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 ❶

[ ] ⊟⊞ Options ▾   Download ▾   **Feature Display Mode** ❓
■ Summary ○ Full

▶ Families

CYCLINS — Representative families

▶ Domains

CYCLIN_CCND1_rpt1   Cyclin_C_2 — Representative domains

▼ Intrinsically Disordered Regions

disorder_predi... — MobiDB-lite: Consensus Disorder Predict
Negative Polyelectrolyte

▼ Conserved Residues

cd20573
CDK Interface

Conserved domains on [lcl|ORF4(ref|NP_444284)]

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

Find similar domain architectures 🗗

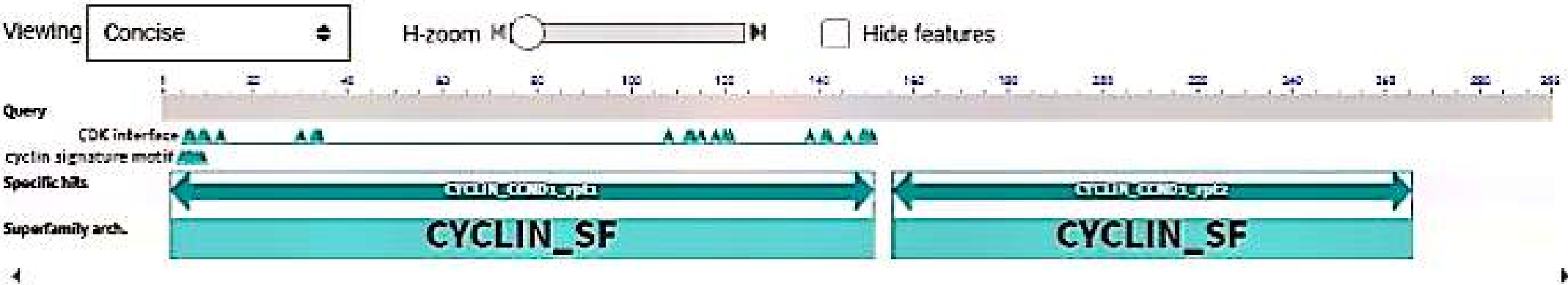| Name	Accession	Description	Interval	E-value
+ CYCLIN_CCND1_rpt1	cd20573	first cyclin box found in G1/S-specific cyclin-D1 (CCND1)	3-151	1.90×10^{-98}
+ CYCLIN_CCND1_rpt2	cd20576	second cyclin box found in G1/S-specific cyclin-D1 (CCND1)	156-265	1.62×10^{-68}

Predicted proteins

Protein type	Other	Signal peptide	Mitochondrial transfer peptide
Likelihood	9.9991	0.0002	0.0007

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$k = 9/23$

```
56.5 %: cytoplasmic
30.4 %: nuclear
 8.7 %: mitochondrial
 4.3 %: Golgi
```

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