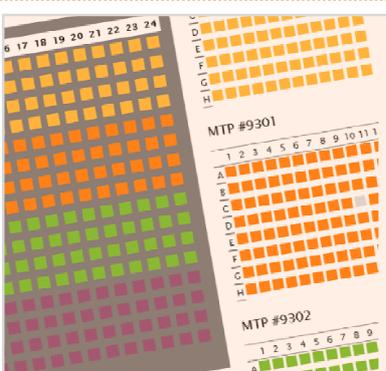


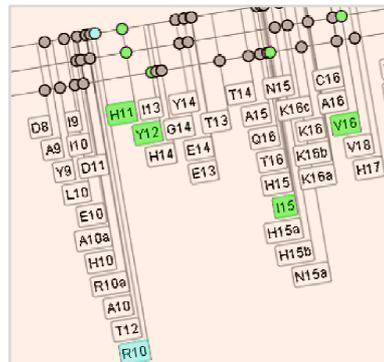


MS Repo

ORGANIZE, ANALYZE, AND SHARE
PROTEIN DATA FROM MALDI MS



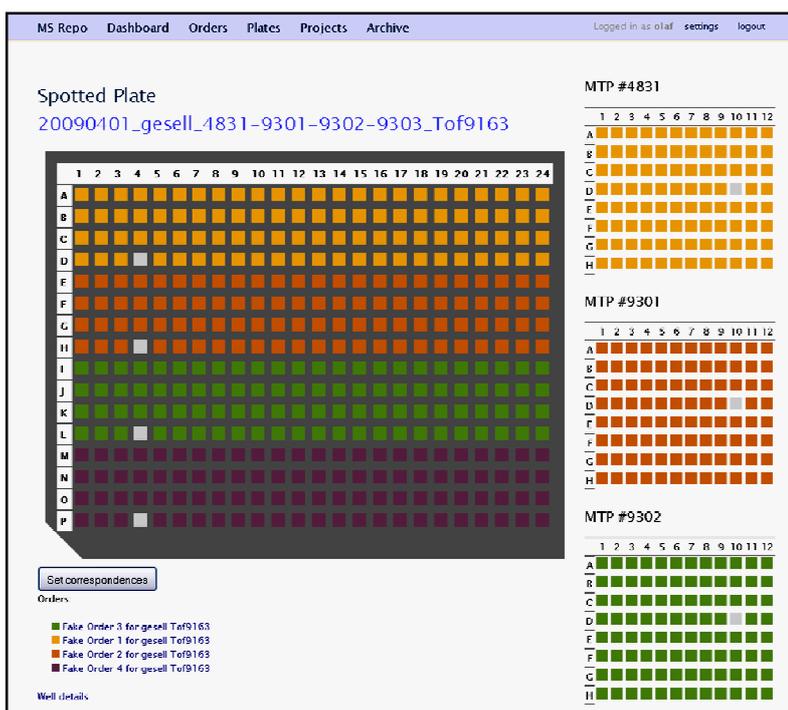
please_check H32_MOUSE *Histone H3.2 OS=Mus*
mcp_guidelines H31_MOUSE *Histone H3.1 OS=M*
mcp_guidelines **OK** RS12_MOUSE *40S ribosomal*
PE=1 SV=2
please_check MIF_MOUSE *Macrophage migration*
PE=1 SV=2
OK H32_MOUSE *Histone H3.2 OS=Mus musculus*
H33_MOUSE *Histone H3.3 OS=Mus musculus GN-*
H31_MOUSE *Histone H3.1 OS=Mus musculus GN-*
NUCL_MOUSE *Nucleolin OS=Mus musculus GN=N*
AMPD2_MOUSE *AMP deaminase 2 OS=Mus muscu*



Organize, analyze, and share MS results

MS Repo is a lab information management system (LIMS) that helps workgroups organize, analyze, and share MALDI mass spectrometry results. From submitting mass spec analysis orders to creating protein hit lists, MS Repo supports day-to-day activities in your lab with minimal overhead. MS Repo makes it easy to conform to publication guidelines of leading journals with its powerful analysis capabilities such as evaluation of protein isoforms and filtering by sequence coverage, number of sequenced peptides etc.

MS Repo tracks samples across the whole protein identification workflow. Here is the correspondence between spots on a MALDI target and wells on a microtiter plate.



