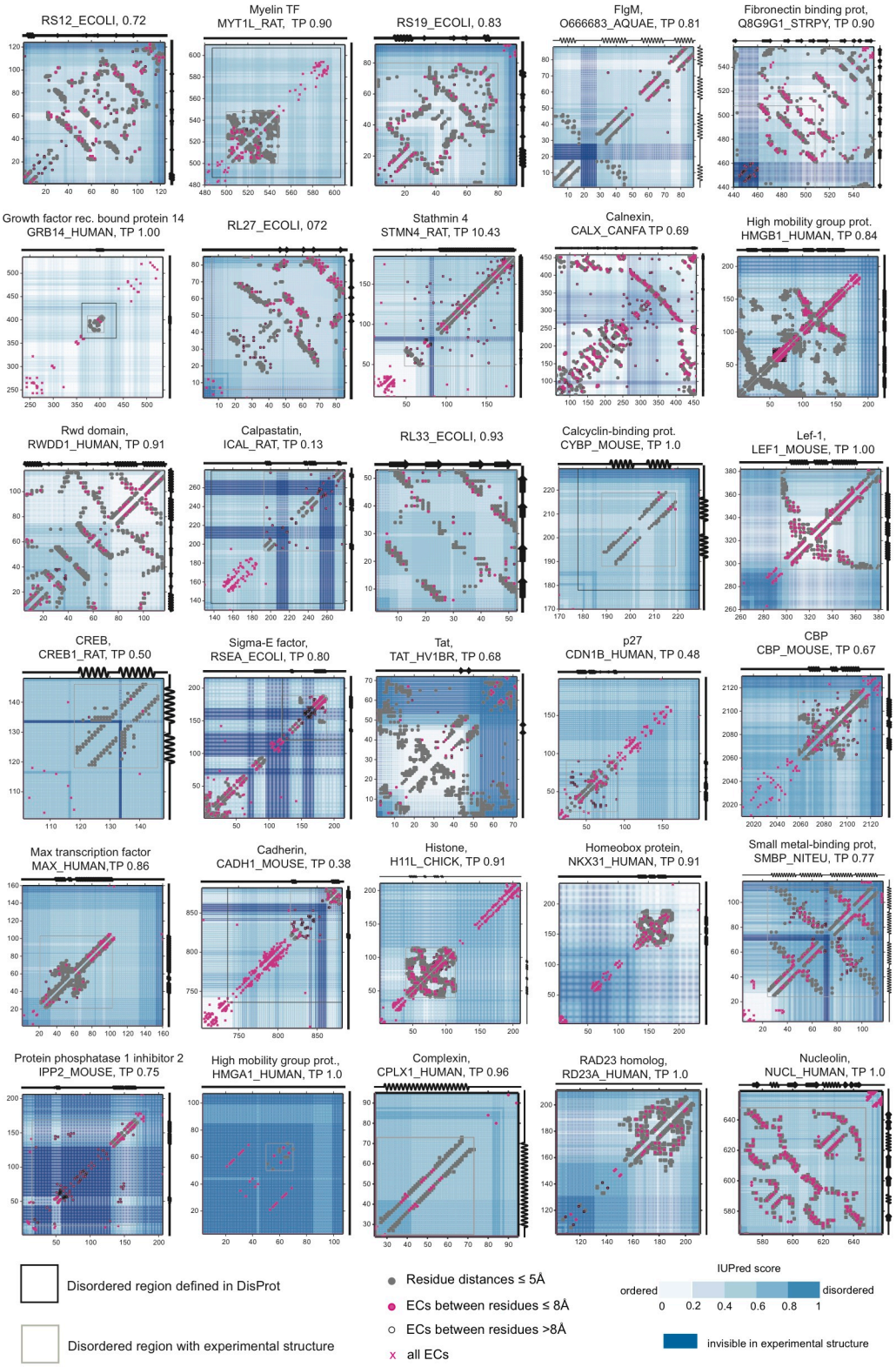Figure S4. Blind prediction of 3D contacts of disordered proteins with known structures captured by evolutionary couplings (30 proteins, Table S2B).