

LCE 1a2 mouse

EMBL mRNA Translation: 1

Nucleotide Sequence (450 nt):

ATGTCCTGCCAGCAGAACCAGCAGCAGTGTGAGCCCCCTCCCAAGTGTCTCCCAAGTGCCAGACCCCAA
AATGCCCTCCAAATGCCCCCTAAGTGTCTCCCAAGTGCCCCCTGTGTCTTCTGCTGTAGCCTGGG
TTCTGGGGGTTGCTGTGGCTCCAGCTCTGGGGGCTGTTGCAGCTCTGGAGGCTGCTGCAGCTCTGGTGGC
TGCTGCAGCTCTGGGGGTGGAGGCTGCTGCCTGAGCCACCACAGACCTCGCAGATCCCTCCGTCGCCATC
GCCATAGCTCTGGATGTTGTAGCAGTGGTGGCAGCAGTGGATGCTGTGGCAGCAGTGGTGGCAGTGGTGG
CTGCTGTGGAAGCAGTGGTGGCAGCAGTGGATGCTGTGGCAGCAGTGGTGGCAGCAGTGGCTGCTGTGGC
AGTAGCCAGCAGTCTGGGGGCTGCTGCTGA

Fasta results for proteins:

<https://blast.ncbi.nlm.nih.gov/Blast.cgi>

>EDL00687.1 small proline rich-like 2, partial [Mus musculus]

GAQGSCTACHLAPEHSPAEMSCQQNQQCQPPPKCPPKCQTPKCPPKCPPKCPPKCPPVSSCCSLGSGGCCGSSSGGC
CSSGGCCSSGGCCSSGGGGCCLSHHRPRRSLRRHRHSSGCCSSGSSGCCGSSGGSGGCCGSSGGSSGCCGSSGGSSG
CCGSSQSGGCC

>NP_082901.1 late cornified envelope 1A2 [Mus musculus]

MSCQQNQQCQPPPKCPPKCQTPKCPPKCPPKCPPKCPPVSSCCSLGSGGCCGSSSGGCCSSGGCCSSGGCCSSGGG
GCCLSHHRPRRSLRRHRHSSGCCSSGSSGCCGSSGGSGGCCGSSGGSSGCCGSSGGSSGCCGSSQSGGCC

>EDL00689.1 small proline rich-like 3, partial [Mus musculus]

PFTHLPRYPKILCTWNLAPEHSPAEMSCQQNQQCQPPPKCPPKCQTPKCPPKCPPKCPPKCPPVSSCCSLGSGGCCGS
SSGGCCSSGGCCSSGGGGCCLSHHRPRRSLRRHRHSSGCCSSGSSGCCGSSGGSSGCCGSSGGSSGCCGSSGGSSG
CGSSQSGGCC

>NP_080260.1 late cornified envelope 1A1 [Mus musculus]

MSCQQNQQCQPPPKCPPKCQTPKCPPKCPPKCPPKCPPVSSCCSLGSGGCCGSSSGGCCSSGGCCSSGGGGCCLSHH
RPRRSLRRHRHSSGCCSSGSSGCCGSSGGSSGCCGSSGGSSGCCGSSGGSSGCCGSSQSGGCC

>XP_036047237.1 late cornified envelope protein 1C-like [Onychomys torridus]

MSCQQNQQCQPPPKCPPKCQTPKCPPKCPPKCPPKCPPVSSCCSLGSGGCCGSSSGGGCGSSSGGCCSSGGGGCCLSH
HHRPRRSLRRHRHSSGCCSSGSSGCCGSSGGSSGCCGSSGGSSGCCGSSGGSSGCCGSSQSGGCC

All of the proteins placed in a multi sequence alignment:

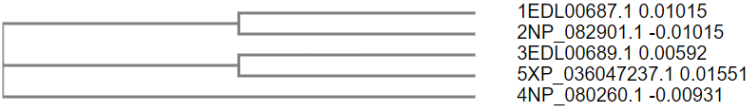
<https://www.ebi.ac.uk/Tools/services/web/toolresult.ebi?jobId=clustalo-I20220223-172034-0384-40568820-p2m&showColors=true&tool=clustalo>

