Estimation of modification efficiency by comparison to simulated fragmentation profiles

1.	M.SssI	0	1:32	1:16	1:8	1:4		0	1:32	1:16	1:8	1:4	ratio enzyme per site
	AdoMet	0	20	20	20	20		0	20	20	20	20	concentration in µM
2.	M.TaqI							1:20	1:20	1:20	1:20	1:20	ratio enzyme per site
	AdoYnTAMRA							40	40	40	40	40	concentration in µM
3.	R.BstUI	10	10	10	10	10							units per µg λ DNA
	R.TaqI							10	10	10	10	10	units per µg λ DNA