

Figure S2. ClustalW analysis: each protein was pasted in the FASTA format.

Address <http://www.ebi.ac.uk/clustalw/index.html?> Go Links

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SEQUENCE ANALYSIS

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ClustalW Submission Form

ClustalW is a general purpose multiple sequence alignment program for DNA or proteins. It produces biologically meaningful multiple sequence alignments of divergent sequences. It calculates the best match for the selected sequences, and lines them up so that the identities, similarities and differences can be seen. Evolutionary relationships can be seen via viewing Cladograms or Phylograms. **New users, please read the FAQ.**

>> Download Software

YOUR EMAIL	ALIGNMENT TITLE	RESULTS	ALIGNMENT	CPU MODE
<input type="text"/>	<input type="text" value="Sequence"/>	<input type="text" value="interactive"/>	<input type="text" value="full"/>	<input type="text" value="single"/>

KTUP (WORD SIZE)	WINDOW LENGTH	SCORE TYPE	TOPDIAG	PAIRGAP
<input type="text" value="def"/>	<input type="text" value="def"/>	<input type="text" value="percent"/>	<input type="text" value="def"/>	<input type="text" value="def"/>

MATRIX	GAP OPEN	END GAPS	GAP EXTENSION	GAP DISTANCES
<input type="text" value="def"/>	<input type="text" value="def"/>	<input type="text" value="def"/>	<input type="text" value="def"/>	<input type="text" value="def"/>

OUTPUT		PHYLOGENETIC TREE		
OUTPUT FORMAT	OUTPUT ORDER	TREE TYPE	CORRECT DIST.	IGNORE GAPS
<input type="text" value="aln w/numbers"/>	<input type="text" value="aligned"/>	<input type="text" value="none"/>	<input type="text" value="off"/>	<input type="text" value="off"/>

Enter or Paste a set of Sequences in any supported format:

Upload a file:

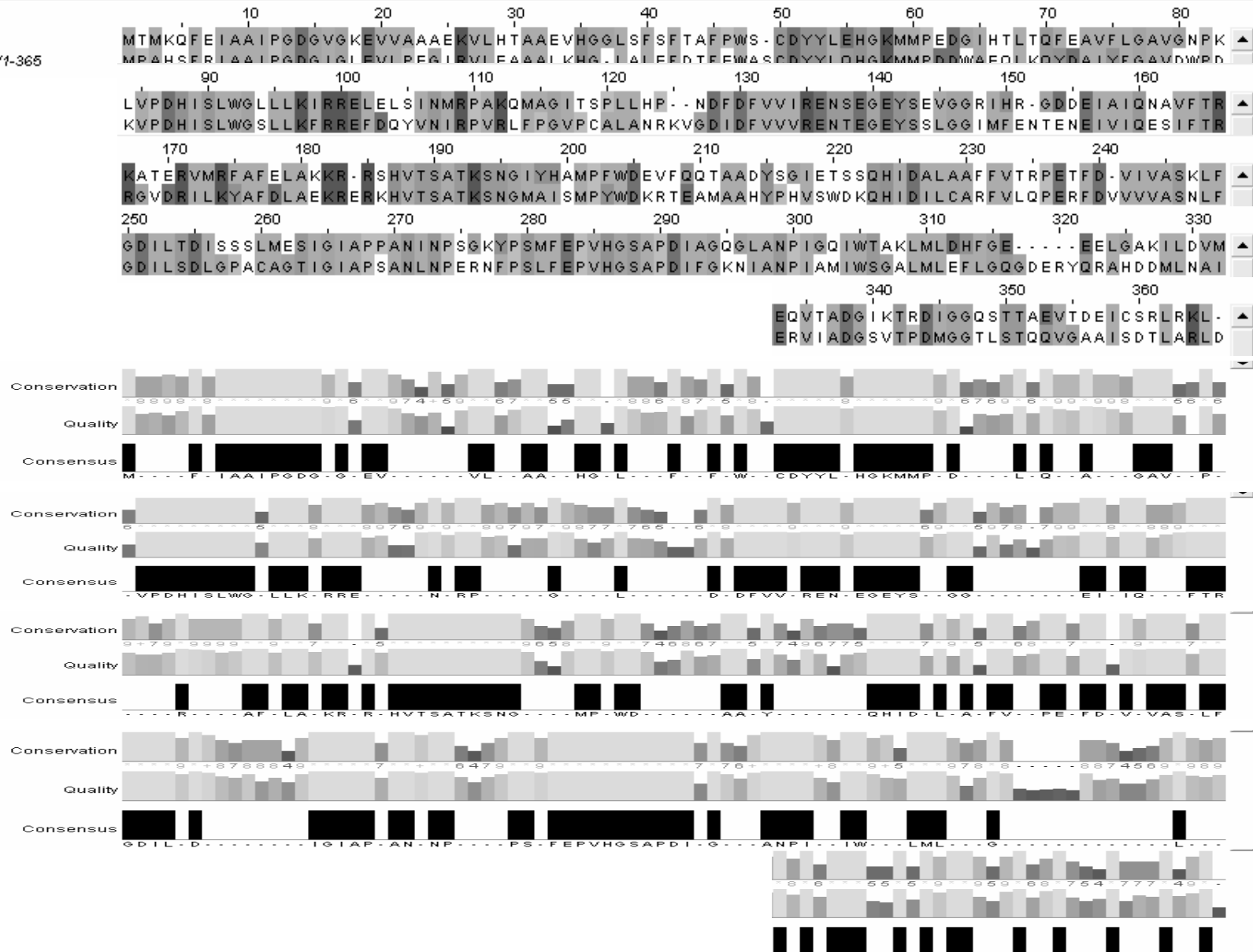
<http://www.ebi.ac.uk/cgi-bin/jobresults/clusterw/clusterw-20060514-07402963.aln>

