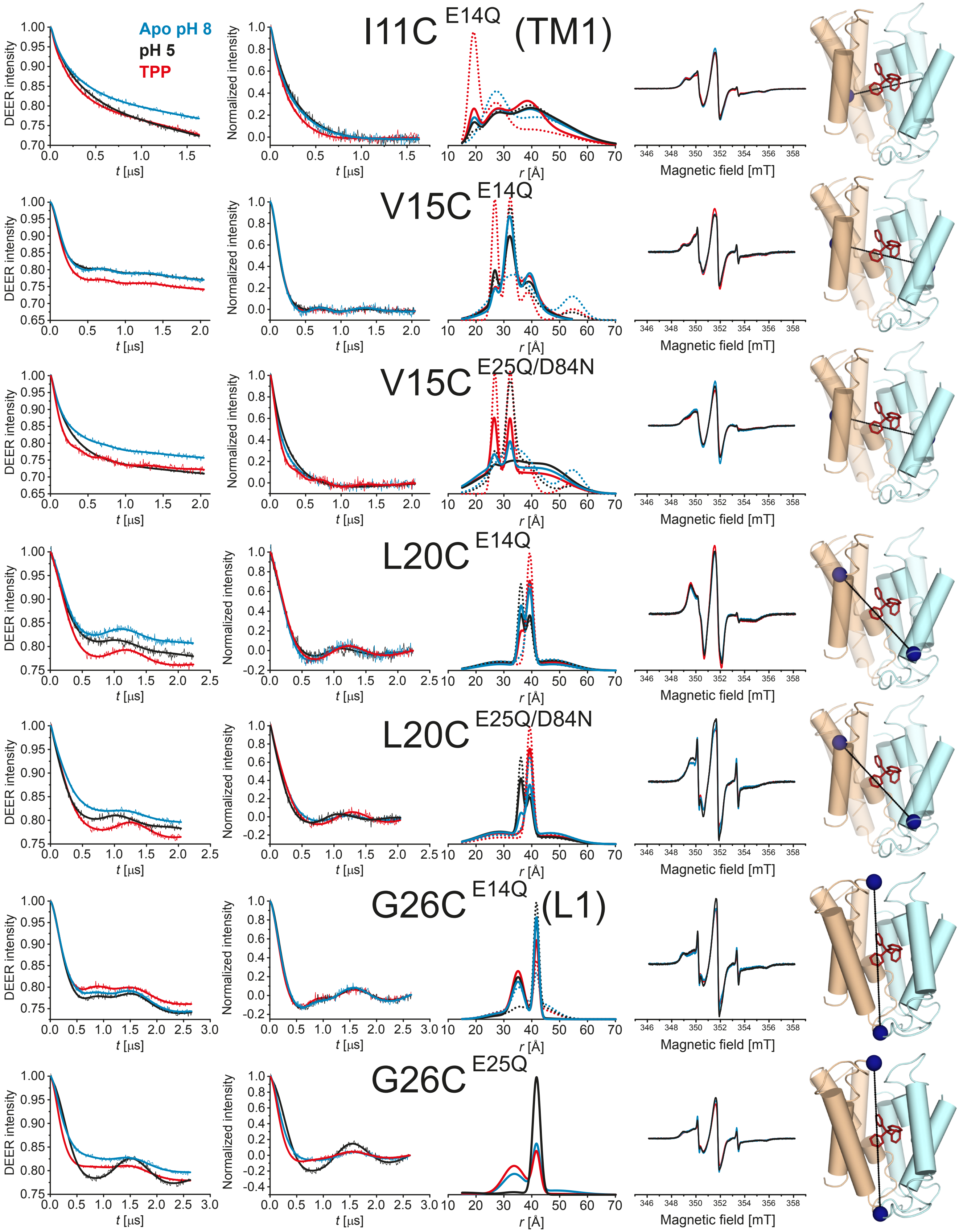
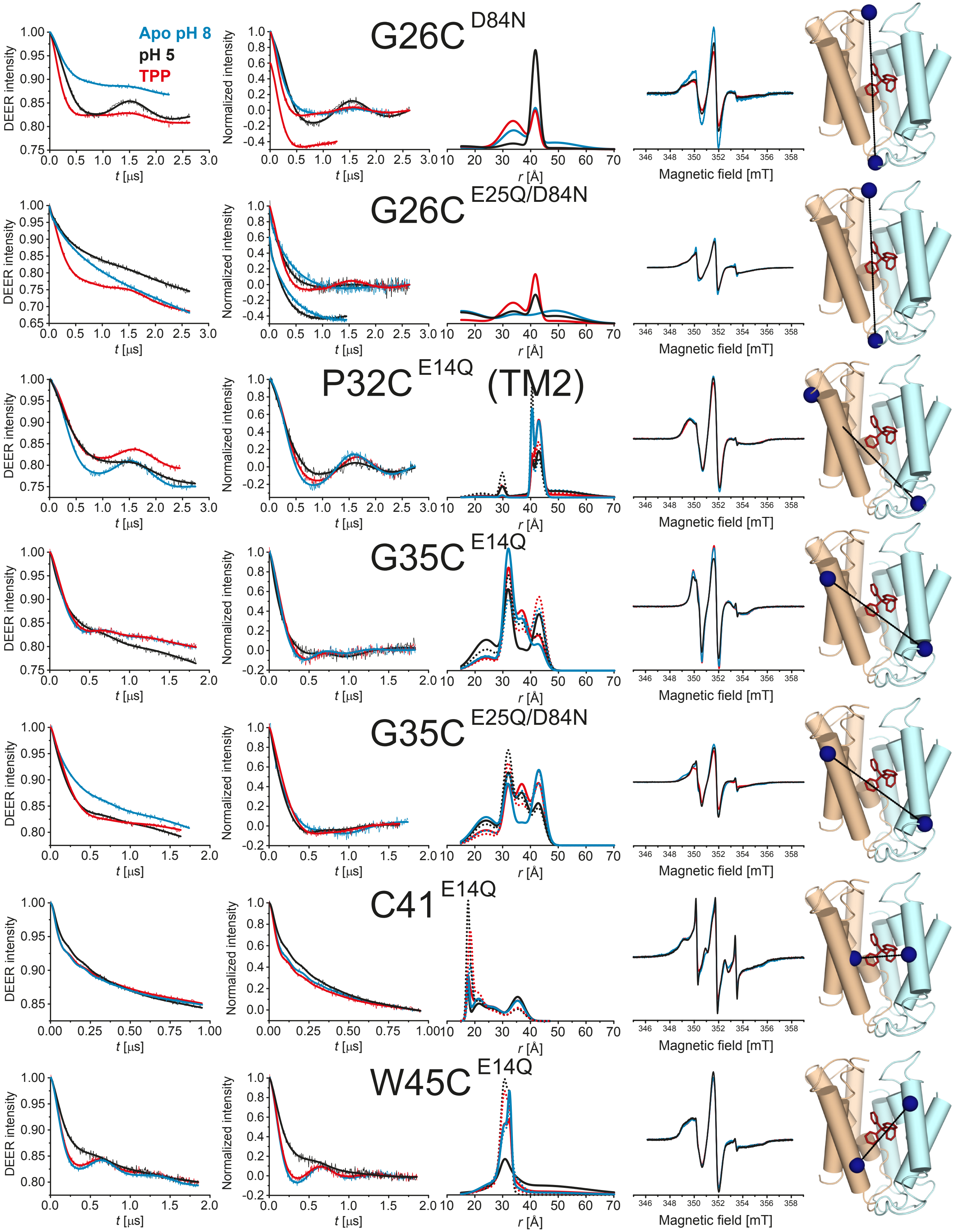
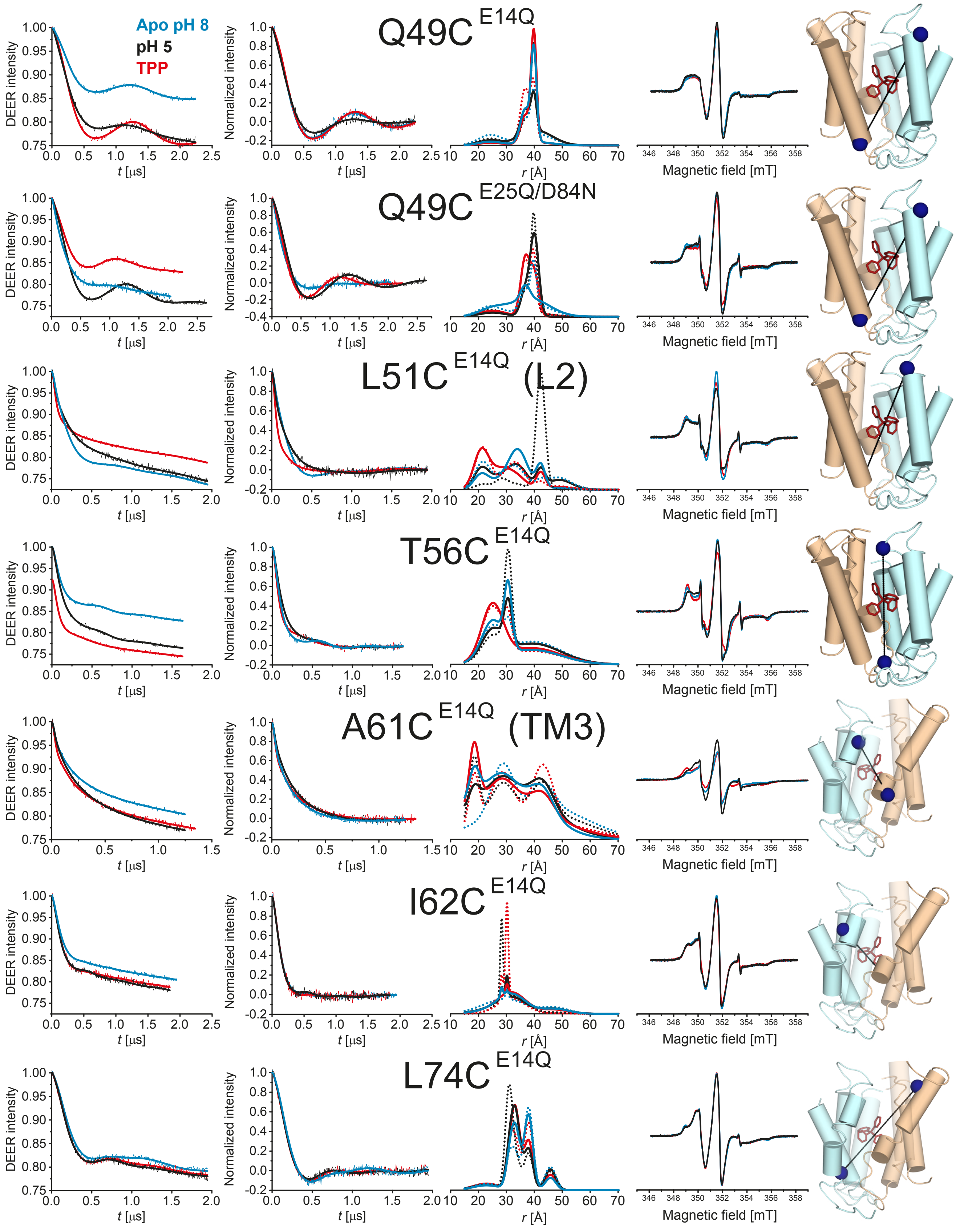


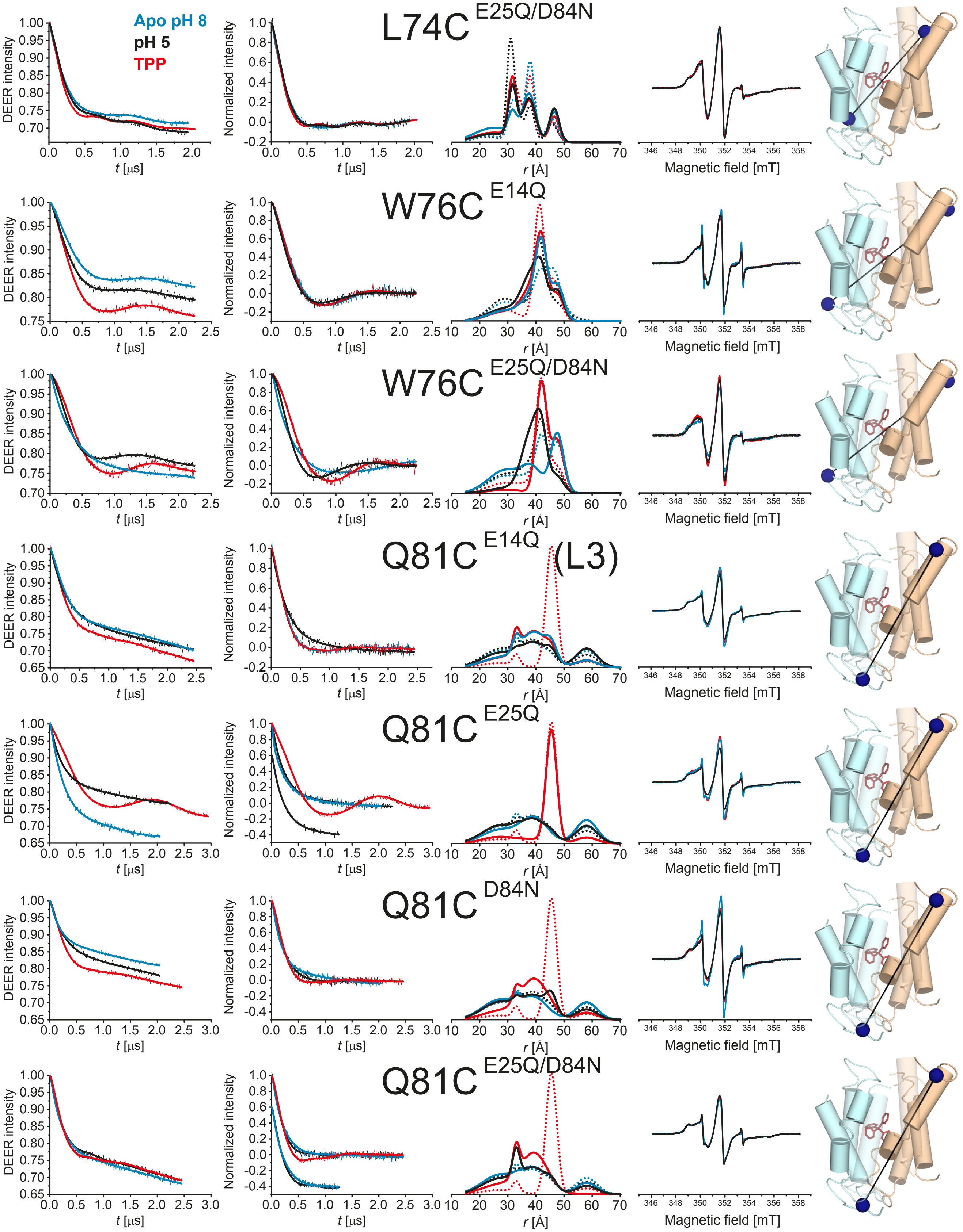
SI Appendix 3A. DEER data analysis for the protonation-mimetic functional mutants in β-DDM micelles. The single (E14Q, E25Q, D84N) or double (E25Q/D84N) mutations were combined with the single-cysteine mutations. For each mutant, from left to right, primary DEER traces with the corresponding fits, baseline-corrected and normalized DEER traces along with the fits, distance distributions, the CW-EPR spectra, and except for non-resolved residues, the position of the mutated residue on the