

Supporting Information for: “Solid-State Nuclear Magnetic Resonance Spectroscopy of Human Immunodeficiency Virus gp41 Protein that Includes the Fusion Peptide: NMR Detection of Recombinant Fgp41 in Inclusion Bodies in Whole Bacterial Cells and Structural Characterization of Purified and Membrane-Associated Fgp41”

Fgp41 amino acid and DNA sequences

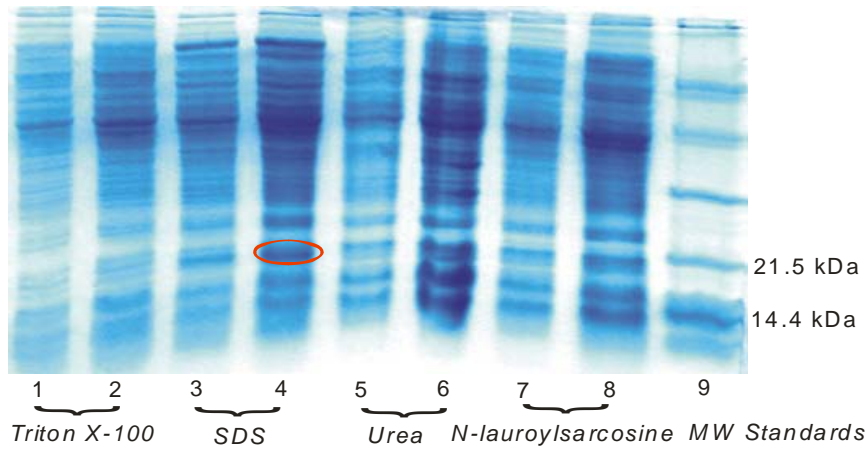
**Start** AVGLGAVFLGFLGAAGSTMGAASMTLTVQARQLLSGIVQQQSNLLKAI  
 IEAQQHLLKLTVWGIKQLQARVLAVERYLQDQQLLGIWGCSSGKLICTSFVP  
 WNNSSWSNKTYNEIWDNMTWLQWDKEISNYTDTIYRLLEDSQNNQKEKNE  
 QDLLALDKLEHHHHHH **Stop**

atggcagttggactaggagctgtcttccttgggttcttgggagcagcagggagcactatgggcgcggcgtcaatgacgctgacg  
 gtacaggccagacaattattgtctggcatagtgaacagcaaagcaatttctgaaggctatagaggctcaacagcatctgttga  
 aactcaggtctggggtattaacagctccaggcaagagtcctggctgtggaagatacctacaggatcaacagctcctgggaa  
 ttggggctgctctggaaaactcatctgcacctctttgtgccctggaacaatagtggagtaacaagactataatgagatttggg  
 acaacatgacctggttgcaatgggataaagaaattagcaattacacagacacaatacaggctacttgaagactcgagaacca  
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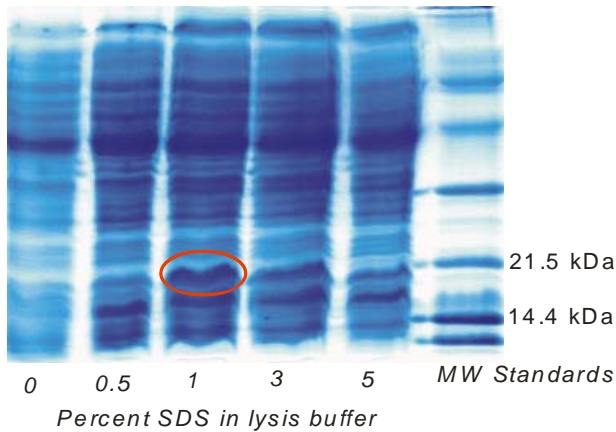
HIV-1 Sequences: Fgp41 (black) and HXB2 (blue)

<b>1</b>	AVGLGAVFLG	FLGAAGSTMG	AASMTLTVQA	RQLLSGIVQQ	QSNLLKAIEA	QQHLLKLTVW
	AVGIGALFLG	FLGAAGSTMG	AASMTLTVQA	RQLLSGIVQQ	QNNLLRAIEA	QQHLLQLTVW
<b>61</b>	GIKQLQARVL	AVERYLQDQQ	LLGIWASGK	LIATSFVPWN	NSWSNKTYNE	IWDNMTWLQW
	GIKQLQARIL	AVERYLKDQQ	LLGIWGCSSGK	LICTTAVPWN	ASWSNKSLWQ	IWNHTTWMEW
<b>121</b>	DKEISNYTDT	IYRLLEDSQN	QQEKNEQDLL	ALDKLEHHHH	HH	
	DREINNYTSL	IHSLIEESQN	QQEKNEQELL	ELDK-----	--	

