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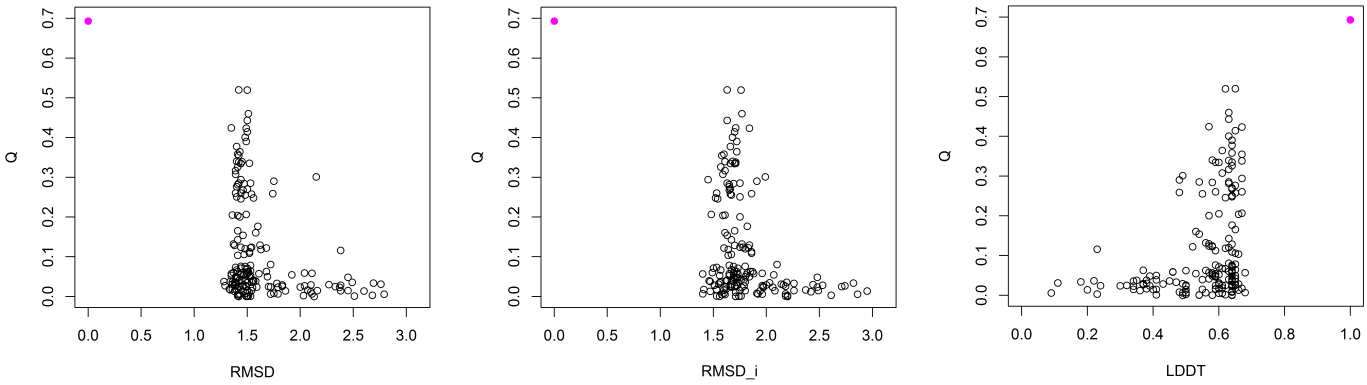

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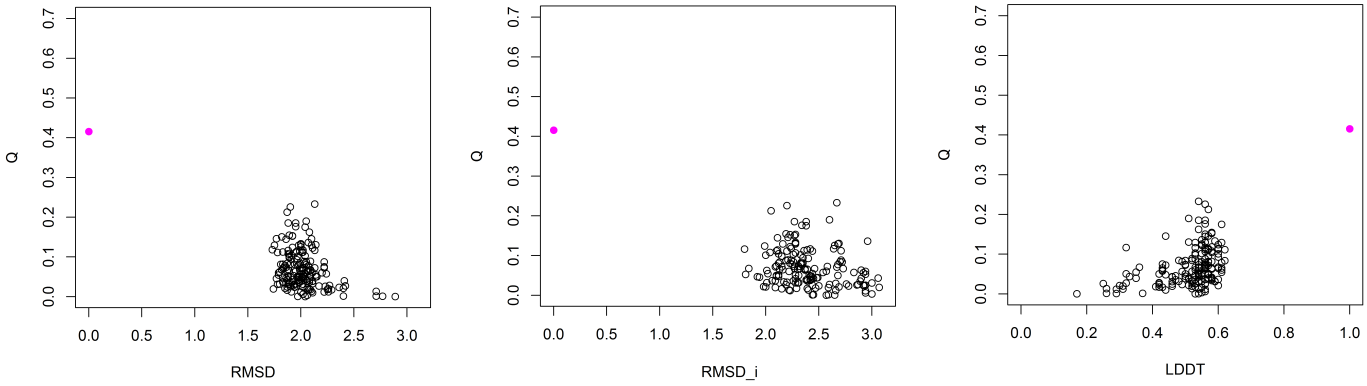

