

CLUSTAL O(1.2.4) multiple sequence alignment

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S. cerevisiae      MQSPYPMT-----QVSNV-----DDGSLLKE--
A. nidulans        MPQPGSSVDFSNNLNPQNNTAIPA-----EVSNATASATMASGASLLPPMV
A. niger           MPPPASSVDFSNNLNPQNNDSTPSTP--VDSSKTPSTPSSTQSNSNMASVSLPPLM
N. crassa          MQRVQSAVDFSNNLNPSESTAIEKRDHSGSPRQQTAPQOQOQOQPEADMATVGLLRPNG
T. atroviride      MQRARSAVDFSNNLNPSSAAP---SQD-----QSGAMSTAATVVIKPNG
T. virens          MORAQSAVDFSNNLNPSSSAGQDSAD-----KSGAMSTAATVVIKPNG
T. reesei          MORAQSAVDFSNNLNPSTAAGQD-----SGAMSTAATVVIKPNG
Crel-96            MORAQSAVDFSNNLNPSTAAGQD-----SGAMSTAATVVIKPNG

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S. cerevisiae      -SKSKSKVAAKSEAPRPHACPICHRLEHQTRHMRIHTGEKPHACDFPGCVKRFSSRS
A. nidulans        KGARPAEEEARQDLPRPYKCPLCERAFHRLEHQTRHIRTHTGEKPHACQFPGCSKRFSRS
A. niger           KGARPATEEVQRDLPRPYKCPLCDRAFHRLEHQTRHIRTHTGEKPHACQFPGCTKRFSRS
N. crassa          PLPGAQATEPANELPRPYKCPLCDKAFHRLEHQTRHIRTHTGEKPHACQFPGCSKKFSRS
T. atroviride      PIPGAQASEANELPRPYKCPLCDKAFRRLEHQTRHIRTHTGEKPHACQFPGCSKKFSRS
T. virens          PLPGAQSTETANELPRPYKCPLCEKAFHRLEHQTRHIRTHTGEKPHACQFPGCSKKFSRS
T. reesei          PIPGTQSTETANELPRPYKCPLCDKAFHRLEHQTRHIRTHTGEKPHACQFPGCSKKFSRS
Crel-96            PIPGTQSTETANELPRPYKCPLCDKAFHRLEHQTRHIRTHTGEKPHACTSITCFFF----

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S. cerevisiae      DELTRHRRRIHTNSHPRGKRGRKKKVVGSP-INSASS-SATSIPDLNTANFSPPLPQQHLS
A. nidulans        DELTRHSRIHNNPNRSR--RGNKAQHAAAAAAAAANQDGSAMANNAGSMPPPSKPITRS
A. niger           DELTRHSRIHNNPNRSR--RSNKAQHAAAAAAAAAG--QDNAMANTASAMPPPSKPMTRS
N. crassa          DELTRHSRIHSNPNSR--RGNKGQQQQQHPLVHN-----HGLQPDMMPPPGPKAIRS
T. atroviride      DELTRHSRIHSNPNSR--RGNKGQQQQHQHQL-HQGM--PHPLHVDGMMAPPPAPKAIRS
T. virens          DELTRHSRIHSNPNSR--RGNKGQQQQHQHQLHHLHQL--PHHMHVDGMMPP-PVPKAIRS
T. reesei          DELTRHSRIHSNPNSR--RGNKGQQQQHQ--LHHQGM--PHPMHVDGLMHPPAAPKAIRS
Crel-96            -----

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S. cerevisiae      P----LIPIAIAPKEN-S-----SRSSTRKGRKTKFEIGESGGNDPVMVSSPKTMAKIPV
A. nidulans        APVSQVGSPDISPPHSFNSYANHMRSNLSPYS--RTSERASSGMDINLLATAASQVERDE
A. niger           APVSQVGSPDISPPHSFNSYASHMRSNLGPYA--RKGERASSGMDINLLATAASQVERDE
N. crassa          APPTAMSSPNVSPPHSYSPYNFAP-SGLNPYSHSRSSAGSQSGPDISLLARAAGQVERDG

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<i>T. atroviride</i>	APASALVSPNVSPPHSYSSFAVPA-VSMPHYG-----RGTDISMLANA AHQIERET
<i>T. virens</i>	APTSTLVSPNVSPPHSYSSFVMPQ-APMPHYN-----RGNDITMLAKA ANQIERET
<i>T. reesei</i>	APPSTLVSPNVSPPHSYSSFVMPH-GPISHYG-----RGNDITMLAKA ANQIERET
Crel-96	-----

<i>S. cerevisiae</i>	SVKPPPSLALNNMNYQTSSASTALSSLSNSHSGSRLKLNALSSSLQMMTP IASSAPRTVFI
<i>A. nidulans</i>	SFGFR--SGQRSHHMYGPR-----H----GSRGLPSLSAYAI SHSMSR----SHSH
<i>A. niger</i>	HFSFH--AGPRNHHLFSSR-----HH----GSGRLPSLSAYAI THNMSR----SHSH
<i>N. crassa</i>	AA---HHHFQPRFQFYGNT-----LHAATASRNQLPGLQAYH----MSR----SHSH
<i>T. atroviride</i>	LSGGPSNHNSRHHPYFSPG-----M---QGPRGHGPSLSSYH----MAR----SHFN
<i>T. virens</i>	LSGGPSNHNSRHHPYFGQS-----M---QNSRGHPPSLSSYH----MAR----SHSN
<i>T. reesei</i>	LSGGPSNHNSRHHPYFGQG-----V---PGSRGHP-SLSSYH----MAR----AHSN
Crel-96	-----

