Figure 11: Multiple sequence alignment of ConA-like lectin/glucanase domains with known 3D structures of lectins. Putative ConA-like domains (amino acid numbering in brackets) of representative CscC proteins of *Enterococcus faecalis* (EF), *Enterococcus faecium* (EFA), *Lactobacillus plantarum* (LPL) and *Lactobacillus brevis* (LBR). Known 3D structures with PDB codes: 1hql, lectin, Glechoma hederacea (Ground-ivy); 1n47, lectin B4, Vicia villosa (Hairy vetch); 1qnw, anti-H(O)lectin 2, Ulex europeus (Furze); 1bqp, lectin(precursor), Pisum sativum (Garden pea). The coloured residues represent conserved ligands of divalent metal ions (Mn^{2+} or Mg^{2+}).

```
1hql                   --IRLTTSHT---WSVGRVMYSKPLTFWG--EGKQVHFKTKISFNITSIAGNKA-DGVAL
1n47                   --LELTKNGKPVPESLGRN------------CTTLASFTTSFSFVMSAPNSLDVADGLAF
1qnw                   --LQVTKVSKPTTTSIGRALYAAPIQIWDSITGKVASFATSFSFVVKADKSDGV-DGLAF
2bqp                   --LQLTKAVK---NSIGRALYSAPIHIWDSKTGDVANFETLFTFAITAPYSSNVADGLAF
EFA03340(125-335)      --LQLNPAER---SQRG-AIWSNK--KIS--LLSDFTFKSYLYLG--NQRDRAG-DGMTF
EF01001(150-359)       --LQLNPAVK---SQKG-AIWSKK--PIS--LLSDFTFKSYLYLG--NEYANAG-DGMTF
LPL0297(66-301)        HVIELTNDD----NQVG-AMWSTPVNRFN--MRVDNQVSMWVNFG----DKAVS-EGLAV
LPL3450(75-333)        QAVQVINGK----KQMG-GFWSNDANRLD--LNKNATFKMWVYLGTSTSTSKAG-DGMAF
LBR01269(64-320)       HGLQITEGN----NHAG-SAWATNNYKVD--LSKDATFSLWLYLG-KGGAGSAG-QGMTF
LBR00625(76-335)       ---MVNNNT----YQFG-SIWSTDENYFD--LTQDETASMWLYFG--NQGTQAA-DGMAF
LBR00331(73-344)       ---SMTRHQ----SEYA-SIWSKHGSEFE--LTKPQTTSMWLYFG--NQYSASG-EGMAF
                           :           .                        . :           :*: .

1hql                   FM--------VPVGPPIPNGGAGGNLGLFDSSGVGKS-------------IFAVKFDTH-
1n47                   FL--------APPDTQP--QKRGGFLGLFKDRKHDIS-----------YQSVAVEFDTY-
1qnw                   FL--------APANSQIPSGSSAGMFGLFSSSDSKSS-----------NQIIAVEFDTYF
2bqp                   FI--------APVDTQPQNIGRAGFLGVFNSETYNKS-----------IQTVAVEIDTF-
EFA03340(125-335)      TLTGDPRMASNPSQVI---GSPGMGIGSYSTRSGQPY----------IANALSIEFDTYK
EF01001(150-359)       TLTNDPRMSTTPQEVI---GSPGMGIGAYSTKAGQPY----------VRNALSIEFDTYK
LPL0297(66-301)        VLQNDPHKMSAISRYGK-KSIIGENLGVYGTDTYTRRTAPATIAKTAIQKSWALELDTKV
LPL3450(75-333)        VLQNDPNGTAASAQVSS-SSIIGETLGVWGVDTDNKLKDGEEFAKTAIQNSWALEFDTYT
LBR01269(64-320)       VLQNAG---ATGFTTIPAGRMAGQSLGTWGLDFNSTAADATAVAAAAISKSWALEFDEQV
LBR00625(76-335)       VLQNDPRGVAAIPDYPTPGKAIGETLGVWGVDMARRQGSVDKLAQTAIQDSWALEFDTNR
LBR00331(73-344)       AIHNDARGVNAMPELNKKGSVPGETLGVWPSDTVRTQGEAADLAKRGIQNSWALEFDTHQ
                        :                       :* :                       :: .*

1hql                   -----------ANVWDPPCR------HIGINVNSRVPVAHKCMDDSVNWEDVTL-----S
1n47                   -----------SNVWDPNTT------HIGIDTNTIESKKITP------------------
1qnw                   G--------KAYNPWDPDFK------HIGIDVNSIKSIKTVK---W-DWRNGEVADVVIT
2bqp                   -----------HNTWDPKINR-----HIGINVNCIKSISTTS---WVLENGREANVLV-R
EFA03340(125-335)      NS-------GSSDRMDREITAD----NRGHGHVAFVTPKPNN------------------
EF01001(150-359)       NT-------GSSNRMDREISQ-----DKGNGHLAFVTPKANN------------------
LPL0297(66-301)        NDGGFWGLYPRGNSFDEKPKKM----HMAASYPASPDTYTQR------------GGLTSS
LPL3450(75-333)        NTSTSYSNAGKGDSFDDGIKKQ----HIATGYPGLASQYENQ---SVRSLDVTGIIWSTR
LBR01269(64-320)       NDSRDG---GDNNGFDYNYINTTTQ-HIASNYPAQVSSYSRN---GTAMSGA-------K
LBR00625(76-335)       NASTGGKAAGYANSFDIGMPPV----HIGSNYPGAGSSYIRHVDHGLPVLGIIQPD---N
LBR00331(73-344)       NIKSGGRAAGQADSFDLEFENSKVGDHIASNHPGSSASFIQHVDSGVLWTGNTPINVM-H
                                   :  *            . .

