

Supplementary Materials

Identification of Allergens in White- and Red-Fleshed Pitaya (*Selenicereus undatus* and *Selenicereus costaricensis*) Seeds Using Bottom-Up Proteomics Coupled with Immunoinformatics

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Table S1. Information of pitaya allergic patients.

Patient number	Age (years old)	Self-reporting symptoms	Symptoms occurring after eating white-fleshed or/and red-fleshed pitaya	Others
P1	23	Vomiting, diarrhea, and abdominal pain	White-fleshed pitaya	Relieved after oral loratadine administration.
P2	23	Vomiting and diarrhea	White-fleshed and red-fleshed pitaya	
P3	6	Wind mass rash, abdominal pain, and watery stools	Red-fleshed pitaya	
P4	33	Swelling of the right eyelid	Red-fleshed pitaya	
P5	14	Urticaria	White-fleshed and red-fleshed pitaya	

Table S2. Information of primers for RT-PCR.

Primers	Sequences (5'-3')
<i>Cupin1</i> (Forward)	ATGATGGCACCCCATTTGAATC
<i>Cupin1</i> (Reverse)	TCACTCAAACCCCATGACCATT
<i>Hsp70</i> (Forward)	TTAATCAACCTCCTCAATCTTGGGA
<i>Hsp70</i> (Reverse)	AAAGGTGAAGGTCCGGCG
<i>Hsp sti 1</i> (Forward)	CATCTGACTTGGACAATGCC
<i>Hsp sti 1</i> (Reverse)	ATGGCCGACGAAGCCAA

Table S3. Full list of the total protein from white-fleshed pitaya seeds protein band hits retrieved with MASCOT discoverer software screening.

N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
1	Uncharacterized protein (Fragment) OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_027930 PE=3 SV=1	A0A0J8DSR1	158	26488	6(6)	24.1
2	Cupin type-1 domain-containing protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8ZNT3	143	18045	2(1)	12.7
3	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_029540 PE=4 SV=1	A0A0K9RTZ6	137	65882	2(1)	4.7
4	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803LTG6	132	19434	4(4)	27.5
5	Heat shock protein 70 OS=Spinacia oleracea OX=3562 GN=HSP70-13 PE=2 SV=1	A0A1I9TK81	106	71808	3(3)	6.1
6	Proteasome subunit beta (Fragment) OS=Spinacia oleracea OX=3562 GN=SOVF_007620 PE=3 SV=1	A0A0K9S2G1	83	29745	1(1)	5.5
7	Histone H4 OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_5g125910 PE=3 SV=1	A0A0J8BUP3	80	11402	1(1)	11.7
8	Formamidase OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9EWT0	77	52325	2(2)	6.1
9	VWFA domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_154600 PE=3 SV=1	A0A0K9QPX4	72	42327	1(1)	4.3
10	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8YYM2	66	16165	1(1)	4.8
11	PLAT domain-containing protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9CMR0	65	19550	1(1)	5.4
12	Proteasome subunit beta OS=Nepenthes alata OX=4376 GN=NaPSB1-1 PE=2 SV=1	A0A286T1W3	64	29511	2(2)	8.1
13	Tr-type G domain-containing protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_2g046240 PE=3 SV=1	A0A0J8BGW2	60	94791	1(1)	1.4
14	ATP synthase subunit alpha OS=Beta vulgaris subsp. vulgaris OX=3555 GN=atpA PE=3 SV=1	A0A023ZQ87	58	55584	1(1)	2.6
15	Proteasome subunit beta OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9D7H1	56	22828	2(2)	10.2
16	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8YRL3	56	15770	2(2)	17.1
17	Uncharacterized protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_9g209070 PE=3 SV=1	A0A0J8BPT8	49	24249	1(1)	4.5
18	D-xylose 1-dehydrogenase (NADP(+)) (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9AF84	48	42687	1(1)	2.6
19	Elongation factor Tu (Fragment) OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_018790 PE=3 SV=1	A0A0J7YLM1	46	44450	2(2)	6.4
20	Dihydrolipoyllysine-residue succinyltransferase OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_009840 PE=3 SV=1	A0A0J8B2D3	45	51446	1(1)	1.7
21	Ferritin OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_2g044700 PE=3 SV=1	A0A0J8BHE5	45	29868	1(1)	3.4
22	Peroxidase OS=Tamarix hispida OX=189793 GN=POD2 PE=2 SV=1	C0KKH7	44	36304	1(1)	1.8

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N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
23	Elongation factor 1-alpha OS=Hylocereus polyrhizus OX=1195597 GN=EF1A PE=2 SV=1	A0A249Y703	43	50180	1(1)	2.6
24	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9CHR1	43	23990	1(1)	5.3
25	Formylglycinamide ribonucleotide amidotransferase OS=Spinacia oleracea OX=3562 GN=SOVF_185900 PE=3 SV=1	A0A0K9QF72	40	149942	1(1)	0.7
26	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9ERX8	40	13642	1(1)	9.8
27	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803KW96	39	65071	1(1)	2.1
28	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_024240 PE=3 SV=1	A0A0K9RVF6	39	36236	1(1)	3.8
29	Histone H2A OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_015930 PE=3 SV=1	A0A0J8B158	38	15362	1(1)	6.2
30	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803LCC3	38	99945	1(1)	0.9
31	Annexin (Fragment) OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8Z5P5	37	36019	1(1)	2.8
32	Lactoylglutathione lyase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9ED66	37	42702	1(1)	1.5
33	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803KPQ9	37	114105	1(1)	0.8
34	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803MK43	36	18155	1(1)	6.4
35	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_117760 PE=4 SV=1	A0A0K9R339	36	101275	1(1)	0.7
36	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_082480 PE=3 SV=1	A0A0K9RCF0	35	20634	1(1)	5.1
37	Ribulose biphosphate carboxylase large chain (Fragment) OS=Persicaria punctata OX=137688 GN=rbcL PE=3 SV=1	A6YSW9	35	49327	1(1)	1.6
38	PPM-type phosphatase domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_154270 PE=4 SV=1	A0A0K9QRN3	34	52513	1(1)	3
39	Tubulin beta chain OS=Spinacia oleracea OX=3562 GN=SOVF_174120 PE=3 SV=1	A0A0K9QIW0	33	50836	1(1)	2.7
40	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_047510 PE=3 SV=1	A0A0K9RPW9	33	35719	1(1)	3.1
41	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8ZTY5	33	12066	1(1)	5.7
42	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803KP77	33	29582	1(1)	4.2
43	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	tr A0A803KM81 A0A803KM81_CHEQI	33	132058	1(1)	0.6
44	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	tr A0A803LHI7 A0A803LHI7_CHEQI	33	84614	1(1)	2.5

Continued Table S3

N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
45	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=3 SV=1	tr A0A7C8ZY03 A0A7C8ZY03_OPUST	33	15483	1(1)	6.3
46	Proteasome subunit beta OS=Opuntia streptacantha OX=393608 PE=3 SV=1	tr A0A7C9DYH2 A0A7C9DYH2_OPUS T	33	29808	1(1)	3.3
47	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	tr A0A7C8ZN49 A0A7C8ZN49_OPUST	32	24996	1(1)	4.6
48	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	tr A0A7C9EA90 A0A7C9EA90_OPUST	32	10670	1(1)	6
49	RING-type E3 ubiquitin transferase OS=Opuntia streptacantha OX=393608 PE=4 SV=1	tr A0A7C8YUS2 A0A7C8YUS2_OPUST	31	34317	1(1)	2.4
50	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_021510 PE=4 SV=1	tr A0A0K9RW14 A0A0K9RW14_SPIOL	31	24723	1(1)	5.2
51	Importin N-terminal domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_181840 PE=4 SV=1	tr A0A0K9QGJ6 A0A0K9QGJ6_SPIOL	28	105505	1(1)	0.8
52	DUF4216 domain-containing protein (Fragment) OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_016490 PE=4 SV=1	tr A0A0J8B0Y1 A0A0J8B0Y1_BETVV	23	57613	1(1)	1
53	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	tr A0A7C9D384 A0A7C9D384_OPUST	19	28239	1(1)	2.5

Table S4. Full list of the total protein from red-fleshed pitaya seeds protein band hits retrieved with MASCOT discoverer software screening.