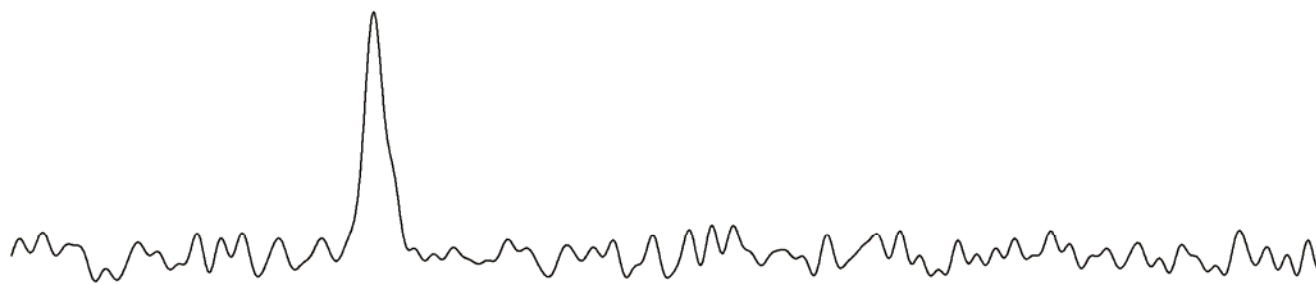
*Representative SDS-PAGE of soluble cell lysates produced using buffers with different detergents or urea.* For each buffer, the left and right lanes respectively correspond to 2 and 5  $\mu$ L aliquots of lysate. The ~19 kDa band apparent in some lanes is assigned to Fgp41. One example is circled in red in lane 4 for lysis in SDS. Bands that may be Fgp41 were also apparent for lysates in either urea or *N*-lauroylsarcosine but purifications of these lysates consistently yielded <1 mg Fgp41/L culture whereas purifications of SDS lysates yielded >1 mg Fgp41/L culture. Subsequent lysates were therefore done with SDS.



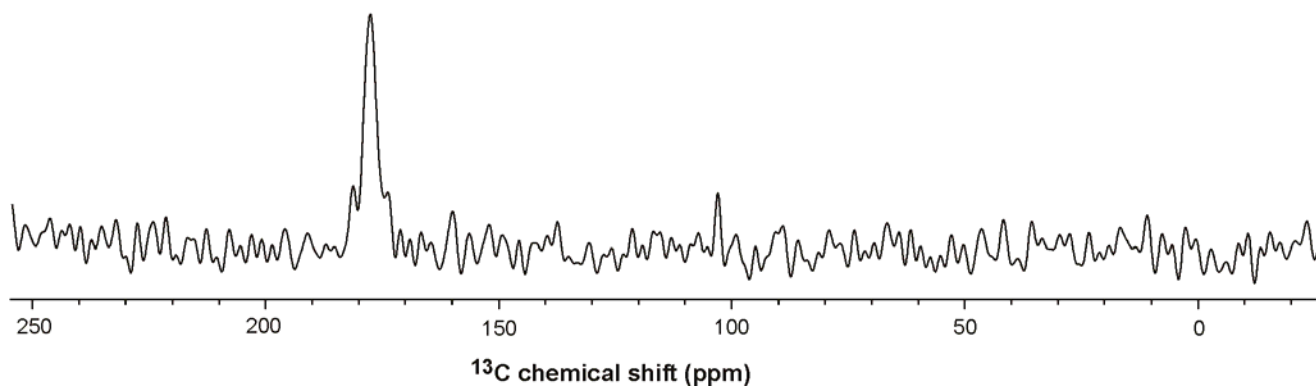
*SDS-PAGE of soluble cell lysates produced using buffers with different [SDS].*



