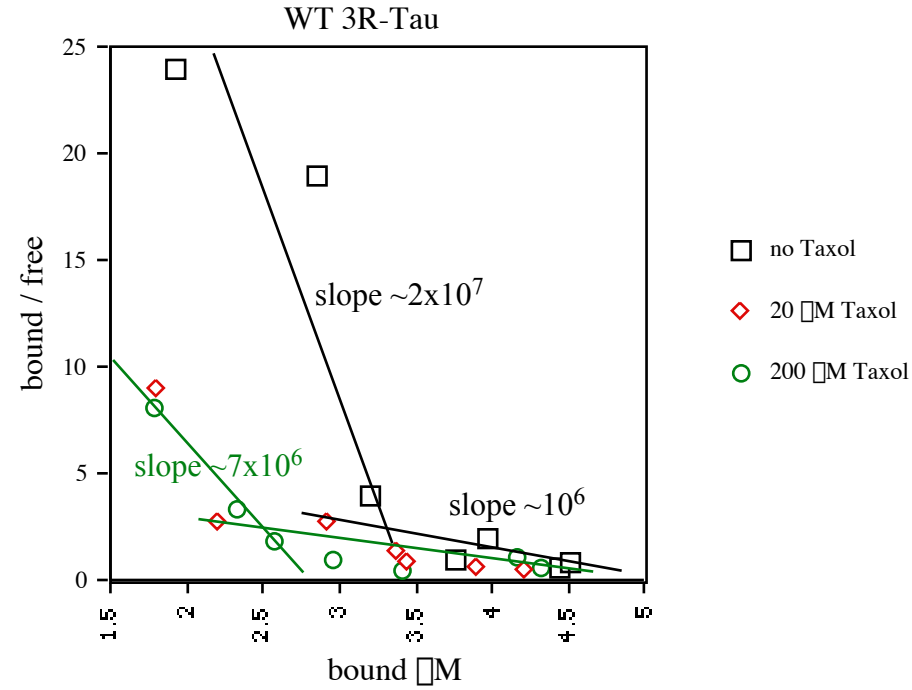
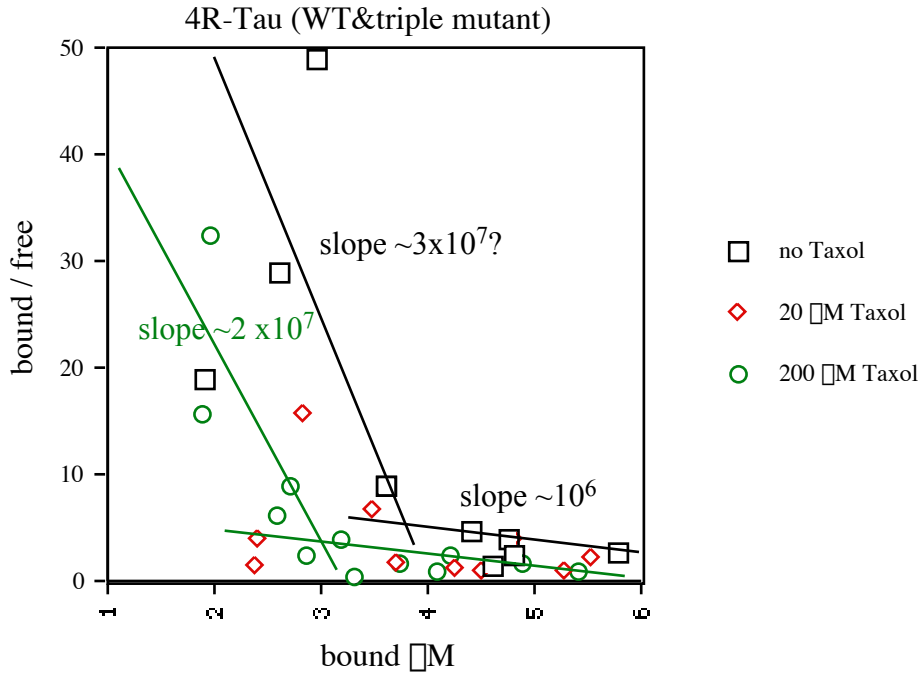
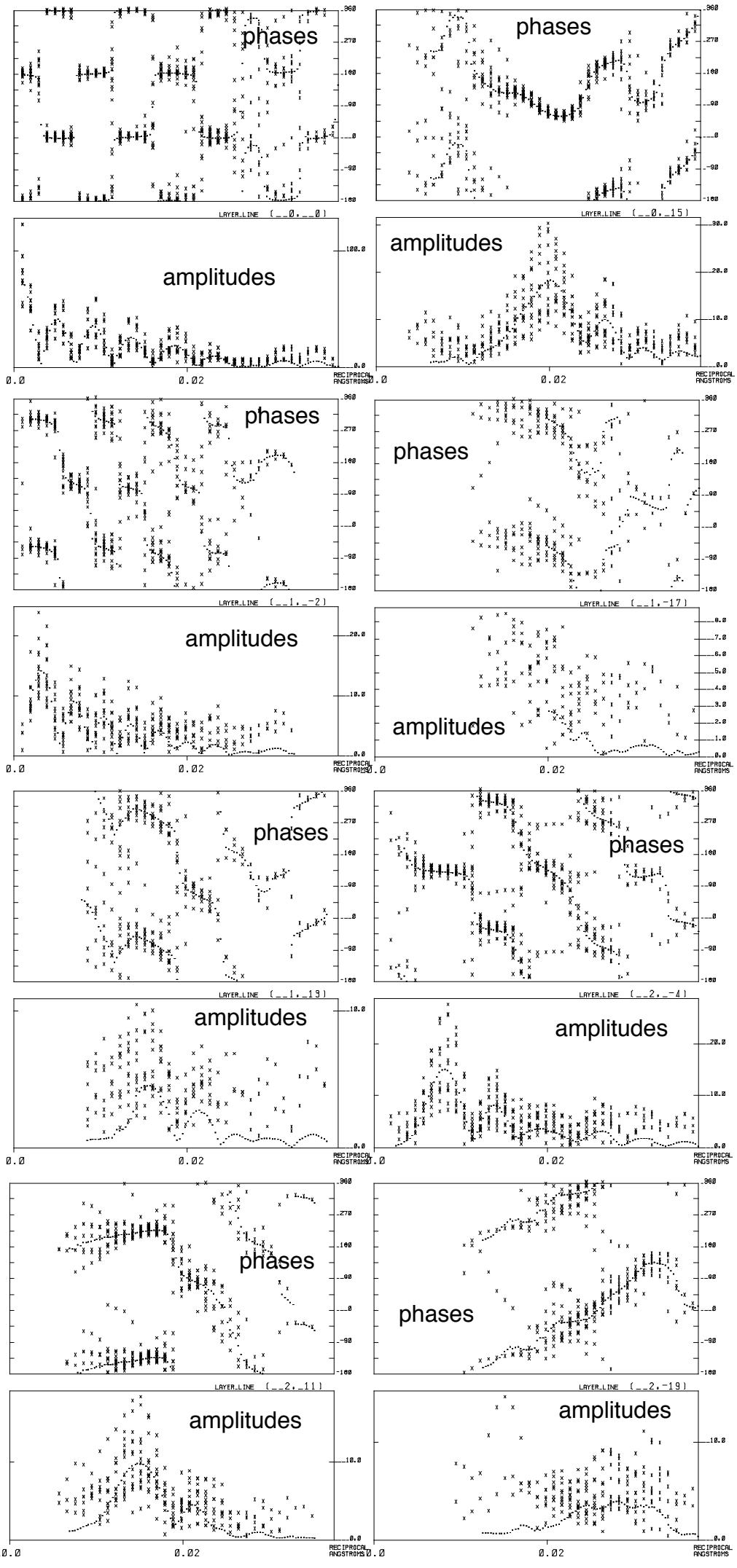




Scatchard plots of the data in Fig. 4 for wild-type 3R-tau and the combined data for triple mutant and wild-type 4R-tau (which were indistinguishable in this assay).
For an enzyme-substrate model: $[tau]_{bound} / [tau]_{free} = (1 / K) [tau]_{bound} + n [tub] / K$
where K is the dissociation constant, n is the number of binding sites for the substrate.
[tub] = 10uM
The initial slopes give K values at low tau concentrations; they are not very accurate because the amounts of free tau measured by densitometry are extremely small (some not detectable by eye). However it is clear that the slopes for the second binding phases are ~10-fold lower and the breaks between the two phases are clear-cut.



Comparison of the phases and amplitudes along the layerlines of different Fourier transforms. Each transform was calculated from a cryo image of a microtubule assembled from tubulin plus gold-labeled 4R-tau and decorated with kinesin. The phases have been adjusted to bring all the specimens into the same orientation. Phases agree best where the amplitudes peak.The data from the other specimens are of a similar quality to these.