MS Repo Dashboard Orders Plates Projects Archive Logged in as olaf settings logout

Select Labels Add to hit list Export as Excel 2003 XML

All None Approved Approve Approve selected Disapprove selected

Filter

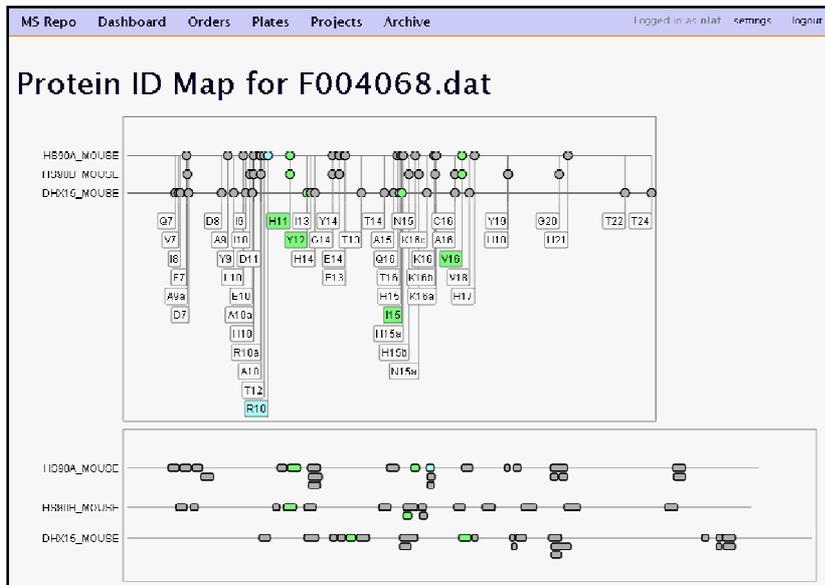
- Peptides above ID >= 2
- Approved hits
- Labels: mcp_guidelines, please_check, tk
- Parameters: Seq cov (10.0), MS/MS seq cov (10.0), MS/MS sig seq cov (10.0), RMS error (15.0), Score (15.0), Ion Score (15.0)
- peptides above ID thr...

Spot	Score	Ion Score	Protein	Cov %	Cov MS/MS %	Cov MS/MS sig %	Pep	IS	Hom	id	RMS Error
A01	995	524.58	please_check BTf3_MOUSE Transcription factor BTf3 OS=Mus musculus CN=BTf3 PE=2 SV=3	52.45	48.53	55.82	9	5	3	3	11.73
A02	134	119.82	mcp_guidelines H33_MOUSE Histone H3.3 OS=Mus musculus CN=H3f3a PE=1 SV=2	26.47	14.71	8.09	4	2	1	1	16.52
A02	133	119.82	please_check H32_MOUSE Histone H3.2 OS=Mus musculus CN=Hist3h3b PE=1 SV=2	26.47	14.71	8.09	4	2	1	1	16.52
A02	132	119.82	mcp_guidelines H31_MOUSE Histone H3.1 OS=Mus musculus CN=Hist3h3a PE=1 SV=2	26.47	14.71	8.09	4	2	1	1	16.52
A03	242	195.53	mcp_guidelines RS12_MOUSE 40S ribosomal protein S12 OS=Mus musculus CN=Rps12 PE=1 SV=2	43.18	17.42	17.42	8	8	3	3	17.93
A04	79.2	70.77	please_check MIF_MOUSE Macrophage migration inhibitory factor OS=Mus musculus CN=Mif PE=1 SV=2	17.39	17.39	9.57	3	2	1	1	1.94
A05	118	104.42	H32_MOUSE Histone H3.2 OS=Mus musculus CN=Hist3h3b PE=1 SV=2	22.79	14.71	8.09	4	2	1	1	21.19
A05	118	104.42	H33_MOUSE Histone H3.3 OS=Mus musculus CN=H3f3a PE=1 SV=2	22.79	14.71	8.09	4	2	1	1	21.19
A05	117	104.42	H31_MOUSE Histone H3.1 OS=Mus musculus CN=Hist3h3a PE=1 SV=2	22.79	14.71	8.09	4	2	1	1	21.19
A06	314	154.41	NUCL_MOUSE Nucleolin OS=Mus musculus CN=Ncl PE=1 SV=2	35.79	5.37	5.37	27	2	2	1	13.58
A06	248	142.05	AMPD2_MOUSE AMP deaminase 2 OS=Mus musculus CN=Ampd2 PE=1 SV=1	29.07	3.88	3.88	26	2	2	2	12.82
A07	445	260.9	NUCL_MOUSE Nucleolin OS=Mus musculus CN=Ncl PE=1 SV=2	35.08	11.74	10.33	29	5	3	4	5.49
A08	486	323.75	PPCE_MOUSE Prolyl endopeptidase OS=Mus musculus CN=Prep PE=2 SV=1	47.32	9.86	7.89	27	5	4	4	15.99
A09	568	362.18	THOP1_MOUSE Thimer oligopeptidase OS=Mus musculus CN=Thop1 PE=1 SV=1	49.2	10.19	8.73	33	5	4	4	11.75
A10	422	271.81	FUBP1_MOUSE Far upstream element-binding protein 1 OS=Mus musculus CN=Fubp1 PE=1 SV=1	47.93	9.52	9.52	25	4	4	4	9.89

