

Protein View: XP_022027330.1

phospholipase SGR2 isoform X2 [Helianthus annuus]

| | |
|--------------------------------------|-----------------------------------|
| Database: | NCBIprot |
| Score: | 86 |
| Expect: | 0.013 |
| Monoisotopic mass (M _r): | 100862 |
| Calculated pI: | 5.35 |
| Taxonomy: | Helianthus annuus |

This protein sequence matches the following other entries:

- XP_022027331.1 from [Helianthus annuus](#)

Sequence similarity is available as [an NCBI BLAST search of XP_022027330.1 against nr](#).

Search parameters

| | |
|-------------------------|---|
| Enzyme: | Trypsin: cuts C-term side of KR unless next residue is P. |
| Fixed modifications: | Carbamidomethyl (C) |
| Variable modifications: | Oxidation (M) |
| Mass values searched: | 22 |
| Mass values matched: | 11 |

Protein sequence coverage: 17%

Matched peptides shown in **bold red**.

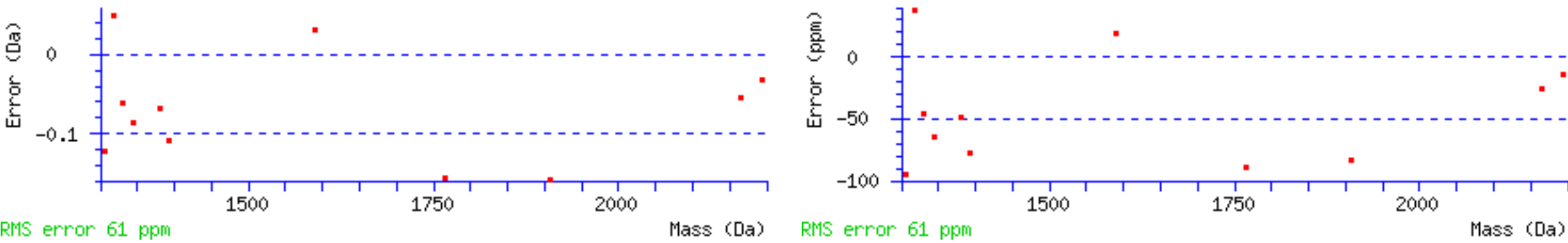
| | | | | | |
|-----|---------------------|--------------------|--------------------|--------------------|---------------------|
| 1 | MAESSGKREM | ATSADMLRNT | PSNIRR LADE | IQQCEGR QKY | LAQTRSPSDG |
| 51 | GDVRWYFSKI | PMAENELAAA | IPPTENVVGKG | DYFRFGMRDS | LAIEASFLQR |
| 101 | EEELLSNWWR | EYGECSVGPK | GSLSSISESN | DSPNAQSSKL | YANEEEERVGV |
| 151 | PVKGGLYEVD | LLRRHSFPVY | WSGDNRRVLR | GHWFARKGSL | DWFPLREDVA |
| 201 | EQLEFAYRSR | IWHRRTFQPS | GLFAARVDMQ | GSSPGLHALF | TGEDDTWDAW |
| 251 | LNIPSSGFSG | VVNFGGTGLK | LRR GYAPSHS | PKPTQDEL RQ | Q KEEEMDDYC |
| 301 | SQVPVR HLVF | MVHGIGQR LQ | KANLVDDVGT | FRLVTQNLAD | LHLTSYQRGT |
| 351 | QR VLFIP CQW | R NLKLSGES | AVEKCTLPGV | RGLRITLSAT | VHDLVYYMSP |
| 401 | IYCQDIIDSV | SNQLNRLYMK | FLKRNPGYDG | KVSLYGHSLG | SVLSYDILCH |
| 451 | QETLSSPFPM | EWMYTDQTHE | VSPERNSSVN | SPENDLVTNN | EGMDTVASHT |
| 501 | EGVNGKLSIA | TDSEK DDSLV | LDEVVVK SGD | DPIEMQSENN | EVLTSDDSSQV |
| 551 | DEEINENDES | VVIKSLKEEI | DCLNARV REL | ESQIAEGTNS | G TRANKQETS |
| 601 | TSRNESVSES | FPSSKNDSRK | SYTPYIKYTK | LLFK VDTFFA | VGSPLGVFLA |
| 651 | L RNVRIIGIK | GKDYWEDENI | IEEMPCCRQM | FNVFHPHDPV | AYRVEPLVSK |
| 701 | EYIDKRFPVII | PYHRGGKRLH | VTYQEFVEGV | ASR SQVVVDK | MSVAK VKVLVT |
| 751 | ICQSRDND DH | EETSEEP EEI | ERSYGSRMLE | RLTGSQDGRV | DHVLQNKTFE |
| 801 | HQYISAVGAH | TKYWR DCDTA | LFILK HLYRD | IPNEPK TSSE | DTLSQENADW |
| 851 | EELFDNEQLP | LTFASEKFMK | QLSVRVKKFA | NQ | |

Unformatted sequence string: [882 residues](#) (for pasting into other applications).

