8 Anhang

8.1 Quantifizierungsdaten der Proteomanalysen

8.1.1 Proteomanalyse des skelettmuskel-spezifischen Titinkinaseregion-KO

Für die Proteomanalyse des skelettmuskel-spezifischen Titinkinaseregion-KO wurden je vier KO- und WT-Tiere zum Zeitpunkt 10 (keine Unterschiede), 20 (Tab. 8.4), 30 Tage (Tab. 8.5) (Quadriceps) und 10 (Tab. 8.1), 20 (Tab. 8.2), 34 Tage (Tab.8.3) (Herz) verwendet.
Die %Volumen (%Vol) Werte der Proteinspots aus den vier WT- und KO-Gelen wurden gemittelt (MW) und die Standardabweichung (STABW) berechnet. Der Quotient aus Mittelwert KO/Mittelwert WT (Ratio), gibt die x-fache Veränderung des KO-Spots gegenüber des WT-Spots an, wobei alle Proteine mit einem Ratio<0,5 im KO vermindert und mit einem Ratio>1,5 vermehrt synthetisiert wurden. Alle Ratios mit einem P<0,1 (Ttest) sind signifikant und in der Tabelle fett gedruckt. Nichtsignifikante Proteine, die zu einem anderen Zeitpunkt der Analyse ebenfalls auftraten, wurden mit aufgeführt und sind normal gedruckt.

Protein	% Vol WT1	% Vol WT2	% Vol WT3	% Vol WT4	MW WT	STABW WT	% Vol KO1	% Vol KO2	% Vol KO3	% Vol KO4	MW KO	STABW KO	Ratio KO/WT	Ttest
Hspb1-2	0,021	0,062	0,017	0,048	0,037	49,615	0,026	0,085	0,08	0,063	0,063	36,048	**1,709**	0,176
Hspb1-3	0,038	0,037	0,013	0,034	0,031	33,793	0,049	0,04	0,046	0,061	0,049	15,376	**1,606**	**0,049**

Tab.8.1: Herzproteomanalyse der 10 Tage alten Titinkinaseregion-KO-Tiere

Protein	% Vol WT1	% Vol WT2	% Vol WT3	% Vol WT4	MW WT	STABW WT	% Vol KO1	% Vol KO2	% Vol KO3	% Vol KO4	MW KO	STABW KO	Ratio KO/WT	Ttest
ApoA1-2	0,087	0,083	0,031	0,139	0,085	44,778	0,016	0,014	0,008	0,027	0,016	42,336	**0,189**	**0,050**
ApoA1-3	0,012	0,011	0,022	0,019	0,016	28,716	0,027	0,027	0,012	0,035	0,025	31,683	**1,585**	0,157
Cryab-1	0,12	0,151	0,17	0,177	0,155	14,254	0,26	0,263	0,304	0,237	0,266	9,127	**1,72**	**0,001**
Gsto1-1	0,014	0,009	0,016	0,019	0,014	25,177	0,032	0,045	0,03	0,025	0,033	21,997	**2,3**	**0,015**
Hspb1-2	0,061	0,034	0,03	0,034	0,04	31,249	0,107	0,094	0,094	0,073	0,092	13,054	**2,304**	**0,002**
Hspb6-1	0,044	0,057	0,038	0,042	0,045	15,254	0,091	0,093	0,095	0,072	0,088	10,626	**1,93**	**0,001**
Hspb7	0,02	0,038	0,025	0,027	0,028	23,947	0,083	0,059	0,035	0,064	0,06	28,617	**2,181**	**0,038**
Psma3	0,003	0,011	0,016	0,02	0,012	49,093	0,013	0,025	0,012	0,03	0,02	38,137	**1,607**	0,243
Psmb4	0,013	0,011	0,009	0,006	0,01	27,023	0,032	0,021	0,008	0,021	0,021	41,198	**2,105**	0,113

Tab. 8.2: Herzproteomanalyse der 20 Tage alten Titinkinaseregion-KO-Tiere

Protein	% Vol WT1	% Vol WT2	% Vol WT3	% Vol WT4	MW WT	STABW WT	% Vol KO1	% Vol KO2	% Vol KO3	% Vol KO4	MW KO	STABW KO	Ratio KO/WT	Ttest
Adprhl1	0,022	0,023	0,034	0,012	0,023	33,912	0,075	0,054	0,088	0,059	0,069	19,206	**3,004**	**0,004**
Akr1b3	0,136	0,073	0,111	0,055	0,094	33,704	0,164	0,153	0,203	0,206	0,181	12,906	**1,94**	**0,010**
Aldh2	0,082	0,066	0,055	0,047	0,062	20,871	0,087	0,076	0,131	0,095	0,097	21,062	**1,559**	**0,056**
Anxa2	0,074	0,028	0,059	0,031	0,048	40,605	0,077	0,072	0,086	0,08	0,079	6,329	**1,642**	**0,066**
Anxa5	0,055	0,042	0,063	0,043	0,051	16,485	0,139	0,094	0,189	0,08	0,126	34,05	**2,474**	**0,053**
Cct5-1	0,012	0,001	0,007	0,007	0,007	53,282	0,028	0,04	0,028	0,02	0,029	24,152	**4,294**	**0,006**
Cfl2-2	0,016	0,005	0,027	0,003	0,013	75,1	0,026	0	0,041	0,017	0,021	69,411	**1,655**	0,455
Cryab-1	0,435	0,29	0,37	0,27	0,341	19,291	0,594	0,584	0,707	0,593	0,62	8,191	**1,815**	**0,001**
Des-2	0,435	0,543	0,556	0,569	0,526	10,137	0,686	1,168	0,88	0,525	0,815	29,377	**1,549**	0,126
Gdi3	0,051	0,033	0,039	0,05	0,043	18,164	0,077	0,048	0,064	0,071	0,065	16,787	**1,515**	**0,033**
Gsto-1	0,021	0,004	0,028	0,004	0,014	73,545	0,056	0,04	0,087	0,057	0,06	28,509	**4,229**	**0,011**
Hk2	0,071	0,071	0,066	0,059	0,067	7,246	0,123	0,099	0,117	0,109	0,112	8,058	**1,672**	**0,001**
Hspb1-2	0,045	0,106	0,134	0,073	0,089	37,709	0,104	0,13	0,258	0,18	0,168	35,054	**1,877**	0,103
Hspb1-3	0,053	0,124	0,151	0,087	0,104	35,892	0,171	0,242	0,254	0,106	0,193	30,81	**1,861**	**0,078**
Hspb6-1	0,043	0,043	0,101	0,05	0,059	40,723	0,118	0,102	0,172	0,152	0,136	20,306	**2,3**	**0,011**
Hspb7	0,011	0,009	0,003	0,018	0,01	55,242	0,028	0,006	0,033	0,031	0,024	43,471	**2,397**	0,104
Rdx/Vil2/Msn-2	0,045	0,037	0,035	0,048	0,041	12,912	0,073	0,046	0,09	0,068	0,069	22,745	**1,689**	**0,048**
Pfkm	0,049	0,065	0,038	0,049	0,05	19,43	0,076	0,05	0,068	0,128	0,081	36,078	**1,604**	0,168
Ppia-1	0,009	0,01	0,018	0,011	0,012	29,029	0,04	0,011	0,035	0,045	0,033	39,356	**2,772**	**0,066**
Psmd7	0,01	0,005	0,026	0,006	0,012	71,605	0,016	0,009	0,032	0,039	0,024	49,462	**2,005**	0,204
Tpt1	0,019	0,026	0,029	0,044	0,029	30,709	0,039	0,019	0,062	0,056	0,044	37,361	**1,503**	0,249
Vcl-1	0,08	0,098	0,073	0,133	0,096	24,371	0,202	0,119	0,091	0,17	0,145	29,654	**1,513**	0,146
Vcl-2	0,053	0,052	0,065	0,064	0,059	9,79	0,125	0,144	0,209	0,115	0,148	24,892	**2,526**	**0,022**
Ywhae	0,003	0,032	0,014	0,007	0,014	79,54	0,073	0,01	0,044	0,053	0,045	50,59	**3,253**	**0,096**
Ywhaq	0,017	0,033	0,02	0,074	0,036	63,372	0,102	0,034	0,076	0,078	0,072	33,697	**2,011**	0,108

Tab.8.3: Herzproteomanalyse der 34 Tage alten Titinkinaseregion-KO-Tiere

Protein	% Vol WT1	% Vol WT2	% Vol WT3	% Vol WT4	MW WT	STABW WT	% Vol KO1	% Vol KO2	% Vol KO3	% Vol KO4	MW KO	STABW KO	Ratio KO/WT	Ttest
Aldh2-2	0,021	0,016	0,026	0,015	0,02	22,316	0,065	0,032	0,065	0,033	0,049	33,901	**2,484**	**0,048**
ApoA1-1	0,055	0,105	0,11	0,104	0,094	23,962	0,174	0,119	0,101	0,203	0,149	27,547	**1,596**	**0,098**
Apobec2	0,005	0,019	0,047	0,016	0,022	72,565	0,034	0,038	0,068	0,043	0,045	29,53	**2,093**	**0,088**
Car3	0,189	0,227	0,193	0,373	0,246	30,552	0,439	0,329	0,331	0,914	0,503	47,998	**2,046**	0,160
Cops4	0,013	0,008	0,015	0,007	0,011	31,618	0,035	0,032	0,03	0,017	0,029	23,684	**2,666**	**0,013**
Cryab	0,065	0,069	0,062	0,067	0,066	4,221	0,387	0,376	0,283	0,634	0,42	30,98	**6,393**	**0,018**
Des-1	0,078	0,068	0,19	0,148	0,121	41,612	0,291	0,08	0,443	0,169	0,246	55,419	**2,029**	0,215
Des-2	0,165	0,264	0,272	0,405	0,277	30,915	0,848	0,576	0,387	0,772	0,646	27,723	**2,334**	**0,029**
Fabp3-2	0,065	0,135	0,093	0,169	0,116	34,554	0,225	0,265	0,15	0,179	0,205	21,495	**1,773**	**0,040**
Hspa5	0,055	0,042	0,134	0,105	0,084	44,447	0,15	0,148	0,144	0,135	0,144	4,11	**1,715**	**0,066**
Hspb1-1	0,045	0,058	0,061	0,056	0,055	11,26	0,144	0,157	0,107	0,35	0,189	49,967	**3,437**	**0,090**
Hspb1-2	0,027	0,034	0,037	0,052	0,037	24,951	0,118	0,15	0,092	0,175	0,134	23,556	**3,568**	**0,010**
Hspb1-3	0,024	0,005	0,013	0,014	0,014	49,776	0,036	0,038	0,042	0,07	0,047	29,702	**3,336**	**0,018**
Hspb7	0,008	0,018	0,01	0,007	0,011	40,644	0,053	0,042	0,027	0,043	0,041	22,379	**3,85**	**0,006**
Hspcb-1	0,32	0,261	0,572	0,408	0,39	30,066	0,581	0,822	0,685	0,634	0,68	13,186	**1,744**	**0,016**
Kbtbd10	0,18	0,171	0,263	0,28	0,223	21,696	0,368	0,487	0,398	0,287	0,385	18,559	**1,724**	**0,021**
LmnA-1	0,032	0,056	0,038	0,032	0,04	24,906	0,067	0,076	0,081	0,087	0,078	9,343	**1,971**	**0,002**
Mb-1	0,138	0,222	0,194	0,238	0,198	19,207	0,79	0,765	0,469	1,19	0,803	31,878	**4,058**	**0,025**
Rdx/Vil2/Msn-1	0,028	0,042	0,04	0,022	0,033	25,203	0,036	0,047	0,055	0,062	0,05	19,508	**1,519**	**0,061**
Myl3/Arhgdia	0,011	0,015	0,057	0,049	0,033	61,183	0,138	0,106	0,124	0,082	0,113	18,368	**3,411**	**0,003**
Myl6	0,842	0,062	0,648	0,809	0,59	53,101	0,131	0,073	0,182	0,45	0,209	69,021	**0,354**	0,125
Nme1/2	0,099	0,151	0,119	0,147	0,129	16,357	0,19	0,179	0,199	0,205	0,193	5,042	**1,499**	**0,008**
Pgm2-2	0,177	0,235	0,187	0,127	0,182	20,976	0,272	0,279	0,321	0,269	0,285	7,424	**1,571**	**0,011**
Ppia-1	0,012	0,024	0,016	0,027	0,02	30,086	0,056	0,033	0,02	0,055	0,041	36,707	**2,087**	**0,089**
Ppia-2	0,044	0,059	0,063	0,068	0,059	15,316	0,116	0,075	0,11	0,132	0,108	19,097	**1,848**	**0,018**
Prdx6-1	0	0,02	0,034	0,024	0,02	63,087	0,054	0,045	0,048	0,136	0,071	53,279	**3,604**	**0,096**
Psma1	0,03	0,018	0,026	0,037	0,028	24,499	0,037	0,044	0,042	0,063	0,046	21,035	**1,669**	**0,040**
Psmb4	0,013	0,03	0,03	0,027	0,025	28,933	0,061	0,089	0,052	0,083	0,071	21,506	**2,844**	**0,008**
Psmb7	0,018	0,012	0,014	0,004	0,012	44,967	0,022	0,037	0,025	0,006	0,023	48,988	**1,88**	0,206
Psmc5	0,003	0,008	0,014	0,012	0,009	46,633	0,019	0,025	0,033	0,031	0,027	20,351	**2,963**	**0,005**
Psmd7	0,017	0,018	0,012	0,023	0,017	21,585	0,029	0,027	0,031	0,124	0,053	77,679	**3,029**	0,235
Ran	0,02	0,028	0,019	0,004	0,018	49,189	0,027	0,035	0,038	0,008	0,027	42,124	**1,522**	0,316
Srl-2	0,094	0,09	0,079	0,079	0,085	7,87	0,117	0,119	0,106	0,172	0,128	19,968	**1,502**	**0,058**
Tnnt3-1	0,371	0,431	0,444	0,385	0,408	7,425	0,506	0,554	0,687	0,732	0,62	14,974	**1,519**	**0,023**
Tpt1	0,02	0,07	0,087	0,059	0,059	41,674	0,115	0,11	0,09	0,109	0,106	9,114	**1,798**	**0,038**
Tuba1/2/7	0,107	0,263	0,264	0,243	0,219	29,832	0,4	0,652	0,357	0,361	0,442	27,555	**2,018**	**0,042**
Vim	0,024	0,062	0,113	0,059	0,064	49,315	0,093	0,089	0,168	0,138	0,122	26,742	**1,9**	**0,072**
Ywhaq	0,02	0,031	0,009	0,017	0,019	41,612	0,049	0,04	0,024	0,019	0,033	36,682	**1,712**	0,157

