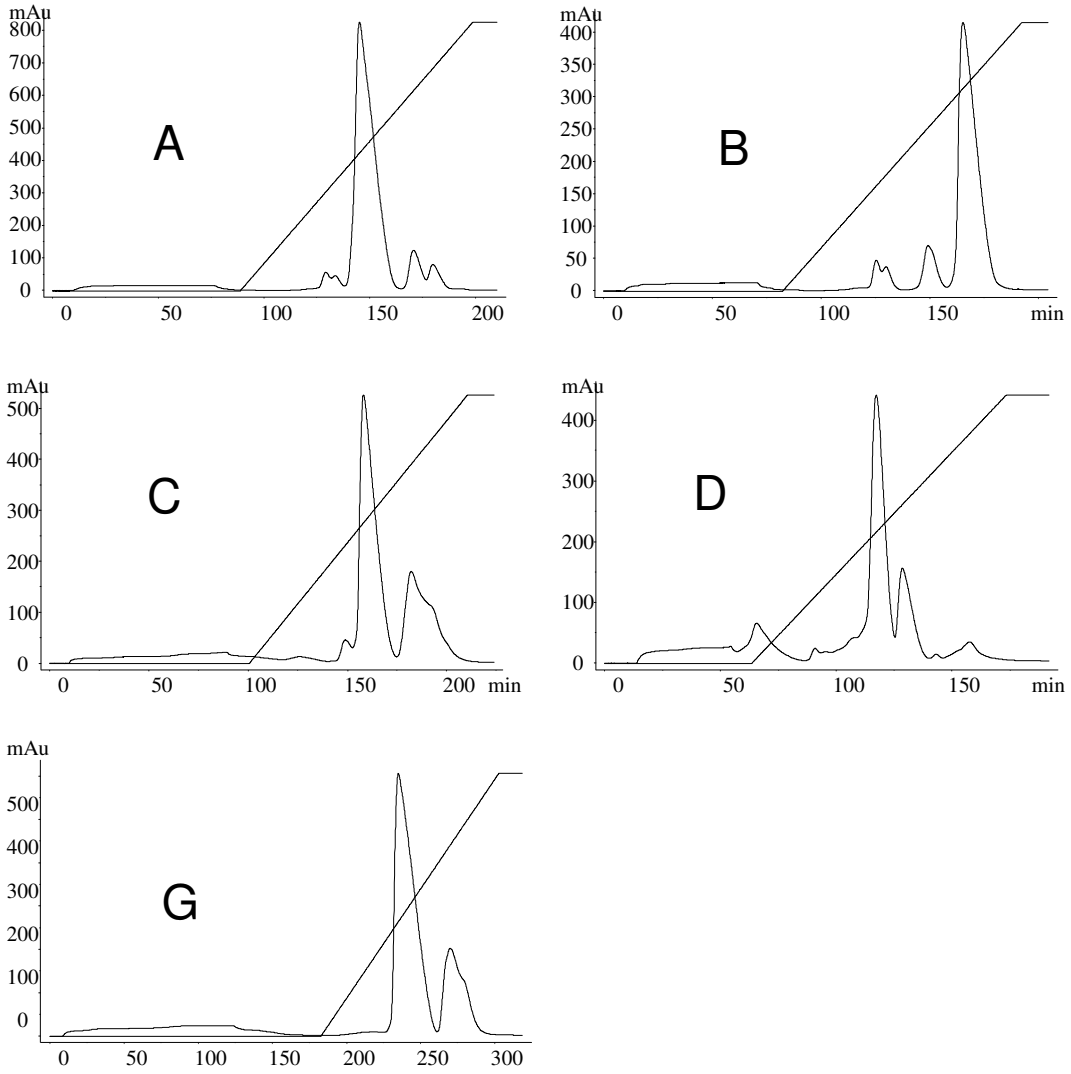

Figure S1. HIC chromatograms of SCX fractions –A, -B, -C, -D, and –G.

Table S1. Characteristics of un-purified proteins.

protein	X!Tandem			top annotated BlastP result (identities)	SignalP cleavage site	theoretical	
	top ranked protein	peptides matched	log(e)			MW	pI
Protein D1 low MW contaminant	gi|225439679|ref|XP_002271116.1| PREDICTED: lipid transfer protein [Vitis vinifera]	16	-184.5		VEA-TI	9060	9.16
SCX-G late eluting peak by HIC	gi|225466093|ref|XP_002265534.1| PREDICTED: hypothetical protein [Vitis vinifera]	32	-228.6	gi|1839578|gb|AAB47171.1| vacuolar invertase 1, GIN1 [Vitis vinifera=grape berries, Sultana, berries, Peptide, 642 aa] (627/649)	not predicted	72051	4.59

Figure S2. Sequences matched by X!Tandem to peptide nanoLC-MS/MS data. Underlined residues indicate sequence coverage by nanoLC-MS/MS data.

