Proteomics Data Collection (ProDaC)
Work Package 4, Deliverable 4.1
Demonstration

The deliverable 4.1 of the ProDaC work package “Proteomics Repository Adaptation“ is the technical possibility to compare datasets based on set operations (intersection, union, difference).

The functionality is implemented on http://www.ebi.ac.uk/pride. This document gives a short demonstration of what to do for a comparison.

ProDaC website: http://www.fp6-prodac.eu

Set-oriented Comparison of PRIDE Datasets

1. Browse datasets on http://www.ebi.ac.uk/pride/startBrowse.do
2. Select datasets to be compared, for example:

This Table Describes 4 Experiments.

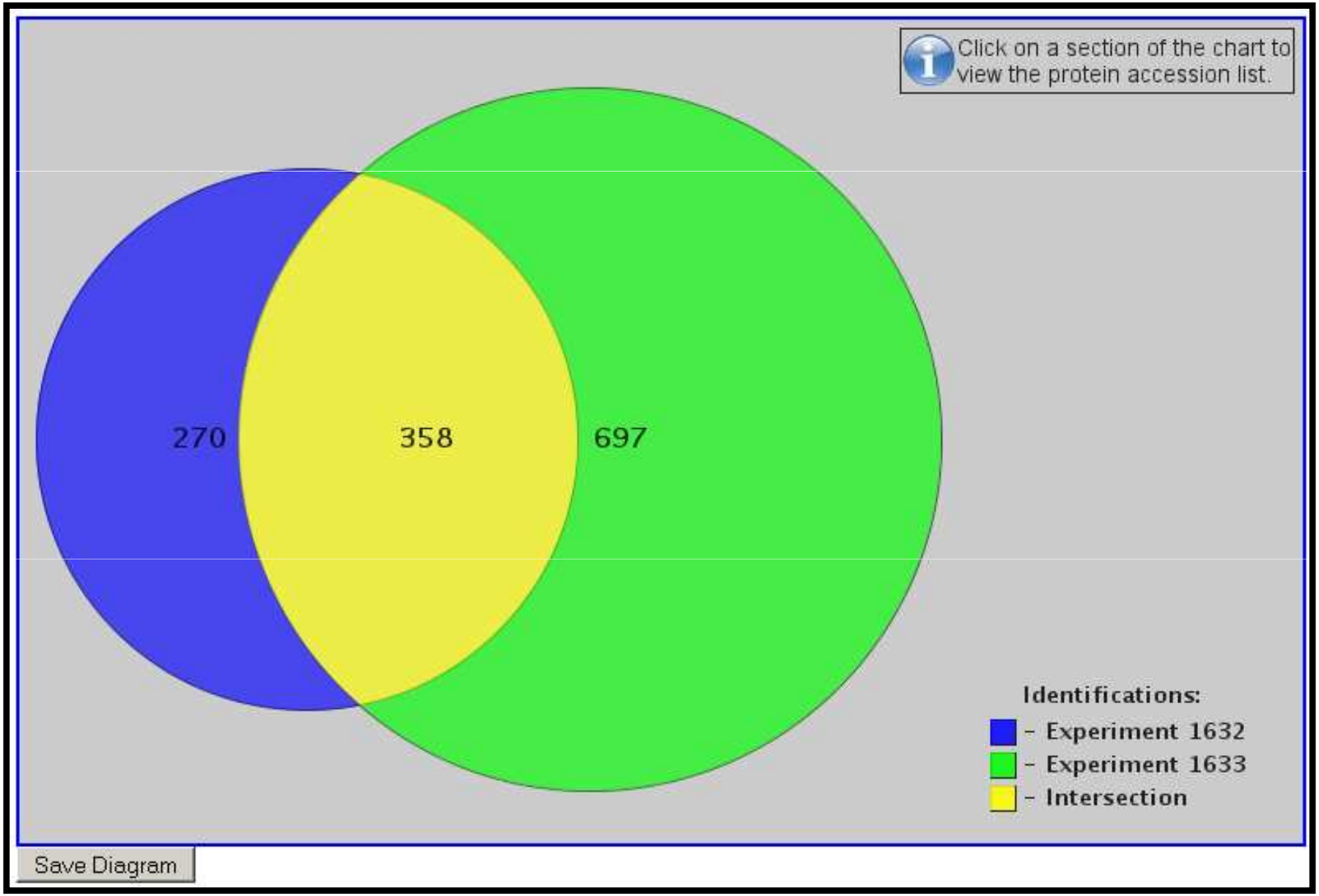
To sort by any of the first seven columns, click the heading.
(Repeated clicking changes the direction of the sort.)

