

LCE 1a2 mouse

EMBL mRNA Translation: 1

Nucleotide Sequence (450 nt):

ATGTCCTGCCAGCAGAACCAGCAGCAGTGTGAGCCCCCTCCCAAGTGTCTCCCAAGTGCCAGACCCCAA
AATGCCCTCCAAAATGCCCCCTAAGTGTCTCCCAAGTGCCCCCTGTGTCTTCTGCTGTAGCCTGGG
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]

GAQGSCTACHLAPEHSPAEMSCQNNQQQCQPPPKCPPKCQTPKCPPKCPPKCPPKCPPVSSCCSLGSGGCCGSSSGG
CCSSGGCCSSGGCCSSGGGGCCLSHHRPRRSLRRHRHSSGCCSSGSSGCCGSSGSSGGCCGSSGGSSGCCGSSGGSS
GCCGSSQSGGCC

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

MSCQNNQQQCQPPPKCPPKCQTPKCPPKCPPKCPPKCPPVSSCCSLGSGGCCGSSSGGCCSSGGCCSSGGCCSSGGG
GCCLSHHRPRRSLRRHRHSSGCCSSGSSGCCGSSGSSGGCCGSSGSSGCCGSSGSSGCCGSSQSGGCC

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

PFTHLPRYPKILCTWNLAPEHSPAEMSCQNNQQQCQPPPKCPPKCQTPKCPPKCPPKCPPKCPPVSSCCSLGSGGCCG
SSSGGCCSSGGCCSSGGGGCCLSHHRPRRSLRRHRHSSGCCSSGSSGCCGSSGSSGCCGSSGSSGCCGSSGSSG
CCGSSQSGGCC

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

MSCQNNQQQCQPPPKCPPKCQTPKCPPKCPPKCPPKCPPVSSCCSLGSGGCCGSSSGGCCSSGGCCSSGGGGCCLSH
HRPRRSLRRHRHSSGCCSSGSSGCCGSSGSSGCCGSSGSSGCCGSSGSSGCCGSSQSGGCC

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

MSCQQNQQCQPPPKCPPKCQTPKCPPKCPPKCPPVSSCCSLGSGGCCGSSSGGGCGSSSGGCCSSGGGGCCL
SHHRPRRSLRRHRHSSGCCSSGSSGCCGSSGSSGCCSSGSSGCCGSSGSSCGSSQQSGGCC

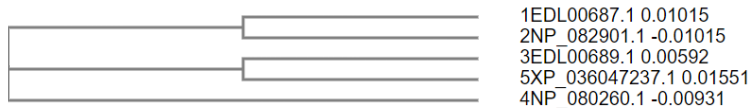
<https://www.ebi.ac.uk/Tools/services/web/toolresult.ebi?jobId=clustalo-l20220223-172034-0384-40568820-p2m&showColors=true&tool=clustalo>

CLUSTAL O(1.2.4) multiple sequence alignment

```
1EDL00687.1      -----GAQGSCTACHLAPLEHSPAEMSCQQNQQCQPPPKCPPKCQTPKCPPKCPP      54
2NP_082901.1     -----MSCQQNQQCQPPPKCPPKCQTPKCPPKCPP      35
3EDL00689.1     PFTHLPKYPKILCTWNLAPLEHSPAEMSCQQNQQCQPPPKCPPKCQTPKCPPKCPP      60
4NP_080260.1     -----MSCQQNQQCQPPPKCPPKCQTPKCPPKCPP      35
5XP_036047237.1 -----MSCQQNQQCQPPPKCPPKCQTPKCPPKCPP      35
                  *****

1EDL00687.1      KCPVSSCCSLGSGGCCGSSSGGCCSSGGCCSSGGCCSSGGGGCCLSHHRPRRSLRRHRH      114
2NP_082901.1     KCPVSSCCSLGSGGCCGSSSGGCCSSGGCCSSGGCCSSGGGGCCLSHHRPRRSLRRHRH      95
3EDL00689.1     KCPVSSCCSLGSGGCCGSSSGGCC-----SSGGCCSSGGGGCCLSHHRPRRSLRRHRH      114
4NP_080260.1     KCPVSSCCSLGSGGCCGSSSGGCC-----SSGGCCSSGGGGCCLSHHRPRRSLRRHRH      89
5XP_036047237.1 KCPVSSCCSLGSGGCCGSSSGGCC-----SSGGCCSSGGGGCCLSHHRPRRSLRRHRH      91
                  *****

1EDL00687.1      SSGCCSSGGSSGCCGSSGGSGCCGSSGGSSGCCGSSGGSSGCCGSSQQSGGCC      168
2NP_082901.1     SSGCCSSGGSSGCCGSSGGSGCCGSSGGSSGCCGSSGGSSGCCGSSQQSGGCC      149
3EDL00689.1     SSGCCSSGGSSGCCGSSGGSGCCGSSGGSSGCCGSSGGSSGCCGSSQQSGGCC      168
4NP_080260.1     SSGCCSSGGSSGCCGSSGGSGCCGSSGGSSGCCGSSGGSSGCCGSSQQSGGCC      143
5XP_036047237.1 SSGCCSSGGSSGCCGSSGGSGCCS-SGGSSGCCGSSGGSS--SCGSSQQSGGCC      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);
```

How similar are the sequences? Are the cysteines conserved? Why is that important?: they are very similar and conserved which is occurring due to the fact that cysteine is a structural components so conservation is naturally attributed to that fact.

