

 **MASCOT Search Results****Protein View: XP_017408189.1****PREDICTED: ethylene-responsive transcription factor ERF098-like [Vigna angularis]****Database:** NCBIprot**Score:** 64**Expect:** 2.8**Monoisotopic mass (M_r):** 15313**Calculated pI:** 5.42**Taxonomy:** Vigna angularis

This protein sequence matches the following other entries:

- KOM27845.1 from Vigna angularis

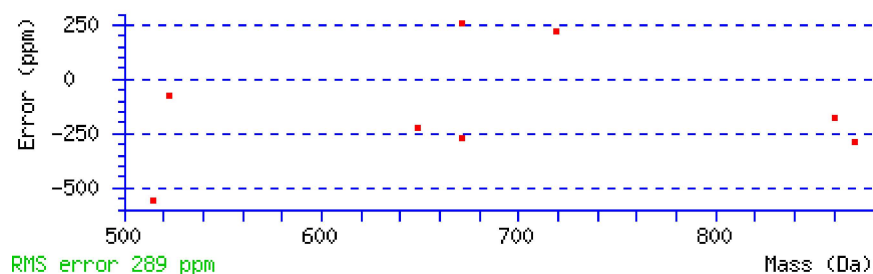
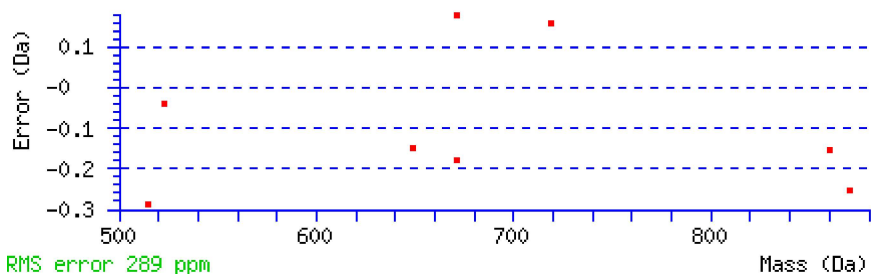
Sequence similarity is available as [an NCBI BLAST search of XP_017408189.1 against nr.](#)**Search parameters****Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.**Fixed modifications:** Carbamidomethyl (C)**Variable modifications:** Oxidation (M)**Mass values searched:** 32**Mass values matched:** 8**Protein sequence coverage: 30%**Matched peptides shown in **bold red**.

1 **MEDPREGEKE** **KEKKKKGEE** **GRYRGVRRRP** WGKFGAEIRD **PTKPTGR**QWL
51 GTFDTAEAAA **RAYDRAAIEL** **RGALAILNFP** DEYHSHLPFL SSSSSSSASV
101 IGSSSTAQGE VIEFEYLDDK VLEDLLESEE KRKKKE

Unformatted sequence string: **136 residues** (for pasting into other applications).Sort by residue number increasing mass decreasing massShow matched peptides only predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
2 - 5	515.9560	514.9487	515.2340	-0.2852 0	M.EDPR.E
6 - 11	719.5150	718.5077	718.3497	0.1580 1	R.EGEKEK.E
15 - 22	861.2500	860.2427	860.3988	-0.1561 1	K.EKGEEGR.Y
23 - 27	650.2260	649.2187	649.3660	-0.1473 1	R.YRGVR.R
40 - 47	871.2080	870.2007	870.4559	-0.2552 0	R.DPTKPTGR.Q
62 - 65	524.2060	523.1987	523.2390	-0.0403 0	R.AYDR.A
66 - 71	672.2250	671.2177	671.3966	-0.1789 0	R.AAIELR.G
66 - 71	672.5800	671.5727	671.3966	0.1761 0	R.AAIELR.G

No match to: 500.1700, 526.3080, 550.3040, 550.7740, 568.3070, 587.3170, 608.0880, 644.2050, 666.1960, 682.1610, 703.6290, 725.5230, 741.5050, 839.2590, 850.7040, 855.2410, 877.2250, 893.1930, 913.8520, 929.7990, 1066.2810, 1082.2530, 1769.1180, 2163.3850



LOCUS XP_017408189 136 aa linear PLN 18-JUL-2016
 DEFINITION PREDICTED: ethylene-responsive transcription factor ERF098-like
 [Vigna angularis].
 ACCESSION XP_017408189
 VERSION XP_017408189.1
 DBLINK BioProject: PRJNA328963
 DBSOURCE REFSEQ: accession XM_017552700.1
 KEYWORDS RefSeq; includes ab initio.
 SOURCE Vigna angularis (adzuki bean)
 ORGANISM Vigna angularis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
 Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae;
 Phaseoleae; Vigna.
 COMMENT MODEL REFSEQ: This record is predicted by automated computational
 analysis. This record is derived from a genomic sequence
 (NW_016115005.1) annotated using gene prediction method: Gnomon.
 Also see:
 Documentation of NCBI's Annotation Process
 ##Genome-Annotation-Data-START##

Annotation Provider :: NCBI
 Annotation Status :: Full annotation
 Annotation Version :: Vigna angularis Annotation Release
 100
 Annotation Pipeline :: NCBI eukaryotic genome annotation
 pipeline
 Annotation Software Version :: 7.1
 Annotation Method :: Best-placed RefSeq; Gnomon
 Features Annotated :: Gene; mRNA; CDS; ncRNA
 ##Genome-Annotation-Data-END##

##RefSeq-Attributes-START##
 ab initio :: 1% of CDS bases
 ##RefSeq-Attributes-END##
 COMPLETENESS: full length.

FEATURES	Location/Qualifiers
source	1..136 /organism="Vigna angularis" /cultivar="Jingnong 6" /db_xref="taxon:3914" /chromosome="Unknown" /tissue_type="seedling" /country="China: Beijing"
Protein	1..136 /product="ethylene-responsive transcription factor ERF098-like" /calculated_mol_wt=15191
Region	22..80 /region_name="AP2" /note="DNA-binding domain in plant proteins such as APETALA2 and EREBPs; smart00380" /db_xref="CDD:197689"
Site	order(24..25,27,29,31,33,37,39,47,49,52) /site_type="DNA binding" /note="DNA binding site [nucleotide binding]" /db_xref="CDD:237985"
CDS	1..136 /gene="LOC108321057" /coded_by="XM_017552700.1:1..411" /db_xref="GeneID:108321057"

Mascot: <http://www.matrixscience.com/>