Tab. 8.4: Quadricepsproteomanalyse der 20 Tage alten Titinkinaseregion-KO-Tiere

Protein	% Vol WT1	% Vol WT2	% Vol WT3	% Vol WT4	MW WT	STABW WT	% Vol KO1	% Vol KO2	% Vol KO3	% Vol KO4	MW KO	STABW KO	Ratio KO/WT	Ttest
Aldh2-2	0,031	0,017	0,016	0,027	0,023	29,311	0,083	0,061	0,081	0,089	0,079	13,108	**3,448**	**0,001**
Anxa5-1	0,034	0,031	0,016	0,016	0,024	33,27	0,041	0,038	0,049	0,037	0,041	11,186	**1,706**	**0,029**
ApoA1-1	0,108	0,05	0,06	0,067	0,071	31,065	0,144	0,082	0,111	0,105	0,11	20,072	**1,546**	**0,073**
Apobec2	0,063	0,049	0,014	0,026	0,038	50,414	0,119	0,093	0,064	0,104	0,095	21,287	**2,505**	**0,012**
Car3	0,582	0,312	0,324	0,391	0,402	26,84	0,929	0,708	0,963	0,781	0,845	12,395	**2,102**	**0,002**
Cfl2	0,146	0,026	0,077	0,095	0,086	50,157	0,138	0,09	0,139	0,16	0,132	19,604	**1,533**	0,175
Cryab	0,105	0,051	0,046	0,123	0,081	41,036	0,568	0,749	0,624	0,648	0,647	10,122	**7,964**	**0,000**
Des-1	1,173	0,317	0,63	0,391	0,628	53,44	0,708	0,927	0,495	1,911	1,01	53,654	**1,609**	0,346
Des-2	0,344	0,178	0,242	0,223	0,247	24,596	0,571	0,599	0,239	0,442	0,463	30,668	**1,876**	**0,072**
Eef1a2	0,08	0,281	0,179	0,345	0,221	45,385	0,301	0,486	0,544	0,383	0,428	21,812	**1,935**	**0,040**
Gdi3	0,076	0,031	0,045	0,073	0,056	33,814	0,11	0,045	0,084	0,104	0,086	29,605	**1,532**	0,162
Gnb2l1	0,034	0,022	0,01	0,025	0,022	38,742	0,033	0,035	0,042	0,042	0,038	11,056	**1,689**	**0,046**
Hadhb	0,004	0,009	0,012	0,03	0,014	69,149	0,019	0,036	0,049	0,029	0,033	32,181	**2,379**	**0,061**
Hspb1-1	0,057	0,045	0,039	0,07	0,053	22,353	0,142	0,117	0,14	0,158	0,139	10,475	**2,649**	**0,000**
Hspb1-2	0,022	0,01	0,021	0,045	0,024	52,101	0,134	0,094	0,143	0,212	0,146	29,088	**5,993**	**0,012**
Hspb1-3	0,015	0,012	0,023	0,012	0,015	29,029	0,065	0,044	0,076	0,102	0,072	29,282	**4,678**	**0,016**
Hspb7	0,011	0,011	0,007	0,009	0,009	18,738	0,047	0,01	0,055	0,064	0,044	46,172	**4,651**	**0,061**
Kbtbd10	0,208	0,103	0,183	0,254	0,187	29,285	0,436	0,644	0,172	0,631	0,471	40,58	**2,517**	**0,078**
Ldh2-1	0,077	0,025	0,046	0,091	0,06	43	0,102	0,05	0,085	0,16	0,099	40,009	**1,653**	0,207
LmnA-1	0,013	0,009	0,046	0,027	0,024	60,736	0,072	0,048	0,064	0,05	0,058	16,997	**2,439**	**0,017**
LOC434885	0,009	0,011	0,009	0,017	0,011	29,933	0,045	0,037	0,02	0,063	0,041	37,946	**3,672**	**0,042**
Mb-1	0,495	0,305	0,413	0,399	0,403	16,74	1,224	1,415	1,403	1,274	1,329	6,176	**3,299**	**0,000**
Mb-2	0,029	0,018	0,053	0,035	0,034	38,014	0,094	0,05	0,108	0,062	0,078	29,798	**2,308**	**0,037**
Myl6	0,872	1,082	1,093	0,609	0,914	21,543	0,258	0,419	0,044	0,205	0,232	57,751	**0,254**	**0,004**
Myoz1-4	0,02	0,004	0,021	0,01	0,014	50,267	0,017	0,015	0,05	0,019	0,025	57,464	**1,822**	0,276
Park7	0,113	0,077	0,116	0,133	0,11	18,646	0,166	0,168	0,193	0,15	0,169	9,117	**1,544**	**0,008**
Pgm2-2	0,146	0,139	0,236	0,177	0,174	21,911	0,236	0,312	0,299	0,245	0,273	11,974	**1,565**	**0,015**
Ppia-1	0,022	0,005	0,008	0,018	0,013	51,607	0,035	0,015	0,019	0,017	0,022	37,299	**1,615**	0,225
Ppia-2	0,057	0,024	0,04	0,044	0,041	29,146	0,094	0,044	0,095	0,061	0,073	29,949	**1,783**	**0,079**
Prdx6-1	0,025	0,027	0,022	0,032	0,026	13,636	0,039	0,058	0,041	0,057	0,049	17,399	**1,854**	**0,015**
Psmb2	0,018	0,002	0,021	0,018	0,015	51,993	0,027	0,02	0,032	0,028	0,027	16,487	**1,814**	**0,063**
Psmb4	0,032	0,009	0,018	0,053	0,028	58,307	0,061	0,028	0,045	0,085	0,055	37,618	**1,952**	0,137
Psmd7	0,019	0,005	0,008	0,019	0,013	50,096	0,033	0,018	0,022	0,035	0,027	26,069	**2,12**	**0,042**
Ran	0,025	0,027	0,014	0,017	0,021	26,419	0,036	0,03	0,046	0,043	0,039	15,74	**1,868**	**0,009**
Sod1	0,084	0,034	0,057	0,093	0,067	34,731	0,13	0,058	0,131	0,111	0,107	27,553	**1,602**	0,115
Srl-1	0,038	0,025	0,016	0,03	0,027	29,37	0,057	0,063	0,039	0,06	0,055	16,61	**2,019**	**0,009**
Srl-2	0,2	0,117	0,162	0,16	0,16	18,342	0,292	0,273	0,259	0,239	0,266	7,235	**1,662**	**0,003**
Tnnt3-1	0,36	0,311	0,284	0,44	0,349	17,075	0,472	0,633	0,525	0,688	0,579	14,751	**1,662**	**0,011**
Tuba1/2/7	0,233	0,189	0,116	0,195	0,183	23,2	0,448	0,502	0,25	0,378	0,395	23,834	**2,154**	**0,022**
Tubb2	0,445	0,442	0,226	0,359	0,368	24,165	0,606	0,695	0,312	0,702	0,579	27,44	**1,573**	0,104
Vcl-1	0,008	0,011	0,001	0,012	0,008	55,867	0,023	0,032	0,016	0,031	0,026	25,607	**3,179**	**0,011**
Vcl-2	0,01	0,009	0,002	0,012	0,008	49,157	0,024	0,024	0,021	0,026	0,024	6,733	**2,911**	**0,002**
Ywhag	0,11	0,024	0,058	0,067	0,065	47,795	0,145	0,126	0,064	0,151	0,122	28,217	**1,883**	**0,078**
Ywhaq	0,055	0,011	0,035	0,05	0,038	45,027	0,085	0,104	0,024	0,105	0,079	41,386	**2,109**	0,116

Tab. 8.5: Quadricepsproteomanalyse der 30 Tage alten Titinkinaseregion-KO-Tiere

8.1.2 Proteomanalyse des induzierbaren herzspezifischen Titinkinaseregion-KO

Für die Proteomanalyse des induzierbaren herzspezifischen Titinkinaseregion-KO wurden je drei Lox homozygote Cre+ Tiere (KO) und Cre- Tiere (WT) 2 x 5 Tage mit 30 mg/kg Tamoxifen behandelt und 30 Tage nach der letzten Injektion analysiert.

Dargestellt sind der Proteinname, die %Volumen (%Vol) Werte der Proteinspots aus den drei WT- und KO-Gelen, der Mittelwert (MW) und die Standardabweichung (STABW) der WT und KO Gele, sowie der Quotient aus Mittelwert KO/Mittelwert WT (Ratio). Alle Ratios mit einem P<0,1 (Ttest) sind signifikant und in der Tabelle fett gedruckt. Nichtsignifikante

Proteine, die in der Proteomanalyse des skelettmuskel-spezifischen Titinkinaseregion-KO ebenfalls auftraten, wurden mit aufgeführt und sind normal gedruckt.

Protein	% Vol WT	% Vol WT	% Vol WT	MW WT	STABW WT	% Vol KO1	% Vol KO2	% Vol KO3	MW KO	STABW KO	Ratio KO/WT	Ttest
Adprhl1	0,082	0,082	0,046	0,07	24,023	0,12	0,131	0,1	0,117	11,091	**1,674**	**0,039**
Cfl2-2	0,027	0,054	0,022	0,034	40,806	0,073	0,039	0,043	0,052	29,307	**1,509**	0,3019
Cryab-1	0,206	0,393	0,3	0,3	25,465	0,713	0,622	0,585	0,64	8,4	**2,136**	**0,009**
Des-2	0,436	0,481	0,489	0,468	4,986	0,594	0,848	0,764	0,735	14,315	**1,57**	**0,0641**
Dlst-1	0,26	0,24	0,194	0,232	11,881	0,622	0,257	0,233	0,371	48,027	**1,601**	0,3836
Dpysl2	0,035	0,038	0,039	0,037	4,246	0,05	0,065	0,068	0,061	13,094	**1,625**	**0,0457**
Eef1a2-1	0,274	0,164	0,271	0,236	21,694	0,312	0,401	0,351	0,355	10,235	**1,504**	**0,0624**
Ehd4	0,04	0,048	0,039	0,042	9,521	0,132	0,12	0,098	0,117	12,213	**2,747**	**0,0124**
Eno1-1	0,189	0,167	0,143	0,166	11,265	0,3	0,255	0,258	0,271	7,671	**1,63**	**0,0062**
Gsn-1	0,021	0,018	0,021	0,02	7,732	0,056	0,032	0,028	0,039	31,605	**1,953**	0,1647
Gsto1-1	0,039	0,043	0,056	0,046	16,065	0,072	0,077	0,06	0,07	9,864	**1,506**	**0,0303**
Gstp1	0,097	0,102	0,069	0,089	16,046	0,182	0,162	0,141	0,161	10,417	**1,808**	**0,0104**
Hspb1-1	0,042	0,026	0,024	0,03	27,032	0,065	0,065	0,039	0,056	21,28	**1,858**	**0,0785**
Hspb1-2	0,122	0,141	0,095	0,119	16,009	0,519	0,246	0,175	0,313	47,219	**2,627**	0,2039
Hspb7	0,029	0,024	0,025	0,026	8,104	0,041	0,045	0,033	0,04	12,928	**1,545**	**0,0442**
Myoz2-1	0,023	0,039	0,026	0,029	23,983	0,067	0,086	0,052	0,068	20,541	**2,325**	**0,0395**
Myoz2-2	0,048	0,07	0,06	0,059	15,512	0,096	0,117	0,104	0,106	8,452	**1,784**	**0,0063**
Nme1/2-1	0,065	0,288	0,153	0,169	54,467	0,342	0,268	0,227	0,279	17,022	**1,655**	0,228
Pgm2	0,072	0,064	0,06	0,065	7,926	0,093	0,102	0,103	0,099	4,314	**1,523**	**0,0021**
Ppia-2	0,015	0,062	0,03	0,036	54,097	0,087	0,044	0,068	0,066	26,143	**1,846**	0,1758
Prdx6-1	0,03	0,03	0,02	0,027	16,909	0,076	0,079	0,033	0,062	33,676	**2,344**	0,1303
Psmd7	0,023	0,024	0,022	0,023	3,813	0,039	0,041	0,03	0,036	13,433	**1,583**	**0,0525**
Rdx/Vil2/Msn-1	0,046	0,014	0,027	0,029	45,023	0,074	0,049	0,028	0,05	37,442	**1,73**	0,2664
Rdx/Vil2/Msn-2	0,028	0,033	0,015	0,026	29,784	0,063	0,038	0,021	0,041	42,213	**1,594**	0,3401
Vcl-1	0,059	0,054	0,033	0,049	23,033	0,106	0,082	0,07	0,086	17,799	**1,765**	**0,0522**
Vcl-2	0,055	0,047	0,045	0,049	8,402	0,097	0,074	0,069	0,08	15,552	**1,63**	**0,0563**

Tab. 8.6: Proteomanalyse des induzierbaren herzspezifischen Titinkinaseregion-KO

8.1.3 Proteomanalyse des Titin-I-Banden-KO (Mdm)

Für die Proteomanalyse des Titin-I-Banden-KO wurden je vier 32 Tage alte WT und KO-Tiere verwendet. Dargestellt sind der Proteinname, die %Volumen (%Vol) Werte der Proteinspots aus den drei WT- und KO-Gelen, der Mittelwert (MW) und die Standardabweichung (STABW) der WT und KO Gele, sowie der Quotient aus Mittelwert KO/Mittelwert WT (Ratio). Alle Ratios mit einem P<0,1 (Ttest) sind signifikant und in der Tabelle fett gedruckt. Nichtsignifikante Proteine, die in der Proteomanalyse des skelettmuskel-spezifischen Titinkinaseregion-KO ebenfalls auftraten, wurden mit aufgeführt und sind normal gedruckt.

Protein	% Vol WT1	% Vol WT2	% Vol WT3	% Vol WT4	MW WT	STABW WT	% Vol KO1	% Vol KO2	% Vol KO3	% Vol KO4	MW KO	STABW KO	Ratio KO/WT	Ttest
Aldh2-2	0,01	0,035	0,018	0,056	0,03	59,818	0,055	0,063	0,042	0,055	0,054	14,07	**1,81**	**0,095**
Apobec2	0,02	0,016	0,019	0,003	0,015	45,808	0,04	0,036	0,058	0,029	0,041	25,695	**2,775**	**0,015**
Arhgdia/Myl3	0,022	0,035	0,022	0,034	0,029	21,907	0,027	0,051	0,047	0,05	0,044	22,028	**1,529**	**0,068**
Car3	0,291	0,268	0,249	0,351	0,29	13,233	0,534	0,469	0,439	0,857	0,575	28,983	**1,982**	**0,056**
Cops4	0,038	0,071	0,101	0,071	0,07	31,61	0,15	0,104	0,12	0,082	0,114	21,456	**1,622**	**0,064**
Cryab	0,165	0,116	0,079	0,116	0,119	25,676	0,588	0,336	0,32	0,17	0,353	42,443	**2,975**	**0,071**
Cs	0,209	0,121	0,136	0,149	0,154	21,735	0,315	0,33	0,375	0,245	0,317	14,751	**2,058**	**0,004**
Des-1	0,098	0,46	0,3	0,334	0,298	43,6	0,611	0,545	0,646	0,278	0,52	27,794	**1,743**	**0,096**
Des-2	0,049	0,131	0,102	0,121	0,101	31,41	0,201	0,228	0,118	0,208	0,189	22,136	**1,879**	**0,030**
Dlst-1	0,09	0,09	0,088	0,082	0,088	3,631	0,158	0,133	0,14	0,153	0,146	6,91	**1,665**	**0,001**
Eno1-2	0,012	0,015	0,016	0,011	0,014	16,381	0,029	0,025	0,027	0,027	0,027	5,166	**2,005**	**0,000**
Gdi3	0,042	0,059	0,046	0,011	0,039	44,949	0,083	0,067	0,083	0,093	0,082	11,439	**2,069**	**0,017**
Hadhb	0,041	0,032	0,037	0,001	0,028	57,608	0,098	0,047	0,086	0,012	0,061	55,967	**2,192**	0,197
Hspb1-1	0,079	0,057	0,038	0,08	0,064	27,398	0,243	0,117	0,12	0,079	0,139	44,258	**2,194**	0,119
Hspb1-2	0,023	0,035	0,02	0,021	0,025	23,687	0,109	0,078	0,067	0,024	0,07	43,655	**2,818**	**0,082**
Hspb7	0,017	0,004	0,008	0,029	0,014	67,794	0,055	0,05	0,037	0,021	0,041	31,798	**2,836**	**0,035**
Idh3a-2	0,015	0,025	0,024	0,029	0,023	21,487	0,052	0,053	0,046	0,046	0,049	6,332	**2,121**	**0,001**
Kbtbd10	0,08	0,223	0,213	0,155	0,168	33,885	0,462	0,351	0,28	0,177	0,317	32,71	**1,89**	**0,084**
Ldh2-1	0,06	0,065	0,035	0,033	0,048	29,593	0,074	0,111	0,068	0,053	0,077	27,686	**1,592**	0,113
LmnA-1	0,015	0,034	0,042	0,037	0,032	32,061	0,048	0,06	0,061	0,052	0,055	9,944	**1,725**	**0,020**
Mb-1	0,39	0,261	0,305	0,414	0,342	18,104	0,574	0,646	0,471	0,476	0,541	13,43	**1,582**	**0,012**
Myoz1-4	0,019	0,017	0,015	0,031	0,02	30,469	0,055	0,04	0,042	0,04	0,044	14,434	**2,161**	**0,003**
Pdhb	0,042	0,071	0,1	0,136	0,088	39,857	0,121	0,138	0,149	0,153	0,14	8,832	**1,604**	**0,072**
Pgam2-2	0,081	0,08	0,08	0,091	0,083	5,404	0,137	0,132	0,175	0,16	0,151	11,465	**1,818**	**0,005**
Ppia-1	0,006	0,021	0,039	0,015	0,02	58,858	0,02	0,045	0,04	0,021	0,032	35,226	**1,562**	0,281
Sod1	0,05	0,08	0,048	0,053	0,058	22,545	0,078	0,091	0,096	0,092	0,089	7,784	**1,541**	**0,016**
Tuba1/2/7	0,109	0,243	0,171	0,15	0,168	28,831	0,293	0,339	0,195	0,262	0,272	19,259	**1,618**	**0,045**

Tab. 8.7: Proteomanalyse des Titin-I-Banden-KO (Mdm)

8.2 Anfertigung eines Herz- und Quadriceps-Mastergels für Proteomanalysen

Die in dieser Arbeit verwendeten Maus-KO-Stämme wurden umfangreichen Proteomanalysen unterzogen. Dazu war es notwendig, Mastergele für die verwendeten Gewebe Herz und Quadriceps anzufertigen, um Proteine, deren Mengen unterschiedlich im KO und WT sind, identifizieren zu können. Für die Anfertigung der Mastergele wurden Herz- und Quadricepslysate von WT-Mäusen unter den gleichen Bedingungen wie die später verwendeten Analyselysate mittels 2D-Gelelektrophorese aufgetrennt und mit Colloidal Coomassie gefärbt. Anschließend wurden alle Proteinspots ausgeschnitten, mit Trypsin verdaut und mit einem MALDI TOF-Massenspektrometer identifiziert. Mit Hilfe einer Bildanalyse-Software (Decodon) wurde dann ein Mastergel für Quadriceps und Herz erstellt, das für alle nachfolgenden Experimente zur Identifizierung der Proteinspots verwendet wurde. Für das Herzmastergel konnten ca. 300 verschiedene Proteine (Abb. 8.1.-8.5, Tab. 8.8) und für das Quadricepsmastergel ca. 200 verschiedene Proteine (Abb. 8.6-8.10, Tab. 8.9) identifiziert werden. Die Mastergele wurden mit den kürzeren Gennamen des Proteins beschriftet. In den Tabellen 8.8 und 8.9 sind der Proteinname und der Genname, sowie das Molekulargewicht (Mw in Da), der isoelektrische Punkt (pI) und die NCBI-

Datenbanknummer aufgeführt. Proteine, denen mehr als ein Spot zugeordnet werden konnte, wurden mit einem Bindestrich hinter dem Gennamen und einer Nummer versehen (Spot1=Genname-1, Spot2=Genname-2, usw.). Aufgrund eines ähnlichen pI und Mw konnten für einige Spots mehrere Proteine identifiziert werden. Diese Spots wurden dann mit den Gennamen der Proteine, getrennt durch einen Schrägstrich beschriftet (Genname1/Genname2/usw.).

