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## Program RSG Belgium Symposium 2015:

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<b>14h00 - 14h05</b>	Introduction
<b>14h05 - 14h50</b>	<b>KEYNOTE: prof. dr. Tomasz BURZYKOWSKI</b> (UHasselt)
<b>14h50 - 15h00</b>	<b>Break</b>
<b>15h00 - 15h15</b>	<i>Connectivity Scores using Factor Analysis</i> by <b>Ewoud De Troyer</b> (UHasselt)
<b>15h15 - 15h30</b>	<i>Structured analysis of unexplained peaks and corresponding patterns in MS/MS spectra</i> by <b>Aida Mrzic</b> (UA)
<b>15h30 - 15h45</b>	<i>Proteoformer: deep proteome coverage through Ribosome profiling and MS integration</i> by <b>Elvis Ndah</b> (UGent)
<b>15h45 - 16h00</b>	<i>Determining the winning SH3 coalition: how cooperative game theory reveals the importance of domain residues in peptide binding</i> by <b>Ashley Conard</b> (ULB)
<b>16h00 - 16h15</b>	<b>Break</b>
<b>16h15 - 16h30</b>	<i>Whole genome phylogenetics: Too much information or not enough?</i> by <b>dr. Conor Meehan</b> (ITM)
<b>16h30 - 16h45</b>	<i>Microbial community analysis using MiSeq sequencing</i> by <b>Sander Wuyts</b> (UA)
<b>16h45 - 17h00</b>	<i>Bioinformatics Algorithms to get accurate 16S rRNA high throughput sequencing data</i> by <b>Mohamed Mysara</b> (SCK-CEN, VUB, VIB)
<b>17h00 - 17h15</b>	<i>Integrated Analysis of Multi-Source Data</i> by <b>Marijke Van Moerbeke</b> (UHasselt)
<b>17h15</b>	Reception

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