<i>S. cerevisiae</i>	DGPEQK-----Q-----LQQQQNSLSPRYSNTVILPRPRSLTDFQGLNNANPNNNGS
<i>A. nidulans</i>	EDED-SY--ASHRVKRSRPNSPNSTAPSSPTFSDSLSPTPDHTP-----LATPAHSPR
<i>A. niger</i>	EDDD-GY---SHRVKRSRPNSPNSTAPSSPTFSDSLSPTPDHTP-----LATPAHSPR
<i>N. crassa</i>	EDHDDHYGQSYRHAKRSRPNSPNSTAPSSPTFSDSLSPTPDHTP-----LATPAHSPR
<i>T. atroviride</i>	D-DDDHYGSMRHAKRSRPNSPNSTAPSSPTFSDSLSPTPDHTP-----IATPAHSPR
<i>T. virens</i>	D-DDDHYS-SMRHAKRSRPNSPNSTAPSSPTFSDSLSPTPDHTP-----IATPAHSPR
<i>T. reesei</i>	D-EDDHYGSLRHAKRSRPNSPNSTAPSSPTFSDSLSPTPDHTP-----IATPAHSPR
Crel-96	-----

<i>S. cerevisiae</i>	LRAQTQSSVQLKRPSSVLSLNDLLVGQRNTNES-----
<i>A. nidulans</i>	LKPLSPSELH-----LPSIRHLSLH---HTPALAPMEPQAE GPNYYNPNQP----HVGP
<i>A. niger</i>	LRPLGSSDLH-----LPSIRHLSLH---HTPALAPMEPQPEGPNYYSPSQG----HHGP
<i>N. crassa</i>	LRPHPG--LE-----LPPFRNLSLGQQHTTPALAPLEPALDGQFSLPQTTPAAPRSSGM
<i>T. atroviride</i>	LRPFSG--YE-----LPSLRNLSLGH-NTTPALAPMEPTLDTHQFPPQAQGLTSRGSGI
<i>T. virens</i>	LRPFSG--YE-----LPSLRNLSLQH-NTTPALAPMEPHLDA PQFPPQLQANNNRSPGM
<i>T. reesei</i>	LRPFSG--YE-----LPSLRNLSLQH-NTTPALAPMEPHLDA PQFHPQLQANTTRSPGM
Crel-96	-----

<i>S. cerevisiae</i>	-DSDFTTGGEDEEDGLKDPSNSSIDNLEQDYLQE QSRKK-SKTSTPTTMLSRSSTSGTNLH
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<i>A. nidulans</i>	SISDIMS RPEGAQRKLPIQV--PKVAVQDMLNP-SGFT-SVSSS----TANSVAGG---
<i>A. niger</i>	SISDIMSKPDGTQRKLPVPQV--PKVAVQDMLNPGSGFS-SVTSS----TANSVAGG---
<i>N. crassa</i>	SLTDIISRPDGTQRKLPVPK-----VAVQDLLGPADGFNPSVRNS----SSTSLSGA---
<i>T. atroviride</i>	SLTDIISRPDGSQRKLPVPQV--PKVAVQDLLSD-GIFTNSGRSS----TTGSLAGG---
<i>T. virens</i>	SLTDIISRPDGSQRKLPVPQV--PKVAVQDLLSD-GVFPNSGRSS----TAGSLAGG---
<i>T. reesei</i>	SLTDIISRPDGSQRKLPVPQV--PKVAVQDLLSD-GVFPNSGRSS----TTGSLAGG---
Cre1-96	-----
<i>S. cerevisiae</i>	TLGYVMNQNHLLHFSSSSPDFQKELNNRLLNVQQQQEQHTLLQSQNTSNQSQNQNQNM
<i>A. nidulans</i>	-----DLAERF-----
<i>A. niger</i>	-----DLAERF-----
<i>N. crassa</i>	-----EMMDRL-----
<i>T. atroviride</i>	-----DLMDRM-----
<i>T. virens</i>	-----DLMDRM-----
<i>T. reesei</i>	-----DLMDRM-----
Cre1-96	-----
<i>S. cerevisiae</i>	ASSSSLSTTPLLLSPRVNMINTAISTQQTPISQSDSQVQELETLPPIRSLPLPFPHMD
<i>A. nidulans</i>	-----
<i>A. niger</i>	-----
<i>N. crassa</i>	-----
<i>T. atroviride</i>	-----
<i>T. virens</i>	-----
<i>T. reesei</i>	-----
Cre1-96	-----

Figure S 4 – Multiple sequence alignment of Cre1 homologues

Multiple sequence alignment of *T. reesei* Cre1, Cre1-96 and Cre1 homologues of *A. nidulans*, *A. niger*, *N. crassa*, *T. atroviride*, *T. virens* and *S. cerevisiae* was conducted using Clustal Omega (<http://www.ebi.ac.uk/Tools/msa/clustalo/>). Protein sequences were retrieved from respective genome databases. The alignment revealed conserved amino acids and protein domains based on sequence similarities.