Protein A:

```
  1 MAAKLLTVLLVGALFGAAVAQNCGCASGLCCSKYGYCGTGSDYCGDGCQSGPCDSSSGSG  60
 61 SSVSDIVTQSFFDGIINQAASSCAGKNFYTRAAFLSALNSYSGFGNDGSTDANKREIAAF  120
121 FAHVTHETGHFCYIEEINGASHNYCDSSNTQYPCVSGQNYYGRGPLQLTWNYNYGAAGNS  180
181 IGFNGLSNPGIVATDVVTSFKTALWFWMNNVHSVIGQGFGATIRAINGAVECNGGNTAAV  240
241 NARVQYYKDYCSQLGVSPGDNLTC                                      264
```

Protein B:

```
  1 MGLCKILSISSFLLTALFFTPSYAATFNIQNHCSYTVWAAAVPGGGMQLGSGQSWSLNVN  60
 61 AGTTGGRVWARTNCNFDASGNGKCETGDCGGLLQCTAYGTPPNTLAEFALNQFSNLDFFD  120
121 ISLVDGFNVPMAFNPTSNGCTRGISCTADIVGECPAALKTTGGCNNPCTVFKTDEYCCNS  180
181 GSCNATDYSRFFKTRCPDAYSYPKDDQTSTFTCPAGTNYEVVFCP                 225
```

Protein C:

```
  1 MRFTTTLPILIPLLLSLLFTSTHEATFDILNKCTYTVWAAASPGGGRRLDSGQSWTITVN  60
 61 PGTTNARIWGRTSCTFDANGRGKCETGDCNGLLECQGYGSPPNTLAEFALNQPNNLDYID  120
121 ISLFDGFNIPMDFSGCRGIQCSADINGQCPSELKAPGGCNNPCTVFKTNEYCCTDGPGSC  180
181 GPTTYSKFFKDRCPDAYSYPQDDKTSLFTCTSGTNYKVTFCP                    222
```

Protein D1:

```
  1 MPLTIMAKEQVCKNHNIFFLSSPFYPINTPLPSPSSHHSFSLLPSTITSPKNGSQALLTI  60
 61 LLVGVLLAALQGSTVAQNCGCASGLCCNKFGYCGTGNAYCGDGCQAGPCYSSGGSSGGVS  120
121 VADVVTQAFFNGIINQAAGNCEGKHFYTRAAFLSALNSYPGFGKDGSADQSKREIAAFFA  180
181 HVTHETGHFCYINEINGASPNYCDSSNTQNPCVAGQKYYGRGPLQISWNYNYGPAGKSIG  240
241 FNGLSNPGIVATNADISFKTALWFWMNNVHSVVNQGFGATIQAIDGAIECNGGSPSSVDA  300
301 RVQYYKNYCSQFGVSPGDYLLRYYVIF                                   327
```

Protein D2:

```
  1 MRFTTTLPILIPLLLSLLFTSTHEATFDILNKCTYTVWAAASPGGGRRLDSGQSWTITVN  60
 61 PGTTNARIWGRTSCTFDANGRGKCETGDCNGLLECQGYGSPPNTLAEFALNQPNNLDYID  120
121 ISLFDGFNIPMDFSGCRGIQCSADINGQCPSELKAPGGCNNPCTVFKTNEYCCTDGPGSC  180
181 GPTTYSKFFKDRCPDAYSYPQDDKTSLFTCTSGTNYKVTFCP                    222
```

Protein F1:

```
  1 MAAKLLTVLLVGALFGAAVAQNCGCASGLCCSKYGYCGTGSDYCGDGCQSGPCDSSSGSG  60
 61 SSVSDIVTQSFFDGIINQAASSCAGKNFYTRAAFLSALNSYSGFGNDGSTDANKREIAAF  120
121 FAHVTHETGHFCYIEEINGASHNYCDSSNTQYPCVSGQNYYGRGPLQLTWNYNYGAAGNS  180
181 IGFNGLSNPGIVATDVVTSFKTALWFWMNNVHSVIGQGFGATIRAINGAVECNGGNTAAV  240
241 NARVQYYKDYCSQLGVSPGDNLTC                                      264
```

Protein F2:

```
  1 MGLCKILSISSFLLTALFFTPSYAATFNIQNHCSYTVWAAAVPGGGMQLGSGQSWSLNVN  60
 61 AGTTGGRVWARTNCNFDASGNGKCETGDCGGLLQCTAYGTPPNTLAEFALNQFSNLDFFD  120
121 ISLVDGFNVPMAFNPTSNGCTRGISCTADIVGECPAALKTTGGCNNPCTVFKTDEYCCNS  180
181 GSCSATDYSRFFKTRCPDAYSYPKDDQTSTFTCTAGTNYEVVFCP                 225
```

