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## Chapter 1

# EXPRESSIVE ARTS THERAPY: AN EVOLVING FIELD

We live in a time and in a culture in which the arts have become separated from the day-to-day lives of ordinary people. Artists, musicians, dancers, and writers are those who have received highly specialized training or those who have become commercially successful with their artistic productions. Works of art often live in galleries, museums, and theaters, but not in the daily lives of human beings. Healing practices, too, have been separated from the purview of ordinary life and are usually performed by highly specialized practitioners, trained in the latest methods of modern science.

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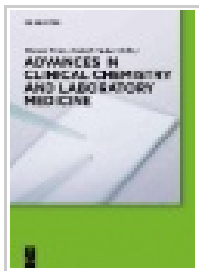
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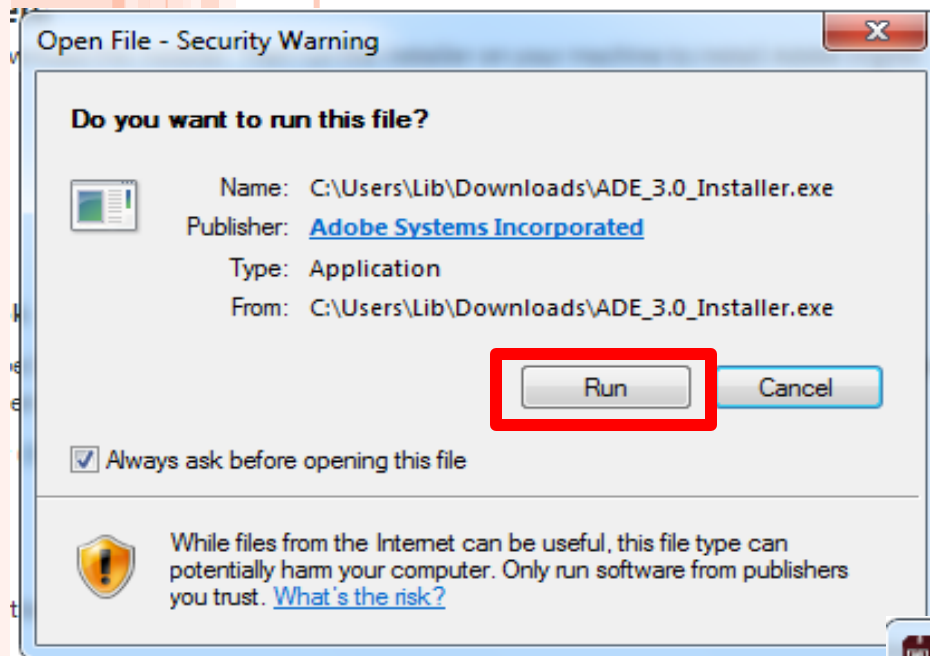
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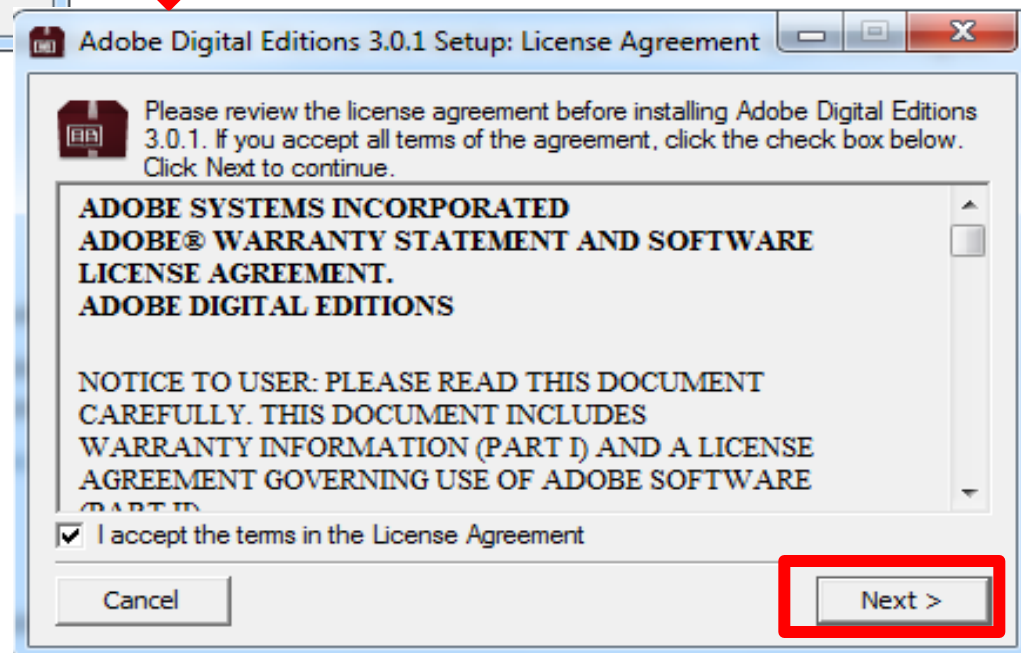
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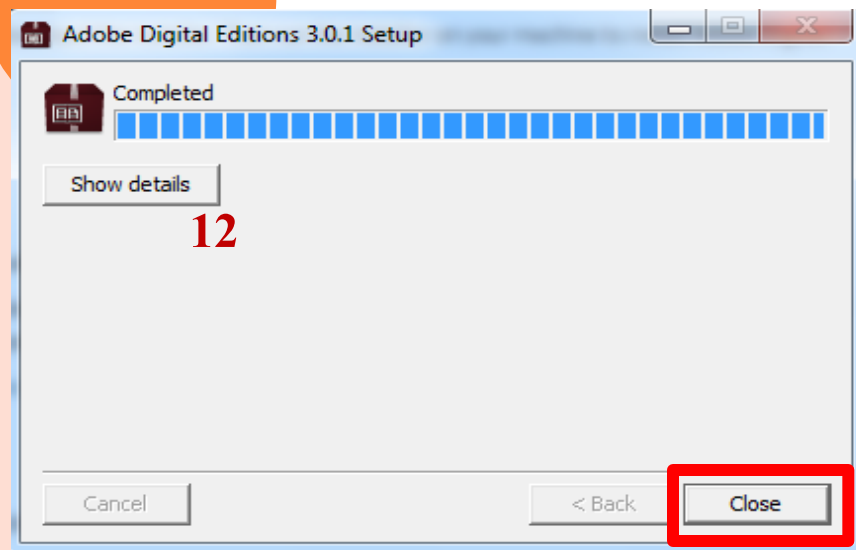
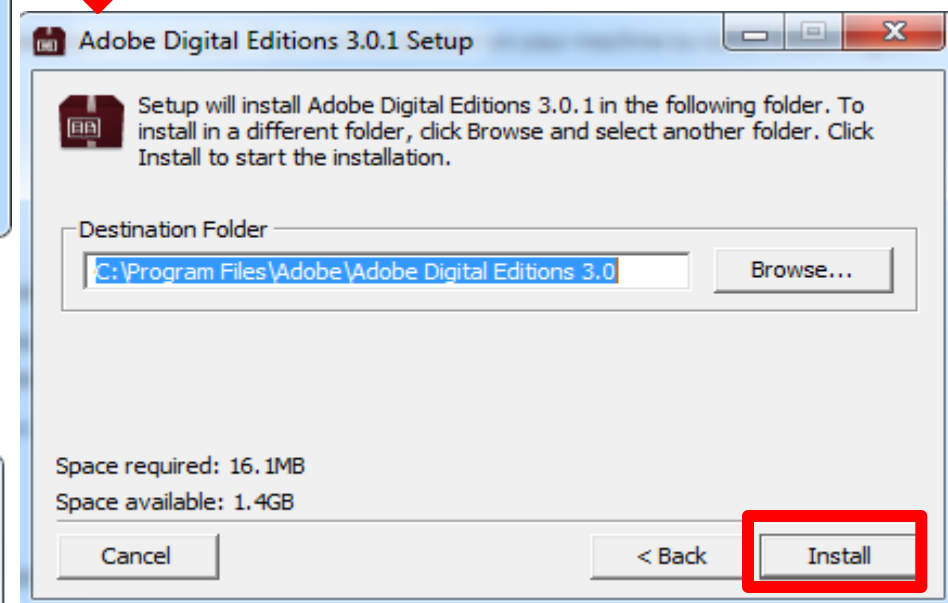
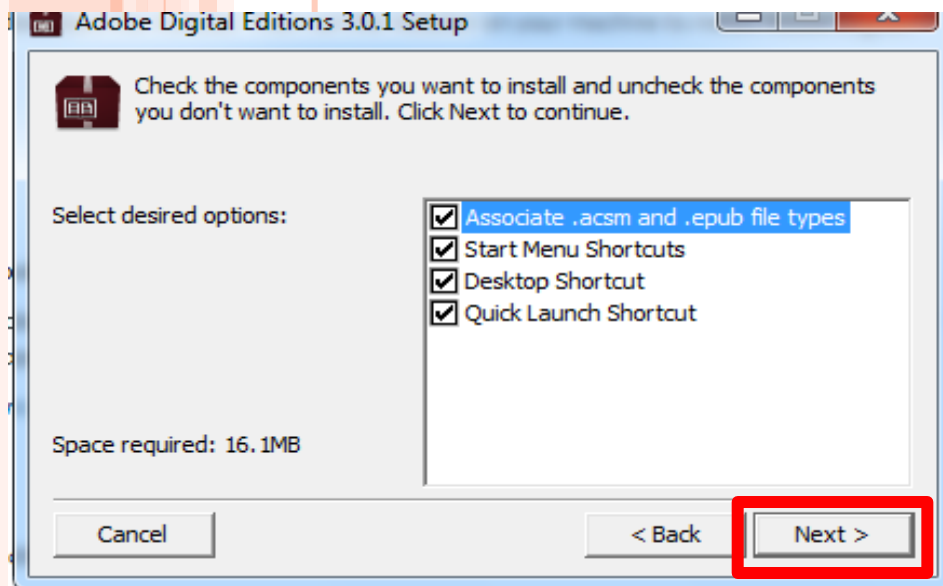
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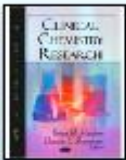
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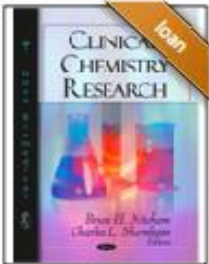
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## 1.1 Proteomics strategies targeting biomarkers for cardiovascular disease

