Title: Mathematical modeling for simulating chromatographic curves of proteins

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Abstract: The most used mathematical models with a phenomenological basis for simulating chromatographic curves of proteins in size exclusion chromatography, ion exchange chromatography, affinity chromatography, and hydrophobic interaction chromatography will be reviewed. The plate model (PM) and the general rate model (GRM) will be briefly described, followed by various applications of these models to the different chromatographic strategies. Based on these examples it is concluded that the GRM is the most complete and informative model, despite the fact that it needs several parameters that have to be estimated from theoretical correlations nonspecific for proteins. The possibility to predict chromatographic curves under different operational conditions similar to those used at industrial scale by applying mathematical models is a challenge because it could contribute to the reduction of costs involved in suitable purification processes.