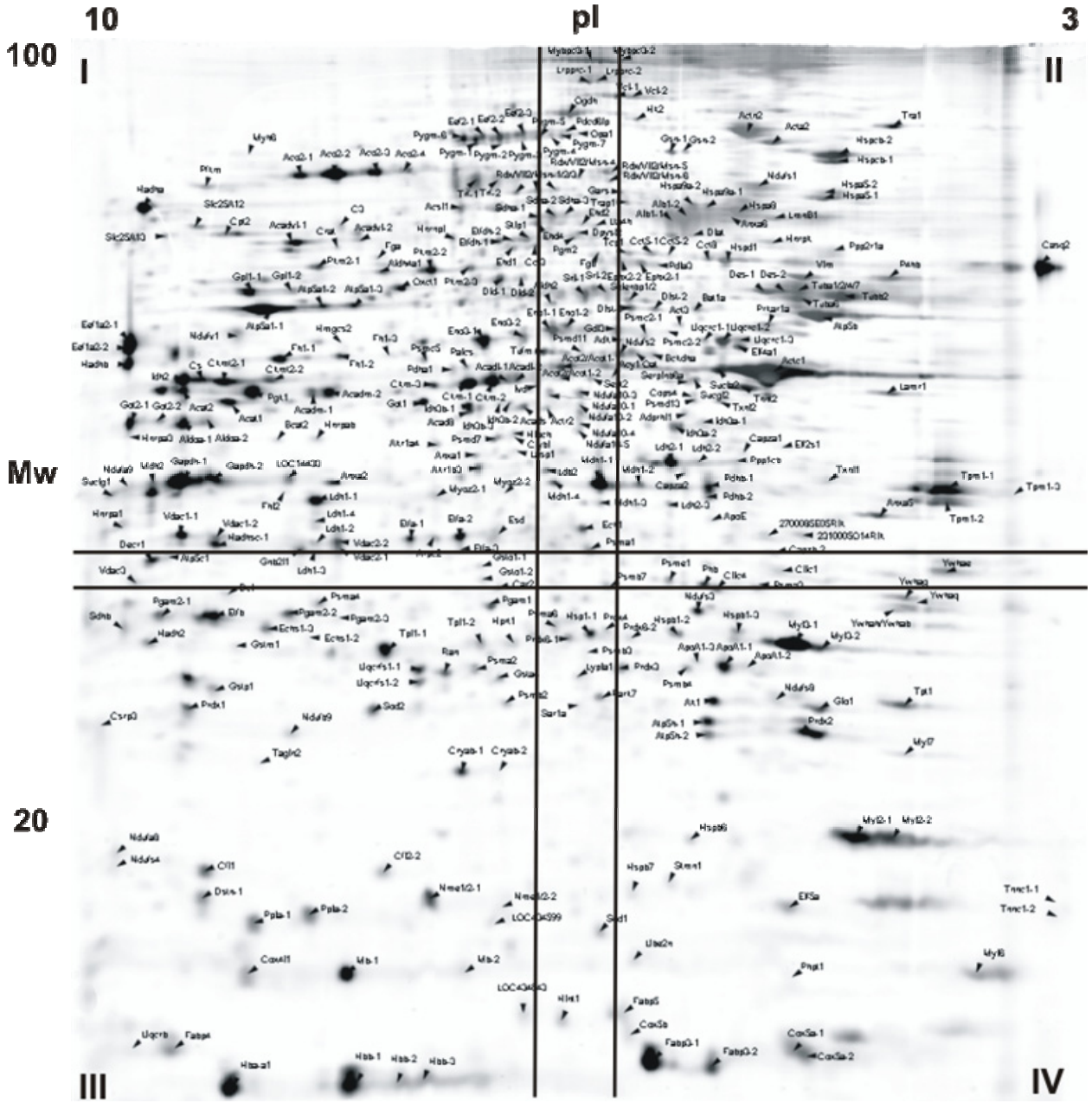

Abb. 8.1: Herzmastergel *Mus Musculus*

Dargestellt ist ein 2D-Gel vom Herzgewebe von *Mus Musculus* mit identifizierten Proteinspots. Die Proteinauftrennung erfolgte zwischen einem pI- Gradienten von 3-10 und einem Mw von 15-100 kDa. Die unterteilten vier Bereiche sind auf den folgenden Seiten vergrößert dargestellt.

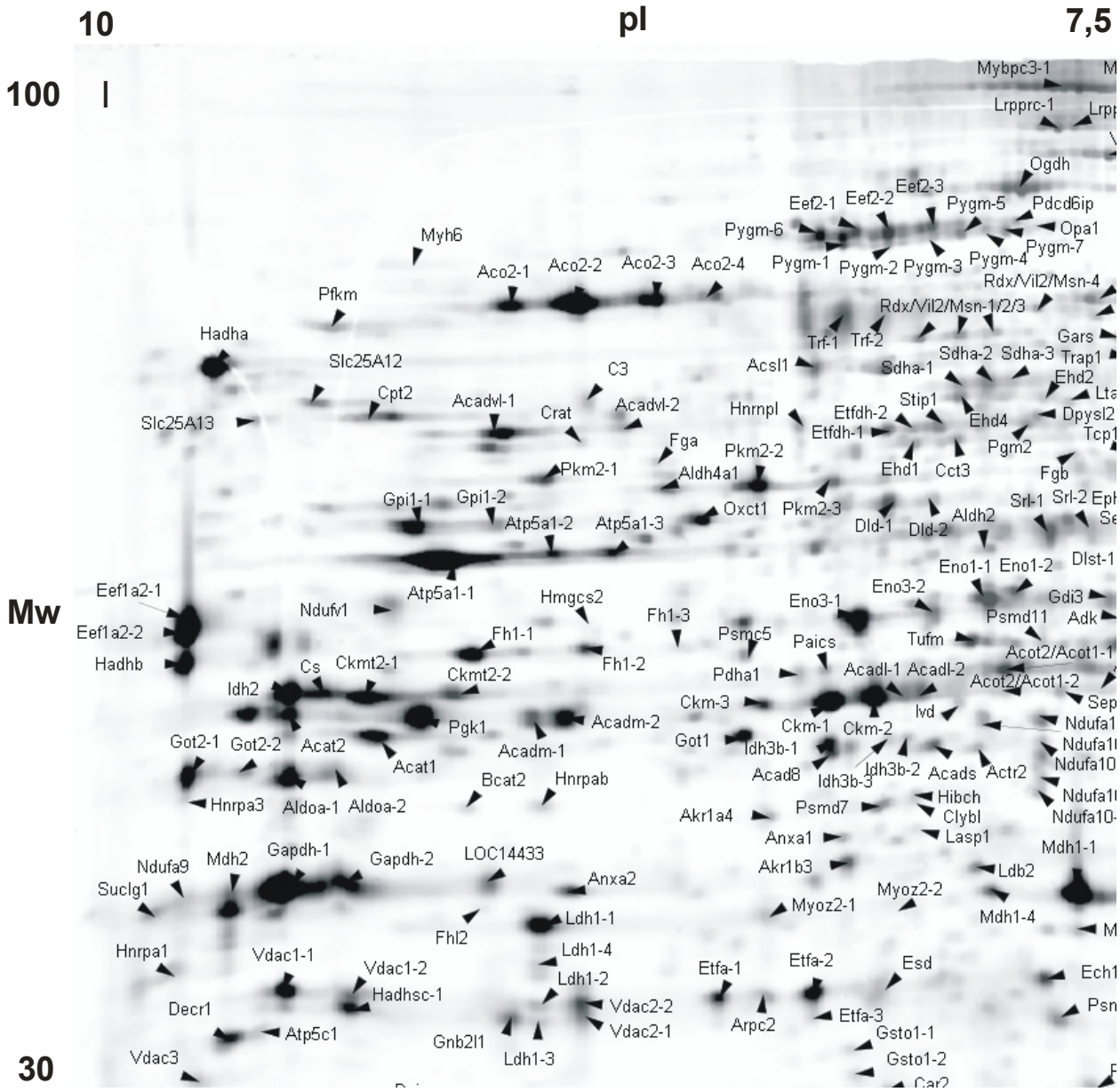

Abb. 8.2: Herzmastergel Teil I

Dargestellt sind die mit Massenspektrometrie identifizierten Proteinspots mit einem pI zwischen 7,5-10 und einem Mw zwischen 30-100 kDa.

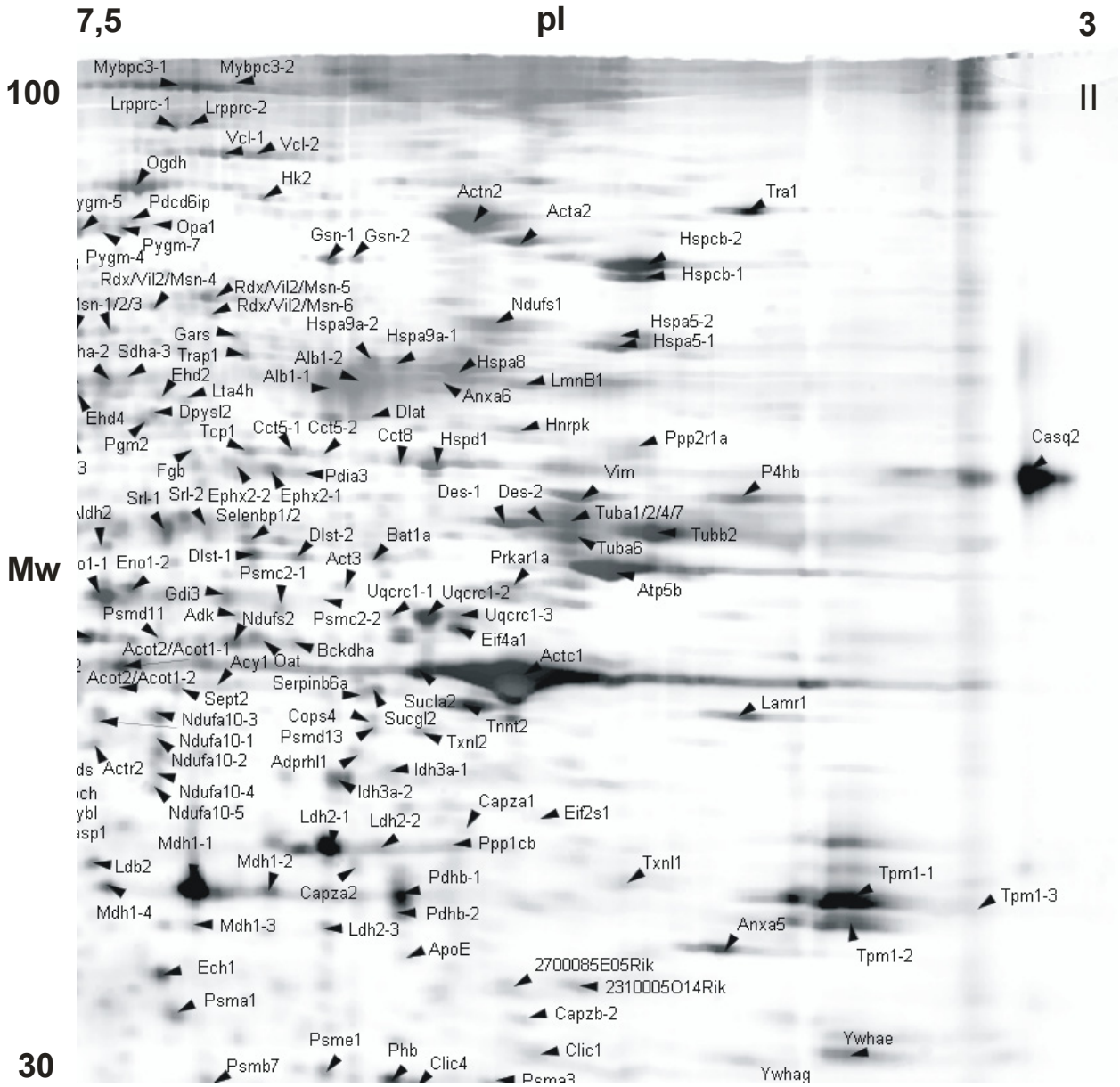

Abb. 8.3: Herzmastergel Teil II

Dargestellt sind die mit Massenspektrometrie identifizierten Proteinspots mit einem pI zwischen 3-7,5 und einem Mw zwischen 30-100 kDa.

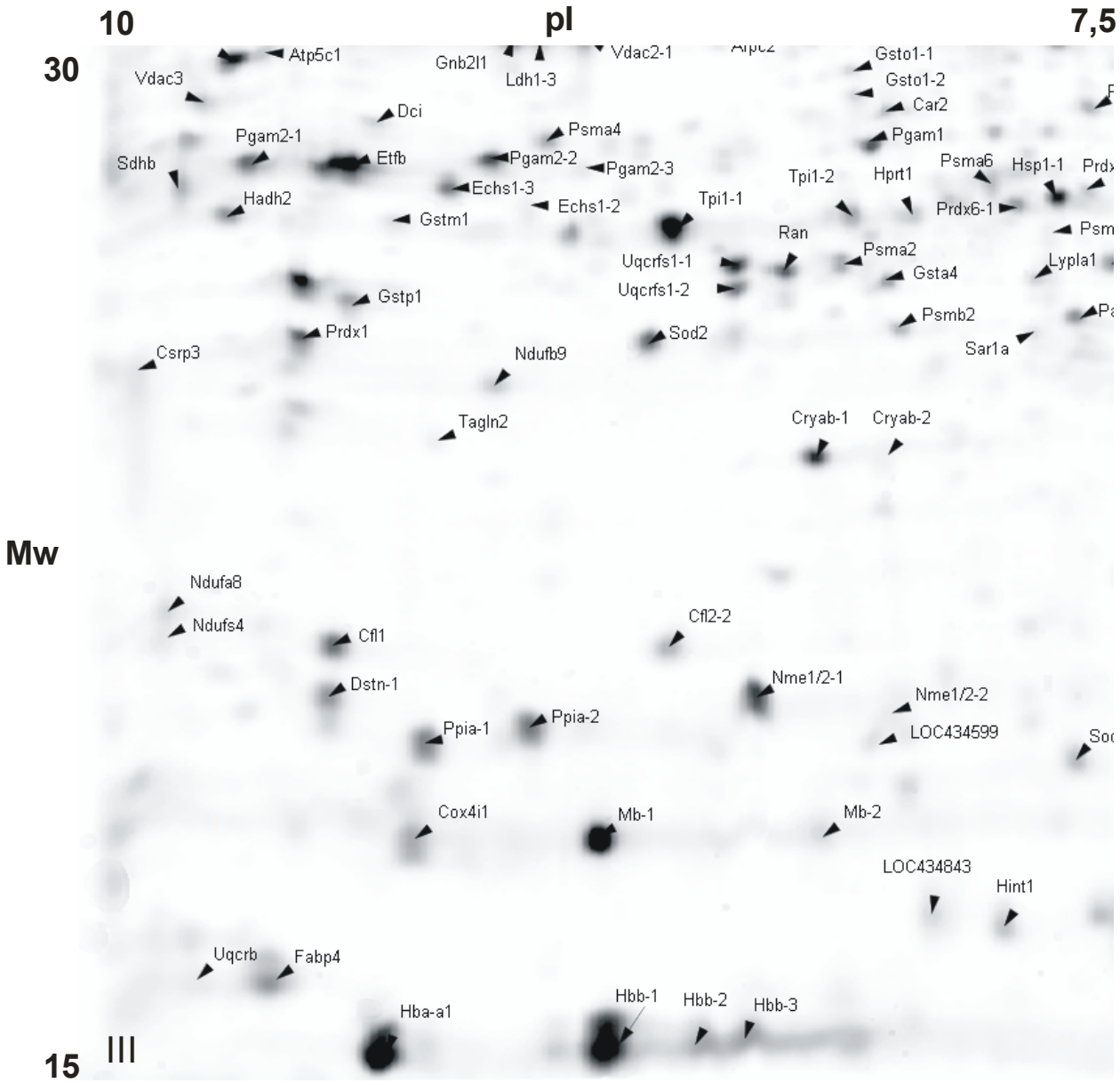

Abb. 8.4: Herzmastergel Teil III

Dargestellt sind die mit Massenspektrometrie identifizierten Proteinspots mit einem pI zwischen 7,5-10 und einem Mw zwischen 15-30 kDa.

