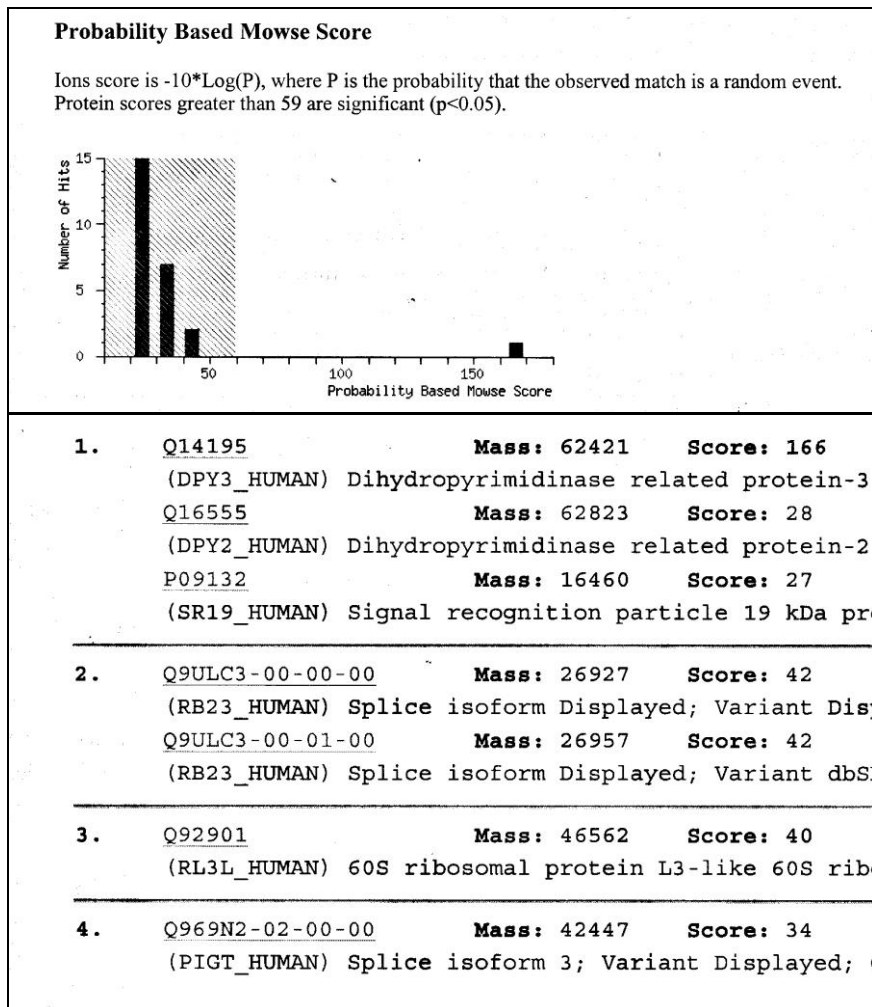
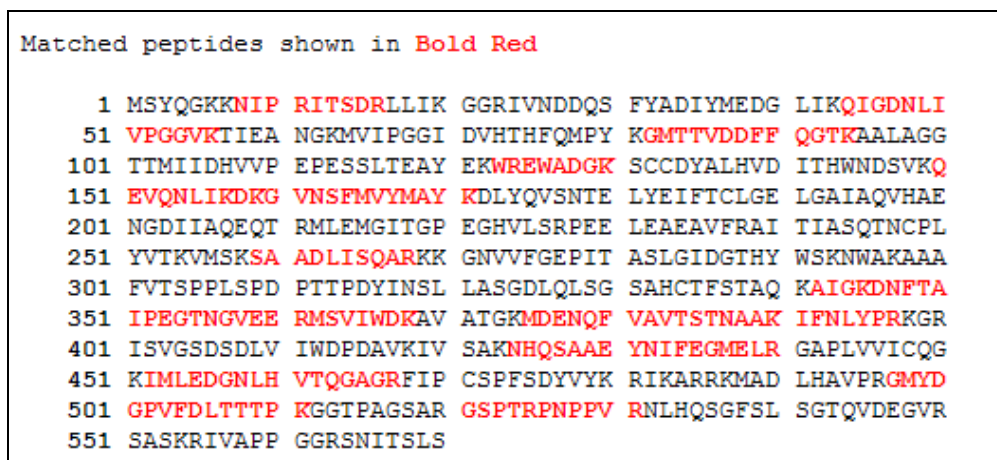


