

Table S1. List of proteins identified in non-diapausing (S2ND and S4ND), diapausing (S2D) and post-diapausing (S4PD) eggs of *Mahanarva spectabilis*.

Egg	Code	Protein name	Protein score	Coverage	Number of peptides	Peptide sequence	Peptide score
S2ND	A0A1B6DHB6	Uncharacterized protein	126.78	2	2	IFAPQHDLEVQYDGTGVK	75.96
	B4IP23	Histone H4	115.59	32	3	YIIQSSVTTNK TVTAMDVVYALK	63.06 74.85
	T1DQ28	Putative hemoglobin subunit alpha	112.65	19	2	ISGLIYEETR DNIQGITKPAIR	39.64 37.79
	A0A1B6L0Y6	Uncharacterized protein	99.34	2	2	IGGHGAEYGAEALER FLASVSTVLTSK	69.79 65.08
	B2BD67	Vitellogenin	83.64	1	2	DAVAQAGTGPALLTIK NLQVNIPIR	71.39 44.91
	A0A1B6CLY7	Uncharacterized protein	77.33	1	1	YTIQSSVTTNK	53.41
	B4IMC5	Histone H2B	73.63	23	2	YPVHAFGR ALGNIAHPR	49.63 47.07
	A0A1B6D741	Uncharacterized protein	60.87	7	1	AMSIMNSFVNDIFER HAVSEGTK	52.45 42.37
	B3GCD7	Peptidyl-prolyl cis-trans isomerase	58.10	9	1	IYTNC(+57.02)C(+57.02)PQSTDR	60.87
	A0A151IEV1	Vitellogenin-1	0	1	1	HVVFGSVVEGM DIVK	58.10
	H9IZ57	Tubulin alpha chain	51.11	3	1	NVPTWELNLLK	55.55
	D2A4R3	ATP synthase subunit beta	50.92	3	1	LIGQIVSSITASLR	51.11
	A0A1B6EGC2	Uncharacterized protein	49.08	3	1	TVLIMELINNVAK	42.41
	A0A146LX34	Spectrin beta chain, brain 4	47.48	0	1	IIGWGEENGVK	49.08
	E3WH90	Vitellogenin	43.92	1	1	LIAENNFR	36.97
	A0A182UHL8	Uncharacterized protein	42.62	0	1	DAVAEAGTGPALLTIK	36.26
	A0A026WAJ5	Uncharacterized protein	38.89	1	1	ASHAAC(+57.02)R	42.61
	D1LBX8	Ribosomal protein S5	38.84	8	1	NAVAQAGTGPALLTIK	38.89
	A0A1B6EBA7	Uncharacterized protein	35.80	1	1	TIAEC(+57.02)VADELINAAK	38.84
	S4ND	A0A1B6DDC2	Uncharacterized protein	143.01	23	8	KIVSALSLSK
						ALDSIQASLEAESK	59.76
						KLEADINELEIALDHANK	49.29
						DVQTALEEEQR	44.85
						SQLELSQVR	43.87
						QIEEAEIEAALNLAK	43.23
						NLADEVKDLLDQIGEGGR	42.28
						DELQAALAEAEAEAELEQEENK	38.31
						ANALQNELEESR	36.20
H9JV50		Tubulin alpha chain	102.81	6	2	TIQFVDWC(+57.02)PTGFK	67.61
A0A026X3R9		Actin, clone	91.19	11	3	IHFPLVTYAPVISAEK	42.31
						AGFAGDDAPR	37.25
						EITALAPSTIK	36.04
						DLYANTVLSGGTTM(+15.99)YPGIADR	34.24
A0A1B6EBM7		Uncharacterized protein	81.41	2	2	YIIQSSVTTNK	58.12
T1E7Z1		Putative hemoglobin subunit alpha	78.81	19	2	IFAPQHDLEVQYDGTGVK FLASVSTVLTSK	46.58 49.29
A0A1B6L0Y6		Uncharacterized protein	71.45	2	2	IGGHGAEYGAEALER DAVAQAGTGPALLTIK	39.56 55.36
A0A154PBX6	Actin, muscle	67.47	5	2	NLQVNIPIR IAPEEHPVLLTEAPLNPK	32.18 37.56	
B4IN83	Histone H2B	66.36	19	2	AGFAGDDAPR HAVSEGTK	37.25 49.48	
					AMSIMNSFVNDIFER	33.75	

Table S1. Continued.