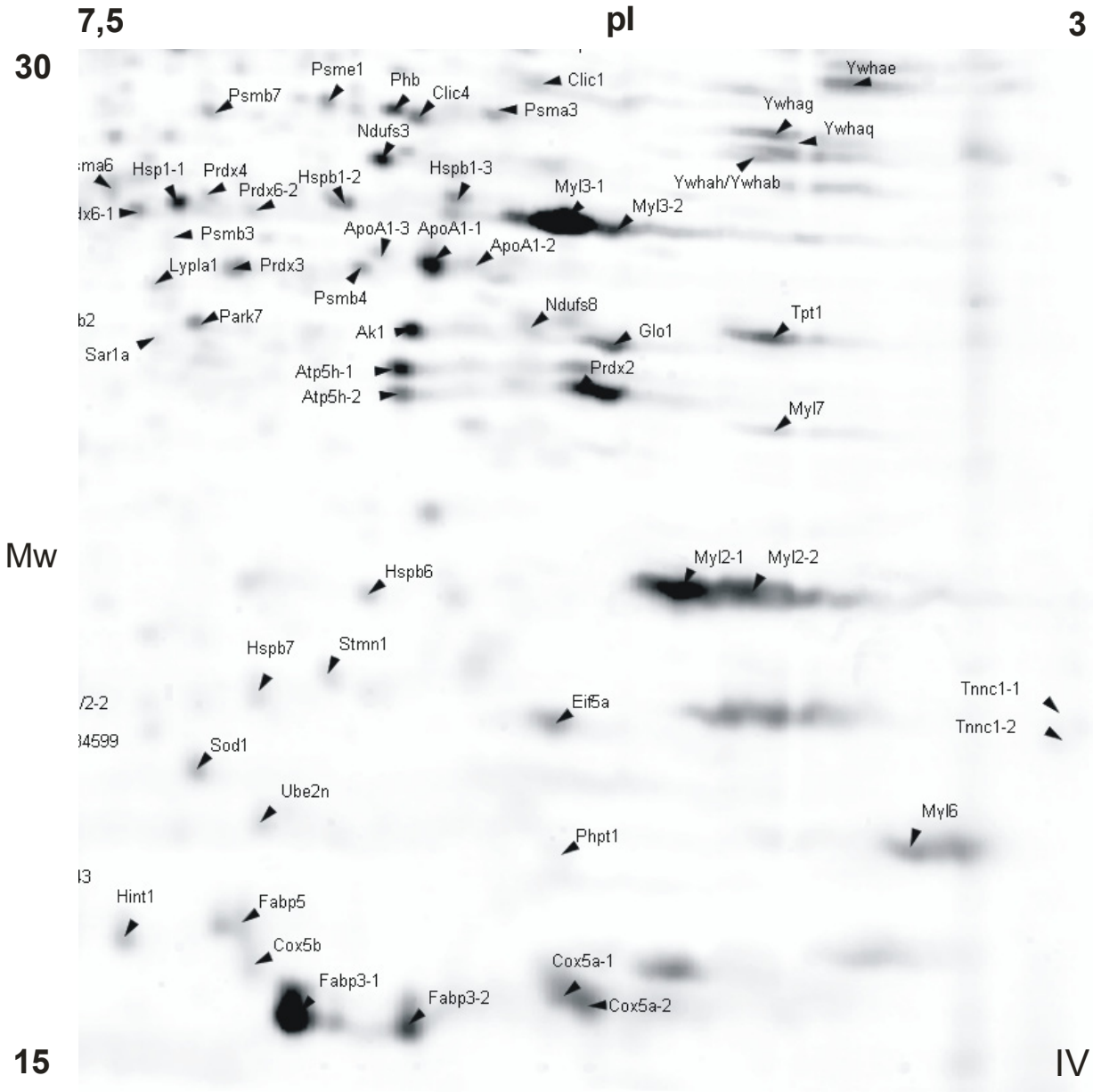

Abb. 8.5: Herzmastergel Teil IV

Dargestellt sind die mit Massenspektrometrie identifizierten Proteinspots mit einem pI zwischen 3-7,5 und einem Mw zwischen 15-30 kDa.

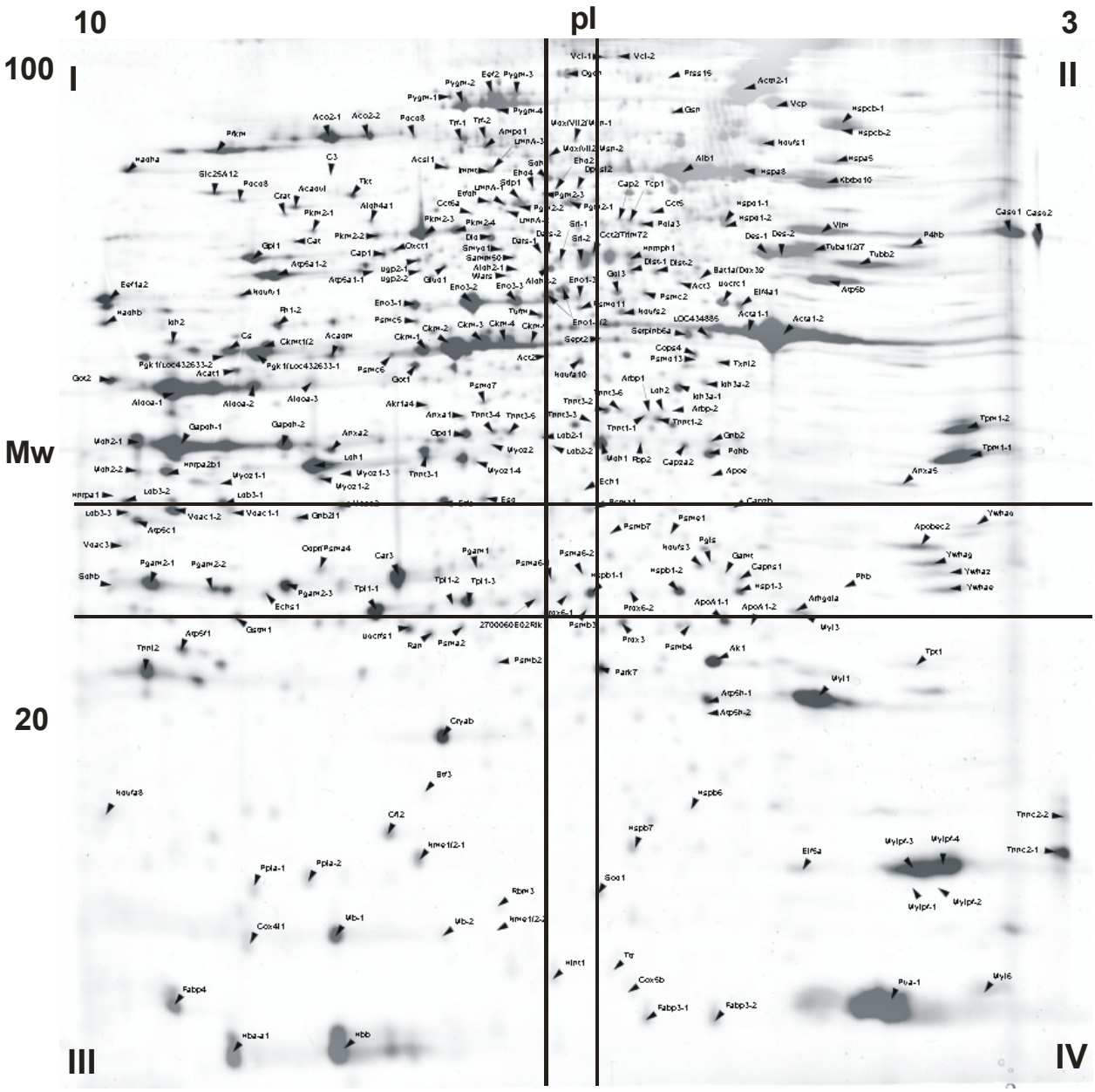

Abb. 8.6: Quadricepsmastergel *Mus Musculus*

Dargestellt ist ein 2D-Gel vom Quadricepsgewebe von *Mus Musculus* mit identifizierten Proteinspots. Die Proteinauftrennung erfolgte zwischen einem pI- Gradienten von 3-10 und einem Mw von 15-100 kDa. Die unterteilten vier Bereiche sind auf den folgenden Seiten vergrößert dargestellt.

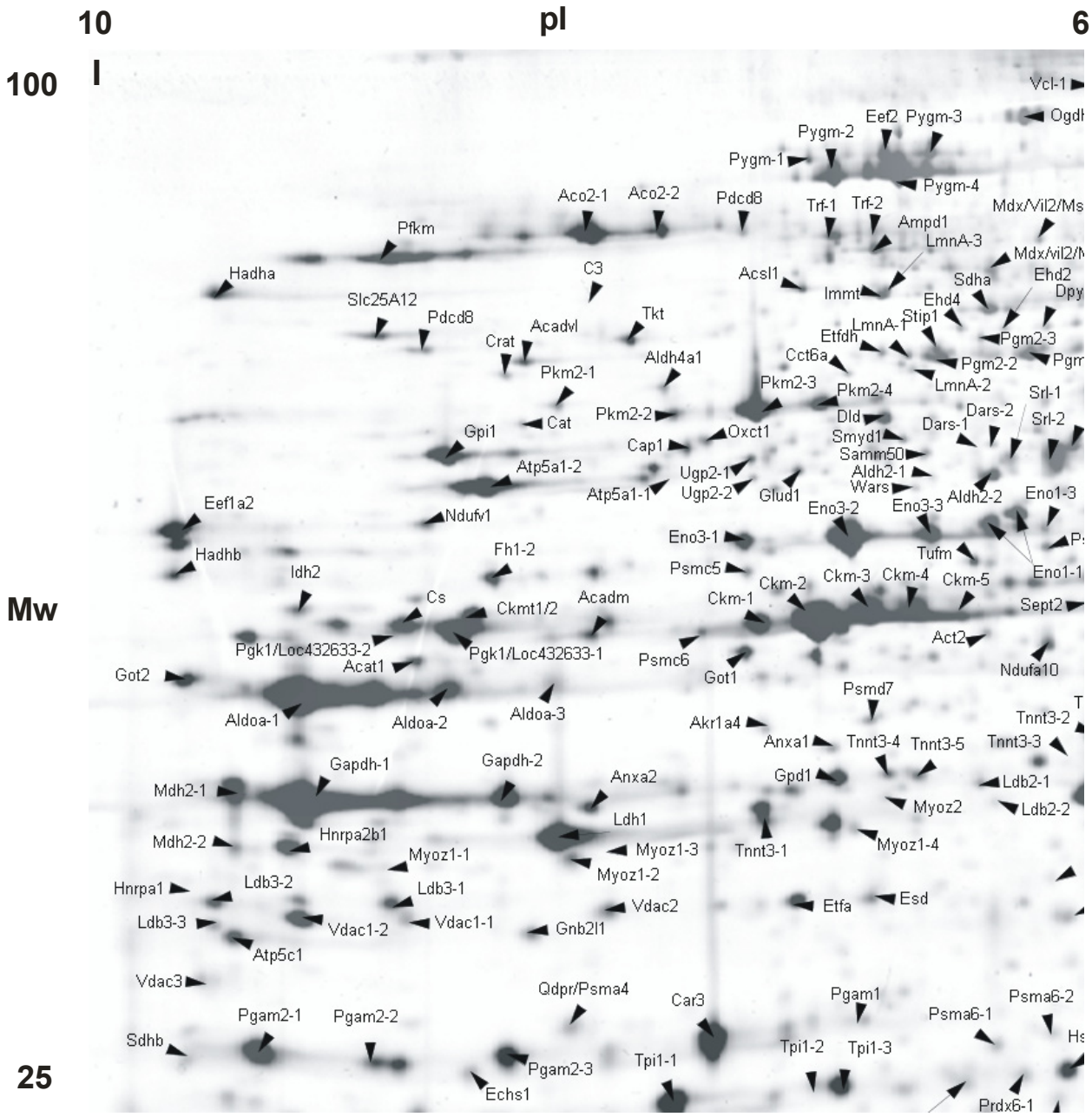

Abb. 8.7: Quadricepsmastergel Teil I

Dargestellt sind die mit Massenspektrometrie identifizierten Proteinspots mit einem pI zwischen 6-10 und einem Mw zwischen 25-100 kDa.

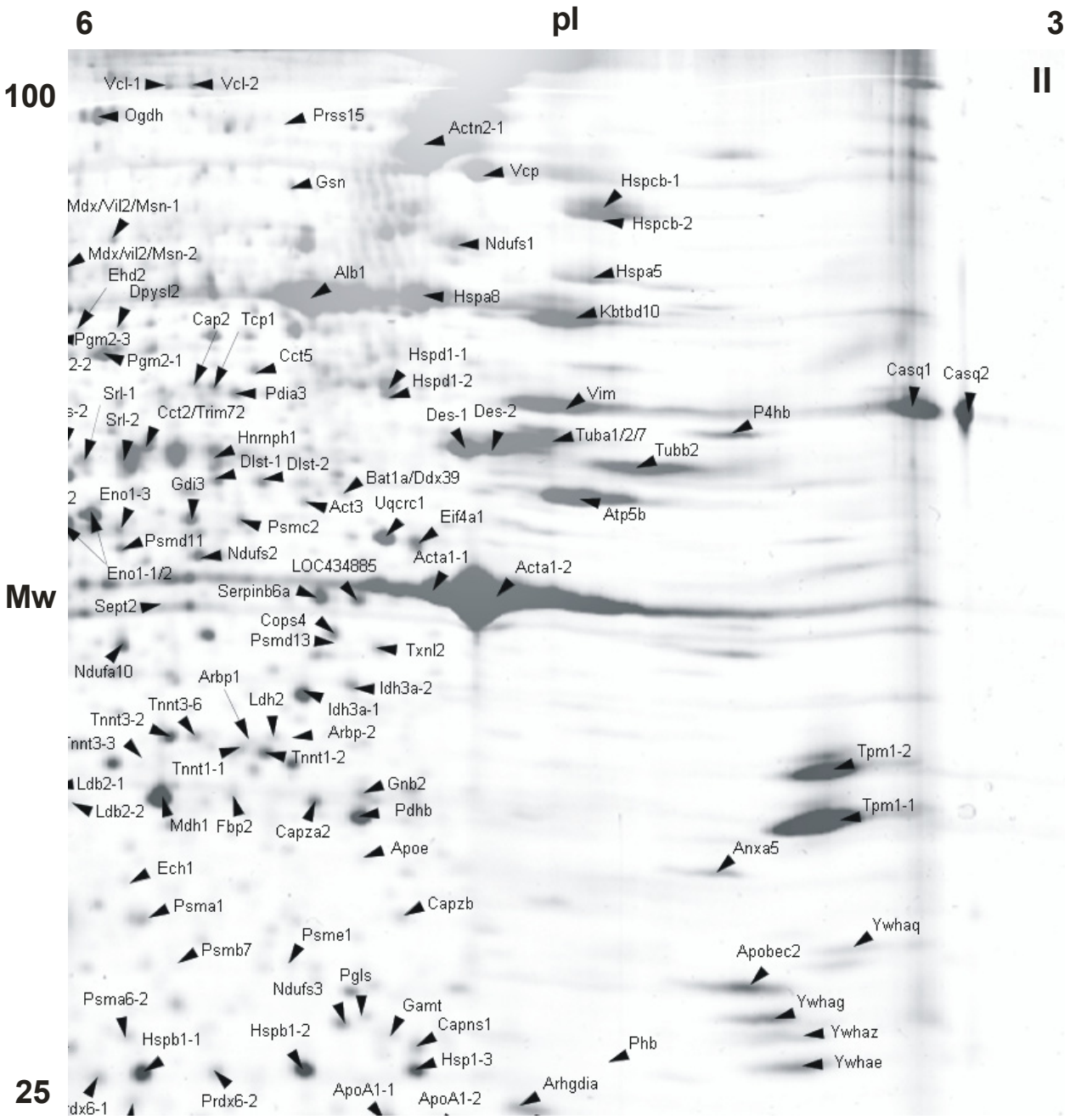

Abb. 8.8: Quadricepsmastergel Teil II

Dargestellt sind die mit Massenspektrometrie identifizierten Proteinspots mit einem pI zwischen 3-6 und einem Mw zwischen 25-100 kDa.

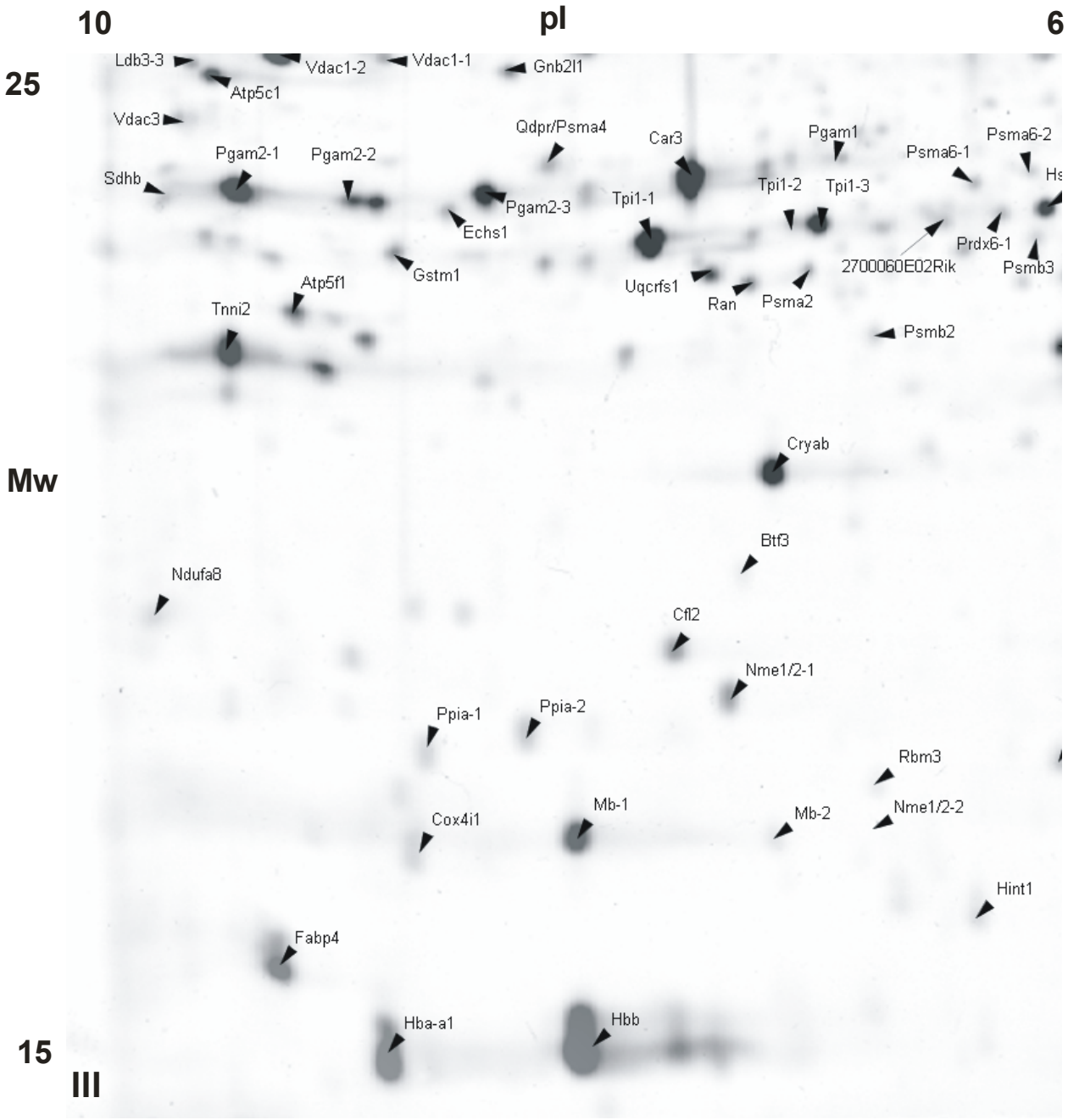

Abb. 8.9: Quadricepsmastergel Teil III

Dargestellt sind die mit Massenspektrometrie identifizierten Proteinspots mit einem pI zwischen 6-10 und einem Mw zwischen 15-25 kDa.

