

Number of amino acids: 295

Theoretical pI: 4.97

Molecular weight: 33729.11

Instability index:

The instability index (II) is computed to be 57.71
This classifies the protein as unstable.

Aliphatic index: 92.92

Grand average of hydropathicity (GRAVY): -0.185

Entry matches to this protein     

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Feature Display Mode 
 Summary Full



 Families



Representative families

 Domains



Representative domains

 Intrinsically Disordered Regions



MobiDB Lite: Consensus Disorder Predictor
Negative Polyelectrolyte

 Conserved Residues



cd20573
CDK Interface

Conserved domains on [1cl]ORF4(ref|NP_444284|)

Icl|ORF4 (G1/S-specific cyclin-D1)

Find similar domain architectures [?]

Precomputed, cdd.v.3.21

Database: RESEARCH.COM

Environ Monit Assess

Composition-based adjustment vs.

Low complexity fiber optic

[Refine parameters
and search again](#)

Viewing | Concise

1

H-zoom H

Hide features

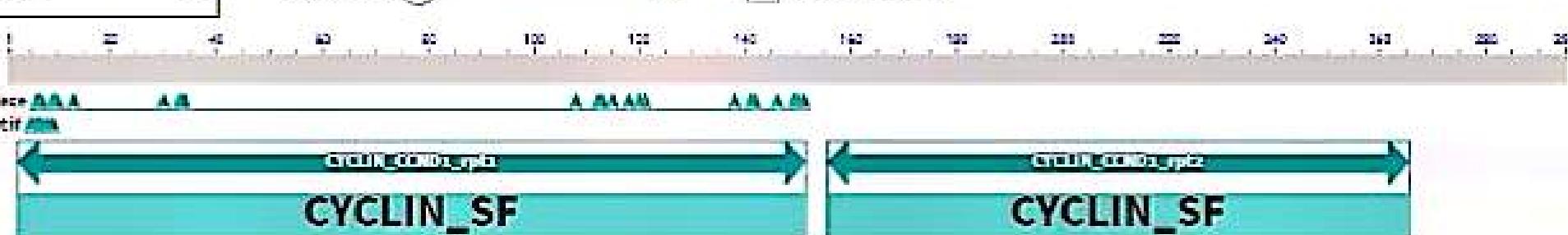
87

CDK Interface 6.0.0

Geplaatst door: [User]

Specifics

Superfamily arch



Name	Accession	Description	Interval	E-value	
+	CYCLIN_CCND1_rpt1	cd20573	first cyclin box found in G1/S-specific cyclin-D1 (CCND1)	3-151	1.90×10^{-98}
+	CYCLIN_CCND1_rpt2	cd20576	second cyclin box found in G1/S-specific cyclin-D1 (CCND1)	156-265	1.62×10^{-68}

Predicted proteins

Sequence
Prediction: Other

Protein type	Other	Signal peptide	Mitochondrial transfer peptide
Likelihood	0.9991	0.0002	0.0007

Download: [PDB](#) | [FASTA](#) | [Tetherer](#)
Protein Domains and Motifs



$$k = 9/23$$

56.5 %: cytoplasmic

30.4 %: nuclear

8.7 %: mitochondrial

4.3 %: Golgi

>> prediction for 176642164122689 is cyt (k=23)