS/MS spectrum for intact wild-type Aurora-A. (b) LC-MS/MS spectrum for intact C290A:C393A Aurora-A. Peaks are

labelled with the average mass (Da) observed. The theoretical intact mass of wild-type and C290A:C393A Aurora-A are 32896.6484 Da and 32832.5273 Da, respectively. The addition of a phosphate group is observed as an increase in mass of 80 Da. Analysis of the spectra indicate wild-type Aurora-A is phosphorylated on 3-6 sites (marked as M+n phospho), while C290A:C393A Aurora-A is phosphorylated on 1-4 sites. Panels (c) and (d) display expanded views of the spectra shown in (a) and (b).