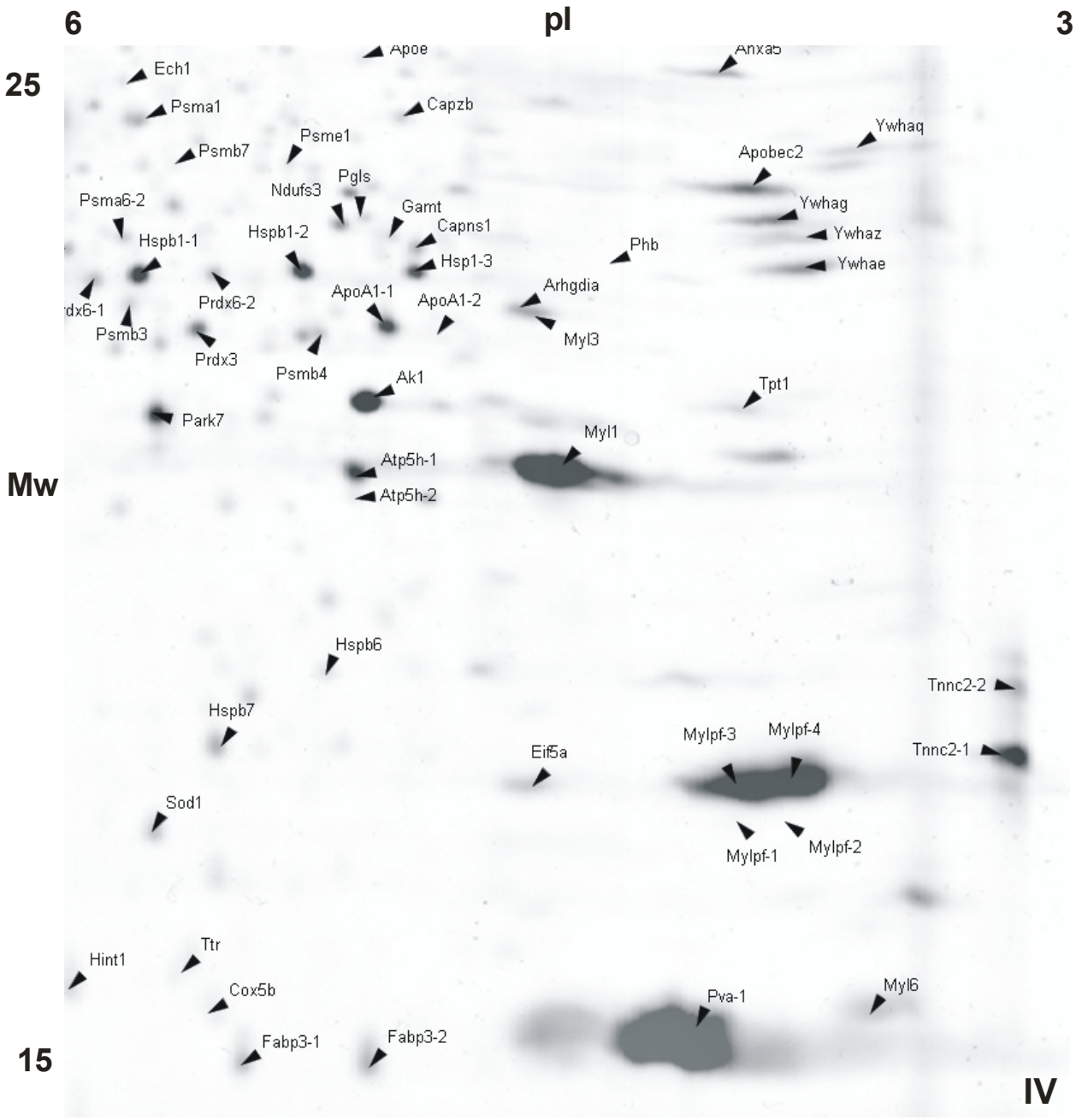

Abb. 8.10: Quadricepsmastergel Teil IV

Dargestellt sind die mit Massenspektrometrie identifizierten Proteinspots mit einem pI zwischen 3-6 und einem Mw zwischen 15-25 kDa.

Protein	Gen	Mw (Da)	pI	NCBI-Nummer
2,4-dienoyl CoA reductase 1	Decr1	36213	9,1	NP_080448
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	Hmgcs2	56822	8,65	NP_032282
3-hydroxyisobutyryl-Coenzyme A hydrolase	Hibch	43037	8,15	NP_666220
3-oxoacid-CoA transferase 1	Oxct1	55988	8,73	NP_077150
acetyl-CoA acetyltransferase 1 precursor	Acat1	44816	8,71	NP_659033
acetyl-CoA acyltransferase 2 (mitochondrial 3-oxoacyl-CoA thiolase)	Acat2	41803	8,33	NP_803421.1
acetyl-CoA dehydrogenase, long-chain	Acadl-1	47866	8,34	NP_031407.2
acetyl-CoA dehydrogenase, long-chain	Acadl-2	47866	8,34	NP_031407.2
acetyl-CoA dehydrogenase, medium chain	Acadm-1	46452	8,6	NP_031408.1
acetyl-CoA dehydrogenase, medium chain	Acadm-2	46452	8,6	NP_031408.1
acetyl-CoA dehydrogenase, short chain	Acads	44861	8,68	NP_031409.2
acetyl-CoA dehydrogenase, very long chain, mitochondrial precursor	Acadvl-1	70830	8,91	NP_059062.1
acetyl-CoA dehydrogenase, very long chain, mitochondrial precursor	Acadvl-2	70830	8,91	NP_059062.1
aconitase 2, mitochondrial	Aco2-1	85410	8,08	NP_542364.1
aconitase 2, mitochondrial	Aco2-2	85410	8,08	NP_542364.1
aconitase 2, mitochondrial	Aco2-3	85410	8,08	NP_542364.1
aconitase 2, mitochondrial	Aco2-4	85410	8,08	NP_542364.1
actin related protein 2 3 complex, subunit 2	Arpc2	34335	6,84	XP_129773.2
acyl-CoA synthetase long-chain family member 1	Acsl1	77901	6,81	NP_032007.2
acyl-Coenzyme A dehydrogenase family, member 8	Acad8	45091	8,32	AAH37644
adenine nucleotide translocator, solute carrier family 25 (mitochondrial carrier), member 4	Slc25a4	32904	9,76	NP_031476
adenosine kinase	Adk	40123	5,84	NP_598840.1
adenylate kinase 1	Ak1	23116	5,7	NP_067490
ADP-ribosylhydrolase 2, ADP-ribosylhydrolase like 1	Adprhl1	41992	5,62	NP_766338
aldehyde dehydrogenase 2, mitochondrial	Aldh2	56537	7,53	NP_033786
aldehyde dehydrogenase 4 family, member A1	Aldh4a1	61772	8,58	NP_780647
aldo-keto reductase family 1, member A4, aldehyde reductase	Akr1a4	35552	6,9	NP_067448
aldo-keto reductase family 1, member B3 (aldose reductase)	Akr1b3	35724	6,71	NP_033788.2
aldolase 1	Aldoa-1	39355	8,3	NP_031464
aldolase 1	Aldoa-2	39355	8,3	NP_031464
alpha actin, cardiac	Actc1	42018	5,23	NP_033738
alpha actinin 2	Actn2	103918	5,31	NP_150371.2
alpha B crystallin	Cryab-1	20068	6,76	NP_034094
alpha B crystallin	Cryab-2	20068	6,76	NP_034094
alpha hemoglobin, adult chain	Hba-a1	15112	7,97	AAH43020
alpha isoform of regulatory subunit A, protein phosphatase 2; serine threonine protein phosphatase	Ppp2r1a	65280	5	NP_058587.1
aminoacylase 1	Acy1	45766	5,81	NP_079647.1
annexin A1; lipocortin 1	Anxa1	38667	6,56	NP_034860.1
annexin A2, calpactin I heavy chain, lipocortin II, chromobindin 8, 33-kDa calcimedin	Anxa2	38676	7,55	NP_031611
annexin A5; annexin V	Anxa5	39860	4,83	NP_033803
annexin A6	Anxa6	75885	5,34	NP_038500
Apolipoprotein A-1	ApoA1-1	30587	5,64	NP_033822
Apolipoprotein A-1	ApoA1-2	30587	5,64	NP_033822
Apolipoprotein A-1	ApoA1-3	30587	5,64	NP_033822
Apolipoprotein E	ApoE	35852	5,56	NP_033826
ARP2 actin-related protein 2 homolog	Actr2	44760	6,29	AAH27799
ARP3 actin-related protein 3 homolog	Act3	47357	5,61	NP_076224.1
ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	Atp5b	56265	5,19	NP_058054.2
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Atp5h-1	18737	5,52	NP_082138.1
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Atp5h-2	18749	5,52	NP_082138
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1-1	59715	9,22	NP_031531.1
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1-2	59715	9,22	NP_031531.1
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1-3	59715	9,22	NP_031531.1
ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Atp5c1	32831	9,06	|NP_065640.1
beta hemoglobin	Hbb-1	15748	7,13	NP_032246
beta hemoglobin	Hbb-2	15748	7,13	NP_032246
beta hemoglobin	Hbb-3	15748	7,13	NP_032246
branched chain aminotransferase 2, mitochondrial	Bcat2	44099	8,61	NP_033867.1
calsequestrin 2, cardiac	Casq2	48324	4,12	NP_033944.1
capping protein (actin filament) muscle Z-line, alpha 2	Capza2	32947	5,57	NP_031630.1
capping protein, alpha 1	Capza1	32939	5,34	NP_033927
carbonic anhydrase 2	Car2	29073	6,52	NP_033931.3
carboxyl terminal LIM domain protein 1	Ldb2	35717	6,38	NP_058557
carnitine acetyltransferase	Crat	70789	8,39	NP_031786.1

Protein	Gen	Mw (Da)	pI	NCBI-Nummer
carnitine palmitoyltransferase 2	Cpt2	73927	8,46	NP_034079
chaperonin subunit 3 (gamma)	Cct3	60629	6,28	NP_033966
chaperonin subunit 5 (epsilon)	Cct5-1	59624	5,72	NP_031663
chaperonin subunit 5 (epsilon)	Cct5-2	59624	5,72	NP_031663
chaperonin subunit 8 (theta)	Cct8	59554	5,57	NP_033970
chloride intracellular channel 1	Clic1	27012	5,09	NP_254279
chloride intracellular channel 4 (mitochondrial)	Clic4	28711	5,44	NP_038913.1
citrate lyase beta like	Clybl	37494	8,76	NP_083832.1
citrate synthase	Cs	51736	8,72	NP_080720
cofilin 1, non-muscle	Cfl1	18559	8,22	NP_031713
cofilin 2, muscle	Cfl2	18697	7,66	NP_031714.1
complement component 3	C3	186364	6,44	NP_033908.1
COP9 signalosome subunit 4	Cops4	46284	5,57	NP_036131
creatine kinase, mitochondrial 2	Ckmt2-1	47443	8,64	NP_940807.1
creatine kinase, mitochondrial 2	Ckmt2-2	47443	8,64	NP_940807.1
creatine kinase, muscle	Ckm-1	43017	6,58	NP_031736.1
creatine kinase, muscle	Ckm-2	43017	6,58	NP_031736.1
creatine kinase, muscle	Ckm-3	43017	6,58	NP_031736.1
cysteine and glycine-rich protein 3	Csrp3	20894	8,9	NP_038836
cytochrome c oxidase, subunit IVa	Cox4i1	19518	9,25	NP_034071
cytochrome c oxidase, subunit Va	Cox5a-1	16101	6,08	NP_031773
cytochrome c oxidase, subunit Va	Cox5a-2	16101	6,08	NP_031773
cytochrome c oxidase, subunit Vb	Cox5b	13846	8,34	NP_034072
cytosolic acyl-CoA thioesterase 1	Acot1	46136	6,12	NP_036136
desmin	Des-1	53497	5,21	NP_034173
desmin	Des-2	53497	5,21	NP_034173
destrin, Sid23p	Dstn-1	18521	8,14	NP_062745
dihydrolipoamide dehydrogenase	Dld-1	54272	7,99	NP_031887
dihydrolipoamide dehydrogenase	Dld-2	54272	7,99	NP_031887
dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase)	Dlat	67902	8,81	NP_663589.2
dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Dlst-1	48964	9,1	NP_084501.1
dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Dlst-2	48964	9,1	NP_084501.1
dihydropyrimidinase-like 2; collapsin response mediator protein 2	Dpysl2	62239	5,95	NP_034085.2
DJ-1 protein, RNA binding protein, regulatory subunit	Park7	20021	6,32	NP_065594
dodecenoyl-CoA delta isomerase (3,2 trans-enoyl-CoA isomerase)	Dci	32078	8,87	CAA78417
EH domain containing protein MPAST2	Ehd4	61480	6,33	NP_598599
EH-domain containing 1	Ehd1	60602	6,35	NP_034249
EH-domain containing 2	Ehd2	57217	6,46	NP_694708.1
electron transferring flavoprotein, alpha polypeptide	Etfa-1	34928	8,42	NP_663590.2
electron transferring flavoprotein, alpha polypeptide	Etfa-2	34928	8,42	NP_663590.2
electron transferring flavoprotein, alpha polypeptide	Etfa-3	34928	8,42	NP_663590.2
electron transferring flavoprotein, beta polypeptide	Etfb	27606	8,24	NP_080971.2
electron transferring flavoprotein, dehydrogenase	Etfdh-1	68007	7,34	NP_080070
electron transferring flavoprotein, dehydrogenase	Etfdh-2	68007	7,34	NP_080070
enolase 1, alpha non-neuron	Eno1-1	47095	6,37	NP_075608.1
enolase 1, alpha non-neuron	Eno1-2	47095	6,37	NP_075608.1
enolase 3	Eno3-1	47024	6,73	NP_031959
enolase 3	Eno3-2	47024	6,73	NP_031959
enoyl CoA hydratase 1, peroxisomal	Ech1	36095	7,6	NP_058052.1
enoyl CoA hydratase 1, short chain, mitochondrial	Echs1-1	31454	8,76	NP_444349.1
enoyl CoA hydratase 1, short chain, mitochondrial	Echs1-2	31454	8,76	NP_444349.1
epoxide hydrolase 2, cytoplasmic	Ephx2-1	62474	5,85	NP_031966.2
epoxide hydrolase 2, cytoplasmic	Ephx2-2	62474	5,85	NP_031966.2
Esterase D formylglutathione hydrolase	Esd	31319	6,7	NP_058599
eukaryotic translation elongation factor 1, alpha 2	Eef1a2-1	95252	6,41	NP_031933.1
eukaryotic translation elongation factor 1, alpha 2	Eef1a2-2	95252	6,41	NP_031933.1
eukaryotic translation elongation factor 2	Eef2-1	95314	6,41	NP_031933
eukaryotic translation elongation factor 2	Eef2-2	95314	6,41	NP_031933
eukaryotic translation initiation factor 2, subunit 1, alpha	Eif2s1	36108	5,02	NP_080390
eukaryotic translation initiation factor 4A1 A2, long form	Eif4a1	46153	5,32	NP_659207
expressed in nonmetastatic cells 1, protein NM23A expressed in nonmetastatic cells 2, protein NM23B	Nme1/Nme2-1	17207 17363	6,84 6,97	XP_126757 NP_032731
expressed in nonmetastatic cells 1, protein NM23A expressed in nonmetastatic cells 2, protein NM23B	Nme1/Nme2-2	17207 17363	6,84 6,97	XP_126757 NP_032731
fatty acid binding protein 3, muscle and heart; fatty acid binding protein heart 4	Fabp3-1	14810	6,11	NP_034304.1
fatty acid binding protein 3, muscle and heart; fatty acid binding protein heart 4	Fabp3-2	14810	6,11	NP_034304.1