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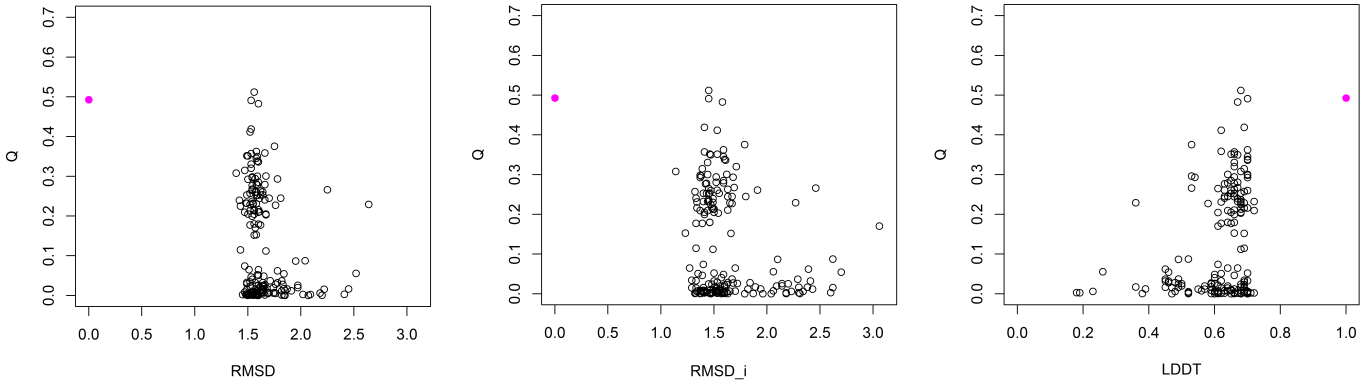
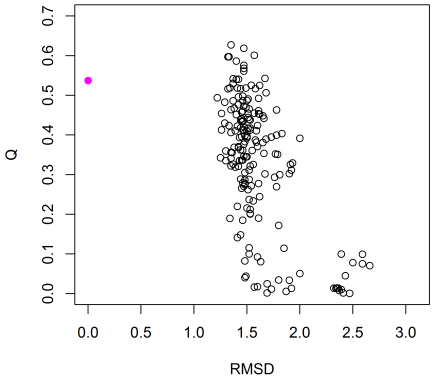
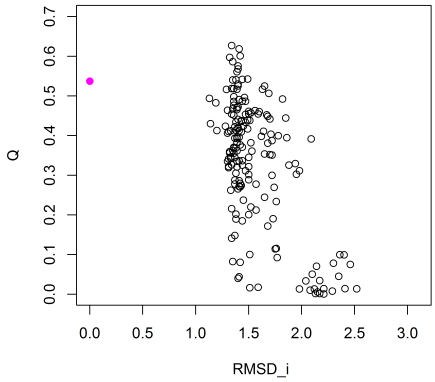


T0801
N2U028_ECOLX

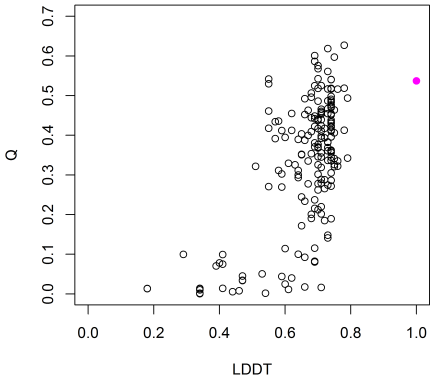
RMSD vs Q



RMSD_i vs Q



LDDT vs Q



T0819
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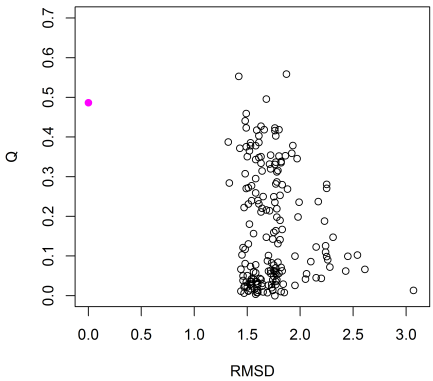

