

1) Align the sequence of the ADP-Glc PPase small subunit with the sequences given in the web page using:

Clustal-W2

T-Coffee

Praline

Praline with secondary structure prediction (PSIPRED).

Identify the conserved residues located in the putative catalytic domain of the potato tuber S subunit (residues 21-290).

Compare the obtained results.

Most of you found 63, 62, and 63 conserved residues using Clustal, T-Coffee, and Praline respectively.

2) Align the sequences of the potato tuber S subunit with the L subunit using global and local alignments (EMBOSS Pairwise Alignment Algorithms).

<http://www.ebi.ac.uk/emboss/align/>

Obtain the %identity and % similarity.

50,1 % Identity

71.1 % Similarity

Why are they different?

3) Find out which of the conserved residues identified in 1), are not conserved in the L subunit. If the L subunit does not have enzymatic activity, but the S subunit does, what can we conclude from this analysis? Arg33, Lys43, Gln126, and Iso232.

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>gi|232164|sp|P23509|GLGS_SOLTU Glucose-1-phosphate adenylyltransferase
small (S) subunit, chloroplast precursor
MAVSQNSQTCLDPDASRSVLGIIILGGGAGTRLYPLTKKRAKPAVPLGANYRLIDIPVSNCLNSNISKIY
VLTQFNSASLNRHLSRAYASNMGYKNEGFVEVLAAQQSPENPDWFQGTADAVRQYLWLFEEHTVLEYLIL
AGDHLRMDYKFIQAHRETDADITVAALPMDEKRATAFGLMKIDEEGRIIEFAEKPQGEQLQAMKVDTTI
LGLDDKRAKEMPFIASMGIYVISKDVMLNLLRDKFPGANDFGSEVIPGATSLGMRVQAYLYDGYWEDIGTI
EAFYNANLGITKKPVPDFSFYDRSAPIYTPRYLPPSKMLDADVTDSVIGEGCVIKNCKIHHSVVGLRSCI
SEGAIIEDSLLMGADYYETDADRKLLAAKGSVPIGIGKNCHIKRAIIDKNARIGDNVKIINKDNVQEAARE
TDGYFIKSGIIVTIKDALIPSGIII
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>gi|232166|sp|Q00081|GLGL1_SOLTU Glucose-1-phosphate
adenylyltransferase large (L) subunit
MAYSVITTENDTQTFVDMRRLERRRANPKDVAAVILGGGEGTKLFPLTSRTATPAVPVGGCYRLIDIPMS
NCINSAINKIFVLTQYNSAPLNRHIARTYFGNGVSFGDGFVEVLAATQTPGEAGKKWFQGTADAVRKFIWV
FEDAKNKNIENIVVLSGDHLRMDYMELVQNHIDRNADITLSCAPAEDSRASDFGLVKIDSRGRVVQFAEK
PKGFDLKAMQVDTTLVGLSPQDAKSPYIASMGVYVFKTDVLLKLLKWSYPTSNDGSEIIPAAIDDYVQ
AYIFKDYWEDIGTIKSFYNASLALTQEFPEFQFYDPKTPFYTSRFLPPTKIDNCKIKDAIISHGCFLRDC
SVEHSIVGERSRLDCGVELKDTFMMGADYYQTESEIASLLAEGKVPPIGIGENTKIRKCIIDKNAKIGKNVS
IINKDGVQEAADRPEEGFYIRSGIIIIILEKATIRDGTVI
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