Egg	Code	Protein name	Protein score	Coverage	Number of peptides	Peptide sequence	Peptide score	
S4ND	B8Y197	Elongation factor 1-alpha	65.50	6	2	M(+15.99)DSTEPPEYSESR	48.22	
						YYVTIIDAPGHR	34.56	
	A0A151IEV1	Vitellogenin-1	62.79	0	1	NVPTWELNLLK	44.28	
	B2BD67	Vitellogenin	62.34	0	1	YPVHAFGR	48.57	
	J9JRM2	Uncharacterized protein	61.23	1	1	AAVTGLGFLLFR	52.12	
	B3NQ25	Calcium-transporting ATPase	60.89	1	1	NILFSGTNVAAGK	34.68	
	A0A1B6E1L5	Uncharacterized protein	57.28	1	1	YSTETDEVYK	49.68	
	A0A1B6C1N7	Uncharacterized protein	50.75	0	1	ALGNIAHPR	38.21	
	K7IRP4	Uncharacterized protein	47.59	7	1	VLEQLTGQQPVFSK	47.59	
	A0A1B6MMG8	Uncharacterized protein	44.79	2	1	ILLELYYK	44.79	
	A0A182MI61	Outer segment 2	44.65	1	1	EYNMVADALR	35.37	
	X1XR84	Uncharacterized protein	40.37	3	1	TPPGGE	40.37	
	A0A075C4X2	Histone H2A	37.11	40	1	VGAGAPVYLAAVM(+15.99)EYLAAEVLELAGNAAR	37.11	
	A0A026WRY7	Ankyrin-2	34.08	2	1	EFAQLADYIDSR	34.08	
A0A084VJ18	AGAP013356-PA-like protein	1	1	1	DLRVTTQR	32.38		
S2D	T1E7Z1	Putative hemoglobin subunit alpha	95.97	19	2	IGGHGAEYGAELER	62.14	
					FLASVSTVLTSK	50.57		
	A0A1B6E1L0	Uncharacterized protein	89.43	23	3	LGQEFDEETPDGR	56.07	
					MILTVDDIVC(+57.02)TR	45.37		
					AIGVGFFTR	32.02		
	A0A1B6EBM7	Uncharacterized protein	88.97	2	2	IFAPQHDLEVQYDGTGVK	53.76	
					YIIQSSVTTNK	50.10		
	A0A0A8KZN4	Histone H4	85.86	18	1	TVTAMDVVYALK	63.82	
	A0A1B6L0Y6	Uncharacterized protein	84.94	2	2	DAVAQAGTGPALLTIK	60.40	
					NLQVNIPIR	49.09		
	H9IZ57	Tubulin alpha chain	72.22	1	1	LIGQIVSSITASLR	72.22	
	A0A1B6CLY7	Uncharacterized protein	64.13	1	3	TNPSMQLLQR	39.64	
					ALGNIAHPR	38.27		
					TNPSM(+15.99)QLLQR	31.71		
	Q6WAW3	Heat shock protein 70	60.60	2	1	VEIANDQGNR	49.28	
	B2BD67	Vitellogenin	59.67	0	1	YPVHAFGR	45.30	
	A0A1A9W425	Histone H2A	58.41	17	1	LLSGVTIAQGGVLPNIQAVLLPK	43.58	
	A0A1B6DMG8	Uncharacterized protein	46.50	8	1	AGGEIITFDELALR	46.50	
	C4WXA0	ACYPI009011 protein	45.21	9	1	MVLTVDDITC(+57.02)TR	45.21	
	A0A182L4P4	Uncharacterized protein	44.65	1	1	GSGGGGGGGGPNRR	35.06	
	A0A182HNE4	Uncharacterized protein	41.77	3	1	DSYVGDEAQS	31.96	
	A0A182MEX8	Uncharacterized protein	38.59	2	1	YWIAVNSWGK	38.59	
	A0A151IEV1	Vitellogenin-1	37.69	0	1	NVPTWELNLLK	37.69	
	A0A1I8MMG5	Amino acid transporter	33.16	2	1	QDAEPTLIR	33.16	
	A0A1B0EM04	Uncharacterized protein	32.22	2	1	LLEVIDR	32.22	
	A0A182LXE1	Uncharacterized protein	32.00	0	1	HAAGDK	32.00	
	A0A069DXP5	Mitogen-activated protein kinase	31.53	0	1	NPPPR	31.53	
	S4PD	A0A0U4B5C7	Heat shock protein 70	120.80	8	4	TTPSYVAFTDTER	57.99
						IINEPTAAAIAYGLDK	51.38	
						VEIANDQGNR	48.61	
					TFFPEEVSSMVLTK	41.03		
A0A1B6DDC2		Uncharacterized protein	120.45	16	5	AQQELEEAER	62.13	
					ALDSIQASLEAESK	45.46		
				GAYEEGQEQLEAVR	45.07			