Arjen Scholten and Albert J.R. Heck

### Summary

Cardiovascular diseases (CVDs) in the broadest sense refer to the dysfunctional conditions of the heart, arteries and veins that supply oxygen to vital, life-sustaining areas of the body. CVD is one of the main killers throughout the Western world; claiming the lives of more than 17 million people each year. According to the World Health Organization, an estimated 30% of mortalities result from various forms of CVD; whereby a certain proportion can be attributed to genetic defects. For instance, hypertrophic cardiomyopathy often originates from a variety of mutations in genes encoding sarcomere proteins, the structural proteins in heart muscle (myocardium) [1]. However, for other CVDs, such as myocardial infarction, congestive heart failure, atherosclerosis, stroke and deep vein thrombosis, specific gene mutations have not yet been implicated or are only partially responsible for the onset and progression of the disease. Other factors, such as level of stress, food and personal lifestyle can contribute to CVDs. In this light, proteins, the functional and dynamic entities of cells and tissues, are useful indicators to identify crucial mediators of the onset, progression and therapeutic intervention options for the various forms of CVDs. Therefore, proteomics, the global study of protein abundances, function and interaction in an organism at different states is an invaluable technique for gaining insights into CVDs. This burgeoning area of research is aptly termed cardiovascular proteomics [2]. It aims to unravel the molecular basis of cardiovascular function to ultimately improve diagnosis, prognosis and the development of novel therapeutic interventions. Proteome strategies, as used in our laboratory, for identifying CVD-mediated alterations in specific parts of the CVD-proteomes are discussed below.