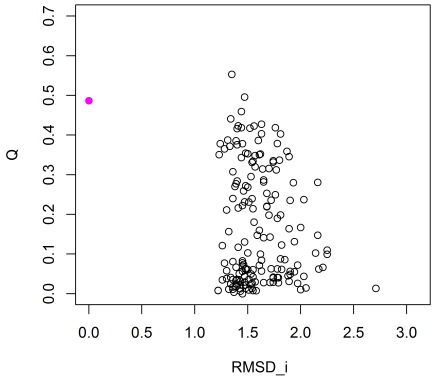

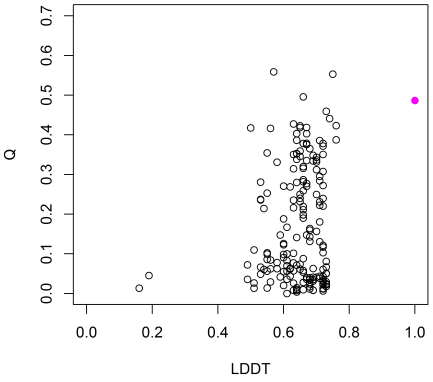

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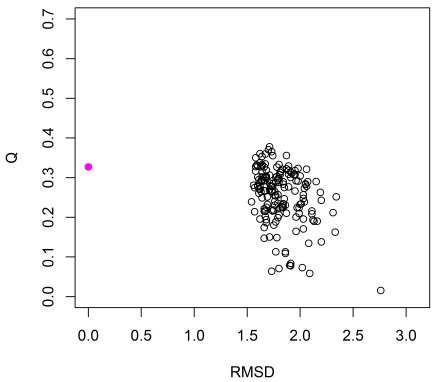