Supplementary figure 3. Protein identification by MALDI-TOF-MS

a. Mascot search results



b. The sequence coverage of identified DRP3 protein



c. Peptides recognized by Peptide Fingerprinting and their position within protein sequence

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence
362 - 368	878.4500	877.4427	877.4368	7	0	R.MSVIWDK.A
391 - 397	922.5200	921.5127	921.5072	6	0	K.IFNLYPR.K
150 - 157	971.5600	970.5527	970.5447	8	0	K.QEVQNLIK.D
259 - 268	1031.5700	1030.5627	1030.5407	21	0	K.SAADLISQAR.K
123 - 130	1047.5300	1046.5227	1046.4934	28	1	K.WREWADGK.S
8 - 16	1071.5600	1070.5527	1070.5832	-29	1	K.NIPRITSDR.L
521 - 531	1177.6200	1176.6127	1176.6364	-20	0	R.GSPTRENPPVR.N
44 - 56	1309.7500	1308.7427	1308.7402	2	0	K.QIGDNLIVPGGVK.T
82 - 94	1446.6900	1445.6827	1445.6497	23	0	K.GMTTVDDFFQGTK.A
82 - 94	1462.6900	1461.6827	1461.6446	26	0	K.GMTTVDDFFQGTK.A Oxidation (M)
497 - 511	1657.8100	1656.8027	1656.7706	19	0	R.GMYDGPVFDLTTTPK.G Oxidation (M)
158 - 171	1668.8500	1667.8427	1667.7687	44	1	K.DKGVNSFMVYMAYK.D Oxidation (M)
452 - 467	1710.8800	1709.8727	1709.8519	12	0	K.IMLEDGNLHVTTQAGR.F
375 - 390	1725.8600	1724.8527	1724.8039	28	0	K.MDENQFVAVTSTNAAK.I
452 - 467	1726.8600	1725.8527	1725.8468	3	0	K.IMLEDGNLHVTTQAGR.F Oxidation (M)
375 - 390	1741.7900	1740.7827	1740.7989	-9	0	K.MDENQFVAVTSTNAAK.I Oxidation (M)
346 - 361	1748.8400	1747.8327	1747.8013	18	0	K.DNFTAIPEGTNGVEER.M
424 - 440	2008.9400	2007.9327	2007.9108	11	0	K.NHQSAAEYNIFEGMELR.G
424 - 440	2024.9400	2023.9327	2023.9057	13	0	K.NHQSAAEYNIFEGMELR.G Oxidation (M)
342 - 361	2118.0700	2117.0627	2117.0389	11	1	K.AIGKDNFTAIPEGTNGVEER.M

