List of Figures

Figure 1. Pictorial representation of normal, osteoarthritis (OA) and rheumatoid arthritis (RA) joints

Figure 2. Involvement of the synovium in OA pathophysiology

Figure 3. Pathological changes in the synovium of RA

Figure 4. Management of OA

Figure 5. Treatment strategies for early active RA

Figure 6. SDS-PAGE analysis of depleted OA synovial fluid

Figure 7. Chromatographic profile of depleted OA synovial fluid by SCX-based fractionation

Figure 8. SCX-based chromatographic profile of the iTRAQ labeled RA and OA synovial fluid

Figure 9. Summary of proteins identified from OA synovial fluid by using different fractionation methods

Figure 10. Relative abundance of proteins in OA synovial fluid

Figure 11. Gene Ontology based classification of proteins identified from OA synovial fluid

Figure 12. Representative MS/MS spectra of peptides from novel proteins identified from OA synovial fluid

Figure 13. Validation of proteins identified in OA synovial fluid by MRM analysis

Figure 14. A schematic workflow illustrating the steps involved in the differential analysis of RA and OA synovial fluid proteome

Figure 15. Gene Ontology-based classification of differentially expressed proteins identified from RA and OA synovial fluid
Figure 16. Representative MS/MS spectra of peptides from novel proteins upregulated in RA and OA synovial fluid

Figure 17. MRM and Western blot analysis of CAPG expression in RA and OA synovial fluid

Figure 18. Glycolytic pathway enriched from GeneSpring analysis