N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
1	Proteasome subunit beta (Fragment) OS=Spinacia oleracea OX=3562 GN=SOVF_007620 PE=3 SV=1	A0A0K9S2G1	315	29745	4(1)	20.4
2	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8YRP5	283	15393	4(1)	37.8
3	Cupin type-1 domain-containing protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8ZNT3	274	18045	2(1)	12.7
4	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9B091	248	64965	5(5)	11
5	Heat shock protein 70 OS=Spinacia oleracea OX=3562 GN=HSP70-13 PE=2 SV=1	A0A1I9TK81	230	71808	6(6)	11
6	Actin 11 OS=Sesuvium portulacastrum OX=221166 PE=2 SV=1	A0A1L5JKA9	206	41929	6(4)	19.2
7	Ribosomal_L18e/L15P domain-containing protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_4g076000 PE=3 SV=1	A0A0J8FEI6	182	20923	4(4)	26.2
8	Formamidase OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9EWT0	182	52325	3(3)	8.7
9	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_029540 PE=4 SV=1	A0A0K9RTZ6	179	65882	2(1)	4.7
10	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8YRL3	170	15770	4(3)	34.2
11	Proteasome subunit beta OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9D7H1	164	22828	4(4)	15.6
12	Cupin_5 domain-containing protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9CU14	156	22754	1(1)	6.5
13	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8ZZS4	146	22123	4(1)	28
14	GTP-binding nuclear protein OS=Spinacia oleracea OX=3562 GN=SOVF_098770 PE=3 SV=1	A0A0K9R796	131	25564	4(3)	20.8
15	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803LTG6	129	19434	3(0)	19.9
16	Thioredoxin-dependent peroxiredoxin OS=Tamarix hispida OX=189793 GN=Prx2 PE=2 SV=1	I0CC94	123	30019	2(1)	10.9
17	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8Z5R6	122	22142	4(1)	22.8
18	Proteasome subunit beta OS=Nepenthes alata OX=4376 GN=NaPSB1-1 PE=2 SV=1	A0A286T1W3	121	29511	3(3)	11.7
19	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803LZK8	118	22897	2(0)	15.4
20	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803N503	114	27087	2(2)	10.1
21	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9DX00	110	17182	3(3)	13
22	Thioredoxin-dependent peroxiredoxin OS=Salicornia europaea OX=206448 PE=2 SV=1	A0A1D8H339	107	30203	2(1)	12
23	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9AUE0	105	16087	4(1)	37

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N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
24	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8YYM2	105	16165	1(1)	4.8
25	Ribosomal_L18e/L15P domain-containing protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9CUT8	105	13740	2(1)	18.9
26	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9D682	96	24843	3(3)	17.9
27	Malate dehydrogenase OS=Spinacia oleracea OX=3562 GN=SOVF_175150 PE=3 SV=1	A0A0K9QKH5	93	36274	1(1)	4.7
28	S4 RNA-binding domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_105660 PE=3 SV=1	A0A0K9R566	92	23031	4(4)	21.3
29	GlutaminyI-tRNA synthetase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8YIH5	89	91277	1(1)	1.6
30	Allene-oxide cyclase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9EZI9	88	30285	3(3)	9.7
31	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9DW78	87	46521	1(1)	3.1
32	Peptidyl-prolyl cis-trans isomerase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9DT77	87	25462	2(2)	10.3
33	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803MK43	86	18155	2(2)	6.4
34	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9ERX8	83	13642	2(2)	9.8
35	ATP synthase subunit alpha OS=Nepenthes ventricosa x Nepenthes alata OX=1744888 GN=atp1 PE=3 SV=1	A0A385Y4B7	77	55587	2(1)	4.3
36	SKP1-like protein OS=Spinacia oleracea OX=3562 GN=SOVF_115630 PE=3 SV=1	A0A0K9R207	77	18890	1(1)	7.2
37	UBX domain-containing protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9DHV8	76	50446	1(1)	3.1
38	Glyceraldehyde-3-phosphate dehydrogenase OS=Spinacia oleracea OX=3562 GN=SOVF_178150 PE=3 SV=1	A0A0K9QJL6	75	45322	1(1)	3.3
39	CN hydrolase domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_119350 PE=3 SV=1	A0A0K9R0Y0	74	37735	1(1)	4.3
40	Ribosomal_L16 domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_064690 PE=3 SV=1	A0A0K9R893	73	25709	1(1)	5.4
41	Ribosomal_L18e/L15P domain-containing protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_6g141790 PE=3 SV=1	A0A0J8C427	72	29125	1(1)	4.1
42	MPN domain-containing protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9DSA4	72	34950	2(2)	7.4
43	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8Z9Z6	71	19831	1(1)	7.8
44	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_074710 PE=4 SV=1	A0A0K9REU3	70	38307	2(2)	6.3
45	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_028400 PE=3 SV=1	A0A0K9RU85	69	23734	1(1)	6.3
46	Superoxide dismutase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8ZWU0	67	26282	3(3)	11.4

Continued Table S4

N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
47	Reticulon-like protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8ZF07	66	33220	2(2)	7.8
48	ATP synthase subunit alpha OS=Beta vulgaris subsp. vulgaris OX=3555 GN=atpA PE=3 SV=1	A0A023ZQ87	66	55584	1(1)	2.6
49	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803MYN6	65	17869	1(1)	8.9
50	Poly [ADP-ribose] polymerase (Fragment) OS=Spinacia oleracea OX=3562 GN=SOVF_124230 PE=4 SV=1	A0A0K9QZG2	65	92270	1(1)	1.6
51	Ubiquitin OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_000430 PE=3 SV=1	A0A0J8B525	64	14906	1(1)	7
52	Acetohydroxy-acid reductoisomerase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9ANA7	64	66498	1(1)	3
53	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_102400 PE=3 SV=1	A0A0K9R865	64	60455	1(1)	2.6
54	Uncharacterized protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_9g209070 PE=3 SV=1	A0A0J8BPT8	63	24249	2(2)	4.5
55	CSD domain-containing protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8ZG77	63	10757	1(1)	15.8
56	Uncharacterized protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_005380 PE=3 SV=1	A0A0J8B417	62	44407	1(1)	3.2
57	Annexin OS=Spinacia oleracea OX=3562 GN=SOVF_164450 PE=3 SV=1	A0A0K9QNT1	62	36187	1(1)	3.5
58	Uncharacterized protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_6g145160 PE=4 SV=1	A0A0J8C319	61	22671	1(1)	5.5
59	Ribosomal_S7 domain-containing protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_3g050700 PE=3 SV=1	A0A0J8CS67	59	23395	2(2)	10.4
60	Adenosinetriphosphatase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9CQ50	59	58332	2(2)	3.3
61	Elongation factor Tu OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9CTD2	58	53499	1(1)	2.3
62	14_3_3 domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_097310 PE=3 SV=1	A0A0K9R7S3	57	29569	1(1)	4.6
63	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803L2U0	56	29434	2(2)	8.8
64	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_128330 PE=3 SV=1	A0A0K9QY28	55	42025	1(1)	2.6
65	40S ribosomal protein S4 OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_004870 PE=3 SV=1	A0A0J8B7M5	54	29968	1(1)	4.2
66	Isocitrate lyase OS=Spinacia oleracea OX=3562 GN=SOVF_042350 PE=3 SV=1	A0A0K9RPI6	54	63996	3(3)	3.2
67	Malate synthase OS=Spinacia oleracea OX=3562 GN=SOVF_184210 PE=3 SV=1	A0A0K9QFS2	54	64615	1(1)	2.1
68	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803MNI3	54	18408	1(1)	4.8
69	Pyruvate kinase OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8Z1C6	54	21590	1(1)	7.6