Protein hits are presented including Mascot scores, sequence coverage, number of peptides, etc. Hits can be filtered based on a variety of criteria. Protein identifications that meet MCP guidelines are labeled with the "mcp_guidelines" label.

Capture data along the whole mass spec workflow

With MS Repo you can capture data along the whole mass spec workflow: location of samples on 2D gels, microtiter plates, digestion, peak lists, Mascot dat files, and GPS Explorer analyses. MS Repo is completely web-based with fine-grained access rights control so results can be shared safely and easily with external collaborators or published on the web.



Protein isoforms can be analyzed using an interactive graphical display of peaks (top) and peptides (bottom). Peptides that were sequenced are highlighted in green.

The screenshot shows the 'Hit List published' interface. It includes a navigation bar at the top and a workspace header. Below the header, there are buttons for 'Move to hit list', 'Copy to hit list', and 'Delete from hitlist'. There are also buttons for 'Download Archive', 'Save as Delta2D annotations', and 'Export as Excel 2003 XML'. The main table lists 16 protein hits with various attributes.

Label	x	y	Gel Image	Sample	Protein	MW	PI	Score	Ions Score	Cov %	Cov MS/MS %	Pep IS	Hom Id	RMS Error	
squl1	100.0	200.0	gel1_sample1	sample1	BTF3_MOUSE Transcription factor BTF3 OS=Mus musculus GN=BTF3 PE=2 SV=3	22017.4	9.51683	395.00	324.58	57.49	48.53	9	5	3	11.73
ID12000	751.0	178.0	control_01	control	RS12_MOUSE 40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=2	14515.6	6.81781	242.00	195.53	43.18	17.42	8	3	3	17.30
ID12002	748.0	213.0	control_01	control	MIF_MOUSE Macrophage migration inhibitory factor OS=Mus musculus GN=MIF PE=1 SV=2	12486.2	6.80098	79.20	70.77	17.39	17.39	3	2	1	1.94
ID12001	772.0	340.0	control_01	control	H31_MOUSE Histone H3.1 OS=Mus musculus GN=Hist1h3a PE=1 SV=2	15394.5	11.127	117.00	104.42	22.79	14.71	4	2	1	21.19
ID12001	772.0	340.0	control_01	control	H32_MOUSE Histone H3.2 OS=Mus musculus GN=Hist1h3b PE=1 SV=2	15378.5	11.2693	118.00	104.42	22.79	14.71	4	2	1	21.19
ID12001	772.0	340.0	control_01	control	H33_MOUSE Histone H3.3 OS=Mus musculus GN=Hist1h3c PE=1 SV=2	15318.5	11.2693	118.00	104.42	22.79	14.71	4	2	1	21.19
ID12008	673.7	348.1	control_01	control	NUCL_MOUSE Nucleolin OS=Mus musculus GN=Ncl PE=1 SV=2	78676.8		314.00	154.41	35.78	5.37	27	2	2	13.58
ID12008	673.7	348.1	control_01	control	AMPD2_MOUSE AMP deaminase 2 OS=Mus	91966.4	5.82382	248.00	142.05	29.07	3.88	26	2	2	12.82

Final hit list after quality control. The hit list includes attributes such as position on 2D gel, isoelectric point, molecular weight, scores, sequence coverage etc. Hit lists can be exported to Excel and archived together with raw data .

Learn more

For more information about MS Repo just call us at +49 (0)3834 515230 or send an email to info@decodon.com. We are looking forward to hearing from you!



DECODON GmbH
Walther-Rathenau-Str. 49a
17489 Greifswald, Germany

www.decodon.com
info@decodon.com

phone: +49(0)3834 515230
fax: +49(0)3834 515239

Copyright and Trademarks

All material in this brochure is Copyright © 2000-2011 DECODON GmbH. All Rights Reserved. DECODON, DECODON logo, Delta2D, MS Repo and Protecs are trademarks or registered trademarks of DECODON GmbH in Germany and in several other countries all over the world. All other products mentioned are trademarks or registered trademarks of their respective companies.