d. Sequence homology between DRP3 and DRP1 demonstrated by BLAST analysis

86.0%	
Graphical alignment	
In original sequence: 1 - 569 (total: 570)	
Raw alignment	
Query	: MSYQGKKNIPRITSDRLLIKGGRIVNDQSFYADIYMEDGLIKQIGDNLIVPGGV 1-55
	: MSYQGKK+IP ITS DRLLIKGGRI+NDDQS YAD+Y+EDGLIKQIG+NLIVPGGV
Q14194	: MSYQGKKSIPHITSDRLLIKGGRIINDDQSLYADVLEDGLIKQIGENLIVPGGV 1-55
Query	: KTIENGKMPVPGGIDVHTHFQMPYKGMTTVDDFFQGTKAALAGGTTMIIDHVVP 56-110
	: KTIENG+MVPVPGGIDV+T+ Q P +GMT DDFQGT+AAL GGTTMIIDHVVP
Q14194	: KTIENGKMPVPGGIDVNTYLQKPSQGMTAADDFFQGTAAALVGGTTMIIDHVVP 56-110
Query	: EPESLLEAYEKWREWADGKSCCDYALHVDIITHWNDSVKQEVQNLIKDKGVNSFM 111-165
	: EP SSL ++EKW E AD KSCCDY+LHVDIT W D V++E++ L++DKGVNSF
Q14194	: EPGSSLLTSFEKWHEAADTKSCCDYSLHVDIITSWYDGVREELEVLVQDKGVNSFQ 111-165
Query	: VYMAYKDLVQVSNTELYEIFTCLGELGAIQVHAENGDIIAQEQTRMLEMGITGP 166-220
	: VYMAYKD+YQ+S+++LYE FT L LGA+ VHAENG+IAQEQ R+LEMGITGP
Q14194	: VYMAYKDVYQMSDSQLYEAFTFLKGLGAVILVHAENGDIIAQEQKRILEMGITGP 166-220
Query	: EGHVLSRPEELEAEAVFRAITIASQTNCPYVTKVMSKSAADLISQARKKGNVVF 221-275
	: EGH LSRPEELEAEAVFRAITIA + NCP+Y+TKVMSKSAAD+I+ ARKKG +VF
Q14194	: EGHVLSRPEELEAEAVFRAITIAGRINCPVYITKVMKSAADIILARKKGPLVF 221-275
Query	: GEPITASLGIDGTHYWSKNWAKAAAFVTSPLSPDPTTDPYINSLLAGDQLQSG 276-330
	: GEPI ASLG DGTHYWSKNWAKAAAFVTSPLSPDPTTDPY+ SLLA GDLQ++G
Q14194	: GEPIAASLGTGTHYWSKNWAKAAAFVTSPLSPDPTTDPYLTSLLAGDQLQVTVG 276-330
Query	: SAHCTFSTAQKAIGKDNFTAIPEGTNGVEERMSVIWDKAVATGKMDENQFVAVTS 331-385
	: S HC +STAQKA+GKDNFT IPEG NG+EERM+V+WDKAVATGKMDENQFVAVTS
Q14194	: SGHCPYSTAQKAVGKDNFTLIEGTVNGIEERMVVDKAVATGKMDENQFVAVTS 331-385
Query	: TNAAKIFNLYPRKGRISVGSDDLVIWDPDAVKIVSAKNHQSAAEYNI FEGMELR 386-440
	: TNAAKIFNLYPRKGRIVGSDD+D+VIWDPD +K ++AK+H+SA EYNI FEGME
Q14194	: TNAAKIFNLYPRKGRIVGSDDADVVIWDPDKLKITAKSHKSAVEYNI FEGMECH 386-440
Query	: GAPLVVICQGGKIMLEDGNLHVTTQAGRFIPCSFSDYVYKRIKARRKQADLHVP 441-495
	: G+PLVVI QGKI+ EDGN++V +G GRFIP F +++Y+R+K R K+ L V
Q14194	: GSPLVVISQGGKIVFEDGNINVNKGMGRFIPRKAFFPEHLYQVVKIRNKVFGVQVGS 441-495
Query	: RGMVDGPFVFDLTTTPKGGT PAGESARGSPTRPN-PPVRNLHQSGFSLSGTQVDE-G 496-548
	: RGMVDGPF+++ TPK TPA SA+ SP++ PP+RNLHQ S FSLSG Q+D+
Q14194	: RGMVDGPFVYEPATPKYAT PAPSAKSSPSKHQPPPIRNLHQSNFSLSGAQIDDNN 496-550
Query	: VRSASKRIVAPPGRSNITSL 549-569
	: R RIVAPPGRSNITSL
Q14194	: PRRIGHRIVAPPGRSNITSL 551-571

e. Sequence homology between DRP3 and DRP2

90.0%	
Graphical alignment	
In original sequence: 1 - 569 (total: 570)	
	