Continued Table S4

N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
70	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8YQ02	53	18764	1(1)	8
71	Ribosomal_S17_N domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_049780 PE=3 SV=1	A0A0K9RPC5	53	17977	1(1)	6.9
72	Aryl-alcohol dehydrogenase (NADP(+)) OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8ZSD4	51	36894	2(2)	6.4
73	KH type-2 domain-containing protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_010820 PE=3 SV=1	A0A0J8B2L2	51	27002	1(1)	5.4
74	Elongation factor Tu (Fragment) OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_018790 PE=3 SV=1	A0A0J7YLM1	51	44450	1(1)	4.7
75	SBP-type domain-containing protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_3g059840 PE=4 SV=1	A0A0J8CTR7	50	111979	1(1)	0.6
76	D-3-phosphoglycerate dehydrogenase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9ER97	50	65170	1(1)	2.6
77	GOLD domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_044590 PE=3 SV=1	A0A0K9RP25	50	24852	1(1)	5.1
78	Elongation factor 1-alpha OS=Hylocereus polyrhizus OX=1195597 GN=EF1A PE=2 SV=1	A0A249Y703	49	50180	2(1)	5
79	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9CR18	49	48442	2(2)	4.7
80	D-xylose 1-dehydrogenase (NADP(+)) (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9AF84	48	42687	1(1)	2.6
81	Glyceraldehyde-3-phosphate dehydrogenase OS=Hylocereus polyrhizus OX=1195597 GN=G3P PE=2 SV=1	A0A249Y796	48	36839	2(2)	6.8
82	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_021510 PE=4 SV=1	A0A0K9RW14	47	24723	1(1)	5.2
83	Ribos_L4_asso_C domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_207050 PE=3 SV=1	A0A0K9Q8R4	47	35669	1(1)	4
84	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9DCD2	47	13894	1(1)	6.7
85	PsbP domain-containing protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9D4B5	47	28412	1(1)	6.8
86	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_123500 PE=3 SV=1	A0A0K9QZL7	46	55585	2(2)	4.3
87	Peroxidase OS=Tamarix hispida OX=189793 GN=POD2 PE=2 SV=1	C0KKH7	46	36304	1(1)	1.8
88	Ubiquitin thioesterase OTU1 OS=Spinacia oleracea OX=3562 GN=SOVF_156820 PE=4 SV=1	A0A0K9QPB3	46	23731	1(1)	5.3
89	TPR_REGION domain-containing protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8ZUV3	45	18155	1(1)	7.3
90	Ribosomal protein S19 OS=Drosera erythrorhiza OX=2005751 GN=tps19 PE=3 SV=1	A0A1Z1GBD9	45	10866	1(1)	8.6
91	Ubiquinone biosynthesis protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8YDY4	45	20731	1(1)	4.9
92	Cysteine proteinase inhibitor OS=Spinacia oleracea OX=3562 GN=SOVF_083420 PE=3 SV=1	A0A0K9RC70	45	32151	1(1)	3.2

Continued Table S4

N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
93	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803N5S8	45	118708	1(1)	1.3
94	Ferritin OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_2g044700 PE=3 SV=1	A0A0J8BHE5	45	29868	1(1)	3.4
95	Germin-like protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_001170 PE=3 SV=1	A0A0J8B8Q5	44	22570	1(1)	7.1
96	CCT-beta OS=Spinacia oleracea OX=3562 GN=SOVF_080100 PE=3 SV=1	A0A0K9RD41	44	57622	1(1)	2.3
97	Uncharacterized protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_9g209130 PE=3 SV=1	A0A0J8BKL6	44	20978	1(1)	4.4
98	Malate dehydrogenase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8ZW35	44	36113	1(1)	6.6
99	CCT-theta OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8ZZY3	44	59064	1(1)	2
100	GrpE protein homolog OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9E1C7	44	29986	1(1)	4.1
101	Peroxiredoxin OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_010570 PE=3 SV=1	tA0A0J8B2B8	43	24516	1(1)	5
102	PRA1 family protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8YMH8	43	23315	1(1)	6.9
103	Non-specific serine/threonine protein kinase OS=Spinacia oleracea OX=3562 GN=SOVF_122500 PE=4 SV=1	A0A0K9R1K3	43	59199	1(1)	2.1
104	Biotin carboxylase OS=Spinacia oleracea OX=3562 GN=SOVF_065980 PE=4 SV=1	A0A0K9RHG8	43	58646	1(1)	2.8
105	Protein kinase domain-containing protein (Fragment) OS=Spinacia oleracea OX=3562 GN=SOVF_192390 PE=4 SV=1	A0A0K9QD95	43	46460	1(1)	1.9
106	Protein translocase subunit SecA OS=Spinacia oleracea OX=3562 GN=SOVF_169110 PE=3 SV=1	A0A0K9QMF2	42	114333	1(1)	1.3
107	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803L847	42	176812	1(1)	0.7
108	D-3-phosphoglycerate dehydrogenase OS=Spinacia oleracea OX=3562 GN=SOVF_126730 PE=3 SV=1	A0A0K9QYI9	41	57587	1(1)	3.1
109	Derlin OS=Spinacia oleracea OX=3562 GN=SOVF_187530 PE=3 SV=1	A0A0K9QGG3	41	27883	1(1)	4.9
110	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8Y LZ9	41	13852	1(1)	10
111	Dihydropolyllysine-residue succinyltransferase OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_009840 PE=3 SV=1	A0A0J8B2D3	41	51446	1(1)	1.7
112	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9DW29	40	36184	1(1)	4.2
113	Allene-oxide cyclase (Fragment) OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9APK0	40	22803	1(1)	6.7
114	Formylglycinamide ribonucleotide amidotransferase OS=Spinacia oleracea OX=3562 GN=SOVF_185900 PE=3 SV=1	A0A0K9QF72	40	149942	1(1)	0.7
115	Uncharacterized protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_007550 PE=3 SV=1	A0A0J8D0R0	40	15837	1(1)	8.5

Continued Table S4

N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
116	Lactoylglutathione lyase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9ED66	39	42702	1(1)	1.5
117	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9DMB2	39	22453	1(1)	7.3
118	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9CHR1	39	23990	2(2)	7.7
119	Ribosomal_L6e_N domain-containing protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8YCZ3	39	25970	1(1)	5.2
120	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9CUJ8	39	26378	1(1)	3.9
121	Lipoaln_cytosolic_FA-bd_dom domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_207970 PE=3 SV=1	A0A0K9Q8I4	39	21646	1(1)	5.3
122	Aspartokinase OS=Spinacia oleracea OX=3562 GN=SOVF_023510 PE=3 SV=1	A0A0K9RXL4	38	100956	1(1)	0.9
123	Reticulon-like protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9DIY1	38	28770	1(1)	5.5
124	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_192730 PE=3 SV=1	A0A0K9QD37	38	38000	1(1)	2
125	Malate dehydrogenase OS=Spinacia oleracea OX=3562 GN=SOVF_046560 PE=3 SV=1	A0A0K9RNG9	38	35899	1(1)	2.7
126	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8ZGD5	38	56683	1(1)	1.5
127	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_107000 PE=4 SV=1	A0A0K9R4R0	36	181965	1(1)	0.4
128	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803KTW4	36	47501	1(1)	2.1
129	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9EID3	36	13180	1(1)	8
130	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803KPQ9	36	114105	1(1)	0.8
131	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8ZY03	36	15483	1(1)	6.3
132	PLAT domain-containing protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9CMR0	36	19550	1(1)	5.4
133	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8ZZR8	36	20251	1(1)	6.7
134	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8YTC3	36	47890	1(1)	2.7
135	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_117760 PE=4 SV=1	A0A0K9R339	36	101275	1(1)	0.7
136	Uncharacterized protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_3g065360 PE=3 SV=1	A0A0J8FG58	36	54945	1(1)	2.2
137	Cellulose synthase OS=Spinacia oleracea OX=3562 GN=SOVF_167560 PE=3 SV=1	A0A0K9QMU6	35	118591	1(1)	0.7
138	Usp domain-containing protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9DG99	35	14923	1(1)	6