### Protein profiling and targeted proteomic analysis

Nowadays, most proteomics experiments use mass spectrometry (MS) to identify proteins. Identification is achieved by extracting proteins from a given sample and digesting these in peptides using specific proteases, such as trypsin (► Fig. 1.1.1). These peptides are then "sequenced" by tandem MS (MS/MS) by measuring both the intact mass and specific peptide fragmentation masses. Subsequently, both intact and fragment masses are used to identify the protein from which the peptide sequence originated in a database search. To reduce complexity and increase coverage, the sample is separated at either the protein level, peptide level or both prior to MS analysis. For the former, gel-based protein separation is often applied, in one and two dimensions. For the latter, a two-dimensional chromatographic MS/MS (2D-LC-MS/MS) separation is mostly used in which peptides are separated based on parameters such as peptide charge and hydrophobicity.



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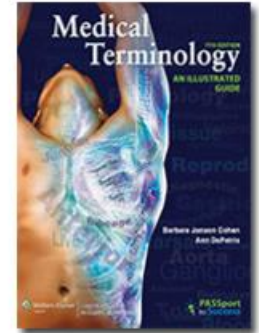
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Barbara Janson Cohen, Ann DePetris



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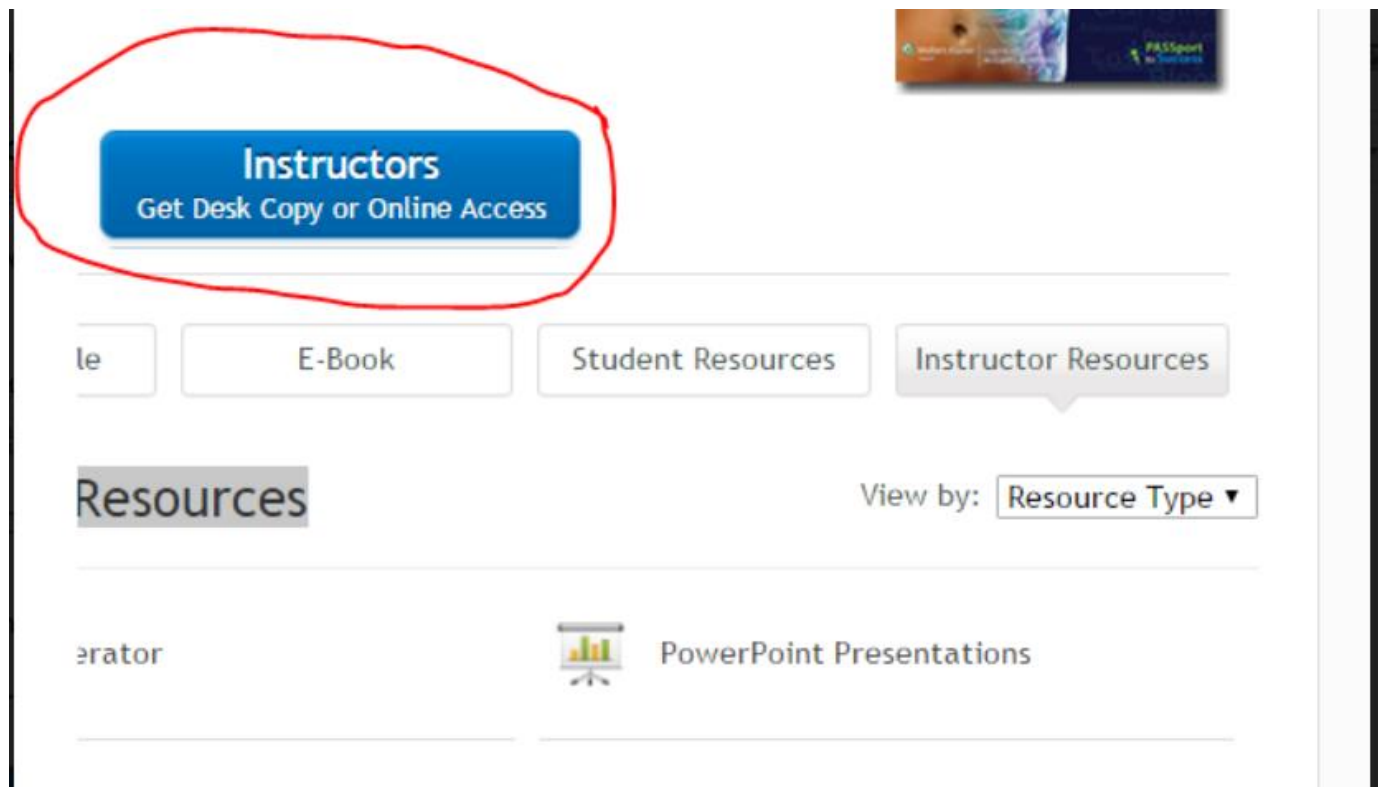