CLUSTAL O(1.2.4) multiple sequence alignment

1EDL00687.1	-----GAQGSCTACHLAPEHSPAEMSCQNNQQCCQPPPKCPPKCQTPKCPPKCPPKCPP	54
2NP_082901.1	-----MSCQNNQQCCQPPPKCPPKCQTPKCPPKCPPKCPP	35
3EDL00689.1	PFTHLPKYPKILCTWNLAPAEHSPAEMSCQNNQQCCQPPPKCPPKCQTPKCPPKCPPKCPP	60
4NP_080260.1	-----MSCQNNQQCCQPPPKCPPKCQTPKCPPKCPPKCPP	35
5XP_036047237.1	-----MSCQNNQQCCQPPPKCPPKCQTPKCPPKCPPKCPP	35

1EDL00687.1	KCPPVSSCCSLGSGGCCGSSGGCCSSGGCCSSGGCCSSGGGGCCLSHHRPRRSLRRHRH	114
2NP_082901.1	KCPPVSSCCSLGSGGCCGSSGGCCSSGGCCSSGGCCSSGGGGCCLSHHRPRRSLRRHRH	95
3EDL00689.1	KCPPVSSCCSLGSGGCCGSSGGCC-----SSGGCCSSGGGGCCLSHHRPRRSLRRHRH	114
4NP_080260.1	KCPPVSSCCSLGSGGCCGSSGGCC-----SSGGCCSSGGGGCCLSHHRPRRSLRRHRH	89
5XP_036047237.1	KCPPVSSCCSLGSGGCCGSSGGGCC-----SSGGCCSSGGGGCCLSHHRPRRSLRRHRH	91

1EDL00687.1	SSGCCSSGGSSGCCGSSGGSSGCCGSSGGSSGCCGSSGGSSGCCGSSQQSGGCC	168
2NP_082901.1	SSGCCSSGGSSGCCGSSGGSSGCCGSSGGSSGCCGSSGGSSGCCGSSQQSGGCC	149
3EDL00689.1	SSGCCSSGGSSGCCGSSGGSSGCCGSSGGSSGCCGSSGGSSGCCGSSQQSGGCC	168
4NP_080260.1	SSGCCSSGGSSGCCGSSGGSSGCCGSSGGSSGCCGSSGGSSGCCGSSQQSGGCC	143
5XP_036047237.1	SSGCCSSGGSSGCCGSSGGSSGCCS-SGGSSGCCGSSGGSS-SGGSSQQSGGCC	142



Tree Data

```
(
(
1EDL00687.1:0.01015,
2NP_082901.1:-0.01015)
:0.01630,
(
3EDL00689.1:0.00592,
5XP_036047237.1:0.01551)
:0.00931,
4NP_080260.1:-0.00931);
```

Each of these proteins hold very similar sequences with highly conservative cysteins which is essential in maintaining a structure.

Results specifically for:

>NP_082901.1 late cornified envelope 1A2 [Mus musculus]

MSCQNNQQCQPPPKCPPKCQTPKCPPKCPPKCPPVSSCCSLGSGGCCGSSSGGCCSSGGCCSSGGCCSSGGG
GCCLSHHRPRRSLRRHRHSSGCCSSGGSSGCCGSSGGSGGCCGSSGGSSGCCGSSGGSSGCCGSSQQSGGCC

Molecular weight: 14042.71

Number of amino acids: 149

Theoretical pI: 8.70

Extinction coefficients:

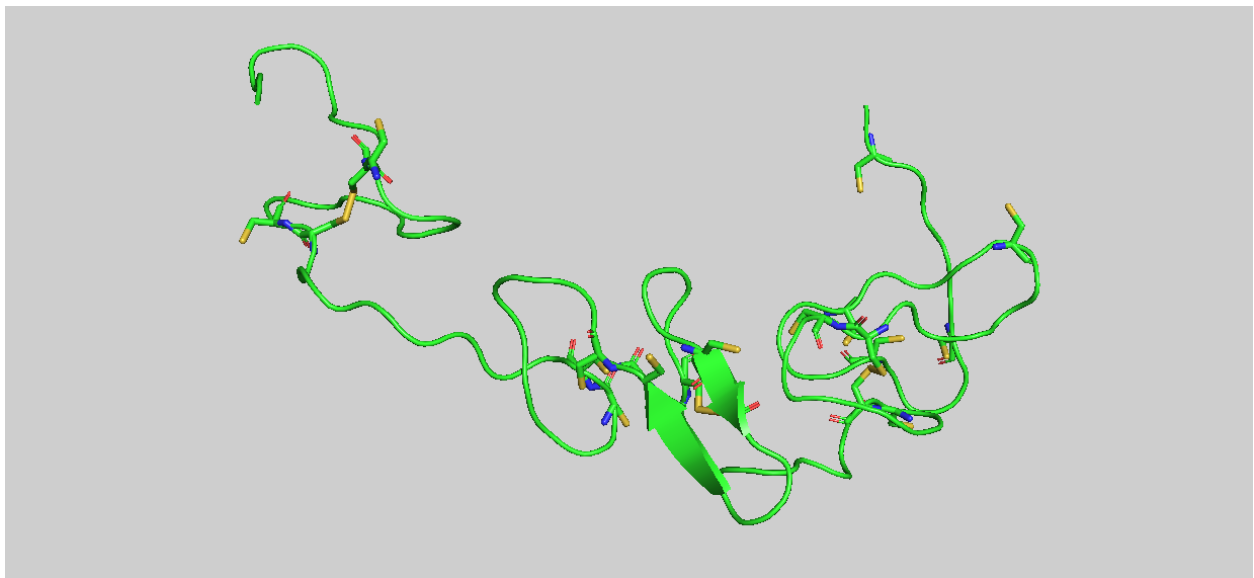
Ext. coefficient 2000

Abs 0.1% (=1 g/l) 0.142, assuming all pairs of Cys residues form cystines

Ext. coefficient 0

Abs 0.1% (=1 g/l) 0.000, assuming all Cys residues are reduced

Number of cysteines: 32 (21.5%)



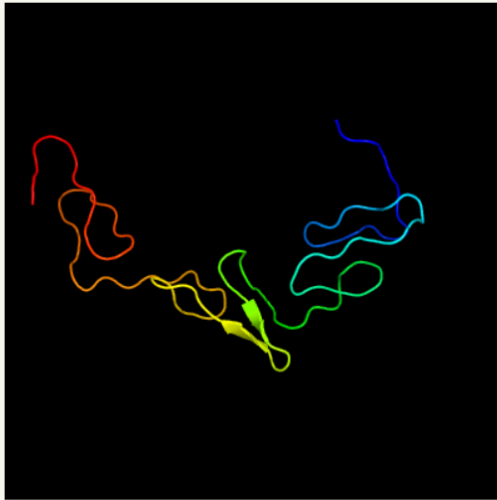


Image coloured by rainbow N → C terminus
Model dimensions (Å): **X**:47.270 **Y**:43.086 **Z**:48.321

Model (left) based on template [c2yggA](#)

Top template information

PDB header:signaling protein

Chain: A; **PDB Molecule:**wnt inhibitory factor 1;

PDBTitle: wif domain-epidermal growth factor (egf)-like domains 1-3 of human wnt2 inhibitory factor 1 in complex with 1,2-3 dipalmitoylphosphatidylcholine

PDB Entry: [PDBe](#) [RCSB](#) [PDBj](#)

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Confidence and coverage

Confidence: **98.2%**

Coverage: **63%**

93 residues (63% of your sequence) have been modelled with 98.2% confidence by the single highest scoring template.

Additional confident templates have been detected (see [Domain analysis](#)) which cover other regions of your sequence.

144 residues (97%) could be modelled at >90% confidence using multiple-templates.

You may wish to try resubmitting your sequence in "intensive" mode to model more of your sequence.

Warning: 60% of your sequence is predicted disordered. Disordered regions cannot be meaningfully predicted.

3D viewing

[Interactive 3D view in JSmol](#)

For other options to view your downloaded structure offline see the [FAQ](#)

