DFR2	MGSSSASESVCVTGASGFIGSWLVMRLIERGYTVRATVRDPANMKKVKHLVELPGAKTKL 60
DFR1	MGSASESVCVTGASGFIGSWLVMRLIERGYTVRATVRDPVNMKKVKHLVELPGAKSKL 58
	** ***********************************
DFR2	SLWKADLAQEGSFDEAIKGCTGVFHVATPMDFDSKDPENEVIKPTINGLLDIMKACVKAK 120
DFR1	SLWKADLAEEGSFDEAIKGCTGVFHVATPMDFESKDPENEVIKPTINGVLDIMKACLKAK 118

DFR2	TVRRLVFTSSAGTVDVTEHPNPVIDENCWSDVDFCTRVKMTGWMYFVSKTLAEQEAWKYA 180
DFR1	TVRRLIFTSSAGTLNVIERQKPVFDDTCWSDVEFCRRVKMTGWMYFVSKTLAEKEAWKFA 178

DFR2	KEHNIDFISVIPPLVVGPFLMPTMPPSLITALSLITGNESHYHIIKQGQFVHLDDLCLGH 240
DFR1	KEQGLDFITIIPPLVVGPFLMPTMPPSLITALSPITGNEDHYSIIKQGQFVHLDDLCLAH 238
	::*::******************************
DFR2	IFVFENPKAEGRYICCSHEATIHDIAKLLNQKYPEYNVLTKFKNIPDELDIIKFSSKKIT 300
DFR1	IFLFEEPEVEGRYICSACDATIHDIAKLINOKYPEYKVPTKFKNIPDOLELVRFSSKKIT 298
	::*:******::::*********************
DFR2	DLGFKFKYSLEDMFTGAVETCREKGLLPKPEETTVNNELLPKPAETTVNDTMQK 354
DFR1	DLGFKFKYSLEDMYTGAIDTCRDKGLLPKPAEKGLFTKPGETPVN-AMHK 347

FIGURE S3.—Alignment of DFR1 with DFR2. "*" represents identical residues; ":" means conserved substitutions between similar residues; "." indicates the semi-conserved substitutions between similar residues.