How good is your model?: very low

Do the cysteines form disulfide bonds?: yes

>tr|Q9D1K4|Q9D1K4_MOUSE Late cornified envelope 1A2 OS=Mus musculus OX=10090 GN=Lce1a2
PE=2 SV=1

MSCQQNQQQCQPPPKCPPKCQTPKCPPKCPPKCPPVSSCCSLGSGGCCGSSSGGCC
SSGGCCSSGGCCSSGGGGCCLSHHRPRLRRHRHSSGCCSSGGSSGCCGSSGGSGGCCG
SSGGSSGCCGSSGGSSGCCGSSQSGGCC

Molecular weight: 14042.71

Number of amino acids: 149

Theoretical pI: 8.70

Extinction coefficients:

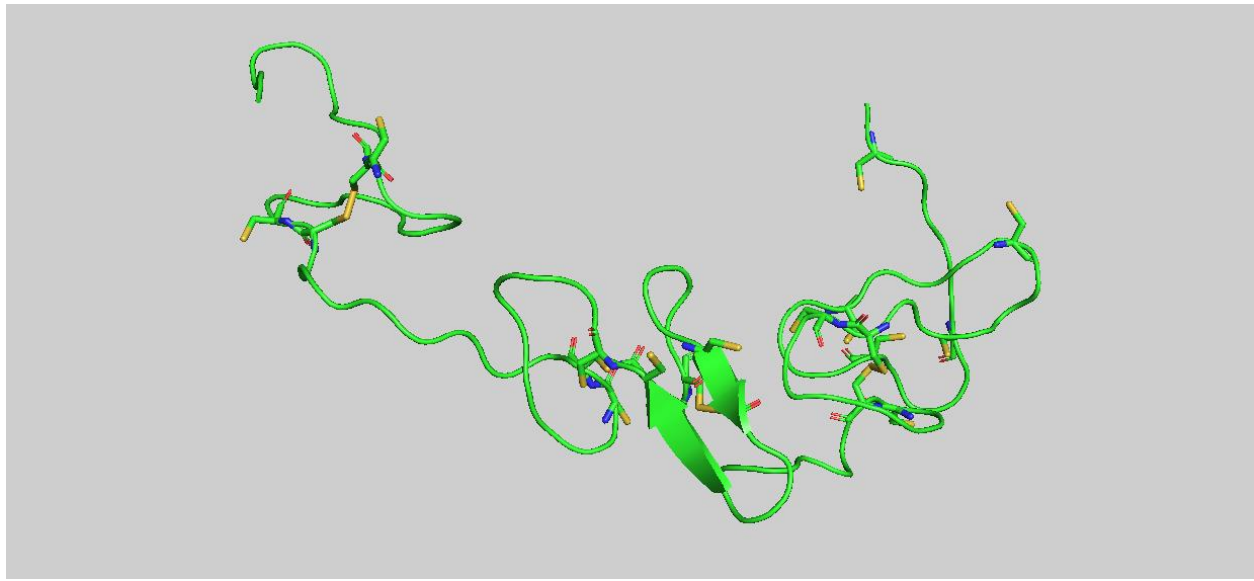
Ext. coefficient 2000

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%)



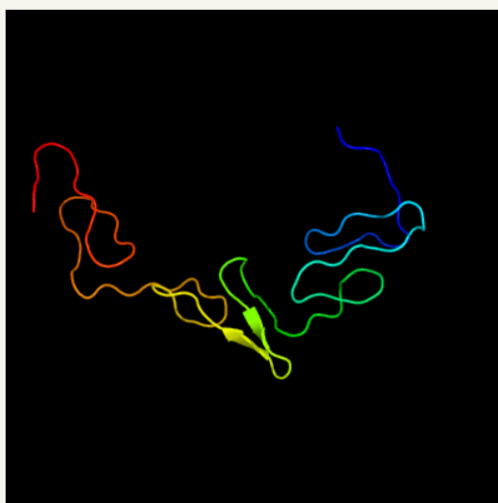


Image coloured by rainbow N → C terminus

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](#)

-

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](#)