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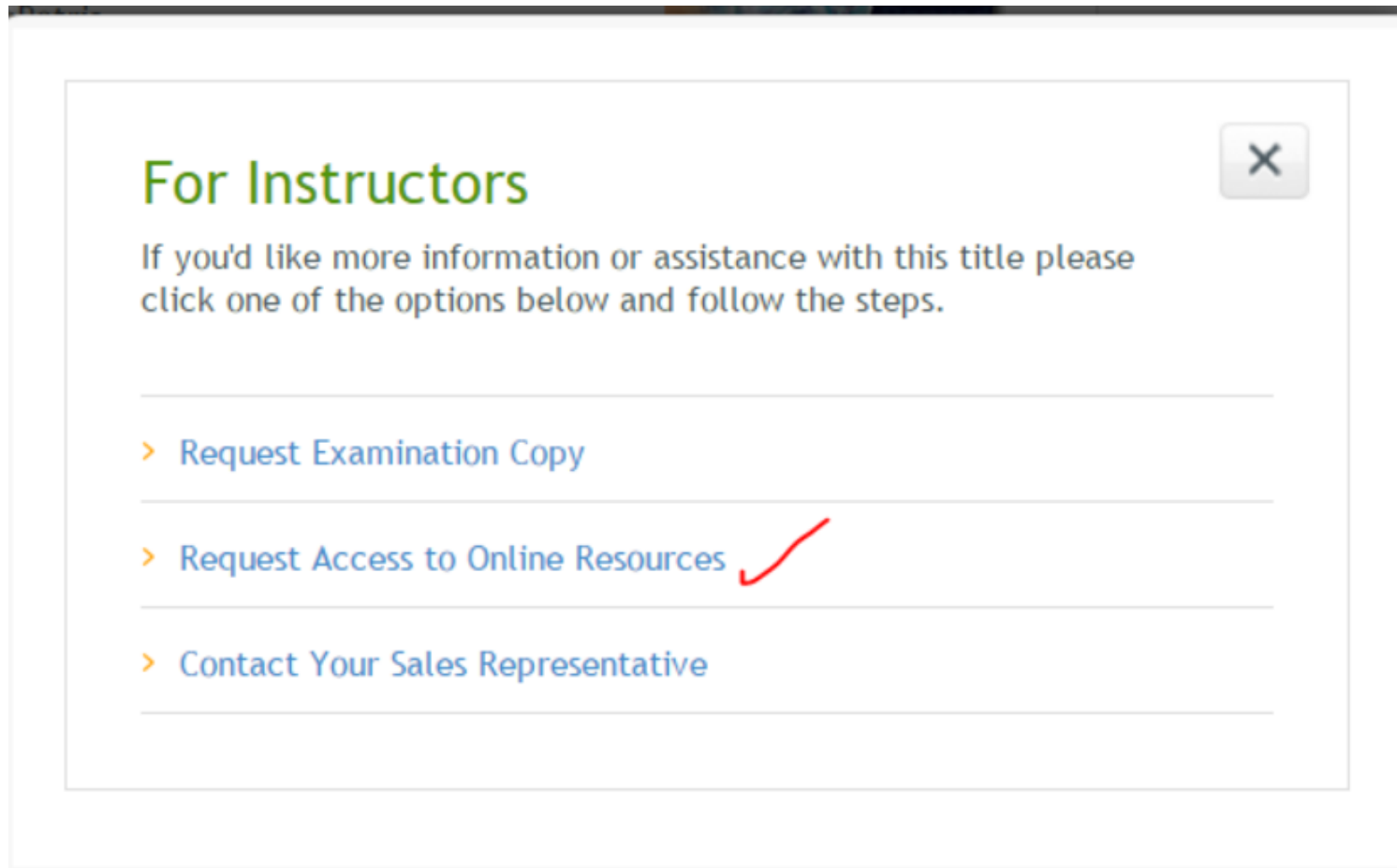