Continued Table S4

N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
139	Alpha-1,4 glucan phosphorylase OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_2g046340 PE=3 SV=1	A0A0J8E823	35	110302	1(1)	0.6
140	Adenosinetriphosphatase (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9DIR4	34	24101	1(1)	6.5
141	NAD(P)H dehydrogenase (quinone) OS=Spinacia oleracea OX=3562 GN=SOVF_195640 PE=4 SV=1	A0A0K9QC65	34	20094	1(1)	7.4
142	Uncharacterized protein (Fragment) OS=Spinacia oleracea OX=3562 GN=SOVF_207490 PE=3 SV=1	A0A0K9Q8M8	34	20562	1(1)	5.1
143	Malate synthase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8ZIT7	34	46998	1(1)	2.4
144	Phosphoenolpyruvate carboxylase (Fragment) OS=Anredera baselloides OX=1038467 GN=ppc-1E1a PE=4 SV=1	A0A075IYP2	34	36088	1(1)	3.2
145	Protein-methionine-S-oxide reductase OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8YWM6	34	12347	2(2)	20.2
146	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803M627	34	22027	1(1)	5.8
147	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9DPF6	33	56110	1(1)	2.2
148	EngB-type G domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_207810 PE=3 SV=1	A0A0K9QA42	33	23645	1(1)	6.6
149	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8ZTY5	33	12066	1(1)	5.7
150	TCTP domain-containing protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9A5U1	33	12322	1(1)	8.3
151	4HBT domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_212720 PE=3 SV=1	A0A0K9Q7A9	33	17040	1(1)	3.8
152	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_092000 PE=3 SV=1	A0A0K9RAQ0	33	17219	1(1)	8.8
153	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_074910 PE=3 SV=1	A0A0K9RG77	33	286882	1(1)	0.7
154	PB1 domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_166830 PE=4 SV=1	A0A0K9QL33	33	85773	1(1)	0.8
155	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8YCZ0	32	27847	1(1)	4.9
156	Reverse transcriptase domain-containing protein OS=Beta vulgaris subsp. vulgaris OX=3555 PE=4 SV=1	F4NCJ4	32	157039	1(1)	1.1
157	60S ribosomal protein L13 OS=Spinacia oleracea OX=3562 GN=SOVF_142670 PE=3 SV=1	A0A0K9QV99	32	23811	1(1)	2.9
158	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C8YK87	32	11461	1(1)	5.9
159	14_3_3 domain-containing protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9F4I6	32	23421	1(1)	7.8
160	Bifunctional dihydrofolate reductase-thymidylate synthase OS=Spinacia oleracea OX=3562 GN=SOVF_062630 PE=3 SV=1	A0A0K9RIF4	32	63193	1(1)	1.4
161	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_131520 PE=4 SV=1	A0A0K9QX48	32	66773	1(1)	2.8

Continued Table S4

N.	Description	Accession	Score	Mass (Da)	Peptides (Unique)	Coverage (%)
162	Ribosomal_L6 domain-containing protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C8ZLQ1	31	15674	1(1)	10.8
163	Phenylcoumaran benzylic ether reductase-like protein I (Fragment) OS=Cylindropuntia imbricata OX=701514 PE=2 SV=1	A0A3G4R8N0	31	32063	1(1)	4.1
164	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha OS=Spinacia oleracea OX=3562 GN=PFP-ALPHA PE=3 SV=1	A0A0K9QFM3	30	68472	1(1)	1.3
165	Malectin_like domain-containing protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9DPM0	30	69601	1(1)	1.3
166	NTP_transferase domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_118350 PE=4 SV=1	A0A0K9R188	30	45858	1(1)	3.2
167	Tubulin alpha chain OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_5g125100 PE=3 SV=1	A0A0J8E3G3	30	50783	1(1)	2.6
168	Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=4 SV=1	A0A803L2J9	30	181673	1(1)	0.4
169	Uncharacterized protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_2g046040 PE=3 SV=1	A0A0J8E851	30	23784	1(1)	5.2
170	Heat shock protein 90 OS=Salicornia europaea OX=206448 PE=2 SV=1	L7QJJ0	29	79996	1(1)	0.9
171	Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1	A0A7C9A5J3	28	13308	1(1)	13.9
172	Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9CDJ2	28	13581	1(1)	6.8
173	40S ribosomal protein S7 OS=Spinacia oleracea OX=3562 GN=SOVF_134950 PE=3 SV=1	A0A0K9QW07	28	22112	1(1)	4.7
174	Purple acid phosphatase OS=Spinacia oleracea OX=3562 GN=SOVF_092830 PE=3 SV=1	A0A0K9R972	28	60725	1(1)	3
175	AAA domain-containing protein OS=Spinacia oleracea OX=3562 GN=SOVF_151020 PE=3 SV=1	A0A0K9QSR5	28	47213	1(1)	3.1
176	Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_002290 PE=3 SV=1	A0A0K9S456	26	17988	1(1)	5.4
177	Protein kinase domain-containing protein OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_1g021560 PE=3 SV=1	A0A0J8BFG4	25	110090	1(1)	0.7
178	Proteasome subunit beta OS=Opuntia streptacantha OX=393608 PE=3 SV=1	A0A7C9DYH2	20	29808	1(1)	3.3

Table S5. Details for top 10% proteins identified via LC–MS/MS from white-fleshed pitaya seeds allergenicity predicted by three online platforms (Allermatchtm, Algpred 2.0, and AllerCatPro).

Unpredicted top 10% protein		Prediction platform			Allergen information	
N.	Description	Allermatchtm	Algpred	AllerCatPro	Allergen code	Allergen source
1	Uncharacterized protein (Fragment) OS=Beta vulgaris subsp. Vulgaris A0A0J8DSR1	-	-	no	-	-
2	Cupin type-I domain-containing protein OS=Opuntia streptacantha A0A7C8ZNT3	+	+	week	Pollen allergen Coc n1	Cocos nucifera (Coconut)
3	Uncharacterized protein OS=Spinacia oleracea A0A0K9RTZ6	+	+	week	Pollen allergen Coc n1	Cocos nucifera (Coconut)
4	Uncharacterized protein OS=Chenopodium quinoa A0A803LTG6	-	-	no	-	-
5	Heat shock protein 70 OS=Spinacia oleracea A0A1I9TK81	+	+	strong	Tyr p 28	Tyrophagus putrescentiae (Storage mite)

Table S6. Details for top 10% proteins identified via LC–MS/MS from red-fleshed pitaya seeds allergenicity predicted by three online platforms (Allermatchtm, Algpred 2.0, and AllerCatPro)

Unpredicted top 10% protein		prediction platform			Allergen information	
N.	Description	Allermatchtm	Algpred	AllerCatPro	Allergen code	Allergen source
1	Proteasome subunit beta (Fragment) OS=Spinacia oleracea A0A0K9S2G1	-	-	no	-	-
2	Uncharacterized protein (Fragment) OS=Opuntia streptacantha A0A7C8YRP5	-	+	no	-	-
3	Cupin type-1 domain-containing protein OS=Opuntia streptacantha A0A7C8ZNT3	+	+	weak	Pollen allergen Coc n1	<i>Cocos nucifera</i> (Coconut)
4	Uncharacterized protein OS=Opuntia streptacantha A0A7C9B091	+	-	strong	Major latex allergen Hev b 5 Gluten-like Q-repeats	<i>Hevea brasiliensis</i> (Para rubber tree (latex))
5	Heat shock protein 70 OS=Spinacia oleracea A0A1I9TK81	+	+	strong	Tyr p 28	<i>Tyrophagus putrescentiae</i> (Storage mite)
6	Actin 11 OS=Sesuvium portulacastrum A0A1L5JKA9	-	-	no	-	-
7	Ribosomal_L18e/L15P domain-containing protein OS=Beta vulgaris subsp. Vulgaris A0A0J8FEI6	-	-	no	-	-
8	Formamidase OS=Opuntia streptacantha A0A7C9EWT0	-	-	no	-	-
9	Uncharacterized protein OS=Spinacia oleracea A0A0K9RTZ6	+	+	weak	Pollen allergen Coc n1 Gly m Bd 28K	<i>Cocos nucifera</i> (Coconut) <i>Glycine max</i> (Soybean)
10	Uncharacterized protein (Fragment) OS=Opuntia streptacantha A0A7C8YRL3	-	+	no	-	-
11	Proteasome subunit beta OS=Opuntia streptacantha A0A7C9D7H1	-	-	no	-	-