Raw alignment	
Query	: MSYQGKKNIPRITSDRLLIKGGRIVNDQSFYADIYMEDGLIKQIGDNLIVPGGV 1-55
	: MSYQGKKNIPRITSDRLLIKGG+IVNDQSFYADIYMEDGLIKQIG+NLIVPGGV
Q16555	: MSYQGKKNIPRITSDRLLIKGGKIVNDQSFYADIYMEDGLIKQIGENLIVPGGV 1-55
Query	: KTIEANGKMVIPGGIDVHTHFQMPYKGMTTVDDFFQGTKAALAGGTTMIIDHVVP 56-110
	: KTIEA+ +MVIPGGIDVHT FQMP +GMT+ DDDFFQGTKAALAGGTTMIIDHVVP
Q16555	: KTIEAHSRMVIPGGIDVHTRFQMPDQGMTSADDDFFQGTKAALAGGTTMIIDHVVP 56-110
Query	: EPESSLTEAYEKWREWADGKSCCDYALHVDITHWNDSVKQEVQNLKDKGVNSFM 111-165
	: EP +SL A+++WREWAD KSCCDY+LHVDI+ W+ +++E++ L+KD GVNSF+
Q16555	: EPGTSLLAAPFDQWREWADSKSCCDYSLHVDISEWHKGIQEEMEALVKDHGVNSFL 111-165
Query	: VYMAKDLYQVSNTELYEIFTCLGELGAIQVHAENGDIIEAQEQTRMLEMGITGP 166-220
	: VYMA+KD +Q+++ ++YE+ + + ++GAIQVHAENGDIIEA+EQ R+L++GITGP
Q16555	: VYMAFKDRFQLTDCQIYEVLSVIRDIGAIQVHAENGDIIEEQQRILDGLGITGP 166-220
Query	: EGHVLSRPEELEAEAVFRAITIASQTNCPYLVTKVMSKSAADLISQARKKGNVVF 221-275
	: EGHVLSRPEE+EAEAV RAITIA+QTNCPY+TKVMSKSA++I+QARKKG VV+
Q16555	: EGHVLSRPEEVEAEAVNRAITIANQTNCPYITKVMSKSAEVIAQARKKGTVVY 221-275
Query	: GEPITASLGIDGTHYWSKNWAKAAAFVTSPPSPDPTTDPDYINSLLASGDLQLSG 276-330
	: GEPITASLG DG+HYWSKNWAKAAAFVTSPPSPDPTTDPD++NSLL+ GDLQ++G
Q16555	: GEPITASLGDGSHYWSKNWAKAAAFVTSPPSPDPTTDFLNSLLSCGDLQVTG 276-330
Query	: SAHCTFSTAQKAIGKDNFTAIPEGTINGVEERMSVIWDKAVATGKMDENQFVAVTS 331-385
	: SAHCTF+TAQKA+GKDNFT IPEGTING EERMSVIWDKAV TGKMDENQFVAVTS
Q16555	: SAHCTFNSTAQKAVGKDNFTLIPPEGTINGTEERMSVIWDKAVVTGKMDENQFVAVTS 331-385
Query	: TNAAKIFNLYPRKGRI+VGSDDLVIWDPDAVKIVSAKHNQSAEYNI FEGMELR 386-440
	: TNAAK+FNLYPRKGRI+VGSDDLVIWDPD+VK +SAK H S+ EYNI FEGME R
Q16555	: TNAAKVFNLYPRKGRIAVGSDADLVIWDPD+VKTISAKTHNSSEYNI FEGMECR 386-440
Query	: GAPLVVICQGKIMLEDGNLHVTQGAGRFPICSPFSDYVYKRIKARRKMDLHAVP 441-495
	: G+PLVVI QGKI+LEDG LHVT+G+GR+IP PF D+VYKRIKAR ++A+L VP
Q16555	: GSPLVVISQGKIVLEDGTLHVTEGSGRYIPRKPFPDFVYKRIKARSRLAELRGVP 441-495
Query	: RGMVDGPFVFDLTTTPKGGTPAGSARGSPTRPN-PPVRNLHQSGFSLSGTQVDEGV 496-549
	: RG+YDGPV +++ TPK TPA SA+ SP + PPVRNLHQSGFSLSG Q+D+ +
Q16555	: RGLYDGPVCEVSVTPKTVTPASSAKTSPAKQQAPPVRNLHQSGFSLSGAQIDDNI 496-550
Query	: -RSASKRIVAPPGGRSNIISL 550-569
	: R ++RIVAPPGGR+NIISL
Q16555	: PRRTTQRIVAPPGGRANITSL 551-571