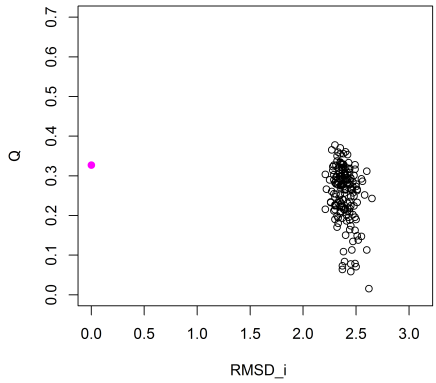

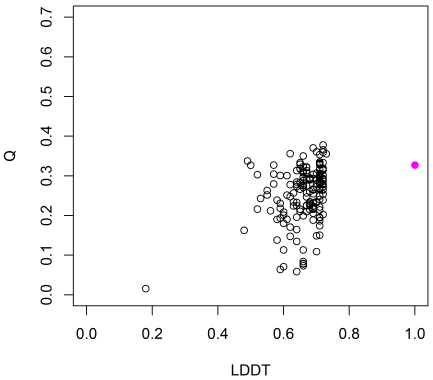

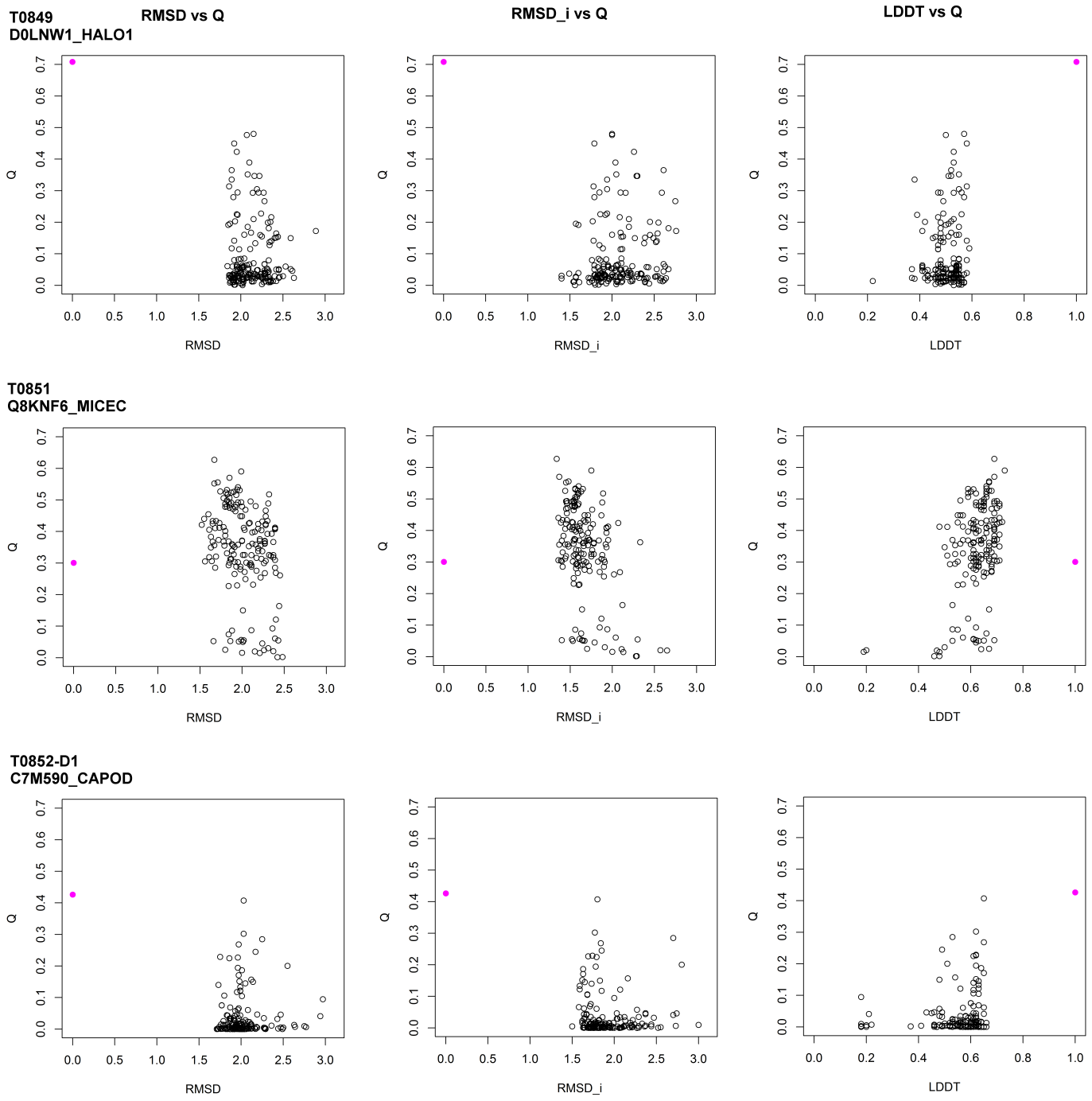

Figure S1. Docking of CASP11 predicted monomer structures into homodimers with ClusPro. The scatterplots show the relationship of the best *Q* score of the top 10 ClusPro clusters with quality metrics of the monomer structures: RMSD, RMSD_i, and LDDT. RMSD is the root-mean-square distance of Cαs between a prediction and the target. RMSD_i is the RMSD of Cαs of interface residues between a prediction and the target after sequence-dependent superposition of these residues with LGA. Interface residues are defined as those residues with Cβ/Cβ distance ≤ 12 Å in two chains of the experimental dimer (Cα in the case of glycines). LDDT is the mean percentage of *i,j* in a prediction, with distance differences less than 0.5 Å, 1 Å, 2 Å, 4 Å, for a list of all *i,j* distances less than 5 Å in target. The *Q* score is a measurement of similarity between the docked dimer and the experimental dimer, based on the corresponding Cβ-Cβ distances of contact residues in each structure. The point colored in magenta is *Q* score of the crystal structure itself, with RMSD = 0 Å, RMSD_i = 0 Å and LDDT = 1.0.