

Newman	40	SENSVTQSDSASNESKSNDSSSVSAAPKTDITNVSDTKTSSNTNNGETSVAQNPAQQETT	99
NRS384	40	SENSVTQSDSASNESKSNDSSSVSAAPKTDITNVSDTKTSSNTNNGETSVAQNPAQQETT	99
N315	40	SENSVTQSDSASNESKSNDSSSVSAAPKTDITNVSDTKTSSNTNNGETSVAQNPAQQETT	99

Newman	100	QSSSTNATTEETPVTGEATTTTNQANTPATTQSSNTNAEELVNQTSNETTFNDTNTVSS	159
NRS384	100	QSSSTNATTEETPVTGEATTTTNQANTPATTQSSNTNAEELVNQTSNETTSDNTNTVSS	159
N315	100	QSSSTNATTEETPVTGEATTTTNQANTPATTQSSNTNAEELVNQTSNETTSDNTNTVSS	159

Newman	160	VNSPQNSTNAENVSTTQDTS TEATPSNNESAPQSTDASNKDVVNQAVNTSAPRMRAFSLA	219
NRS384	160	VNSPQNSTNAENVSTTQDTS TEATPSNNESAPQSTDASNKDVVNQAVNTSAPRMRAFSLA	219
N315	160	VNSPQNSTNAENVSTTQDTS TEATPSNNESAPQNTDASNKDVVSQAVNPSTPRMRAFSLA	219
		***** .***** .*** .*:*****	
Newman	220	AVAADAPAAGTDITNQLTNVTVGIDSGTTVYPHQAGYVKLNYGFSVPNSAVKGDTFKITY	279
NRS384	220	AVAADAPAAGTDITNQLTNVTVGIDSGTTVYPHQAGYVKLNYGFSVPNSAVKGDTFKITY	279
N315	220	AVAADAPAAGTDITNQLTDVKVTIDSGTTVYPHQAGYVKLNYGFSVPNSAVKGDTFKITY	279
		***** : * *****	
Newman	280	PKELNLTGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFDYVNTKDDVKATLTM PAYI	339
NRS384	280	PKELNLTGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFDYVNTKDDVKATLTM PAYI	339
N315	280	PKELNLTGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFDYVDNKENVTANITM PAYI	339
		***** : . * : * . : *****	
Newman	340	DPENVKKTGNVTLATGIGSTTANKTVLVDYEKYGKFYNLSIKGTIDQIDKTNNTYRQTIY	399
NRS384	340	DPENVKKTGNVTLATGIGSTTANKTVLVDYEKYGKFYNLSIKGTIDQIDKTNNTYRQTIY	399
N315	340	DPENVTKTGNVTLTTGIGTNTASKTVLIDYEKYGFHNLSIKGTIDQIDKTNNTYRQTIY	399
		***** .***** :*** : . * . ***** :***** : * .*****	
Newman	400	VNPSGDNVIAPVLTGNLKPNTDSNALIDQQNTSIKVYKVDNAADLSESYFVNPNFEDVT	459
NRS384	400	VNPSGDNVIAPVLTGNLKPNTDSNALIDQQNTSIKVYKVDNAADLSESYFVNPNFEDVT	459
N315	400	VNPSGDNVVLPALVTGNLIPNTKSNALIDAKNTDIKVYRVDNANDLSESYVNPSPDFEDVT	459
		***** : * .***** *** .***** :** .**** :**** ***** :*** . : *****	
Newman	460	NSVNITFPNPQYKVEFNTDDQITTPYIVVNGHIDPNSKGDALRSTLYGYNLSNI IWR	519
NRS384	460	NSVNITFPNPQYKVEFNTDDQITTPYIVVNGHIDPNSKGDALRSTLYGYNLSNI IWR	519
N315	460	NQVRISFPNANQYKVEFPTDDQITTPYIVVNGHIDPASTGDALRSTFYGYDSNFIWR	519
		* . * . : * * . ***** * ***** * . ***** . * * : * * . * * *	
Newman	520	SMSWDNEVAFNN	531
NRS384	520	SMSWDNEVAFNN	531
N315	520	SMSWDNEVAFNN	531

Figure S1. Amino acid alignment of ClfA₄₀₋₅₃₁. Shown are amino acid sequences for the fibrinogen binding region of ClfA for strains Newman, NRS384, and N315. Newman is used as a surrogate for NRS384 in analyzing the location of amino acid differences with N315 ClfA on the crystal structure of the protein.