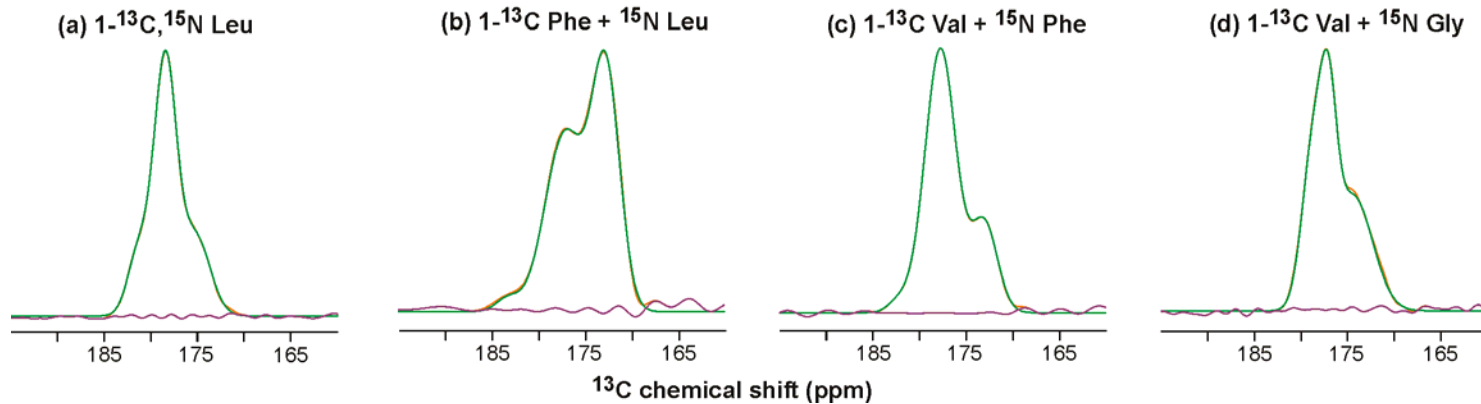
$\Delta S$  spectrum of lyophilized cells labeled with  $1\text{-}^{13}\text{C}$ ,  $^{15}\text{N}$  Leu



$\Delta S$  spectrum of membrane-reconstituted Fgp41 labeled with  $1\text{-}^{13}\text{C}$ ,  $^{15}\text{N}$  Leu



$S_0$  spectra of membrane-reconstituted Fgp41  
experiment (orange); best-fit deconvolution sum (green); difference (purple)

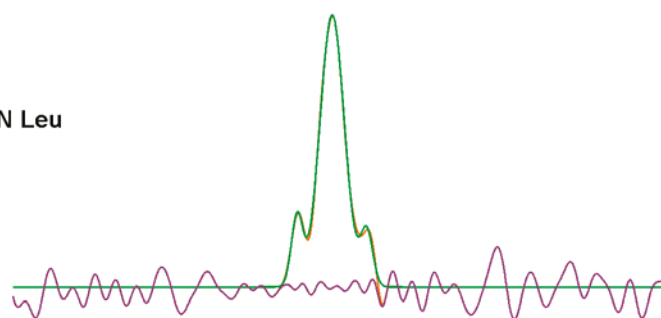
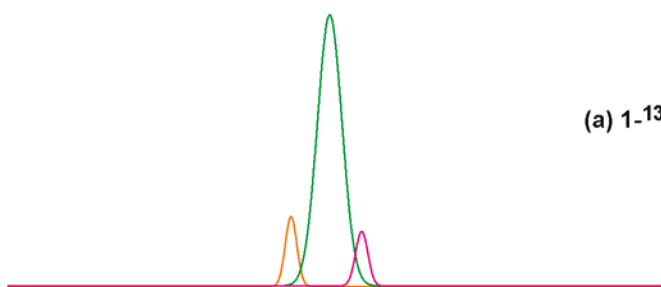


$\Delta S$  spectra of membrane-reconstituted Fgp41

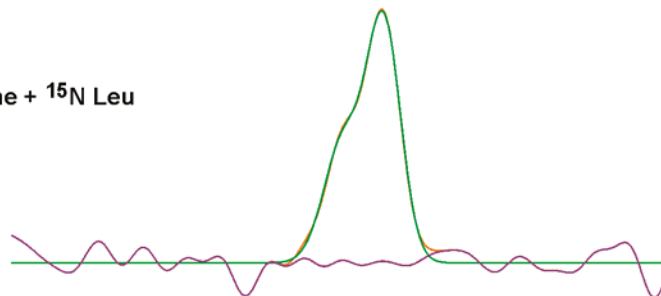
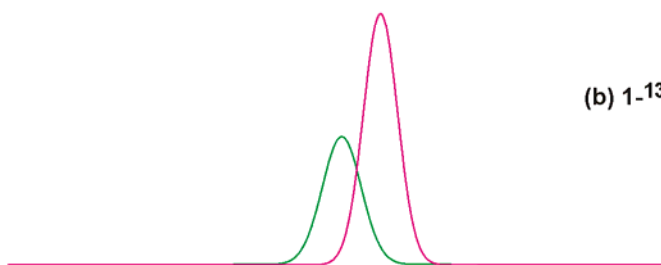
best-fit deconvolution

experiment (orange); best-fit deconvolution sum (green); difference (purple)