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fatty acid binding protein 4, adipocyte protein aP2	Fabp4	14649	8,53	NP_077717
fibrinogen B	Fgb	54752	6,68	NP_862897
fibrinogen, alpha polypeptide	Fga	61325	7,16	NP_034326
fumarate hydratase 1	Fh1-1	54336	9,12	NP_034339
fumarate hydratase 1	Fh1-2	54336	9,12	NP_034339
fumarate hydratase 1	Fh1-3	54336	9,12	NP_034339
gelsolin	Gsn-1	85941	5,83	NP_666232
gelsolin	Gsn-2	85941	5,83	NP_666232
glucose phosphate isomerase 1 complex	Gpi1-1	62767	7,75	NP_032181
glucose phosphate isomerase 1 complex	Gpi1-2	62767	7,75	NP_032181
glutamate oxaloacetate transaminase 1, soluble, cytosolic aspartate aminotransferase	Got1	46231	6,68	NP_034454
glutamate oxaloacetate transaminase 2, mitochondrial aspartate aminotransferase	Got2-1	47411	9,13	NP_034455
glutamate oxaloacetate transaminase 2, mitochondrial aspartate aminotransferase	Got2-2	47411	9,13	NP_034455
glutathione S-transferase omega 1	Gsto1-1	27480	6,92	NP_034492.1
glutathione S-transferase omega 1	Gsto1-2	27480	6,92	NP_034492.1
glutathione S-transferase, alpha 4	Gsta4	25559	6,77	NP_034487.1
glutathione S-transferase, mu1	Gstm1	25953	7,71	NP_034488
glutathione S-transferase, pi 1	Gstp1	23594	7,68	NP_038569
glyceraldehyde-3-phosphate dehydrogenase	Gapdh-1	35810	8,44	NP_001001303
glyceraldehyde-3-phosphate dehydrogenase	Gapdh-2	35810	8,44	NP_001001303
glycyl tRNA synthetase	Gars	81799	6,24	NP_851009.1
glyoxalase 1	Glo1	20826	5,24	NP_079650.2
guanine nucleotide binding protein, beta 2, related sequence 1	Gnb2l1	35055	7,6	NP_032169.1
guanosine diphosphat (GDP) dissociation inhibitor 3, GDI beta, RAB	Gdi3	50495	5,93	NP_032138
Heat shock protein family, member 7, (cardiovascular), HSP 25 kDa 2	Hspb7	18623	5,95	NP_038896.2
heat shock protein, A; heat shock protein cognate 74	Hspa9a-1	73482	5,91	NP_034611.1
heat shock protein, A; heat shock protein cognate 74	Hspa9a-2	73482	5,91	NP_034611.1
heat shock protein, alpha-crystallin-related, B6	Hspb6	17510	5,64	NP_001012401
heterogeneous nuclear ribonucleoprotein A B	Hnrpab	30812	7,68	NP_034578.1
heterogeneous nuclear ribonucleoprotein A1	Hnrpa1	34196	9,27	NP_034577.1
heterogeneous nuclear ribonucleoprotein A3, isoform b	Hnrpa3	39651	9,1	NP_666242
heterogeneous nuclear ribonucleoprotein K	Hnrpk	50976	5,39	NP_079555
heterogeneous nuclear ribonucleoprotein L	Hnrnpl	60123	6,65	NP_796275
hexokinase 2	Hk2	102535	5,77	NP_038848
histidine triad nucleotide binding protein 1; protein kinase C inhibitor 1	Hint1	13768	6,36	NP_032274.1
HSP 1, 60 kDa	Hspd1	60956	5,67	NP_034607
HSP 1, beta, 84 kDa, 86 kDa, HSP 1, 90 kDa	Hspcb-1	83229	4,97	NP_032328.2
HSP 1, beta, 84 kDa, 86 kDa, HSP 1, 90 kDa	Hspcb-2	83229	4,97	NP_032328.2
HSP 70 kDa protein 5 (glucose regulated protein), 78 kDa HSP	Hspa5-1	72423	5,01	NP_071705
HSP 70 kDa protein 5 (glucose regulated protein), 78 kDa HSP	Hspa5-2	72423	5,01	NP_071705
HSP 8, 70 kDa	Hspa8	70871	5,37	NP_112442
HSP1, 25 kDa, HSP1, 27 kDa	Hspb1-1	22887	6,44	NP_038588.1
HSP1, 25 kDa, HSP1, 27 kDa	Hspb1-2	22887	6,44	NP_038588.1
HSP1, 25 kDa, HSP1, 27 kDa	Hspb1-3	22887	6,44	NP_038588.1
hydroxyacyl-Coenzyme A dehydrogenase beta subunit	Hadhb	51386	9,43	NM_145558
hydroxyacyl-Coenzyme A dehydrogenase type II	Hadh2	27764	8,76	NP_058043.1
hydroxyacyl-Coenzyme A dehydrogenase 3-ketoacyl-Coenzyme A thiolase enoyl-Coenzyme hydratase	Hadha	82617	9,24	NP_849209.1
hypoxanthine guanine phosphoribosyl transferase	Hprt1	24554	6,51	NP_038584.1
isocitrate dehydrogenase 2 (NADP+), mitochondrial	Idh2	50902	8,88	NP_766599.1
isocitrate dehydrogenase 3, (NAD+) alpha	Idh3a-1	39638	6,27	NP_083849
isocitrate dehydrogenase 3, (NAD+) alpha	Idh3a-2	39638	6,27	NP_083849
isocitrate dehydrogenase 3, beta subunit	Idh3b-1	42168	8,76	NP_570954.1
isocitrate dehydrogenase 3, beta subunit	Idh3b-2	42168	8,76	NP_570954.1
isocitrate dehydrogenase 3, beta subunit	Idh3b-3	42168	8,76	NP_570954.1
isovaleryl coenzyme A dehydrogenase	Ivd	46296	8,53	NP_062800.1
L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	Hadhsc	33067	7,74	NP_032238.1
lactate dehydrogenase 1, A chain	Ldh1	36475	7,62	NP_034829.1
lactate dehydrogenase 2, B chain	Ldh2-1	36572	5,7	NP_032518
lactate dehydrogenase 2, B chain	Ldh2-2	36572	5,7	NP_032518
lactate dehydrogenase 2, B chain	Ldh2-3	36572	5,7	NP_032518
lamin B1	LmnB1	66884	5,11	NP_034851
laminin receptor 1	Lamr1	32914	4,8	NP_035159
leucine-rich PPR motif-containing protein; leucine rich protein LRP130	Lrpprc-1	147331	5,92	NP_082509.1
leucine-rich PPR motif-containing protein; leucine rich protein LRP130	Lrpprc-2	147331	5,92	NP_082509.1

Protein	Gen	Mw (Da)	pI	NCBI-Nummer
leukotriene A4 hydrolase, LTA4	Lta4h	69004	5,91	NP_032543
LIM and SH3 protein 1	Lasp1	29975	6,61	NP_034818.1
lysophospholipase 1	Lypla1	24671	6,14	NP_032892.1
malate dehydrogenase, mitochondrial	Mdh2	35596	8,82	CAA30274
malate dehydrogenase, soluble	Mdh1-1	36468	5,92	NP_032644
malate dehydrogenase, soluble	Mdh1-2	36468	5,92	NP_032644
malate dehydrogenase, soluble	Mdh1-3	36468	5,92	NP_032644
malate dehydrogenase, soluble	Mdh1-4	36468	5,92	NP_032644
mitochondrial acyl-CoA thioesterase 1 cytosolic acyl-CoA thioesterase 1	Acot2/Acot1-1	49609 46136	7,21 6,12	NP_598949 NP_036136
mitochondrial acyl-CoA thioesterase 1 cytosolic acyl-CoA thioesterase 1	Acot2/Acot1-2	49609 46136	7,21 6,12	NP_598949 NP_036136
muscle glycogen phosphorylase	Pygm-1	97224	6,65	NP_035354
muscle glycogen phosphorylase	Pygm-2	97224	6,65	NP_035354
muscle glycogen phosphorylase	Pygm-3	97224	6,65	NP_035354
muscle glycogen phosphorylase	Pygm-4	97224	6,65	NP_035354
muscle glycogen phosphorylase	Pygm-5	97224	6,65	NP_035354
muscle glycogen phosphorylase	Pygm-6	97224	6,65	NP_035354
muscle glycogen phosphorylase	Pygm-7	97224	6,65	NP_035354
myoglobin	Mb-1	17069	7,06	NP_038621
myoglobin	Mb-2	17069	7,06	NP_038621
myosin binding protein C	Mybpc3-1	140632	6,06	NP_032679
myosin binding protein C	Mybpc3-2	140632	6,06	NP_032679
myosin light chain, alkali, nonmuscle	Myl6	16961	4,46	NP_034990
myosin light, polypeptide 7, regulatory, A	Myl7	19345	4,8	NP_075017
myosin, light polypeptide 2, regulatory, cardiac, slow, phosphorylatable	Myl2-1	18870	4,71	NP_034991.1
myosin, light polypeptide 2, regulatory, cardiac, slow, phosphorylatable	Myl2-2	18870	4,71	NP_034991.1
myosin, light polypeptide 3	Myl3-1	22421	5,03	NP_034989
myosin, light polypeptide 3	Myl3-2	22421	5,03	NP_034989
myozenin-like 2, calsarcin-1	Myoz2-1	29761	8,53	NP_067478
myozenin-like 2, calsarcin-1	Myoz2-2	29761	8,53	NP_067478
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	Ndufa10-1	40578	7,63	NP_077159.1
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	Ndufa10-2	40578	7,63	NP_077159.1
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	Ndufa10-3	40578	7,63	NP_077159.1
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	Ndufa10-4	40578	7,63	NP_077159.1
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	Ndufa10-5	40578	7,63	NP_077159.1
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	Ndufa8	19992	8,76	NP_080979
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	Ndufa9	42509	9,75	NM_025358
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	Ndufb9	21970	7,67	NP_075661.1
NADH dehydrogenase (ubiquinone) Fe-S protein 1	Ndufs1	79776	5,51	CAI24120
NADH dehydrogenase (ubiquinone) FE-S protein 2, NADH coenzyme Q reductase	Ndufs2	52592	6,52	NP_694704.1
NADH dehydrogenase (ubiquinone) Fe-S protein 3	Ndufs3	30149	6,67	NP_080964
NADH dehydrogenase (ubiquinone) Fe-S protein 8	Ndufs8	24023	5,89	NP_659119.2
NADH dehydrogenase (ubiquinone) flavoprotein 1	Ndufv1	50834	8,51	NP_598427
NADH dehydrogenase (ubiquinone), Fe-S-protein 4	Ndufs4	18568	9,9	NP_035017
optic atrophy 1 homolog	Opa1	111270	7,18	NP_598513.1
ornithine aminotransferase	Oat	48324	6,19	NP_058674.1
oxoglutarate dehydrogenase (lipoamide)	Ogdh	116448	6,36	NP_035086
peptidylprolyl isomerase A, cyclophilin A	Ppia-1	17970	7,73	NP_032933
peptidylprolyl isomerase A, cyclophilin A	Ppia-2	17970	7,73	NP_032933
peroxiredoxin 1	Prdx1	22162	8,26	NP_035164.1
peroxiredoxin 2; thioredoxin peroxidase 1; Prx II-1; thioredoxin reductase	Prdx2	21834	5,19	NP_035693.2
peroxiredoxin 3, anti-oxidant protein 1	Prdx3	28127	7,15	NP_031478
peroxiredoxin 4, antioxidant enzyme AOE372, Prx IV	Prdx4	31052	6,67	NP_058044
peroxiredoxin 6, anti-oxidant protein 2, acidic calcium independent phospholipase A2,	Prdx6-1	24811	5,98	NP_031479.1
peroxiredoxin 6, anti-oxidant protein 2, acidic calcium independent phospholipase A2	Prdx6-2	24811	5,98	NP_031479.1
phosphofructokinase, muscle	Pfkm	85302	8,24	NP_067489
phosphoglucomutase 2	Pgm2	61479	6,3	NP_082408.2
phosphoglycerate kinase 1	Pgk1	44550	8,02	NP_032854
phosphoglycerate mutase 1	Pgam1	28918	6,19	NP_075907.1
phosphoglycerate mutase 2, muscle specific subunit	Pgam2-1	28809	8,7	NP_061358.1
phosphoglycerate mutase 2, muscle specific subunit	Pgam2-2	28809	8,7	NP_061358.1
phosphoglycerate mutase 2, muscle specific subunit	Pgam2-3	28809	8,7	NP_061358.1
phosphohistidine phosphatase 1	Phpt1	13996	5,27	AAH28657
phosphoribosylaminoimidazole carboxylase	Paics	47006	6,94	AAH52691
programmed cell death 6 interacting protein	Pdcd6ip	95950	6,15	NP_035182.1

Protein	Gen	Mw (Da)	pI	NCBI-Nummer
prohibitin	Phb	29820	5,57	NP_032857
prolyl 4-hydroxylase, beta polypeptide	P4hb	57058	4,77	NP_035162
proteasome (prosome, macropain) 26S subunit, ATPase 2	Psmc2-1	52833	5,97	NP_035318
proteasome (prosome, macropain) 26S subunit, ATPase 2	Psmc2-2	52833	5,97	NP_035318
proteasome (prosome, macropain) 26S subunit, ATPase 5	Psmc5	45626	7,11	NP_032976
proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	Psmd7	36539	6,29	NP_034947
proteasome (prosome, macropain) 28 subunit, alpha	Psme1	28672	5,73	NP_035319
proteasome (prosome, macropain) subunit, alpha type 1	Psma1	29546	6	NP_036095
proteasome (prosome, macropain) subunit, alpha type 2	Psma2	25926	6,91	AAH26768
proteasome (prosome, macropain) subunit, alpha type 3	Psma3	28490	5,4	NP_035314
proteasome (prosome, macropain) subunit, alpha type 4	Psma4	29452	7,59	NP_036096.1
proteasome (prosome, macropain) subunit, alpha type 6	Psma6	27372	6,35	NP_036098
proteasome (prosome, macropain) subunit, beta type 2	Psmb2	22906	6,52	NP_032970
proteasome (prosome, macropain) subunit, beta type 2	Psmb2	22852	6,43	NP_036100.2
proteasome (prosome, macropain) subunit, beta type 7	Psmb7	29891	8,14	NP_035317
proteasome (prosome, macropain) subunit, beta type, 4	Psmb4	29069	5,47	NP_032971.1
proteasome 26S non-ATPase subunit 11	Psmd11	47494	6,08	NP_848731
proteasome 26S non-ATPase subunit 13; 26S proteasome subunit p40.5	Psmd13	42782	5,46	NP_036005.1
proteasome beta 3 subunit	Psmb3	22949	6,15	NP_036101.1
protein disulfide isomerase associated 3	Pdia3	56678	5,88	NP_031978
protein kinase, cAMP dependent regulatory, type I, alpha	Prkar1a	43185	5,27	NP_068680
protein phosphatase 2a, catalytic subunit, beta isoform	Ppp1cb	35575	5,21	NP_059070
pyruvate dehydrogenase E1 alpha 1	Pdha1	43203	8,49	NP_032836
pyruvate dehydrogenase, beta	Pdhb-1	38937	6,41	NP_077183
pyruvate dehydrogenase, beta	Pdhb-2	38937	6,41	NP_077183
pyruvate kinase 3	Pkm2-1	57844	7,17	NP_035229
pyruvate kinase 3	Pkm2-2	57844	7,17	NP_035229
pyruvate kinase 3	Pkm2-3	57844	7,17	NP_035229
Radixin villin2 moesin	Rdx/Vil2/Msn-1	68485 69303 66440	5,84 5,83 5,94	NP_033067 NP_033536 NP_034963
Radixin villin2 moesin	Mdx/Vil2/Msn-2	68485 69303 66440	5,84 5,83 5,94	NP_033067 NP_033536 NP_034963
Radixin villin2 moesin	Mdx/Vil2/Msn-3	68485 69303 66440	5,84 5,83 5,94	NP_033067 NP_033536 NP_034963
Radixin villin2 moesin	Mdx/Vil2/Msn-4	68485 69303 66440	5,84 5,83 5,94	NP_033067 NP_033536 NP_034963
Radixin villin2 moesin	Mdx/Vil2/Msn-5	68485 69303 66440	5,84 5,83 5,94	NP_033067 NP_033536 NP_034963
Radixin villin2 moesin	Mdx Vil2 Msn-6	68485 69303 66440	5,84 5,83 5,94	NP_033067 NP_033536 NP_034963
RAN, member RAS oncogene family	Ran	24423	7,01	NP_033417
RIKEN cDNA 2700085E05	2700085E05Rik	33316	5,28	AAH61012
SAR1a gene homolog (S. cerevisiae)	Sar1a	22385	6,21	NP_033146.1
sarcalumenin	Srl-1	99183	4,39	NP_780556
sarcalumenin	Srl-2	99183	4,39	NP_780556
selenium binding protein 1 selenium binding protein 2	Selenbp1/2	52480 52628	5,87 5,78	NP_033176 NP_062287
septin2	Sept2	41499	6,1	NP_035021.1
serine (or cysteine) proteinase inhibitor, clade B, member 6	Serpinb6a	42598	5,53	NP_033280
serum albumin 1	Alb1-1	68677	5,75	NP_033784.1
serum albumin 1	Alb1-2	68677	5,75	NP_033784.1
similar to eukaryotic translation initiation factor 5A (eIF-5A)(eIF-4D), Ref binding factor	Eif5a	16832	5,07	P63242
similar to glyceraldehyde-3-phosphate dehydrogenase, phosphorylating	LOC14433	35810	8,44	NP_032110
similar to putative RNA-binding protein 3	LOC434599	16685	5,91	XP_486442.1
similar to putative RNA-helicase HLA-B-associated transcript 1A	Bat1a	49035	5,44	NP_062667
similar to ribosomal protein S12	LOC434843	14480	6,81	XP_486761.1
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	Slc25A13	74466	8,77	NP_056644
solute carrier family 25 (mitochondrial carrier, Aralar), member 12	Slc25A12	74569	8,43	NP_766024
stathmin 1; leukemia-associated gene p18; metablastin	Stmn1	17264	5,76	NP_062615.1
stress-induced phosphoprotein 1, HSP70 HSP90 organizing protein	Stip1	62582	6,4	NP_058017
succinate dehydrogenase, Fp subunit	Sdha-1	72585	7,06	NP_075770
succinate dehydrogenase, Fp subunit	Sdha-2	72585	7,06	NP_075770
succinate dehydrogenase, Fp subunit	Sdha-3	72585	7,06	NP_075770
succinate-CoA ligase, ADP-forming, beta subunit	Sucla2	50113	6,57	Q9Z2I9
succinate dehydrogenase Ip subunit	Sdhb	31813	8,96	NP_075863