Compare Experiments

Accession	Title	Species	Tissue / Disease	Protein Count	Peptide Count	Spectra Count	Retrieve Details (Output format set above.)	Compare Protein Identification Sets	Select Reference Experiment
1632	Differential COFRADIC N-terminal proteomic analysis of Fas-induced apoptotic protein cleavage in Jurkat cells (2/4)	Homo sapiens	apoptosis, Jurkat cells, Antigens, CD95	628	1105	1105	Download	☑	
1633	Differential COFRADIC N-terminal proteomic analysis of Fas-induced apoptotic protein cleavage in Jurkat cells (3/4)	Homo sapiens	apoptosis, Jurkat cells, Antigens, CD95	1055	1808	1808	Download	☐	
1634	Differential COFRADIC N-terminal proteomic analysis of Fas-induced apoptotic protein cleavage in Jurkat cells (4/4)	Homo sapiens	apoptosis, Jurkat cells, Antigens, CD95	1032	1869	1869	Download	☑	
1635	Differential COFRADIC N-terminal proteomic analysis of Fas-induced apoptotic protein cleavage in Jurkat cells (1/4)	Homo sapiens	apoptosis, Jurkat cells, Antigens, CD95	833	1584	1584	Download	☑	

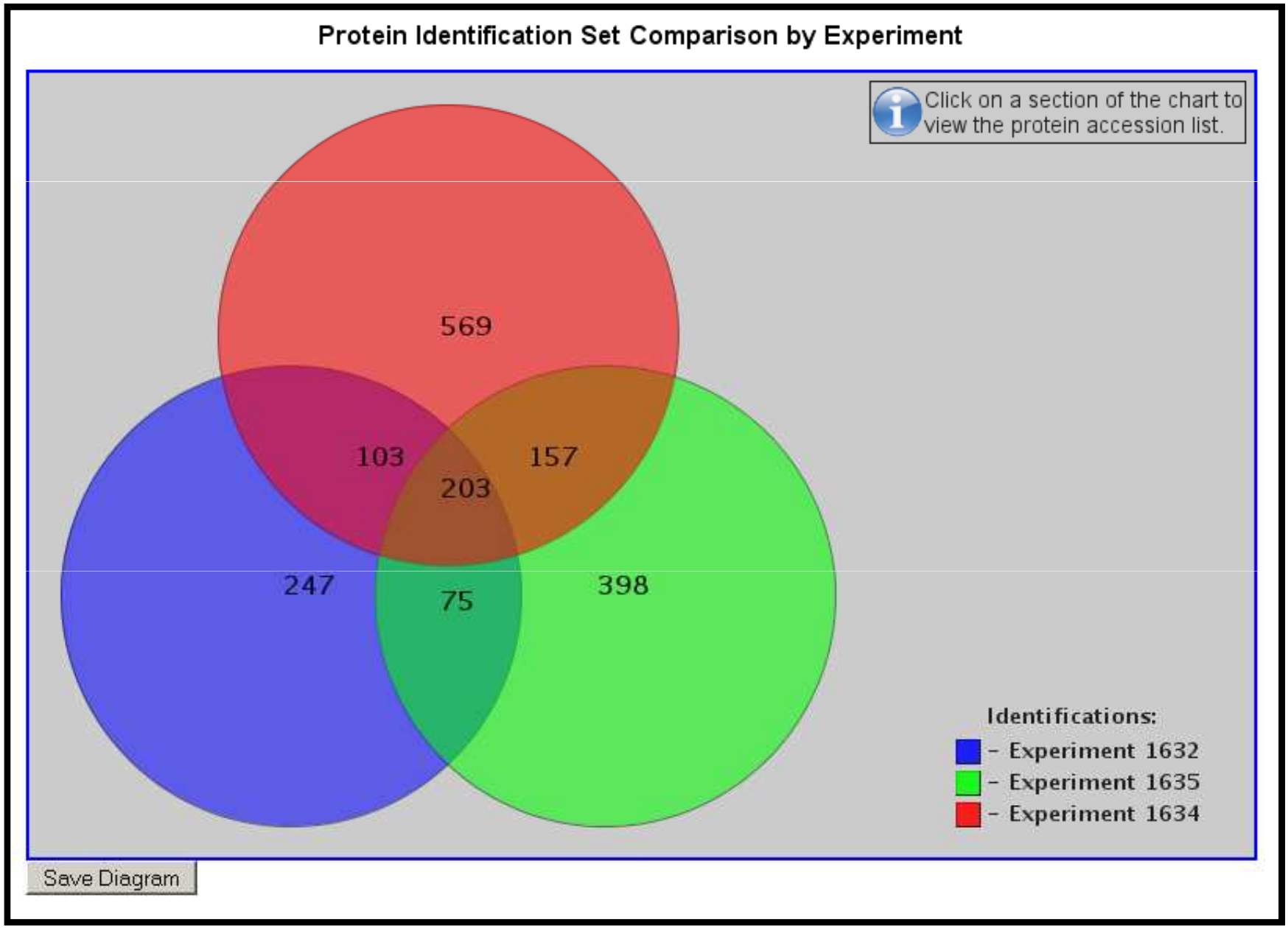
Set-oriented Comparison of PRIDE Datasets

Resulting plot when comparing two experiments:



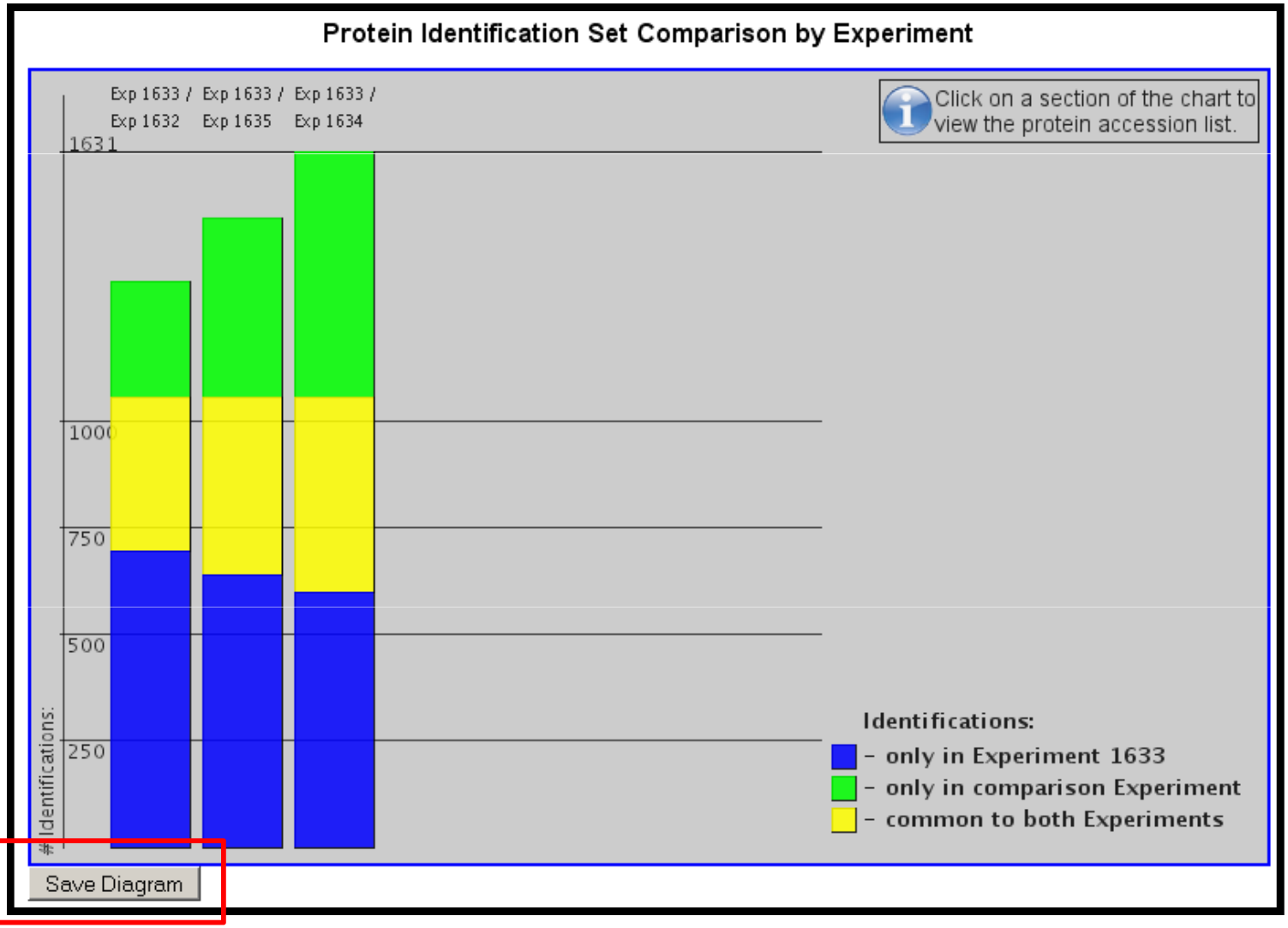
Set-oriented Comparison of PRIDE Datasets

Resulting plot when comparing three experiments:



Set-oriented Comparison of PRIDE Datasets

Resulting plot when comparing more than three experiments;
one experiment (here: 1633) is compared to all others:



Each diagram can be saved.

Set-oriented Comparison of PRIDE Datasets

Click on a section of one of the charts to view a protein accession list, here: intersection of experiment 1635 and experiment 1634

Intersection of Exp.1635 and Exp.1634

Experiment 1635:

Title:	Differential COFRADIC N-terminal proteomic analysis of Fas-induced apoptotic protein cleavage in Jurkat cells (1/4)
Sample description:	NEWT: Homo sapiens
	MeSH: apoptosis
	MeSH: Jurkat cells
	MeSH: Antigens, CD95

Experiment 1634:

Title:	Differential COFRADIC N-terminal proteomic analysis of Fas-induced apoptotic protein cleavage in Jurkat cells (4/4)
Sample description:	NEWT: Homo sapiens
	MeSH: apoptosis
	MeSH: Jurkat cells
	MeSH: Antigens, CD95
Total Identification count:	157
Similarity Score {B∩C}/{B∪C}:	0.23920266

Protein accession:	Protein version:	Database:
Q93079		SWISS-PROT
P24752		SWISS-PROT
P49591		SWISS-PROT
Q92817		SWISS-PROT
P43034		SWISS-PROT
Q02978		SWISS-PROT
P12236		SWISS-PROT
P30101		SWISS-PROT
P45974		SWISS-PROT
Q13283		SWISS-PROT
Q16550		SWISS-PROT
P52597		SWISS-PROT
P11229		SWISS-PROT
Q96BY6		SWISS-PROT
P35270		SWISS-PROT
Q13586		SWISS-PROT