Table S1. Continued.

Egg	Code	Protein name	Protein score	Coverage	Number of peptides	Peptide sequence	Peptide score
S4PD						NLADEVKDLLDQIGEGGR	40.32
	A0A0P4VVE9	Putative actin muscle isoform x2	119.00	5	5	KLEGELQTLHADLDELLNEAK	39.64
						DSYVVGDEAQS	50.42
						AGFAGDDAPR	45.60
						DLYANTVLSGGTTM(+15.99)YPGIADR	44.16
						HQGVVM(+15.99)VGMGQK	40.23
						EITALAPSTIK	37.80
	H9JV50	Tubulin alpha chain	114.30	8	3	TIQFVDWC(+57.02)PTGFK	70.35
						LIGQIVSSITASLR	43.68
	B4IQA5	Histone H4	108.76	21	2	DVNAAIATIK	41.25
						TVTAM(+15.99)DVVYALK	65.70
	A0A158P200	Delta-aminolevulinic acid dehydratase	103.48	4	3	ISGLIYEETR	57.17
						IINEPTAAAIAYGLDK	51.38
						VEIANDQGNR	48.61
	A0A1B6DHB6	Uncharacterized protein	93.44	2	2	DVDEIVLVGGSTR	35.76
						YIIQSSVTTNK	56.46
	B2BD67	Vitellogenin	88.94	1	2	IFAPQHDLEVQYDGTGVK.	48.12
						YTIQSSVTTNK	56.55
	A0A1B6CLY7	Uncharacterized protein	81.10	1	1	YPVHAFGR	50.09
	A0A0K8W1R2	ATP synthase subunit beta	80.59	7	2	ALGNIAHPR	55.07
						IINVIGEPIDER	49.25
						FTQAGSEVSALLGR	49.12
	F6M9L9	Tubulin beta chain	79.60	3	1	IM(+15.99)NTYSVVPSPK	46.85
	A0A1B6L0Y6	Uncharacterized protein	79.20	2	2	DAVAQAGTGPALLTIK	54.40
						NLQVNIPIR	49.59
	A0A0L7RDX3	Histone H2A	70.15	17	1	LLSGVTIAQGGVLPNIQAVLLPK	48.47
	A0A1B6FW63	Citrate synthase	67.01	3	1	ALGTLASLVWDR	57.22
	A0A067R2J7	Spectrin beta chain	66.18	1	1	VQQLEDAYAELVK	54.08
	A0A1B6EFU4	Uncharacterized protein	63.57	4	1	TNDIAGDGTATVLAQAIVR	52.34
	A0A193PCD1	Adenine nucleotide translocase insect2	57.88	4	1	GFGVSVQGIYR	39.48
	A0A0Z7	Enolase	55.10	4	1	AVDNINKSIAPELLK	39.02
	A0A1B6CC82	Uncharacterized protein	52.97	3	1	YFTILEAGSR	52.97
	A0A1B6CGM1	Uncharacterized protein	52.28	0	1	LWLVDGAPDFLK	44.67
	A4V3G1	Fructose-bisphosphate aldolase	49.49	3	1	VTETVLAAVYK	49.49
	J9JVQ8	Serine/threonine-protein phosphatase	48.56	5	1	EIFLSQPILLEEAPLK	48.56
	T1DQ28	Putative hemoglobin subunit alpha	48.53	9	1	FLASVSTVLTSK	48.53
	K7JMJ3	Uncharacterized protein	42.99	2	1	SNPTVSYFFLK	42.99
	A0A1B6EGC2	Uncharacterized protein	42.20	3	1	IIGWGEENGVK	42.20
	Q5PXZ1	Putative IDGF	37.75	2	1	TLLESVESR	37.75