Continued Table S6

Unpredicted top 10% protein		prediction platform			Allergen information	
N.	Description	Allermatchtm	Algpred	AllerCatPro	Allergen code	Allergen source
12	Cupin_5 domain-containing protein OS=Opuntia streptacantha A0A7C9CU14	-	-	no	-	-
13	Uncharacterized protein OS=Opuntia streptacantha A0A7C8ZZS4	-	-	no	-	-
14	GTP-binding nuclear protein OS=Spinacia oleracea A0A0K9R796	-	-	no	-	-
15	Uncharacterized protein OS=Chenopodium quinoa A0A803LTG6	-	-	no	-	-
16	Thioredoxin-dependent peroxiredoxin OS=Tamarix hispida I0CC94	+	+	week	thiol peroxiredoxin	<i>Bombyx mori</i> (domestic silkworm)
17	Uncharacterized protein OS=Opuntia streptacantha A0A7C8Z5R6	-	-	no	-	-

Table S7. CDSs for potential allergens in white- and red-fleshed pitaya seeds.

CDS name	Sequences	Length (bp)	Location on the genome
<i>Su-cupin1</i> Or <i>Sc-cupin1</i>	ATGATGGCACCCCATTTGAATCCAACGGCCACAGAGTATGCCG TAGTTTTTAAGCGGACGAGGAAACATCCAGGTAGTCTACCCAA ACGGAAGCTCAGCGATGAGTGCCAGAGTCAGTGAAGGTGATG TCTTCTGGATTCCAAAGTACTTCCCTTTCTGCCAGATTGCTTCC AGGGCTGGCCCATTCGAGTTCTTGGGATTCACCACCTCAGCTC ACCGGAACCGGCCCCAGTTCTAGTGGGTGCCTCCTCAATCCT GAACACCATGCGAGCCCCGAACTTGCAACTGCTTTTGGCTTA ACCGAAGAGAGGTTTCGGCGAGATTGTGGGTGCTCAGAGAGA GGCGGTCATTCTCCGTCTCCTGCAGCTGCTCCACCCGATGGG AAGGAGCGGTCAAAGTCGGAGGGGGAGGGGTCAAATCCGA GGTGGAGGAAAAGAACAAGCTAGAGGTGCCAAAGTTGACTA GGACTTTAGGTCCAGATATGGTCATGGGTTTTGAGTGA	504	From 65759275 to 65759778

Su and *Sc* are the abbreviations for *Selenicereus undatus* (white-fleshed pitaya) and *Selenicereus costaricensis* (red-fleshed pitaya), respectively.

Continued Table S7

CDS name	Sequences	Length (bp)	Location on the genome
<i>Su-hsp70</i> Or <i>Sc-hsp70</i>	ATGGCCGGTAAAGGTGAAGGTCCGCGCATCGGAATCGATCTCGGAACGACATACTCATGCGTCGGTGTCTGG CAGCATGATCGTGTGAGATCATCGCAATGATCAAGGAAATCGTACCACACCGTCTTATGTTGCTTTCACCGA CACTGAGCGTTTGATCGGTGATGCTGCTAAGAATCAGGTCGCCATGAATCCTACCAACACCGTATTGATGCTA AGAGGCTTATCGGAAGGAGGTTTCAGTGACTCATCTGTTTCAGAATGACATGAAACTCTGGCCATTAAAGGTCAT TGCTGGTGTGGTGACAAGCCTATGATTGTGGTAACATATAAGGGTGAGGAGAAGCAATTTGCAGCTGAAGA GATCTCTCAATGGTCCTCACAAAGATGAAAGAGATTGCGGAGGCCTACCTTGGCTCAACGGTGAAAAACGC TGTTGTCACTGTTCTGCTTACTTCAACGATTCCCAGCGTCAAGCTACAAAGGATGCTGGTGTCAATTGCTGGC TTGAATGTTATGCGAATCATCAACGAGCCAACCGCTGCTGCTATTGCCTATGGTCTTGACAAGAAGGCCACCA GCATTGGCGAGAAGAACGTCCTGATCTTTGATCTTGGTGGTGGTACCTTTGATGTCTCGTTGCTTACTATTGAG GAGGGTATCTTTGAGGTGAAAGCCACAGCTGGAGACACCCATCTTGGTGGTGAGGATTTTGACAACCGAATG GTAAACCATTTTGTCCAGGAGTTCAAGAGAAAAGCACAAAGAAGGATATCAGCGGCAGCCCAAGGGCTCTTAGG AGGCTGAGGACTGCATGTGAGAGGGCAAAGAGGACTCTCTCATCCACTGCCCCAAACCACCATGAAATTGAC TCCCTCTATGAGGGTGTGATTTCTACACCACCATACCCGTGCTCGTTTGGAGGAGCTGAACATGGATTGTT TAGGAAATGTATGGAGCCAGTGGAGAAGTGTGAGGGATGCTAAGATGGACAAGAGTAGCGTGATGATGT TGTCTTGTGGAGGATCCACTAGGATTCCCAAGGTCCAGACGCTGTTGCAGGACTTCTTCAACGGCAAGGA GCTGTGCAAAAGCATTAACCCAGATGAGGCGGTTGCCTATGGTGCCGCTGTGCAAGCTGCCATCTTGAGTGGT GAAGGGAACGAGAAGGTCCAGGACCTCCTGTTGCTCGATGTCACTCCTCTCTCCCTTGGTTTGAAACCGCT GGTGGAGTCATGACTGTGTTGATCCCTAGGAATACCACCATTCCAACCAAGAAAAGAGCAGGTCTTCTCAACG TACTCGGACAACCAGCCGGGTGTGTTGATCCAGGTTTACGAGGGTGAGAGAACTCGGACACGGGATAACAAC TTGCTGGGAAAAGTTTGAGCTTTCCGGCATCCCTCCCGCCCTAGAGGTGTACCCAGATTACAGTGTGCTTTG ACATTGATGCCAATGGTATCTTGAATGTTTCTGCTGAGGACAAGACTACTGGGCAGAAGAACAAGATCACCAT CACCAACGACAAGGGCAGGTGTCAAAAGAAGAGATCGAGAAGATGGTCCAGGAGGCTGAGAAGTACAAG ACTGAAGATGAGGAGCACAAAGAAGAAGGTGGAGGCAAAGAATGCTTTGGAGAACTACGCCTACAACATGAG GAATACTGTAAGGGATGAGAAGATTGGTGCGAAGTTGCGCAGAGGCCGACAAGAAGAAGATCGAGGATGCTAT CGACAATGCCATCCAGTGGTTGGATAATAATCAGCTTGCTGAGGCTGATGAATTTGAGGACAAAATGAAGGAG CTCGAGAGTATCTGCAACCCCATATTGCCAAGATGTACCAGGGTGTGCTGGGGGTGACATGGGTGGTGCC ATGGATGATGATGCCCCCTCTGCTGGTGCAAGTGGCGCTGGTCCCAAGATTGAGGAGGTTGATTAA	1949	From 32343233 to 32344969 and from 32345659 to 32345870
<p><i>Su</i> and <i>Sc</i> are the abbreviations for <i>Selenicereus undatus</i> (white-fleshed pitaya) and <i>Selenicereus costaricensis</i> (red-fleshed pitaya), respectively.</p>			