f. Sequence homology between DRP3 and DRP4

86.0%	
Graphical alignment	
In original sequence: 1 - 570 (total: 570)	
Raw alignment	
Query	: MSYQGKKNIPRITSDRLLIKGGRIVNDDQSFYADIYMEDGLIKQIGDNLIVPGGV 1-55
	: MS+QGKK+IPRITSDRLLI+GGRIVNDDQSFYAD+++EDGLIKQIG+NLIVPGG+
O14531	: MSFQGKKSIPRITSDRLLIRGGRIVNDDQSFYADVHVEDGLIKQIGENLIVPGGI 1-55
Query	: KTIEANGKMVIPGGIDVHTHFQMPYKGMTTVDDFFQGTKAALAGGTMIIDHVVP 56-110
	: KTI+A+G MV+PGG+DVHT QMP GMT DDF QGTKAALAGGTMI+DHV P
O14531	: KTIDAHGLMVLPGGVDVHTRLQMPVLGMTPADDFCQGTKAALAGGTMIIDHVFP 56-110
Query	: EPESLLEAYEKREWADGKSCCDYALHVDITHWNDSVKQEVQNLIKDKGVNSFM 111-165
	: + SL AYE+WRE AD +CCDY+LHVDIT W++S+K+E++ L+K+KGVNSF+
O14531	: DTGVSLLAAYEQWRERADSAACCDYSLHVDITRWHEHSIKEELEALVKEKGVNSFL 111-165
Query	: VYMAYKDLYQVSNTELYEIFTCLGELGAIQVHAENGDI IAQEQTRMLEMGITGP 166-220
	: V+MAYKD Q S++++YEIF+ + +LGA+AQVHAENGDI+ +EQ R+LE+GITGP
O14531	: VFMAYKDRQCSDSQMYEIFSIIIRDLGALAQVHAENGDIVEEEQKRLELGITGP 166-220
Query	: EGHVLSRPEELEAEAVFRAITIASQTNCPYVTKVMSKSAADLISQARKKGNVVF 221-275
	: EGHVLS PEE+EAEAV+RA+TIA Q NCPLYVTKVMSK AAD I+QA+++G VVF
O14531	: EGHVLSHPVEEAEAVYRAVTIAKQANCPYVTKVMSKGAADAIAQAKRRGVVVF 221-275
Query	: GEPITASLGIDGTHYWSKNWAKAAAFVTSPPSPDPTTPDYINSLASGDLQLSG 276-330
	: GEPITASLG DG+HYWSKNWAKAAAFVTSPP++PDPTT D++ LL+SGDLQ++G
O14531	: GEPITASLGTGSHYWSKNWAKAAAFVTSPPVNPDPPTADHLTCLLSSGDLQVTG 276-330
Query	: SAHCTFSTAQKAIGKDNFTAIPEGTINGVEERMSVIWDKAVATGKMDENQFVAVTS 331-385
	: SAHCTF+TAQKA+GKDNF IPEGTING+EERMS++W+K VA+GKMDEN+FVAVTS
O14531	: SAHCTFTTAQKAVGKDNFALIPEGTINGIEERMSMVWEKCVASGKMDENEFVAVTS 331-385
Query	: TNAAKIFNLYPRKGRISVGSDDLVIWDPDAVKIVSAKNHQSAEYNI FEGMELR 386-440
	: TNAAKIFN YPRKGR++VGSD+DLVIW+P A KI+SAK H EYNIFEG+E R
O14531	: TNAAKIFNFYPRKGRVAVGSDADLVIWNPKATKIISAKTHNLNVEYNI FEGVECR 386-440
Query	: GAPLVVICQGKIMLEDGNLHVTQAGGRFIPCSFSDYVYKRIKARRKMADLHAVP 441-495
	: GAP VVI QG++ LEDG + VT GAGRF+P F D+VYKRIKAR ++A++H VP
O14531	: GAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPDFVYKRIKARNRLAEIHGVP 441-495
Query	: RGMVDGPFVDLTTTPKGGTPAGSARGSPTRPN-PPVRNLHQSGFSLSGTQVDEGV 496-549
	: RG+YDGPV ++ K G+ A + P + + PPVRNLHQSGFSLSG+Q D+ +
O14531	: RGLYDGPVHEVMVPAKPGSGAPARASCPGKISVPPVRNLHQSGFSLSGSQADDHI 496-550
Query	: -RSASKRIVAPPGGRSNITSLS 550-570
	: R +++I+APPGGRSNITSLS
O14531	: ARRTAQKIMAPPGGRSNITSLS 551-572