

## Suppl. Table II:

### Conservation of the Hsp20 domain in *Arabidopsis* sHsps and Acd proteins

For 16 sHsp and 25 Acd proteins (Scharf et al., 2001) the E value of the Hsp20 domain was determined (HMMER, hmmer.wustl.edu,) and the proteins listed according to sequence conservation of the Hsp20 domain. If the size of the predicted polypeptide was altered according to improved gene prediction, the new predicted molecular mass was calculated and the former acronym adapted. (e.g. for At1g52560 AtHsp26.5-P to AtHsp19.9- P). For the two peroxisomal sHsp identified in this study the acronyms AtHsp15.7-Px (formerly AtHsp15.7-CI) and AtAcd31.2-Px are suggested. Note that the previous protein classification into Hsps and Acd proteins introduced by Scharf et al. (2001) is not related to phylogenetic relationship or Hsp20 domain conservation (see also Suppl. Fig. 1). AtAcd44.3, AtAcd48.0, and AtAcd86.6 are annotated ARID/BRIGHT DNA-binding domain-containing proteins. Abbreviations: CI/II/III: cytosolic class I/II/III; M: mitochondrium; n.d.: E value <1 not detected; P: plastid; Px: peroxisome.

Acronym		Gene locus	Size	Hsp20 domain	
new	former		(aa)	E value	location
<b>E &lt; e-2</b>					
AtHsp17.6-CII	identical	At5g12020	155	2.7e-52	48 to 153
AtHsp17.4-CI	identical	At3g46230	156	2.4e-51	52 to 155
AtHsp17.6C-CI	identical	At1g53540	157	4.4e-51	53 to 156
AtHsp18.1-CI	identical	At5g59720	161	5.5e-51	55 to 158
AtHsp17.7-CII	identical	At5g12030	156	7.7e-50	49 to 154
AtHsp17.8-CI	identical	At1g07400	157	1.8e-49	51 to 151
AtHsp17.6B-CI	identical	At2g29500	153	1.3e-48	49 to 152
AtHsp17.6A-CI	identical	At1g59860	155	1.9e-48	49 to 154
AtHsp25.3-P	identical	At4g27670	227	8.6e-46	130 to 227
AtHsp22.0-ER	identical	At4g10250	195	1.1e-43	74 to 178
AtHsp19.9-P	AtHsp26.5-P	At1g52560	232	3.1e-27	128 to 232
<b>AtHsp15.7-Px</b>	<b>AtHsp15.7-CI</b>	<b>At5g37670</b>	<b>137</b>	<b>3.2e-24</b>	<b>25 to 134</b>
AtHsp17.4-CIII	identical	At1g54050	155	6.5e-23	45 to 153
AtHsp23.6-M	identical	At4g25200	210	1.7e-21	110 to 210
AtHsp23.5-M	identical	At5g51440	210	1.7e-19	112 to 210
AtHsp15.4-CI	identical	At4g21870	134	1.3e-10	29 to 121
<b>AtAcd31.2-Px</b>	<b>identical</b>	<b>At1g06460</b>	<b>285</b>	<b>5.8e-06</b>	<b>189 to 284</b>
AtAcd41.3	identical	At5g04890	366	7.3e-06	24 to 121
AtAcd28.1	identical	At5g20970	249	8.8e-06	18 to 113
AtAcd28.7	identical	At1g76770	244	0.00034	34 to 133
AtHsp18.5-CI	identical	At2g19310	162	0.00036	63 to 158
AtHsp14.7-P	AtHsp14.2-P	At5g47600	131	0.00036	33 to 125
AtAcd25.1	identical	At2g27140	224	0.00091	21 to 114
AtAcd54.2	identical	At3g10680	490	0.00094	31 to 124
AtAcd25.4	identical	At4g16540	232	0.0021	149 to 185
AtAcd27.7	AtAcd26.0	At2g03020	247	0.0084	182 to 208
AtAcd22.3	AtAcd21.4	At1g54850	206	0.0088	103 to 124
<b>E &gt; e-2</b>					
AtAcd86.6	AtAcd32.4	At2g17410	786	0.011	701 to 786
AtHsp21.7-CI	identical	At5g54660	192	0.014	90 to 191
AtAcd28.9	identical	At5g47590	264	0.015	168 to 264
AtAcd48.0	AtAcd55.2	At1g76510	434	0.02	351 to 434
AtAcd16.6	identical	At1g54400	153	0.023	48 to 74
AtAcd216.9	identical	At1g76780	1871	0.034	9 to 39
AtAcd44.3	identical	At1g20910	398	0.042	315 to 398
AtAcd22.1	identical	At3g22530	198	0.062	144 to 177
AtAcd56.6	AtAcd55.5	At5g02480	508	0.13	384 to 501
AtAcd81.4	identical	At4g16550	743	0.17	189 to 282
AtAcd57.5	AtAcd114.3	At4g16560	532	0.17	35 to 128
AtAcd39.4/30.4*	AtAcd39.0	At1g54840	349 and 268*	0.95	244 to 347
AtAcd51.9	identical	At1g20870	463	n.d.	
AtAcd15.5	identical	At1g76440	143	n.d.	
AtAcd55.8/39.8	AtAcd55.8	At2g37570	494 and 351	n.d.	
AtAcd55.3	identical	At3g12570	489	n.d.	
AtAcd16.9	identical	At4g14830	152	n.d.	