Continued Table S7

CDS name	Sequences	Length (bp)	Location on the genome
<i>Sc- hsp sti 1</i>	ATGGCTGAAGAGGCCAAAGCCAAAGGCAACGCCGCCTTCGC CGCCGGCAACTACACGGAGGCCATTAAGCACTTCACGGAGGG GATCATCCTGGCCCCACCAACCACGTCTCTACTCCAACAGA TCCGCCGCATACGCCTCCCTCCACAATACTCCGACGCCCTCT CCGATGCCAAGAAGACGGTCGACCTCAAGCCCGACTGGTCCA AGGGCTACAGCCGCCTTGGCGCCGCCTATCTCGGCCTCCATAA CTACTCCGAAGCCATCGCCGCCTACAAGCATGGCCTTGAAATC GACCCCAATAACGAGGCTCTGAAATCCGGCTTAGCCGATGCG CAAGCAGCCGCCGCCGCCCGAGCCAGGTCGACCTCGCCGCCT TCCCCCTTCGGCGACGTCTTCTCCGGGCAGGAGATGTGGGCC AAGCTCACGGCGGACCCCACTCGGGCATTCCTCCAGCAG CCTGATTTCTGTCAGCATGATGCAGGACATTCAGAAGAACCCTA ATAATCTGAATCTATACTTGAAGGATCAGAGGGTTATGCAGGC TCTTGGGGCTCTTTGAATGTCAAATTGAGGACTGCAACTGAG GATATGGAAGTGGAACACCTTTTCTGAGGAGGAGCCGGTG AAGAAGCCCGAGCCAGAGCCTCGACGGGAGCCGGAGCCTGA GCCCATCGAGCTGGCGGAGGAGAGAGAGAAAGGAAGGAA AAGAAGGCATTGGCCCAGAAGGAGAAAAGAGGCTGGCAATGC TGCTTATAAGAAGAAGGATTTTGAAGGCTGCTATTCAGCATTAC ACCAAGGCCATTGAATTGGATGATGAGGATATTTCCTTCTTCA CTAATCGTGCTGCTGTTTACTTGGAGATGGGAAAGGTACGATG AGTGTATCAAAGACTGTGACAAAGCTGTTGAAAGAGGAAGG GAACTTCGATCAGACTACAAGATGATAGCAAGGGCTTTGACC AGGAAAGGAACTGCCTTGGTTAAGATGGCAAAGACTTCAAAG GACTTTGAGACGGCTATTGAAGCTTTTCAGAAAGCTCTCACTG AGCATCGCAATCCTGATACATTGAAAAAGTTGAACGATGCTGA AAGAGCAAAGAAAGAACTAGAGCAGCAGGAGTACTTTGATC CAAAAATAGCCGATCAGGAACGTGAAAAAGGAGGCATATAGC AACAGAGCTGCATGTTACACGAAATTGGGGGCATTGCCAGAA GCTCTAAAAGATGCAGAGAAGTGATCAAGCTTGATCCTACAT TTGTGAAGGGATATACTAGGAAGGGTGCTGCCAGTTTTTGAT GAAGGAGCATGATAAAGCATTGGAAACCTATCAAGAAGGGCT TAAGCATGATCCCAACAACCAGGAATTGTTGGATGGGGTGCG GAGGTGTGTCAGGTATTGATTGACTTCCAAGAGAATCCAAAG GCAGCACAAAGAGCATATGAAGAACCCAATGGTGATGAACAAG ATCCAGAAGCTGGTCAGCGCTGGAATTGTCCAAGTCAGATGA	1519	From 8614836 to 8615721, from 8616533 to 8616816, from 8617196 to 8617427, from 8617842 to 8617958

Su and *Sc* are the abbreviations for *Selenicereus undatus* (white-fleshed pitaya) and *Selenicereus costaricensis* (red-fleshed pitaya), respectively.

Supplement information S8. The distribution of identified peptides in the top 10% of protein identified via LC–MS/MS in excised gel spot from white-fleshed pitaya seeds (The peptides coverages have been marked with highlight).

>tr|A0A0J8DSR1|A0A0J8DSR1_BETVV Uncharacterized protein (Fragment) OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_027930 PE=3 SV=1

SIRVAPLRAMCDDEVQALVVDNGSGMVKAGFAGDDAPRAVFPISVGRPRHTGIMVGATQ
KDAYVGDEAQAKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAP
LNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASGRRTGIVLDCGDGVSHTVPIYEGYA
LPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDIKEKLAYCALDFDTEM

>tr|A0A7C8ZNT3|A0A7C8ZNT3_OPUST Cupin type-1 domain-containing protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1

MMAPHLNPMATEYGIVLSGRGKIQVVYPNGSSAMNARVSEGDVFWIPKYFPFCQIASRTG
PFEFFGFTTSAHRNRPQFLVGASSILNAMRGPELATAFGLTEERFDEIVSAQREAVILPSPAA
APPDESGGSKSEQEGLDSETEKKKTVVPKLIRTLGPAMVMGFE

>tr|A0A0K9RTZ6|A0A0K9RTZ6_SPIOL Uncharacterized protein OS=Spinacia oleracea OX=3562 GN=SOVF_029540 PE=4 SV=1

MGRLKGVLLVALVVCYAMQVVVSQS YEERRRERELMSPEEEERRAKEEDWRRREKTAEE
ERRHRSWEEEEEEEEERGRKWDEDEEEQEEEEERGRQPRPKPRPEPYRPGGRGEGMF
VLRDSKKVISTQAGEMRVVRGYGGKIVENPLDIGFITMEPRSLFVPQYLDSSLIIFLRRGEA
KLGFYDDELSEKQLKMGDVYRIPAGSTFYIVNTGETQRLHIICSIDPSEGLGFSTFQSFFIGG
GTNPVSVLAGFDPETLSTAFNVSIGELRGFMTGQDAGPIIFADTTTHSPSLWANFLKVKGEEER
LERLKTVAESGEQKEEEEEEPKSWWNIFDSLIGSENKKGEKKGDTRTGSSPDSYNLLDRE
PSYRNNYGWSIAVDKHEYKPLKKSIGGVYLVNLTAGSMMPHVNPIMATEYGVVLSGVGT
IQVVYPNGTSAMNTNVKEGDVFWIPRYFPFCQIASRSGSFEFFGFTTSAHRNRPQFLVGAS
SILRSMRGPEFATAFGLTEDRYNEIVDAQREALILPSPSAASGDTREFEEKEQSSQEKKPESK
EQEKEKPGIEKVPKFMRTLGPIMMGFE

>tr|A0A803LTG6|A0A803LTG6_CHEQI Uncharacterized protein OS=Chenopodium quinoa OX=63459 PE=3 SV=1

MRQCLIYDSPEADARLIGIEYIVSEDLFMTLPDAEKRLWHSHEYEVKSGVLFLPGVPGAM
QRPDLAKVAQTYGKTIHFQVDRGDNLPGLPQIMMALTRDGQLYTHLASDVEKKYNV
NFEKERENRAYMKGLEHGIHPLANAEKGKLRTELREVDCHGGAGAHSTPRVFV

>tr|A0A1I9TK81|A0A1I9TK81_SPIOL Heat shock protein 70 OS=Spinacia oleracea OX=3562 GN=HSP70-13 PE=2 SV=1

MSGKGEGPAIGIDLGTYSVGVWQHDRVETIANDQGNRTTPSYVAFTDTERLIGDAAKN
QVAMNPTNTVFDAKRLIGRRVSDPSVQADMKLWPFKVIPGPADKPMIVVNYKGEEKQFS
AEEISSMVLTKMKEIAEAFLGTTIKNAVVTVPAYFNDSQRQATKDAGVISGLNVMRIINEPT
AAAIAYGLDKKASSSGEKHVLIFDLGGGTDFVSLLTIEEGIFEVKATAGDTHLGGEDFDNR
MVNHVQVEFRKHKKDISGNPRSLRRLRTACERAKRTLSSTAQTIEIDSLYEGVDFTTIT
RARFEELNMDLFRKCMPEVVEKCLRDAKMDKGNVDDVVLVGGSTRIPKVQQLQDFFNG

KELCKSINPDEAVAYGAAVQAAILS GEGNEKVQDLLLLDVTPLSLGLETAGGVMTVLIPRN
TTIPTKKEQVFSTYSDNQPGVLIQVFEGERTTRDNNLLGKFELTGIPPAPRGVPQINVCFDI
DANGILNVSAEDKTTGQKNKITITNDKGRLSKEEIEKMQEAERYKSEDEEHKKKVEAKN
ALENYAYNMRNTIKDDKINSKLDAADKKKIEEAIEQAIQWLDGNQLAEADEFDKMKEL
EGICNP IAKMYQGGAGAGPDMGGTMDEDAPSAGGASGAGPKIEEVD

Supplement information S9. The distribution of identified peptides in the top 10% of protein identified via LC–MS/MS in excised gel spot from red-fleshed pitaya seeds (The peptides coverages have been marked with highlight).

