Supplementary table 1. Sequences of the primers used for the generation of CrmD mutants. The substituted bases are underlined.

Primer	Mutation	Sequence (5´-3´)
CrmD37	K44A	GGTACAGACTATAACAGTAATAATCTATGTTGTGCACAATGCAATCCTGGAAT
CrmD38	K44A	ATTCCAGGATTGCATTGTGCACAACATAGATTATTACTGTTATAGTCTGTACC
CrmD39	P68A	TACAAAATGTGACAAGTGCGCAGATGACACCTTTACATC
CrmD40	P68A	GATGTAAAGGTGTCATCTGCGCACTTGTCACATTTTGTA
CrmD41	N77A	AGATGACACCTTTACATCCATTCCTGCTCATAGTCCCGCGTG
CrmD42	N77A	CACGCGGGACTATGAGCAGGAATGGATGTAAAGGTGTCATCT
CrmD43	N77F	AGATGACACCTTTACATCCATTCCTTTTCATAGTCCCGCGTG
CrmD44	N77F	CACGCGGGACTATGAAAAGGAATGGATGTAAAGGTGTCATCT
CrmD45	Q93A/E95A	AAGTTGTCGAGGCAAATGTAGCAGTAATGCAGTAGCGACTAAATCGTGTAGTAAC
CrmD46	Q93A/E95A	GTTACTACACGATTTAGTCGCTACTGCATTACTGCTACATTTGCCTCGACAACTT
CrmD47	Q103A/D104A/R105A	GTAATCAAGTAGAGACTAAATCGTGTAGTAACACAGCGGCCGCAGTATGTGTCTGTGCATC
CrmD48	Q103A/D104A/R105A	GATGCACAGACACATACTGCGGCCGCTGTGTTACTACACGATTTAGTCTCTACTTGATTAC
CrmD49	Y141A/S142A/S143A	GTGGTTCTGGTTACGGTGTATATGGCGCCGCAGCTAAAGGAGATGTAATATGTAAAAAGT
CrmD50	Y141A/S142A/S143A	ACTTTTTACATATTACATCTCCTTTAGCTGCGGCGCCATATACACCGTAACCAGAACCAC
CrmD51	D35A/Y36A	CCCATTAATGGGAAATGTAACGGTACAGCCGCTAACAGTAATAATCTATGTTGTAAACAA
CrmD52	D35A/Y36A	TTGTTTACAACATAGATTATTACTGTTAGCGGCTGTACCGTTACATTTCCCATTAATGGG
CrmD53	F72A/T73A/S74A	GACAAGTGCCCAGATGACACCGCTGCAGCCATTCCTAATCATAGTCCCG
CrmD54	F72A/T73A/S74A	CGGGACTATGATTAGGAATGGCTGCAGCGGTGTCATCTGGGCACTTGTC
CrmD55	H78A/S79A	CCCAGATGACACCTTTACATCCATTCCTAATGCTGCTCCCGCGTGTCTAAGT
CrmD56	H78A/S79A	ACTTAGACACGCGGGAGCAGCATTAGGAATGGATGTAAAGGTGTCATCTGGG
CrmD57	R86A/K86A	TAGTCCCGCGTGTCTAAGTTGTGCAGGCGCATGTAGCAGTAATCAAGTAGAG
CrmD58	R86A/K86A	CTCTACTTGATTACTGCTACATGCGCCTGCACAACTTAGACACGCGGGACTA
CrmD59	S90A/S91A	GTGTCTAAGTTGTCGAGGCAAATGTGCCGCTAATCAAGTAGAGACTAAATCGTGT
CrmD60	S90A/S91A	ACACGATTTAGTCTCTACTTGATTAGCGGCACATTTGCCTCGACAACTTAGACAC
CrmD61	E116A/F117A/E118A	TGCATCCGGATACTACTGCGCAGCTGCAGGATCAAACGGTTGCAGGC
CrmD62	E116A/F117A/E118A	GCCTGCAACCGTTTGATCCTGCAGCTGCGCAGTAGTATCCGGATGCA
CrmD63	D146A/I148A	GTATATGGCTACTCATCTAAAGGAGCTGTAGCATGTAAAAAGTGTCCGGGTAATATA
CrmD64	D146A/I148A	TATATTACCCGGACACTTTTTACATGCTACAGCTCCTTTAGATGAGTAGCCATATAC

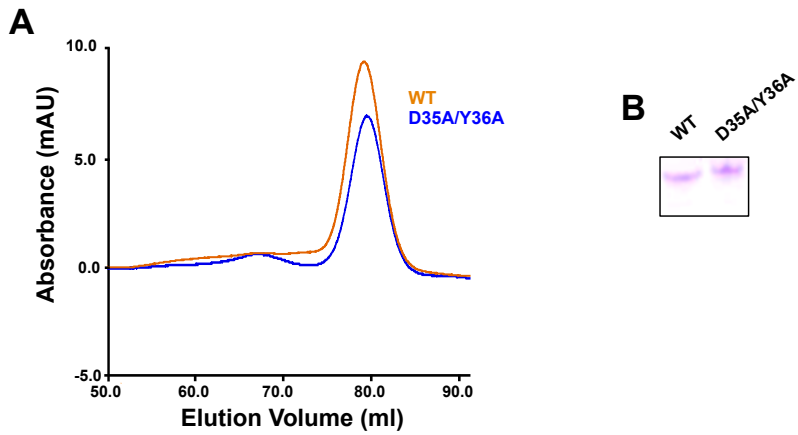

Figure S1. CrmD D35A/Y36A mutant displays the same oligomeric state than wild type CrmD. The oligomeric state of wild type CrmD (WT) and the CRD1 mutant D35A/Y36A was compared by size exclusion chramathography (A) and electrophoresis in native gel (B). In A, 100 µg of WT (orange) and D35A/Y36A (blue) CrmD mutant in 1 ml of PBS were eluted in a Superdex 200 gel filtration column. In B, 500 ng of WT and D35A/Y36A were analyzed in a native gel using the PhastGel System. Proteins were loaded in a 12.5% homogeneous gel with native buffer strips. Subsequently, the gel was stained with coomasie blue.