X-ray structure (PDB code 3B5D) are shown. The dotted distance distributions are the corresponding wild type distributions.



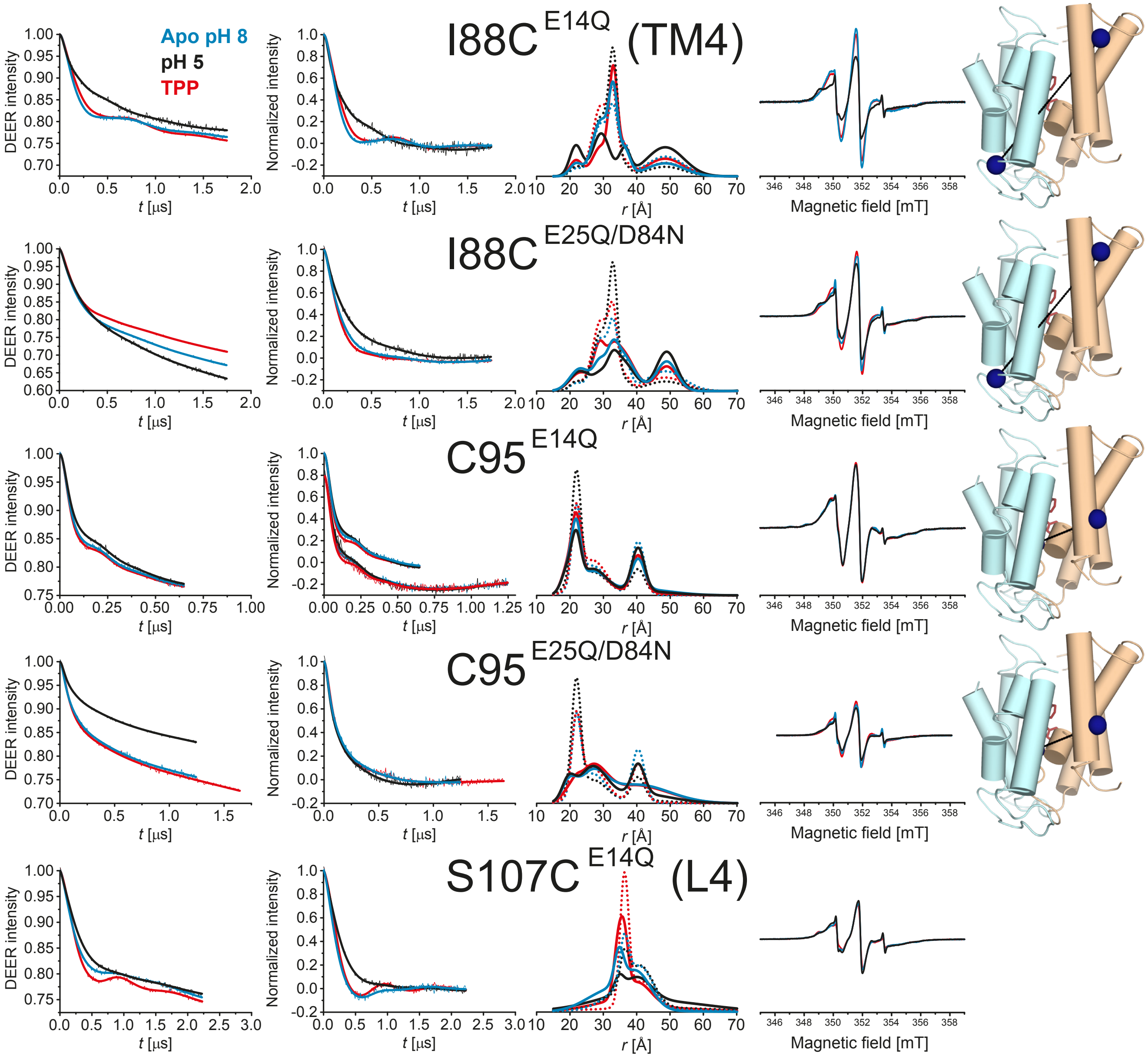
SI Appendix 3B. DEER data analysis for the protonation-mimetic functional mutants in β-DDM micelles. The single (E14Q, E25Q, D84N) or double (E25Q/D84N) mutations were combined with the single-cysteine mutations. For each mutant, from left to right, primary DEER traces with the corresponding fits, baseline-corrected and normalized DEER traces along with the fits, distance distributions, the CW-EPR spectra, and except for non-resolved residues, the position of the mutated residue on the