Protein	Gen	Mw (Da)	pI	NCBI-Nummer
succinate-CoA ligase, GDP-forming, alpha subunit	Suclg1	34975	9,45	NP_063932
superoxide dismutase 1	Sod1	15933	6,02	NP_035564
superoxide dismutase 2	Sod2	24602	8,8	NP_038699
t-complex protein 1	Tcp1	60303	5,76	NP_038714.1
thioredoxin-like 2, PKC interacting cousin of thioredoxin	Txnl2	37778	5,42	Q9CQM9
thioredoxin-like, 32 kDa	Txnl1	32237	4,84	Q8CDN6
TNF receptor-associated protein 1 (Trap1)	Trap1	80208	6,25	NM_026508
transferrin	Trf	76673	6,94	NP_598738.1
transgelin 2	Tagln2	22395	8,4	NP_848713
transthyretin	Ttr	15766	5,77	NP_038725.1
triosephosphate isomerase	Tpi1-1	26712	6,9	NP_033441
triosephosphate isomerase	Tpi1-2	26712	6,9	NP_033441
tropomyosin 1, alpha	Tpm1-1	32689	4,71	NP_077745.2
tropomyosin 1, alpha	Tpm1-2	32689	4,71	NP_077745.2
tropomyosin 1, alpha	Tpm1-3	32689	4,71	NP_077745.2
troponin C, cardiac slow skeletal	Tnnc1-1	18420	4,04	NP_033419
troponin C, cardiac slow skeletal	Tnnc1-2	18420	4,04	NP_033419
troponin T2, cardiac	Tnnt2	34219	5,24	NP_035749
Tu translation elongation factor, mitochondrial	Tufm	49477	7,23	NP_766333
tubulin, alpha 1 tubulin, alpha 2 tubulin, alpha 4 tubulin alpha 6	Tuba1/Tuba2/Tuba4/ Tuba7	50104 50119 49892 49959	4,94 4,94 4,95 4,98	NP_035783.1 NP_035784.1 NP_033473.1 NP_033475
tubulin, alpha 6	Tuba6	49877	4,96	NP_033474
tubulin, beta, 2	Tubb2	49831	4,79	NP_666228
tumor protein, translationally-controlled 1, 21 kDa polypeptide	Tpt1	19449	4,76	NP_033455.1
tumor rejection antigen gp96, 1	Tra1	92475	4,74	NP_035761
tyrosine 3-monooxygenase tryptophan 5-monooxygenase activation protein, epsilon, 14-3-3	Ywhae	29188	4,63	NP_033562
tyrosine 3-monooxygenase tryptophan 5-monooxygenase activation protein, eta, 14-3-3 tyrosine 3-monooxygenase tryptophan 5-monooxygenase activation protein beta, 14-3-3	Ywhah/Ywhab	28211 28086	4,81 4,77	NP_035868 NP_061223
tyrosine 3-monooxygenase tryptophan 5-monooxygenase activation protein, gamma, 14-3-3	Ywhag	28284	4,8	NP_061359.2
tyrosine 3-monooxygenase tryptophan 5-monooxygenase activation protein, theta, 14-3-3	Ywhaq	27778	4,69	NP_035869
ubiquinol-cytochrome c reductase binding protein	Uqcrb	13561	9,1	AAI00602
ubiquinol-cytochrome c reductase, core protein 1	Uqcrc1-1	52768	5,75	Q9CZ13
ubiquinol-cytochrome c reductase, core protein 1	Uqcrc1-2	52768	5,75	Q9CZ13
ubiquinol-cytochrome c reductase, core protein 1	Uqcrc1-3	52768	5,75	Q9CZ13
ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Uqcrfs1-1	29367	8,92	NP_079986
ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Uqcrfs1-2	29367	8,92	NP_079986
ubiquitin-conjugating enzyme E2N	Ube2n	17127	6,13	NP_542127.1
vimentin	Vim	53687	5,06	NP_035831
vinculin, metavinculin	Vcl-1	116717	5,77	NP_033528
vinculin, metavinculin	Vcl-2	116717	5,77	NP_033528
voltage dependent anion channel 1	Vdac1-1	30737	8,62	NP_035824.1
voltage dependent anion channel 1	Vdac1-2	30737	8,62	NP_035824.1
voltage dependent anion channel 2	Vdac2-1	31712	7,44	NP_035825.1
voltage dependent anion channel 2	Vdac2-2	31712	7,44	NP_035825.1
voltage dependent anion channel 3	Vdac3	30752	8,96	NP_035826

Tab. 8.8: Identifizierte Proteine des Herz-Mastergels von *Mus Musculus*

Protein	Gen	Mw	pI	NCBI-Nummer
3-oxoacid CoA transferase 1	Oxct1	55953	8,73	NP_077150.1
6-phosphogluconolactonase	Pgls	27237,4	5,55	NP_079672.1
acetyl-CoA acetyltransferase 1 precursor	Acat1	44816	8,71	NP_659033
acetyl-CoA dehydrogenase, very long chain, mitochondrial precursor	Acadvl	70830	8,91	NP_059062.1
acetyl-Coenzyme A dehydrogenase, medium chain	Acadm	46451,6	8,6	NP_031408.1
acidic ribosomal phosphoprotein P0	Arbp-1	34195	5,91	NP_031501.1
acidic ribosomal phosphoprotein P0	Arbp-2	34195	5,91	NP_031501.1
aconitase 2	Aco2-1	85410	8,08	NP_542364.1
aconitase 2	Aco2-2	85410	8,08	NP_542364.1
actin-related protein 2	Act2	44732	6,3	NP_666355.1
acyl-CoA synthetase long-chain family member 1	Acsl1	77901,4	6,81	NP_032007.2
adenylate kinase 1, cytosolic	Ak1	23116	5,7	NP_067490
albumin 1; serum albumin variant	Alb1	68677,7	5,75	NP_033784.1
aldehyde dehydrogenase 2, mitochondrial	Aldh2-1	56537	7,53	NP_033786
aldehyde dehydrogenase 2, mitochondrial	Aldh2-2	56537	7,53	NP_033786
aldehyde dehydrogenase 4 family, member A1	Aldh4a1	61771,6	8,58	NP_780647.2
aldo-keto reductase family 1, member A4, aldehyde reductase	Akr1a4	35552	6,9	NP_067448.1
aldolase 1, A isoform	Aldoa-1	39355	8,3	NP_031464
aldolase 1, A isoform	Aldoa-2	39355	8,3	NP_031464
aldolase 1, A isoform	Aldoa-3	39355	8,3	NP_031464
alpha actin 1, skeletal muscle	Acta1-1	42051	5,23	NP_033736.1
alpha actin 1, skeletal muscle	Acta1-2	42051	5,23	NP_033736.1
alpha actinin 2	Actn2	103918	5,31	NP_150371.2
alpha hemoglobin, adult chain 1	Hba-a1	15075,8	7,97	NP_032244.1
alpha tropomyosin 1	Tpm1-1	32689	4,71	NP_077745.2
alpha tropomyosin 1	Tpm1-2	32689	4,71	NP_077745.2
alphaB-crystallin	Cryab	20068	6,76	NP_034094
annexin A1; lipocortin 1	Anxa1	38667	6,56	NP_034860.1
annexin A2, calpactin I heavy chain, annexin II, lipocortin II, chromobindin 8, calcimedin	Anxa2	38676	7,55	NP_031611
annexin A5; annexin V	Anxa5	39860	4,83	NP_033803
apolipoprotein A-1	ApoA1-1	30587	5,64	NP_033822
apolipoprotein A-1	ApoA1-2	30587	5,64	NP_033822
apolipoprotein B editing complex 2	Apobec2	25644	4,75	NP_033824.1
apolipoprotein E	Apoe	35830,3	5,56	NP_033826.1
ARP3 actin-related protein 3 homolog	Act3	47357	5,61	NP_076224.1
aspartyl-tRNA synthetase	Dars-1	57081	6,07	NP_663482.1
aspartyl-tRNA synthetase	Dars-2	57081	6,07	NP_663482.1
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Atp5h-1	18737	5,52	NP_082138.1
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Atp5h-2	18737	5,52	NP_082138.1
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1-1	59715,6	9,22	NP_031531.1
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1-2	59715,6	9,22	NP_031531.1
ATP-synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	Atp5f1	28930	9,11	NP_033855
ATP-synthase, H+ transporting, mitochondrial F1 complex, beta subunit	Atp5b	56265,5	5,19	NP_058054.2
ATP-synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide	Atp5c1	32831,2	9,06	NP_065640.1
basic transcription factor 3	Btf3	17688,2	6,85	NP_663430.1
beta enolase 3, muscle	Eno3-1	47024	6,73	NP_031959
beta enolase 3, muscle	Eno3-2	47024	6,73	NP_031959
beta enolase 3, muscle	Eno3-3	47024	6,73	NP_031959
beta hemoglobin, adult major chain	Hbb	15748	7,13	NP_032246
calpain, small subunit 1; calpain 4	Capns1	28444,9	5,41	NP_033925.1
calsequestrin 1	Casq1	45618,9	3,93	NP_033943.1
calsequestrin 2	Casq2	48324	4,12	NP_033944.1
CAP, adenylate cyclase-associated protein 1	Cap1	51542,5	7,16	NP_031624.1
CAP, adenylate cyclase-associated protein, 2	Cap2	52862	6,0	NP_080332.1
capping protein 1, actin filament, muscle Z-line, capping protein beta 1	Capzb	33344,6	5,28	AAH02053
capping protein, actin filament, muscle Z-line, alpha 2	Capza2	32947	5,57	NP_031630.1
carbonic anhydrase 3	Car3	29366	6,89	NP_031632
carboxyl terminal LIM domain protein 1	Ldb2-1	35695	6,38	NP_058557.1
carnitine acetyltransferase	Crat	70789,3	8,39	NP_031786.1
catalase 1	Cat	59696,7	8,1	NP_033934.1
chaperonin subunit 2 (beta) similar to tripartite motif protein 50A	Cct2/Trim72	57411 52783	5,97 6,01	NP_031662.1 XP_486011.1
chaperonin subunit 5 (epsilon)	Cct5	59586	5,72	NP_031663.1
chaperonin subunit 6a (zeta); chaperonin containing TCP-1	Cct6a	57967,7	6,63	NP_033968.1
citrate synthase	Cs	51736	8,72	NP_080720
cofilin 2, muscle	Cfl2-1	18697,8	7,66	NP_031714.1
complement component 3	C3	186364	6,44	NP_033908.1
COP9 signalosome subunit 4; COP9 complex S4	Cops4	46284	5,57	NP_036131.1
creatine kinase, mitochondrial 1 creatine kinase, mitochondrial 2	Ckmt1/2	46974 47443	8,39 8,64	NP_034027.1 NP_940807.1

Protein	Gen	Mw (Da)	pI	NCBI-Nummer
creatine kinase, mitochondrial 1 creatine kinase, mitochondrial 2	Ckmt1/2	46974 47443	8,39 8,64	NP_034027.1 NP_940807.1
creatine kinase, musle	Ckm-1	43017,8	6,58	NP_031736.1
creatine kinase, musle	Ckm-2	43017,8	6,58	NP_031736.1
creatine kinase, musle	Ckm-3	43017,8	6,58	NP_031736.1
creatine kinase, musle	Ckm-4	43017,8	6,58	NP_031736.1
creatine kinase, musle	Ckm-5	43017,8	6,58	NP_031736.1
cytochrome c oxidase, subunit IVa	Cox4i1	19518	9,25	NP_034071
cytochrome c oxidase, subunit Vb	Cox5b	13846	8,34	NP_034072
desmin	Des-1	53497	5,21	NP_034173
desmin	Des-2	53497	5,21	NP_034173
dihydrolipoamide dehydrogenase	Dld	54272	7,99	NP_031887
dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Dlst-1	48964	9,11	NP_084501.1
dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Dlst-2	48964	9,11	NP_084501.1
dihydropyrimidinase-like 2, collapsin response mediator protein 2	Dpysl2	62239	5,95	NP_034085.2
DJ-1 protein, RNA binding protein regulatory subunit	Park7	20021	6,32	NP_065594
EH-domain containing 2	Ehd2	57216,8	6,46	NP_694708.1
EH-domain containing 4	Ehd4	61480	6,33	NP_598599.2
electron transferring flavoprotein, alpha polypeptide	Etfa	34928	8,42	NP_663590.2
electron transferring flavoprotein, dehydrogenase	Etfdh	68007	7,34	NP_080070.1
enolase 1, alpha non-neuron	Eno1-1	47095	6,37	NP_075608.1
enolase 1, alpha non-neuron	Eno1-2	47095	6,37	NP_075608.1
enolase 1, alpha non-neuron	Eno1-3	47095	6,37	NP_075608.1
enoyl CoA hydratase 1, peroxisomal; dienoyl-CoA isomerase	Ech1	36095	7,6	NP_058052.1
enoyl coenzyme A hydratase 1, peroxisomal	Echs1	36095,2	7,6	NP_058052
Esterase D formylglutathione hydrolase	Esd	31319	6,7	NP_058599
eukaryotic translation elongation factor 1 alpha 2	Eef1a2	95252,9	6,41	NP_031933.1
eukaryotic translation elongation factor 1 gamma	Eef1g	50033	6,31	NP_080283.2
eukaryotic translation elongation factor 2	Eef2	95314	6,41	NP_031933
eukaryotic translation initiation factor 4A1 A2, long form	Eif4a1	46153	5,32	NP_659207
fatty acid binding protein 3, muscle and heart	Fabp3-1	14818	6,11	NP_034304
fatty acid binding protein 3, muscle and heart	Fabp3-2	14818	6,11	NP_034304
fatty acid binding protein 4, adipocyte protein aP2	Fabp4	14649	8,53	NP_077717
fumarate hydratase 1	Fh1-1	54336,1	9,12	NP_034339
Gelsolin	Gsn	85941	5,83	NP_666232
glucose phosphate isomerase 1	Gpi1	62767	7,75	NP_032181
glucose-regulated protein, endoplasmatic reticulum, 58 kDa, phosphorylated	Pdia3	56678	5,88	NP_031978
glutamate dehydrogenase	Glud1	61336	8,05	NP_032159
glutamate oxaloacetate transaminase 1, soluble, cytosolic aspartate aminotransferase	Got1	46231	6,68	NP_034454
glutamate oxaloacetate transaminase 2, mitochondrial aspartate aminotransferase	Got2	47411	9,13	NP_034455
glutathione S-transferase, mu1	Gstm1	25953	7,71	NP_034488
glyceraldehyde-3-phosphate dehydrogenase	Gapdh-1	35810	8,44	NP_001001303
glyceraldehyde-3-phosphate dehydrogenase	Gapdh-2	35810	8,44	NP_001001303
glycerol-3-phosphate dehydrogenase 1 (soluble)	Gpd1	37572	6,75	NP_034401
guanidinoacetate methyltransferase	Gamt	26319	5,43	NP_034385.1
guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	Gnb2l1	35055	7,6	NP_032169.1
guanine nucleotide-binding protein, beta-2 subunit	Gnb2	37307,1	5,6	NP_034442.1
guanosine diphosphat (GDP) dissociation inhibitor 3, GDI beta, RAB	Gdi3	50495	5,93	NP_032138
heat shock 70 kDa protein 5 (glucose regulated protein), 78 kDa	Hspa5	72423	5,01	NP_071705
heat shock protein 1 (chaperonin), heat shock protein 60 kDa	Hspd1-1	60956	5,67	NP_034607
heat shock protein 1 (chaperonin), heat shock protein 60 kDa	Hspd1-2	60956	5,67	NP_034607
heat shock protein 1, beta, 84 kDa, heat shock 90 kDa protein 1, beta	Hspcb-1	83229,1	4,97	NP_032328.2
heat shock protein 1, beta, 84 kDa, heat shock 90 kDa protein 1, beta	Hspcb-2	83229,1	4,97	NP_032328.2
heat shock protein 8; heat shock protein cognate 70	Hspa8	70827,2	5,37	NP_112442.2
Heat shock protein family, member 7, (cardiovascular), HSP 25 kDa 2	Hspb7	18623	5,95	NP_038896.2
heat shock protein, alpha-crystallin-related, B6	Hspb6	17510	5,64	NP_001012401
heterogeneous nuclear ribonucleoprotein A1	Hnrpa1	34196	9,27	NP_034577.1
heterogeneous nuclear ribonucleoprotein A2 B1 isoform 1	Hnrpa2b1	35992	8,67	NP_058086.1
heterogeneous nuclear riboprotein H1	Hnrnph1	49168,4	5,89	NP_067485.1
histidine triad nucleotide binding protein 1; protein kinase C inhibitor 1	Hint1	13768,1	6,36	NP_032274.1
HLA-B-associated transcript 1A; nuclear RNA helicase Bat1 DEAD (Asp-Glu-Asp) box polypeptide 39; UAP56-related helicase, 49 kDa	Bat1a/Ddx39	49003 49036	5,44 5,46	NP_062667.1 NP_932099.2
HLA-B-associated transcript 1A; nuclear RNA helicase Bat1 DEAD (Asp-Glu-Asp) box polypeptide 39; UAP56-related helicase, 49 kDa	Bat1a/Ddx39	49003 49036	5,44 5,46	NP_062667.1 NP_932099.2
HSP1, 25 kDa, HSP1, 27 kDa	Hspb1-1	22887	6,44	NP_038588.1
HSP1, 25 kDa, HSP1, 27 kDa	Hspb1-2	22887	6,44	NP_038588.1
HSP1, 25 kDa, HSP1, 27 kDa	Hspb1-3	22887	6,44	NP_038588.1
hydroxyacyl-Coenzyme A dehydrogenase beta subunit RIKEN cDNA 4930479F15	Hadhb	51382	9,42	NM_145558
hydroxyacyl-Coenzyme A dehydrogenase 3-ketoacyl-Coenzyme A thiolase	Hadha	82617,5	9,24	NP_849209.1
inner membrane protein, mitochondrial	Immt	25573,2	6	NP_083949.1
isocitrate dehydrogenase 2 (NADP+), mitochondrial	Idh2	50902	8,88	NP_766599.1