1hql                   INYDEADKIITVRAQ----VGLTKHYDLSHKLDLSTI-----------------------
1n47                   --FDMVYGEKILFAS--------------LVFPVSQD-----------------------
1qnw                   YRAPTKSLTVCLSYP-----SDGTSNIITASVDLKAI-----------------------
2bqp                   FDAHTNVLSVVLSYP-----GLPDSYILSDVVPLKDI-----------------------
EFA03340(125-335)      NNYSGEHTGVTVAPT---FLSNGTWRLLIIKWDAEQR------SLTYDLEGV--------
EF01001(150-359)       NNYTGEHSGVTVAPT---YLSNGTWRMLTVHWNAATK------ALTYDLEGV--------
LPL0297(66-301)        YRFEQNHGSIADKLP----LADGNWHHLVLKWVASKQ------IMSYTLDQ---------
LPL3450(75-333)        YYFTQKHTNLVTNMS----LGDSKWHHLVMDWHAATK------TMTYTYNDINPDGSATG
LBR01269(64-320)       YFYYLNHQGKLNATL-----SDGTWHHLTLAWTAPTD-NSNTGSVTYTFNDKNPTTGASQ
LBR00625(76-335)       YYYGLNHLGVIADESQPNFLSNGQWHHVTLSWKAATK------QMTYTFNDKDPQTGAMQ
LBR00331(73-344)       YYYHIQHVGMIGDKSNSNYLSNGQWRHLTLKWQPANHEGNSYGQMTYVFDDKDPKTGERL
```

```
1hql                   ----------------------LEKKVQVGLSASTG---TNIALHDINYWEF
1n47                   ---------------------ILPEYVRVGFSATTGLNEGVVETH-------
1qnw                   ----------------------LPEWVSVGFSGGVGNA-AEFETHDVLSWYF
2bqp                   ----------------------VPEWVRIGFSAATG—--AEFAEHDIRYWSF
EFA03340(125-335)      -GRSSRIIPDLIRQFG-------STEVNWGFTSSTGTFFQEN-AVAVTRLPS
EF01001(150-359)       -GTNTYVVSDLNAQFG-------ATTVYWGFTSSTGGKYQEN-ALAMTQIPT
LPL0297(66-301)        -GPTRMTTIDTTVFGK------DIRNVTWGLTSTATTANART-LVVFDRLPQ
LPL3450(75-333)        SGFTQSEVLDTSQFNS------SDGLVRWGFMGATGSNSGNN-MVVIESAPN
LBR01269(64-320)       SGQSATISLDLSKLGI--NVTDVTKIVTWGFTGVSGTFGTNN-VVAFEHIPG
LBR00625(76-335)       PGVSRTVTLDPAKIDP-----NNTGKIRWGFTGATGSRYENN-LVVFESVPG
LBR00331(73-344)       NGREQTVNVNVNTIDP-----DRNGKARWGLAGTTTTKFASNQLVVFEKAP-
                                                   *:
```

1hql.pdb: Lectin, Glechoma hederacea (Ground-ivy)
1n47.pdb: Lectin B4, Vicia villosa (Hairy vetch)
1qnw.pdb: Anti-H(O)lectin 2, Ulex europeus (Furze)
1bqp.pdb: Lectin(precursor), Pisum sativum (Garden pea)