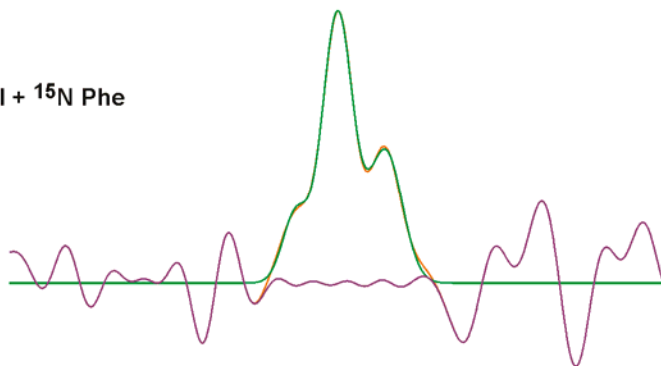
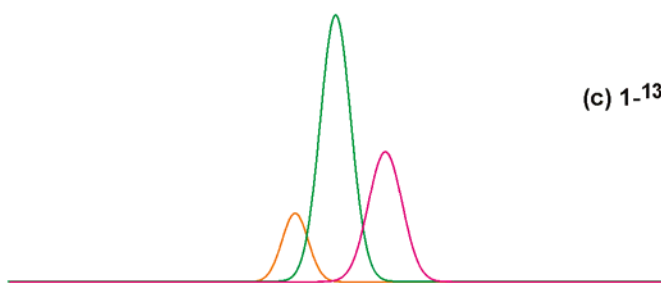
(a)  $1\text{-}^{13}\text{C}, ^{15}\text{N}$  Leu



(b)  $1\text{-}^{13}\text{C}$  Phe +  $^{15}\text{N}$  Leu



(c)  $1\text{-}^{13}\text{C}$  Val +  $^{15}\text{N}$  Phe

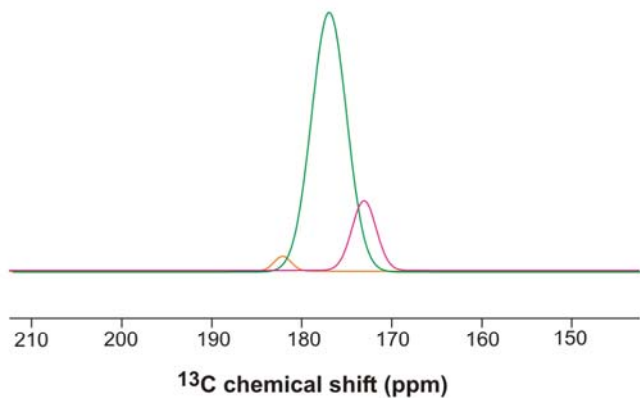


210 200 190 180 170 160 150  
 $^{13}\text{C}$  chemical shift (ppm)

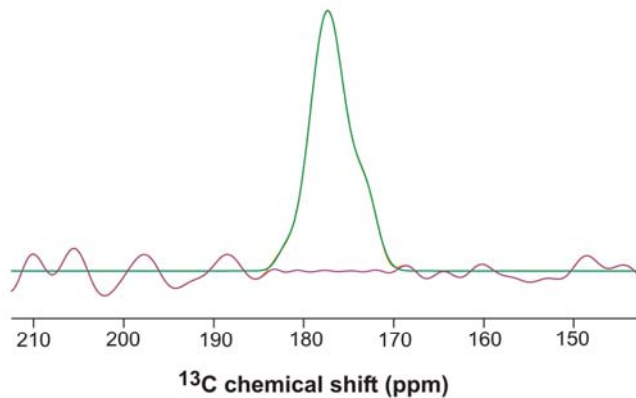
210 200 190 180 170 160 150  
 $^{13}\text{C}$  chemical shift (ppm)

**Analysis of  $\Delta S$  spectrum of lyophilized cells labeled with  $1\text{-}^{13}\text{C}$ ,  $^{15}\text{N}$  Leu**

**best-fit deconvolution**

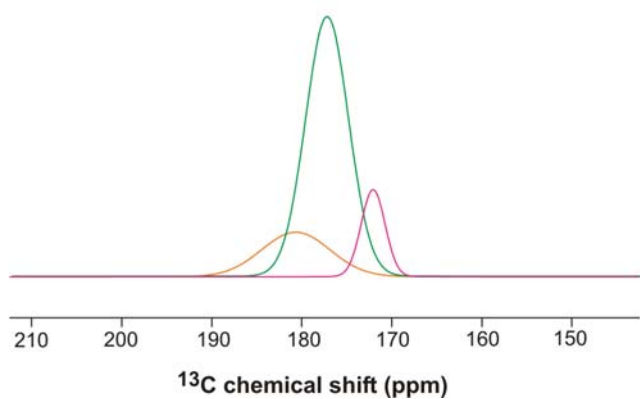


**experiment (orange); best-fit deconvolution sum (green); difference (purple)**



**Analysis of  $S_0$  spectrum from difference data between lyophilized cells with  $1\text{-}^{13}\text{C}$ ,  $^{15}\text{N}$  Leu and cells with unlabeled Leu**

**best-fit deconvolution**



**experiment (orange); best-fit deconvolution sum (green); difference (purple)**