>tr|A0A0K9S2G1|A0A0K9S2G1_SPIOL Proteasome subunit beta (Fragment) OS=Spinacia oleracea OX=3562 GN=SOVF_007620 PE=3 SV=1
VLCDLHLYSPLSSFPFHHLQNRPIQLQPLSLSPQHTKMEDLGLNAPHSMGTTIIGVTYKDG
VILGADSRTSTGVYVANRASDKITQLTDNVYVCRSGSAADSQIVSDYVRYFLHQHTIQLGQ
PATVKVAANLVRLAYGNKDTLQTMIVGGWDKYEGGKIYGIPLGGTIIQQPFSIGSGSS
YLYGFLDQAWKDGMSKDEAEELVKKAVSLAIARDGASGGVVRTVIINEEGVTRNFYPGD
QLPLWHEELEPQNSLLDIWGAAAASPVPMTE

>tr|A0A7C8YRP5|A0A7C8YRP5_OPUST Uncharacterized protein (Fragment) OS=Opuntia streptacantha OX=393608 PE=4 SV=1
VYVCRSGSAADSQIVSDYVRYFLHQHTIQLGQPATVKVAANLVRLAYNNKNMLQTGLIV
GGWDKYEGGKIYGIPLGGTIIQQPFAIGSGSSYLYGFFDQAWREGMTKEEAEQLVVKAVS
LAIARDGASGGVVRTVINSEG

>tr|A0A7C8ZNT3|A0A7C8ZNT3_OPUST Cupin type-1 domain-containing protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1
MMAPHLNPMATEYIGIVLSGRGKIQVVYPNGSSAMNARVSEGDVFWIPKYFPFCQIASRTG
PFEFFGFTTSAHRNRPQFLVGASSILNAMRGPELATAFGLTEERFDEIVSAQREAVILPSPAA
APPDESGGSKSEQEGLDSETEKKKTVVPKLI RTLG PAMVMGFE

>tr|A0A7C9B091|A0A7C9B091_OPUST Uncharacterized protein OS=Opuntia streptacantha OX=393608 PE=4 SV=1
MADEAKAKGNAAFSAGNYTEAIKHFTAINLAPTNHVLYSNRSAAYASLHNYSDALSDA
KKTVELKADWSKGY SRLGAAYLGLHQYSDAIAAYKQGLEIDPNNEALKSGLADAQAAA
RAKSTPLPSPFGDVFSGPEMWAKLTADPATRAFLQQPDFVSMQDIQKNPSNLNLYLKDQ
RVMQALGVLLNVKLRTAPEDMEVPPAEELPLKKEEPAKKPEPKPQPQPEPEPEPVAEEEEKE
KKERKALAQKEKEAGNAAYKKKDFETAIQHYTKAIELDDEDISFLTNRAAVYLEMGKYD
ECIKDCDKAVERGRELRSDFKMIARALTRKGTA FVKMAKTSKDYEP AIEAFQKALTEHRN
PDTLKKLNEAGRAKKELEQQEYFDPKIADEEREKGNEYFKEQKYPEAVKHYTEAIKRNP
DPKAYS NRAACYTKLGALPEGLRDAEKCIELDPTFVKGYTRKGAVQFFMKEYDKALETY
QEGCLKLDPNNQELLDGVRRCVEQINKASRGDLSPEELKERQAKAMQDPEIQTILTDPMR
QVLIDFQENPKAAQEHMKNPMVMNKKIQLVSAGIVQVR

>tr|A0A1I9TK81|A0A1I9TK81_SPIOL Heat shock protein 70 OS=Spinacia oleracea OX=3562 GN=HSP70-13 PE=2 SV=1
MSGKGEGPAIGIDLGTYS CVGVWQHDRVEIIANDQGNRTTPSYVAFTDTERLIGDAAKN
QVAMNPTNTVFDAKRLIGRRVSDPSVQADMKLWPFKVIPGPADKPMIVVNYKGEEKQFS
AEEISSMVLTKMKEIAEAF LGTTIKNAVVTVPAYFNDSQRQATKDAGVISGLNVMRIINEPT
AAAIAYGLDKKASSSGEKHVLIFDLGGGTFDVSLLTIEEGIFEVKATAGDTHLGGEDFDNR
MVNHVFQEFRRKHKKDISGNPRSLRRLRTACERAKRTLSSTAQT TIEIDSLYEGVDFYTTIT

RARFEELNMDLFRKCMEPVEKCLRDAKMDKGNVDDVVLVGGSTRIPKVQQLLQDFFNG
KELCKSINPDEAVAYGAAVQAAILSGEGNEKVQDLLLLDVTPLSLGLETAGGVMTVLIPRN
TTIPTKKEQVFSTYSNDQPGVLIQVFEGERTRTDNNLLGKFELTGIPPAPRGVQPINVCFDI
DANGILNVSAEDKTTGQKNKITITNDKGRLSKEEIEKMQEAERYKSEDEEHKKKVEAKN
ALENYAYNMRNTIKDDKINSKLDAAADKKKIEEAIEQAIQWLDGNQLAEADEFDKMKEL
EGICNPPIAKMYQGGAGAGPDMGGTMDDEDAPSAGGASGAGPKIEEVD

>tr|A0A1L5JKA9|A0A1L5JKA9_SESPO Actin 11 OS=Sesuvium portulacastrum OX=221166
PE=2 SV=1

MCDDVQALVIDNGSGMCKAGFAGDDAPRAVFPISVGRPRHTGVMVGMGQKDSYVGDEA
QSKRGILTLYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREK
MTQIMFETFNTPAMYVAIQAVLSLYASGRITGIVMDSGDGVTHTVPIYEGYALPHAILRLD
LAGRDLTDYLMKILTERGYSFTTTAEREIVRDIKEKLAYVALDFEQEMQTAASSSSLEKSYE
LPDGQVITIGNERFRCPEALFQPSFLGMEAAGVHETTYNSIMKCDVDIRKDLYGNVVLSG
GSTMFPGIADRMQKELTALAPSTIKIKIIPPERKYSVWIGGSILASLSTFQQMWISKEEYDE
SGPSIVHRKCF

>tr|A0A0J8FEI6|A0A0J8FEI6_BETVV Ribosomal_L18e/L15P domain-containing protein
OS=Beta vulgaris subsp. vulgaris OX=3555 GN=BVRB_4g076000 PE=3 SV=1

MGIDLKAGGKSKTKRTAPKSNVDVYLKLLVKLYRFLVRRTGSSFNQVVLKRLFMKINKA
PLSLRLITYMKGKEDKIAVIVGAVTDDIRVYEVPAKVTALRFTETARARIEKAGGECLTF
DQLALRAPLGQNTVLLRGPKNAREAVKHFGKAPGVPHSHTKPYVRANGRKFERARGRR
NSRGYRV

>tr|A0A7C9EWT0|A0A7C9EWT0_OPUST Formamidase OS=Opuntia streptacantha
OX=393608 PE=4 SV=1