X-ray structure (PDB code 3B5D) are shown. The dotted distance distributions are the corresponding wild type distributions.



SI Appendix 3C. DEER data analysis for the protonation-mimetic functional mutants in β-DDM micelles. The single (E14Q, E25Q, D84N) or double (E25Q/D84N) mutations were combined with the single-cysteine mutations. For each mutant, from left to right, primary DEER traces with the corresponding fits, baseline-corrected and normalized DEER traces along with the fits, distance distributions, the CW-EPR spectra, and except for non-resolved residues, the position of the mutated residue on the X-ray structure (PDB code 3B5D) are shown. The dotted distance distributions are the corresponding wild type distributions.



SI Appendix 3D. DEER data analysis for the protonation-mimetic functional mutants in β-DDM micelles. The single (E14Q, E25Q, D84N) or double (E25Q/D84N) mutations were combined with the single-cysteine mutations. For each mutant, from left to right, primary DEER traces with the corresponding fits, baseline-corrected and normalized DEER traces along with the fits, distance distributions, the CW-EPR spectra, and except for non-resolved residues, the position of the mutated residue on the X-ray structure (PDB code 3B5D) are shown. The dotted distance distributions are the corresponding wild type distributions.



SI Appendix 3E. DEER data analysis for the protonation-mimetic functional mutants in β-DDM micelles. The single (E14Q, E25Q, D84N) or double (E25Q/D84N) mutations were combined with the single-cysteine mutations. For each mutant, from left to right, primary DEER traces with the corresponding fits, baseline-corrected and normalized DEER traces along with the fits, distance distributions, the CW-EPR spectra, and except for non-resolved residues, the position of the mutated residue on the X-ray structure (PDB code 3B5D) are shown. The dotted distance distributions are the corresponding wild type distributions.