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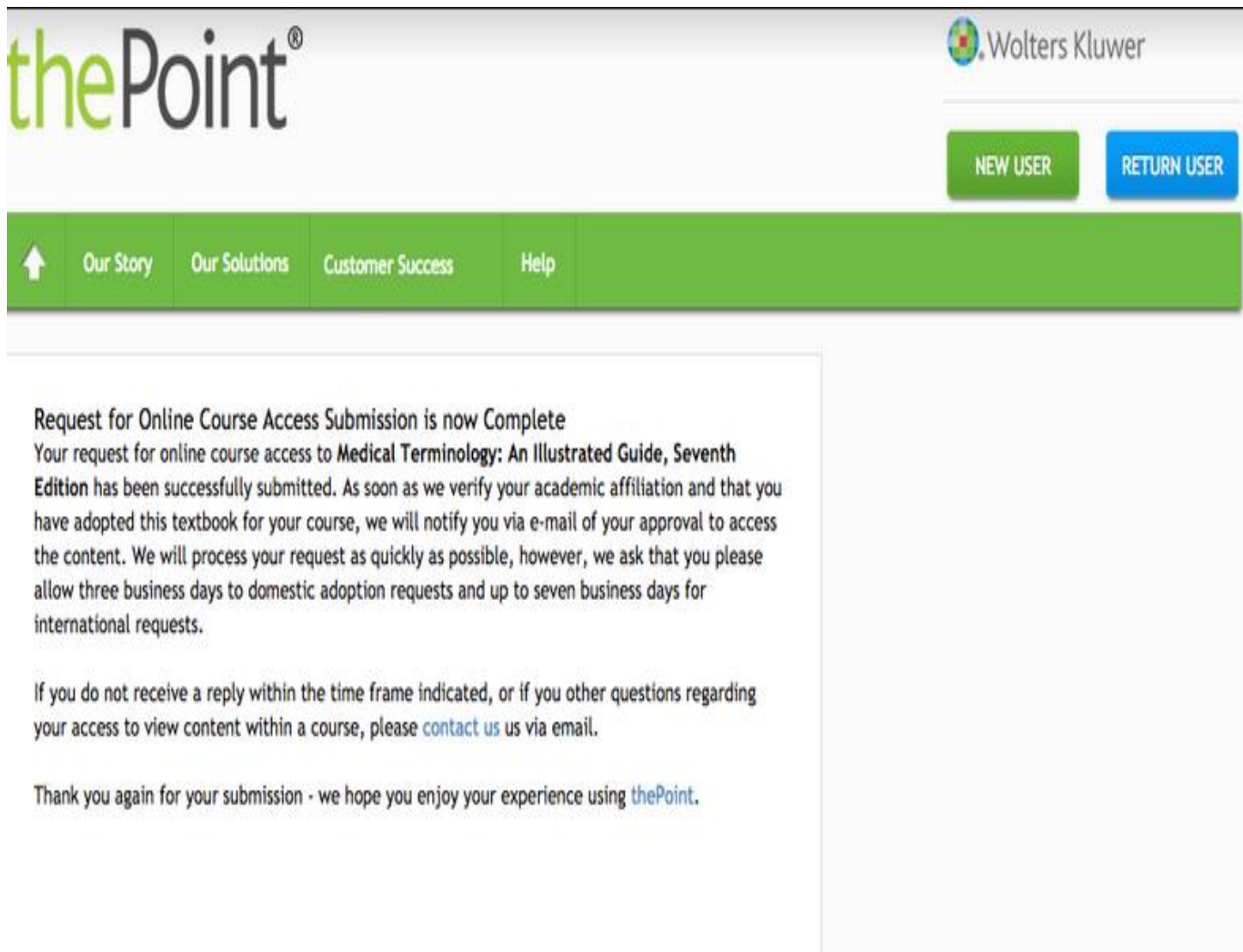
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