Sort by ☒ residue number ☐ increasing mass ☐ decreasing mass
Show ☒ matched peptides only ☐ predicted peptides also

| Start – End | Observed | Mr (expt) | Mr (calc) | Delta | M | Peptide |
|-------------|-----------|-----------|-----------|---------|---|---|
| 27 – 37 | 1318.6559 | 1317.6486 | 1317.5983 | 0.0503 | 0 | R.LADE IQQCEGR .Q |
| 274 – 292 | 2167.0344 | 2166.0272 | 2166.0818 | -0.0546 | 1 | R.GYAPSHS PKPTQDEL RQ QK .E |
| 307 – 318 | 1393.6438 | 1392.6365 | 1392.7449 | -0.1084 | 0 | R.HLVFM MVHGIGQR .L |
| 353 – 362 | 1346.6529 | 1345.6456 | 1345.7329 | -0.0873 | 1 | R.V LFI PCQ WRK .N |
| 516 – 527 | 1330.6485 | 1329.6412 | 1329.7028 | -0.0616 | 0 | K.DDSLVL DEVVVK .S |
| 579 – 593 | 1591.7866 | 1590.7793 | 1590.7485 | 0.0308 | 0 | R.E LESQIAEGTNS G TR .A |
| 635 – 652 | 1908.8997 | 1907.8925 | 1908.0509 | -0.1585 | 0 | K.VDTFFAV GSPLGVFLALR .N |
| 734 – 745 | 1306.5803 | 1305.5731 | 1305.6962 | -0.1232 | 1 | R.SQVVVDK MSVAK .V + Oxidation (M) |
| 782 – 797 | 1766.7578 | 1765.7505 | 1765.9071 | -0.1566 | 1 | R.LTGSQDGRVD HVLQNK .T |
| 798 – 815 | 2194.0504 | 2193.0431 | 2193.0756 | -0.0325 | 1 | K.TFE HQYISAVGAH TKYWR.D |
| 826 – 836 | 1381.6547 | 1380.6475 | 1380.7150 | -0.0675 | 1 | K.HLYRD IPNEPK .T |

No match to: 870.4201, 1014.4370, 1261.5736, 1276.6542, 1326.6287, 1608.8216, 1646.7789, 2062.8520, 2077.9626, 2162.0488, 2211.1040



| | | | | |
|------------|---|--------|--------|-----------------|
| LOCUS | XP_022027330 | 882 aa | linear | PLN 07-AUG-2017 |
| DEFINITION | phospholipase SGR2 isoform X2 [Helianthus annuus]. | | | |
| ACCESSION | XP_022027330 | | | |
| VERSION | XP_022027330.1 | | | |
| DBLINK | BioProject: PRJNA396063 | | | |
| DBSOURCE | REFSEQ: accession XM_022171638.1 | | | |
| KEYWORDS | RefSeq. | | | |
| SOURCE | Helianthus annuus (common sunflower) | | | |
| ORGANISM | Helianthus annuus | | | |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae; Pentapetalae; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae alliance; Heliantheae; Helianthus. | | | |
| COMMENT | MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from a genomic sequence (NC_035435.1) annotated using gene prediction method: Gnomon, supported by EST evidence. Also see: Documentation of NCBI's Annotation Process ##Genome-Annotation-Data-START## Annotation Provider :: NCBI Annotation Status :: Full annotation Annotation Version :: Helianthus annuus Annotation Release 100 Annotation Pipeline :: NCBI eukaryotic genome annotation pipeline Annotation Software Version :: 7.4 Annotation Method :: Best-placed RefSeq; Gnomon Features Annotated :: Gene; mRNA; CDS; ncRNA ##Genome-Annotation-Data-END## COMPLETENESS: full length. | | | |
| FEATURES | Location/Qualifiers | | | |
| source | 1..882 /organism="Helianthus annuus" /specimen_voucher="SF193" /db_xref="taxon:4232" /tissue_type="leaves" /dev_stage="4 leaves" /country="France" /collected_by="INRA, LIPM" /linkage_group="3" /genotype="XRQ/B" | | | |
| Protein | 1..882 /product="phospholipase SGR2 isoform X2" /calculated_mol_wt=100109 | | | |
| Region | 535..>586 /region_name="GrpE" /note="nucleotide exchange factor GrpE; c103075" /db_xref="CDD:322182" | | | |
| Region | 634..828 /region_name="DDHD" /note="DDHD domain; pfam02862" /db_xref="CDD:308481" | | | |
| CDS | 1..882 /gene="LOC110928610" /coded_by="XM_022171638.1:762..3410" /db_xref="GeneID:110928610" | | | |