Protein	Gen	Mw	pI	NCBI-Nummer
isocitrate dehydrogenase 3 (NAD+) alpha	Idh3a-1	39613,1	6,27	NP_083849.1
isocitrate dehydrogenase 3 (NAD+) alpha	Idh3a-2	42785	9,17	NP_032349
lactate dehydrogenase 1, A chain	Ldh1	36475,2	7,62	NP_034829.1
lactate dehydrogenase 2, B chain	Ldh2	36549	5,7	NP_032518.1
lamin A isoform C2, lamin A C	LmnA-1	52652	6,22	NP_062263
lamin A isoform C2, lamin A C	LmnA-2	52652	6,22	NP_062263
lamin A isoform C2, lamin A C	LmnA-3	52652	6,22	NP_062263
LIM domain binding 3, Z-band alternatively spliced PDZ-motif protein, cypher 1, cypher 2	Ldb3-1	77134	8,47	O75112
LIM domain binding 3, Z-band alternatively spliced PDZ-motif protein, cypher 1, cypher 2	Ldb3-2	77134	8,47	O75112
LIM domain binding 3, Z-band alternatively spliced PDZ-motif protein, cypher 1, cypher 2	Ldb3-3	77134	8,47	O75112
malate dehydrogenase 1, NAD (soluble)	Mdh1-1	36445,1	5,92	NP_032644.2
malate dehydrogenase 1, NAD (soluble)	Mdh1-2	36445,1	5,92	NP_032644.2
malate dehydrogenase, mitochondrial	Mdh2-1	35596	8,82	CAA30274
malate dehydrogenase, mitochondrial	Mdh2-2	35596	8,82	CAA30274
muscle glycogen phosphorylase	Pygm-1	97225	6,65	NP_035354.1
muscle glycogen phosphorylase	Pygm-2	97225	6,65	NP_035354.1
muscle glycogen phosphorylase	Pygm-3	97225	6,65	NP_035354.1
muscle glycogen phosphorylase	Pygm-4	97225	6,65	NP_035354.1
myoglobin	Mb-1	17069	7,06	NP_038621
myoglobin	Mb-2	17069	7,06	NP_038621
myomesin 1, skelemin	Myom1-1	185331	5,83	NP_034997.1
myomesin 1, skelemin	Myom1-2	185331	5,83	NP_034997.1
myomesin 2	Myom2	164519	5,51	NP_032690.1
myosin heavy polypeptide 7, cardiac muscle, beta, myosin heavy chain, fetal	Myh7	222878	5,59	NP_542766.1
myosin light chain, phosphorylatable, fast skeletal muscle, myosin light chain 2	Mylpf-1	18955	4,82	NP_058034.1
myosin light chain, phosphorylatable, fast skeletal muscle, myosin light chain 2	Mylpf-2	18955	4,82	NP_058034.1
myosin light chain, phosphorylatable, fast skeletal muscle, myosin light chain 2	Mylpf-3	18955	4,82	NP_058034.1
myosin light chain, phosphorylatable, fast skeletal muscle, myosin light chain 2	Mylpf-4	18955	4,82	NP_058034.1
myosin light polypeptide 3, myosin light chain, alkali, cardiac ventricles, skeletal, slow	Myl3	22407,3	5,03	NP_034989.1
myosin, light polypeptide 1, alkali, fast skeletal muscle	Myl1	20581	5,0	NP_067260.1
myosin, light polypeptide 1; myosin light chain, alkali, fast skeletal muscle; myosin	Myl1	20581,4	4,98	NP_067260.1
myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	Myl6	16961	4,46	NP_034990
myozenin 1, calsarcin-2, calcineurin-2, skeletal muscle-specific protein	Myoz1-1	31457	8,57	NP_067483.1
myozenin 1, calsarcin-2, calcineurin-2, skeletal muscle-specific protein	Myoz1-2	31457	8,57	NP_067483.1
myozenin 1, calsarcin-2, calcineurin-2, skeletal muscle-specific protein	Myoz1-3	31457	8,57	NP_067483.1
myozenin 1, calsarcin-2, calcineurin-2, skeletal muscle-specific protein	Myoz1-4	31457	8,57	NP_067483.1
myozenin 2; calsarcin-1; myozenin-like 2	Myoz2	29743	8,53	NP_067478.1
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	Ndufa8	19992	8,76	NP_080979
NADH dehydrogenase (ubiquinone) Fe-S protein 1	Ndufs1	79776	5,51	CAI24120
NADH dehydrogenase (ubiquinone) FE-S protein 2, NADH coenzyme Q reductase	Ndufs2	52592	6,52	NP_694704.1
NADH dehydrogenase (ubiquinone) Fe-S protein 3	Ndufs3	30149	6,67	NP_080964
NADH dehydrogenase (ubiquinone) flavoprotein 1, 24 kDa	Ndufv1	50834	8,51	NP_598427
NADH dhg (ubiquinone) 1 alpha subcomplex 10	Ndufa10	40578	7,63	NP_077159.1
nucleoside-diphosphate kinase 1; A nucleoside-diphosphate kinase 2; B	Nme1 2/1	17196 17352	6,84 6,97	NP_032730.1 NP_032731
nucleoside-diphosphate kinase 1; A nucleoside-diphosphate kinase 2; B	Nme1 2/2	17196 17352	6,84 6,97	NP_032730.1 NP_032731
oxoglutarate dehydrogenase (lipoamide)	Ogdh	116043	6,51	NP_035086.1
parvalbumin	Pva-1	11937	5,02	NP_038673
peptidylprolyl isomerase A, cyclophilin A	Ppia-1	17970	7,73	NP_032933
peptidylprolyl isomerase A, cyclophilin A	Ppia-2	17970	7,73	NP_032933
peroxiredoxin 3, anti-oxidant protein 1, mitochondrial Trx dependent peroxide reductase	Prdx3	28127	7,15	NP_031478
peroxiredoxin 6; acidic calcium-independent phospholipase A2; peroxiredoxin 5; 1-Cys Prx	Prdx6-1	24811	5,98	NP_031479.1
peroxiredoxin 6; acidic calcium-independent phospholipase A2; peroxiredoxin 5; 1-Cys Prx	Prdx6-2	24811	5,98	NP_031479.1
phosphofructokinase, muscle, -1 A isozyme	Pfkm	85302	8,24	NP_067489
phosphoglucomutase 2	Pgm2-1	61517	6,3	NP_082408
phosphoglucomutase 2	Pgm2-2	61517	6,3	NP_082408
phosphoglucomutase 2	Pgm2-3	61517	6,3	NP_082408
phosphoglycerate kinase 1 similar to phosphoglycerate kinase 1	Pgk1/ LOC432633-1	44508 44550	7,53 8,02	NP_032854.1 XP_484116.1
phosphoglycerate kinase 1/ similar to phosphoglycerate kinase 1	Pgk1/ LOC432633-2	44508 44550	7,53 8,02	NP_032854.1 XP_484116.1
phosphoglycerate mutase 1	Pgam1	28918,9	6,19	NP_075907.1
phosphoglycerate mutase 2, muscle specific subunit	Pgam2-1	28809	8,7	NP_061358.1
phosphoglycerate mutase 2, muscle specific subunit	Pgam2-2	28809	8,7	NP_061358.1
phosphoglycerate mutase 2, muscle specific subunit	Pgam2-3	28809	8,7	NP_061358.1
phosphogucomutase 2	Pgm2-1	61479	6,3	NP_082408.2
phosphogucomutase 2	Pgm2-2	61479	6,3	NP_082408.2
phosphogucomutase 2	Pgm2-3	61479	6,3	NP_082408.2
programmed cell death 8; programmed cell death 8 (apoptosis inducing factor)	Pdcd8	66723,8	9,23	NP_036149.1
prohibitin	Phb	29802	5,57	NP_032857.1
prolyl 4-hydroxylase, beta polypeptide	P4hb	57058	4,77	NP_035162

Protein	Gen	Mw	pI	NCBI-Nummer
protease (prosome, macropain) 26S subunit, ATPase 5	Psmc5	45597,1	7,11	NP_032976.1
protease, serine, 15	Prss15	105776	6,15	XP_128721.3
proteasome (prosome, macropain) 26S subunit, ATPase 2	Psmc2	52833,2	5,97	NP_035318.1
proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	Psmd7	36517,2	6,29	NP_034947.1
proteasome (prosome, macropain) 28 subunit, alpha	Psme1	28672	5,73	NP_035319
proteasome (prosome, macropain) subunit, alpha type 1	Psma1	29528	6	NP_036095.1
proteasome (prosome, macropain) subunit, alpha type 2	Psma2	25909,3	8,39	NP_032970.1
proteasome (prosome, macropain) subunit, alpha type 6	Psma6-1	27355	6,34	NP_036098.1
proteasome (prosome, macropain) subunit, alpha type 6	Psma6-2	27355	6,34	NP_036098.1
proteasome (prosome, macropain) subunit, beta type 2	Psmb2	22851,7	6,43	NP_036100.2
proteasome (prosome, macropain) subunit, beta type 7	Psmb7	29872	8,14	NP_035317.1
proteasome (prosome, macropain) subunit, beta type, 4	Psmb4	29069,3	5,47	NP_032971.1
proteasome 26S ATPase subunit 6	Psmc6	44172	7,09	NP_080235.2
proteasome 26S non-ATPase subunit 11	Psmd11	47494	6,08	NP_848731
proteasome 26S non-ATPase subunit 13; 26S proteasome subunit p40.5	Psmd13	42782,1	5,46	NP_036005.1
proteasome beta 3 subunit	Psmb3	22949,4	6,15	NP_036101.1
pyruvate carboxylase, pyruvate decarboxylase	Pcx	129684	6,25	NP_032823.1
pyruvate dehydrogenase (lipoamide), beta	Pdhb	38937	6,41	NP_077183
pyruvate kinase 3, muscle	Pkm2-1	57844	7,17	NP_035229
pyruvate kinase 3, muscle	Pkm2-2	57844	7,17	NP_035229
pyruvate kinase 3, muscle	Pkm2-3	57844	7,17	NP_035229
pyruvate kinase 3, muscle	Pkm2-4	57844	7,17	NP_035229
Quininoid dihydropteridine reductase proteasome (prosome, macropain) subunit, alpha type 4	Qdpr/Psma4	25554 29452	7,67 7,59	NP_077198.1 NP_036096.1
Radixin villin2 moesin	Rdx/Vil2/Msn-1	68485 69303 66440	5,84 5,83 5,94	NP_033067 NP_033536 NP_034963
Radixin villin2 moesin	Rdx/Vil2/Msn-2	68485 69303 66440	5,84 5,83 5,94	NP_033067 NP_033536 NP_034963
RAN, member RAS oncogene family	Ran	24407,6	7,01	NP_033417.1
Rho GDP dissociation inhibitor (GDI) alpha	Arhgdia	23393	5,12	NP_598557.3
RIKEN cDNA 2700060E02	2700060E02Rik	28134,8	6,4	BC096571
RNA binding motif protein 3	Rbm3	16750,8	7,98	NP_058089.2
sarcalumenin	Srl-1	99123	4,39	NP-780556.2
sarcalumenin	Srl-2	99123	4,39	NP-780556.2
septin 2; neural precursor cell expressed, developmentally down-regulated gene 5	Sept2	41499,3	6,1	NP_035021.1
serine (or cysteine) proteinase inhibitor, clade B, member 6a	Serpin6a	42571,2	5,53	NP_033280.1
SET and MYND domain containing 1	Smyd1	54436	6,41	NP_033892
similar to AMP deaminase 1 (Myodeadenylate deaminase) isoform M	Ampd1	83392	6,31	XP_131103.2
similar to eukaryotic translation initiation factor 5A (eIF-5A)(eIF-4D), Ref binding factor	Eif5a	16832	5,07	P63242
similar to GTP-specific succinyl-CoA synthetase beta subunit	LOC434885	46904,7	6,3	XP_486811.1
similar to Kelch repeat and BTB domain containing protein 10	Kbtbd10	68146,8	5,05	XP_130293.2
solute carrier family 25 (mitochondrial carrier, Aralar), member 12	Slc25A12	74522,7	8,43	NP_766024.1
sorting and assembly machinery component 50 homolog	Samm50	51863	6,34	NP_848729
stress-induced phosphoprotein 1, IEF SSP 3521, HSP70 HSP90 organizing protein	Stip1	62582	6,4	NP_058017.1
succinate dehydrogenase Fp subunit	Sdha	72585	7,06	NP_075770
succinate dehydrogenase Ip subunit	Sdhb	31813	8,96	NP_075863
superoxide dismutase 1, soluble, Cu(2+)-Zn2+ superoxide dismutase	Sod1	15933	6,02	NP_035564.1
t-complex protein 1	Tcp1	67531,5	6,63	XP_487508.1
thioredoxin-like 2, PKC interacting cousin of thioredoxin	Txnl2	37754	5,42	NP_075629.2
transferrin	Trf-1	76673,7	6,94	NP_598738.1
transferrin	Trf-2	76673,7	6,94	NP_598738.1
transketolase	Tkt	67587,6	7,23	NP_033414.1
transthyretin	Ttr	15766	5,77	NP_038725.1
triose phosphate isomerase	Tpi1-1	26696	6,9	NP_033441.1
triose phosphate isomerase	Tpi1-2	26696	6,9	NP_033441.1
triose phosphate isomerase	Tpi1-3	26696	6,9	NP_033441.1
troponin C, fast skeletal	Tnnc2-1	18110	4,07	NP_033420
troponin C, fast skeletal	Tnnc2-2	18110	4,07	NP_033420
troponin I, skeletal fast 2	Tnni2	21357	8,65	NP_033431.1
troponin T1, skeletal, slow; skeletal muscle slow-twitch TnT	Tnnt1-1	31196,1	5,85	NP_035748.1
troponin T1, skeletal, slow; skeletal muscle slow-twitch TnT	Tnnt1-2	31196,1	5,85	NP_035748.1
troponin T3, skeletal fast	Tnnt3-1	29358	9,01	NP_035750.1
troponin T3, skeletal fast	Tnnt3-2	29358	9,01	NP_035750.1
troponin T3, skeletal fast	Tnnt3-3	29358	9,01	NP_035750.1
troponin T3, skeletal fast	Tnnt3-4	29358	9,01	NP_035750.1
troponin T3, skeletal fast	Tnnt3-5	29358	9,01	NP_035750.1
troponin T3, skeletal fast	Tnnt3-6	29358	9,01	NP_035750.1
tryptophanyl-tRNA synthetase	Wars	54291,1	6,44	NP_035840.2
Tu translation elongation factor, mitochondrial	Tufm	49477	7,23	NP_766333.1
Tubulin beta-2	Tubb2	49831	4,79	NP_666228

Protein	Gen	Mw	pI	NCBI-Nummer
tubulin, alpha 1 tubulin, alpha 2 tubulin, alpha 7	Tuba1/2/7	50104 50119 49928	4,94 4,94 4,97	NP_035783.1 NP_035784.1 NP_033475.1
tubulin, alpha 1 tubulin, alpha 2 ubulin, alpha 7	Tuba1/2/7	50104 50119 49928	4,94 4,94 4,97	NP_035783.1 NP_035784.1 NP_033475.1
tubulin, alpha 1 ubulin, alpha 2 ubulin, alpha 7	Tuba1/2/7	50104 50119 49928	4,94 4,94 4,97	NP_035783.1 NP_035784.1 NP_033475.1
tumor protein, translationally-controlled 1; 21 kDa polypeptide	Tpt1	19449,6	4,76	NP_033455.1
tyrosine 3-monooxygenase tryptophan 5-monooxygenase activation protein, theta, 14-3-3	Ywhaq	27778	4,69	NP_035869
tyrosine 3-monooxygenase tryptophan 5-monooxygenase activation protein, zeta, 14-3-3	Ywhaz	27754	4,73	NP_035870.1
tyrosine 3-monooxygenase tryptophan 5-monooxygenase activationprotein, epsilon 14-3-3	Ywhae	29188	4,63	NP_033562
tyrosine 3-monooxygenase tryptophan 5-monooxygenase activationprotein, gamma, 14-3-3	Ywhag	28285	4,8	NP_061359.2
ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Uqcrfs1	29367	8,92	NP_079986
ubiquinol-cytochrome c-reductase core protein 1	Uqcrc1	52768	5,75	Q9CZ13
UDP-glucose pyrophosphorylase 2	Ugp2-1	56979	7,18	NP_647458
UDP-glucose pyrophosphorylase 2	Ugp2-2	56979	7,18	NP_647458
valosin containing protein	Vcp	89363	5,14	NP_033529
vimentin	Vim	53687	5,06	NP_035831
vinculin, metavinculin	Vcl-1	116644	5,77	NP_033528.3
vinculin, metavinculin	Vcl-2	116644	5,77	NP_033528.3
voltage dependent anion channel 1	Vdac1-1	30737	8,62	NP_035824.1
voltage dependent anion channel 1	Vdac1-2	30737	8,62	NP_035824.1
voltage dependent anion channel 2	Vdac2	31712,6	7,44	NP_035825.1
voltage dependent anion channel 3	Vdac3	30733	8,96	NP_035826.1

Tab. 8.9: Identifizierte Proteine des Quadriceps-Mastergels von *Mus Musculus*