

**Table S1:** The native sesame OAPs fractions was analysed by mass spectrometry using peptide mass fingerprint. The table shows the identified proteins in this fraction.

Band	Protein (Accession number)	Cut-Off	Protein Score	Sequence coverage [%]	Molecular Mass [kDa]
<b>Sesame OAPs: HIC-Elution-Fraction 3</b>					
1	uncharacterized protein LOC105177100 (NP_001292915.1)	49	45	10	17,4
	15 kDa oleosin (AAD42942.1)	49	23	6	15,2
	PREDICTED: oleosin 1-like (XP_011076526.1)	49	23	4	24,0
2	11-beta-hydroxysteroid dehydrogenase-like 5 (NP_001291330.1)	79/50	169/55	54/4	41,3
3	11-beta-hydroxysteroid dehydrogenase 1B-like (NP_001291322.1)	79/50	125/31	50/2	39,7
	11-beta-hydroxysteroid dehydrogenase-like 5 (NP_001291330.1)	79/50	87/20	41/4	41,3
4	peroxygenase (NP_001291323.1)	79/50	76/115	40/23	27,8
5	PREDICTED: legumin B-like (XP_011083024.1)	79/50	93/59	35/8	52,1
	Peroxygenase (NP_001291323.1)	79/50	80/81	32/10	27,8
	11S globulin precursor isoform 4 (ABB60055.1)	79/50	80/59	32/8	53,0
6	PREDICTED: legumin B-like (XP_011083024.1)	79	72	33	52,1
	11S globulin precursor isoform 4 (ABB60055.1)	79	60	28	53,0
	15 kDa oleosin (AAD42942.1)	50	22	6	15,2
	PREDICTED: oleosin 1-like (XP_011076526.1)	50	22	4	24,0
7	15 kDa oleosin (AAD42942.1)	50	61	6	15,2
	PREDICTED: oleosin 1-like (XP_011076526.1)	50	61	4	24,0
8	uncharacterized protein LOC105177100 (NP_001292915.1)	51	43	10	17,4
9	uncharacterized protein LOC105177100 (NP_001292915.1)	49	40	10	17,4
	15 kDa oleosin (AAD42942.1)	49	35	6	15,2
	PREDICTED: oleosin 1-like (XP_011076526.1)	49	35	4	24,0
	PREDICTED: oleosin 16.4 kDa (XP_011097414.1)	49	20	10	17,4

**Sesame OAPs: HIC-Elution-Fraction 4**

10	Peroxygenase ( <i>NP_001291323.1</i> )	79/49	108/27	41/8	27,8
11	Peroxygenase ( <i>NP_001291323.1</i> )	51	81	10	27,8
12	uncharacterized protein LOC105177100 ( <i>NP_001292915.1</i> )	79	57	39	17,4
	15 kDa oleosin ( <i>AAD42942.1</i> )	50	47	6	15,2
	PREDICTED: oleosin 1-like ( <i>XP_011076526.1</i> )	50	47	4	24,0
13	uncharacterized protein LOC105177100 ( <i>NP_001292915.1</i> )	51	24	10	17,4
	PREDICTED: oleosin 1-like ( <i>XP_011081346.1</i> )	51	22	7	14,8
	15 kDa oleosin ( <i>AAD42942.1</i> )	51	21	6	15,2
	PREDICTED: oleosin 1-like ( <i>XP_011076526.1</i> )	51	21	4	24,0
14	PREDICTED: DDB1- and CUL4-associated factor 8 ( <i>XP_011089371.1</i> )	79	58	22	54,1
	uncharacterized protein LOC105177100 ( <i>NP_001292915.1</i> )	49	15	10	17,4

**Sesame OAPs: HIC-Elution-Fraction 5**

15	-	-	-	-	-
16	11-beta-hydroxysteroid dehydrogenase-like 5 ( <i>NP_001291330.1</i> )	79/50	190/70	53/7	41,3
17	Peroxygenase ( <i>NP_001291323.1</i> )	79/50	119/73	53/13	27,8
18	Peroxygenase ( <i>NP_001291323.1</i> )	79/50	80/63	27/10	27,8
19	uncharacterized protein LOC105177100 ( <i>NP_001292915.1</i> )	50	67	10	17,4
	15 kDa oleosin ( <i>AAD42942.1</i> )	50	52	6	15,2
	PREDICTED: oleosin 1-like ( <i>XP_011076526.1</i> )	50	52	4	24,0
20	PREDICTED: oleosin 1-like ( <i>XP_011081346.1</i> )	51	46	7	14,8
	uncharacterized protein LOC105177100 ( <i>NP_001292915.1</i> )	51	43	10	17,4
21	PREDICTED: DDB1- and CUL4-associated factor 8 ( <i>XP_011089371.1</i> )	79	91	36	54,1
	uncharacterized protein LOC105177100 ( <i>NP_001292915.1</i> )	49	17	10	17,4

Cut-off, protein-score and sequence coverage are highlighted in green if the results were obtained from MS/MS experiments

**Table S2:** The native walnut OAPs fractions was analysed by mass spectrometry using peptide mass fingerprint. The table shows the identified proteins in this fraction.

Band	Protein (Accession number)	Cut-Off	Protein Score	Sequence coverage [%]	Molecular Mass [kDa]
<b>Walnut OAPs: HIC-Elution-Fraction 3</b>					
22	-	-	-	-	-
23	-	-	-	-	-
24	-	-	-	-	-
25	-	-	-	-	-
26	Oleosin (AET74077.1)	79	40	38	14,7
<b>Walnut OAPs: HIC-Elution-Fraction 4</b>					
27	-	-	-	-	-
28	-	-	-	-	-
29	-	-	-	-	-
30	-	-	-	-	-
31	-	-	-	-	-
32	-	-	-	-	-
33	Oleosin (AET74077.1)	79	48	38	14,7
<b>Walnut OAPs: HIC-Elution-Fraction 5</b>					
34	-	-	-	-	-
35	Oleosin (AET74077.1)	79	53	35	14,7

Cut-off, protein-score and sequence coverage are highlighted in green if the results were obtained from MS/MS experiments

**Table S3:** The native pecan nut OAPs fractions was analysed by mass spectrometry using peptide mass fingerprint. The table shows the identified proteins in this fraction.

Band	Protein (Accession number)	Cut- Off	Protein Score	Sequence coverage [%]	Molecular Mass [kDa]
<b>Pecan nut OAPs: HIC-Elution-Fraction 3</b>					
1	-	-	-	-	-
2	-	-	-	-	-
3	-	-	-	-	-
4	-	-	-	-	-
5	-	-	-	-	-
6	-	-	-	-	-
7	-	-	-	-	-
<b>Pecan nut OAPs: HIC-Elution-Fraction 4</b>					
8	-	-	-	-	-
9	-	-	-	-	-
10	-	-	-	-	-
11	-	-	-	-	-
12	-	-	-	-	-
13	-	-	-	-	-
<b>Pecan nut OAPs: HIC-Elution-Fraction 5</b>					
14	-	-	-	-	-
15	-	-	-	-	-
16	-	-	-	-	-
17	-	-	-	-	-
18	-	-	-	-	-
19	-	-	-	-	-

Cut-off, protein-score and sequence coverage are highlighted in green if the results were obtained from MS/MS experiments