

Pf1 dialysis protocol / buffer conditions for RDC

We also provide a protocol which explains how one can dialyse our Pf1 preparation (solubilized in 10mM Potassiumphosphate, 2mM Magnesiumchloride, pH 7.6) if someone prefers another buffer composition. Please fill in your [contact data](#) and the actual pdf-version will be sent to your email account.

Buffer condition used for alignment of macromolecules with Pf1 filamentous phage:

Buffer conditions	Normalized ^2H residual coupling (Hz) ^a
10 mM NaH ₂ PO ₄ , 1.5 mM EDTA, pH 8, ~17 mg/ml Pf1, 0.3 mM IRE RNA	8.2
40 mM NaH ₂ PO ₄ , 0.5 mM EDTA, pH 8, ~13 mg/ml Pf1, 1.8 mM DNA 16-mer	6.0
10 mM NaH ₂ PO ₄ , 100 mM NaCl, pH 6.8, ~6 mg/ml Pf1, 1 mM DNA 10-mer	7.7
10 mM Tris(d ₁₁), 0.5 mM EDTA, pH 8, ~22 mg/ml Pf1, 0.9 mM IRE RNA	6.1
10 mM imidazole(d ₄), 5 mM KCl, 0.5 mM EDTA, pH 6.5, ~22 mg/mg Pf1, 1.9 mM apocalmodulin	7.2
10 mM succinate, 0.1 mM EDTA, pH 5.5, ~19 mg/ml Pf1	8.2 (7.3)
10 mM succinate, 100 mM NaCl, 0.1 mM EDTA, pH 5.5, ~19 mg/ml Pf1	7.8 (5.0)
10 mM succinate, 100 mM NaCl, 2.0 mM MgCl ₂ , 0.1 mM EDTA, pH 5.5, ~20 mg/ml Pf1	6.9 (4.6)
10 mM Tris(d ₁₁), 0.1 mM EDTA, pH 8, ~15 mg/ml Pf1	8.8
10 mM Tris(d ₁₁), 0.1 mM EDTA, pH 7, ~15 mg/ml Pf1	5.5
10 mM Tris(d ₁₁), 0.1 mM EDTA, pH 6, ~15 mg/ml Pf1	4.4

^aThe residual quadrupole coupling constants for the D₂O signal were measured by 1-D ^2H spectra. Because all buffers conditions did not have the same Pf1 concentration, the values given are normalized to a Pf1 phage concentration of 10 mg/ml. Values in parentheses indicate that the sample was prepared by dialysis, whereas the other samples were prepared by pelleting the phage in the given buffer.

The table is an outline from *Mark R. Hansen, Paul Hanson and Arthur Pardi. Filamentous bacteriophage for aligning RNA, DNA, and proteins for measurement of nuclear magnetic resonance dipolar coupling interactions. Methods in Enzymology, Volume 317, 2000, Pages 220-240.*