Protein G:

```
  1 MRFTTTLPILIPLLLSLLFTSTHAATFDILNKCTYTVWAAASPGGGRRLDSGQSWTITVN  60
 61 PGTTNARIWGRTSCTFDANGRGKCETGDCNGLLECQGYGSPPNTLAEFALNQPNNLDYID  120
121 ISLVDGFNIPMDFSGCRGIQCSVDINGQCPSELKAPGGCNNPCTVFKTNEYCCTDGPGSC  180
181 GPTTYSKFFKDRCPDAYSYPQDDKTSLFTCPSGTNYKVTFCP                    222
```

Protein H1:

```
  1 MPLTIMAKEQVCKNHNIFFLSSPFYPINTPLPSPSSHHSFSLLPSTITSPKNGSQALLTI  60
 61 LLVGVLLAALQGSTVAQNCGCASGLCCNKFGYCGTGNAYCGDGCQAGPCYSSGGSSGGVS  120
121 VADVVTQAFFNGIINQAAGNCEGKHFYTRAAFLSALNSYPGFGKDGSADQSKREIAAFFA  180
181 HVTHETGHFCYINEINGASPNYCDSSNTQNPCVAGQKYYGRGPLQISWNYNYGPAGKSIG  240
241 FNGLSNPGIVATNADISFKTALWFWMNNVHSVVNQGFGATIQAIDGAIECNGGSPSSVDA  300
301 RVQYYKNYCSQFGVSPGDYLLRYYVIF                                   327
```

Protein H2:

```
  1 MRFTTTLPILIPLLLSLLFTSTHAATFDILNKCTYTVWAAASPGGGRRLDSGQSWTITVN  60
 61 PGTTNARIWGRTSCTFDANGRGKCETGDCNGLLECQGYGSPPNTLAEFALNQPNNLDYID  120
121 ISLVDGFNIPMDFSGCRGIQCSVDINGQCPSELKAPGGCNNPCTVFKTNEYCCTDGPGSC  180
181 GPTTYSKFFKDRCPDAYSYPQDDKTSLFTCPSGTNYKVTFCP                    222
```

Protein I:

```
  1 MRFTTTLPILIPLLLSLLFTSTHAATFDILNKCTYTVWAAASPGGGRRLDSGQSWTITVN  60
 61 PGTTNARIWGRTSCTFDANGRGKCETGDCNGLLECQGYGSPPNTLAEFALNQPNNLDYID  120
121 ISLVDGFNIPMDFSGCRGIQCSVDINGQCPSELKAPGGCNNPCTVFKTNEYCCTDGPGSC  180
181 GPTTYSKFFKDRCPDAYSYPQDDKTSLFTCPSGTNYKVTFCP                    222
```

Protein D1 low molecular weight contaminant (lipid transfer protein):

```
  1 MGSSGAVKLACVMVICMVVAAPAAVEATITCGQVASAVGPCASYLQKGGSVPAGCCSGIK  60
 61 SLNSAAKTTVDRQAACKCLKTFSGSIPGINFGLASGLPGKCGVSVPYKISPSTDCSKVT  119
```

SCX-G late eluting fraction by HIC (invertase):

```
  1 MDTHHATSHDLLHDEAYAPLPYSPLPDHPVPAGAPALGQRRPLKVFAVTLASLMFLASLV  60
 61 ALVIHQSPQTPVTVDNDGPSMEREGRGVAQGVSEKSFLGFSGRRLSYNWTTAMFAWQRTA  120
121 FHFQPEKNWMNDPDGPLFHMGWYHLFYQYNPDSAVWGNITWGHAVSRDMIHWLYLPLAMV  180
181 PDRWFDLNGVWTGSATILPNGQIIMLYTGDTNDSVQVQNLAYPANLSDPLLLHWIKYENN  240
241 PVMVPPAGIGSDDFRDPTTMWVGADGNWRVAVGSLVNTTGIVLVFQTTNFTDFELLDGEL  300
301 HGVPGTGMWECVDFYPVSINGVYGLDTSAHGPGIKHVLKASMDDNRHDYYALGEYDPMTD  360
361 TWTPDDPELDVGIGLRLDYGKYYASKTFYDQVKKRRILYGWISEGDIESDDLKKGWASLQ  420
421 SIPRTVLHDNKTGTYLLLWPIEEVESLRTNSTEFEDVLLEPGSVVPLDIGSASQLDIVAE  480
481 FEVDNETLEAMVEADVIYNCSTSAGAAGRGALGPFGILVLADDTLSELTPIYFYIAKDTD  540
541 GSYKTFFCTDLSRSSLAVDDVDQRIYGSIVPVLDDEKPTMRVLVDHSIVEGFSQGGRSCI  600
601 TTRVYPTEAIYGAARLFLFNNATGVNVTASIKIWEMASADIHPYPLDQP              649
```