NTLARSERPSIPRSPEGTKEMATSYGARTVIAVDVTKKPWEQKPPLHNRWHPDIPPVAVK
AGEVFRVEMVDFSGGITKDYTAEDVKYADPSVVHYLSGPIKVCDEAGVPAKPGDLLAVE
ICNLGPLPGDEWGYTATFDRENGGGFLTDHFPCATKAIWYFEGIYAYSPHIPGVRFPGLTHP
GIIGTAPSKQLLDIWNERRDVEENGLQSLKLCEVLHSRPLANLPSPKGCLLGKIEKGTPE
WEKIAREAARTIPGRENGGNCIDIKNLSRSGKIYLPVFVEGANLSTGDMHFSQGDGEVSFC
GAIEMSGFLELKCDIIRGGMKEYLTPMGPTPLHVNPIFEIGPVEPRFSEWLVEGISVDESGR
QHFLDASIAYKRAVLNAIDYLSKFYSKEQVYLLSCCPCEGRISGIVDAPNAVATLAIPTSI
FDQDIRPKTSKVPVGPRLVRKADVCLKCTYDGHLPVTRNPAASS

>tr|A0A0K9RTZ6|A0A0K9RTZ6_SPIOL Uncharacterized protein OS=Spinacia oleracea
OX=3562 GN=SOVF_029540 PE=4 SV=1

MGRLKGVLLVALVVCYAMQVVVSQSYEERRRERELMSPEEEERRAKEEDWRRREKTAEE
ERRHRRSWEEEEEEEEERGRKWDEDEEEQEEEEERGRQPRPKRPEPYRPGGRGGEGMF
VLRDSKKVISTQAGEMRVVRGYGGKIVENPLDIGFITMEPRSLFVPQYLDSSLIIFLRGEA
KLGFIYDDELSEKQKMGDVYRIPAGSTFYIVNTGETQRLHIICSIDPSEGLGFSTFQSFFIGG
GTNPVSVLAGFDPETLSTAFNVSIGELRGFMTGQDAGPIIFADTTTHSPSLWANFLKVKGEER
LERLKTVAESGEQKEEEEEPRKSWWNIFDSLIGSENKKGEKKGDTRTGSSPDSYNLLDRE
PSYRNNYGWSIAVDKHEYKPLKKSIGIGVYLVNLTAGSMMAHPVNPIMATEYGVVLSGVGT

IQVVYPNGTSAMNTNVKEGDVFWIPRYFPFCQIASRSGSFEFFGFTTSAHRNRPQFLVGAS
SILRSMRGPEFATAFGLTEDRYNEIVDAQREALILPSPSAASGDTREFEEKEQSSQEKKPESK
EQEKEKPGIEKVPKFMRTLGPPEMIMGFE

>tr|A0A7C8YRL3|A0A7C8YRL3_OPUST Uncharacterized protein (Fragment) OS=Opuntia
streptacantha OX=393608 PE=4 SV=1

CRSGSAADSQVVSDYVRYFLHQHTIQLGQPATVKVAANLVRLLAYNNKNMLQTGLIVGG
WDKYDGGKIYGIPLGGTLIEQPFAIGGSGSTYLYGFFDQAWKEGMDKDEAEQLVVKAIVSL
AIARDGASGGVVRTVIINSEGVTRNFY

>tr|A0A7C9D7H1|A0A7C9D7H1_OPUST Proteasome subunit beta OS=Opuntia
streptacantha OX=393608 PE=3 SV=1

MECVFGLVGNGFAIIAADTSVHLSILVHKSNEKDIMILDSHKLMDGASGESGDRVQFTEYIQ
KNVALYQFRNGIPLTAAAAANFTRGELATALRKSPYFVNILLAGYDKETGPSLYFIDYIATL
HKVDKGAFGYGSYFALSMMDRHYHSGMSVEEAIDLVDKCIVEIRSRLVVAPPNFVIKIVDE
KGAREYGWRESVKDTTFPRVS

>tr|A0A7C9CU14|A0A7C9CU14_OPUST Cupin_5 domain-containing protein OS=Opuntia
streptacantha OX=393608 PE=4 SV=1

EREREREREREMVGTSQLVEKLNKKAHVEGGYFHETFRDHSITLSKSHLPPQYKVDRPVST
AIYFLLPAGSVSKLHRIPMAETWHFYLGEPIMIVELNEKDASVKLTCLGPNLMENQQPQYT
VPPNVWFGSFPTKDISISPNGVATKAEPDPETHFSLVGCTCAPAFQFEDFELAKRSELVSLF
PNYESLISLLTSSD

>tr|A0A7C8ZZS4|A0A7C8ZZS4_OPUST Uncharacterized protein OS=Opuntia
streptacantha OX=393608 PE=3 SV=1

MFLVDWIFYGILASLGLWQKEAKILFLGLDNAGKTTLLHMLKDERLVQHQPQYPTSEELS
IGKIKFKAFDLGGHQIARRVWKDYAKVDVYLVLDAYDKERFAESKKELDALLSDEAL
ANVPFLILGNKIDIPYAASEEELRYHLGLTNFTTGKGVNLADSNVRPMEVFMCSIVKKM
GYGEGFRWLSQYIK

>tr|A0A0K9R796|A0A0K9R796_SPIOL GTP-binding nuclear protein OS=Spinacia oleracea
OX=3562 GN=SOVF_098770 PE=3 SV=1

MALPNQQTVDYPSFKLVLVGDGGTGKTTFVKRHLSGEFEKKYEPTIGVEVHPLDFHTNCG
QIRFYCWDTAGQEKFGGLRDGYIYGQCAIIMFDVTARLTYKNVPTWHRDLRCVCENIPI
VLCGNKVDVKNRQVKAKQVTFHRKKNLQYYEISAKSNYNFEKPFLYLARKLAGDQNLH
FVESPALAPPEVQIDLAEQQRHEQELAVAAAQPLPDDDDDAFE

>tr|A0A803LTG6|A0A803LTG6_CHEQI Uncharacterized protein OS=Chenopodium quinoa
OX=63459 PE=3 SV=1

MRQCLIYDSPEADARLIGIEYIVSEDLFMTLPDAEKRLWHSHEYEVKSGVLFLPGVPGAM
QRPDLAKVAQTYGKTIHFWQVDRGDNPLGLPQIMMALTRDGQLYTHLASDVEKKYNV
NFEKERENRAYMKGLEHGIHPLANAEGKGLRTELREVDCHGGAGAHSTPRVVF

**>tr|I0CC94|I0CC94_9CARY Thioredoxin-dependent peroxiredoxin OS=Tamarix hispida
OX=189793 GN=Prx2 PE=2 SV=1**

MACAAPTSAAVLSPSSSNPRAAGKLAAASIAKPFAQTLTAQNSFSGLRSSSSLRHFPLPASS
CRSSHSARRSFVVRAGELPLVGNEAPDFEAEAVFDQEFINVKLSDYRGKKYVILFFYPLDF
TFVCPTEITAFSDRCAEFEKLNTEVLGVSVDSVFSHLAWVQTDRKSGGLGDLKYPLISDVT
KSVSKAYNVLIPDQGIALRGLVIIDKEGIIQHSTINNLAIGRSVDETLRTLQALQYVQENPDE
VCPAGWKPGEEKSMKPDPKLSKEYFAAI

**>tr|A0A7C8Z5R6|A0A7C8Z5R6_OPUST Uncharacterized protein OS=Opuntia
streptacantha OX=393608 PE=3 SV=1**

MFLVDWIFYGILASLGLWQKEAKILFLGLDNAGKTTLLHMLKDERLAQHQPQTQYPTSEELS
IGRIKFKAFDLGGHQIARRVWKDYAQAQVDAVVYLVDAFDRERFAESKRELDALLSDESLA
KVPFLILGNKIDIPYAASEEELRYALGLMNCTSGKGTVNLEGTNVRPLEVFMCSIVRKMGY
GEGFKWMSQYIK