File Edit Search View Colour Calculate Help

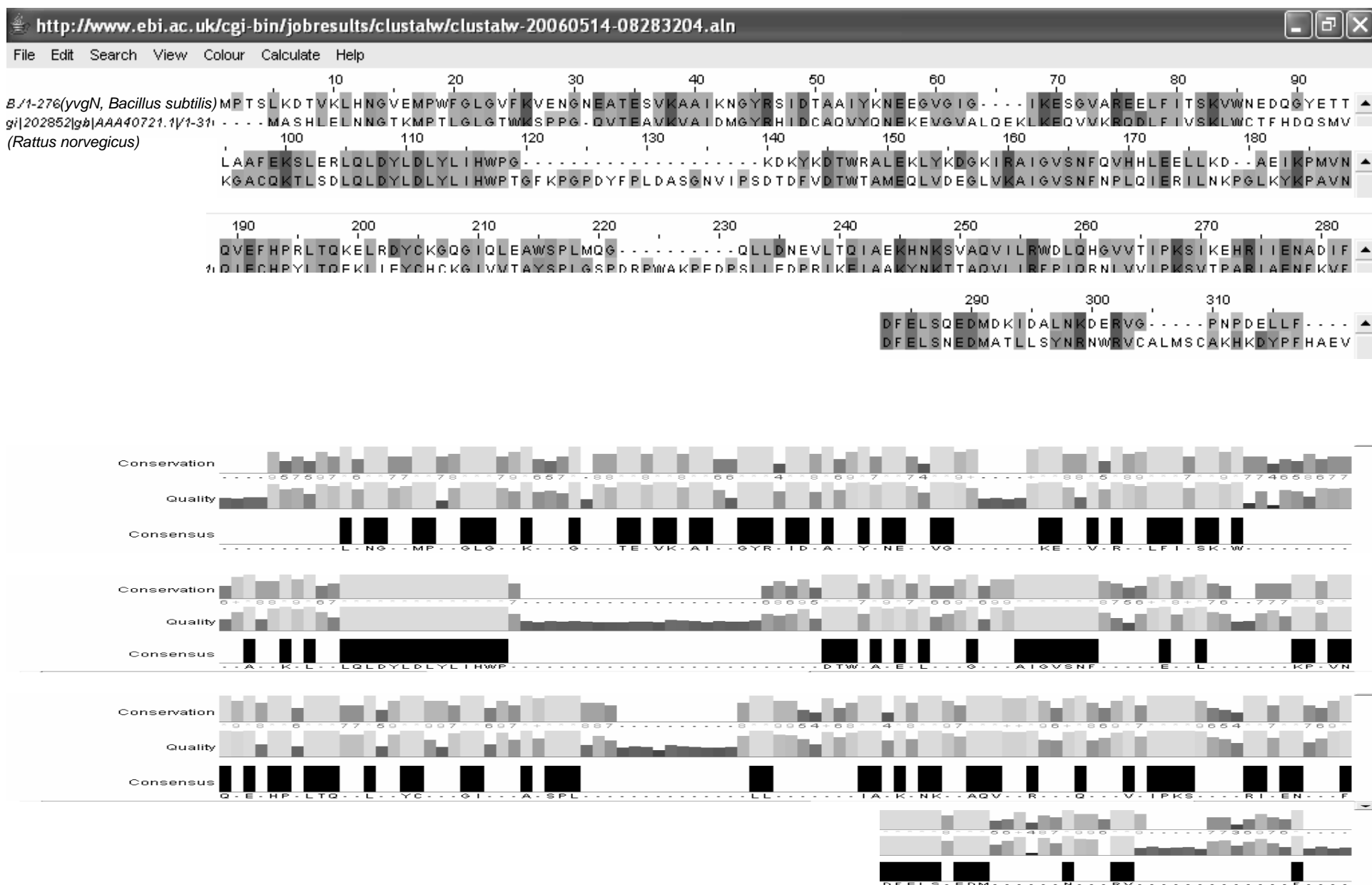
B/1-354 (*ycaA*, *Bacillus subtilis*)

gi|3024771|sp|Q51945|TTUC_PSEP/1-365

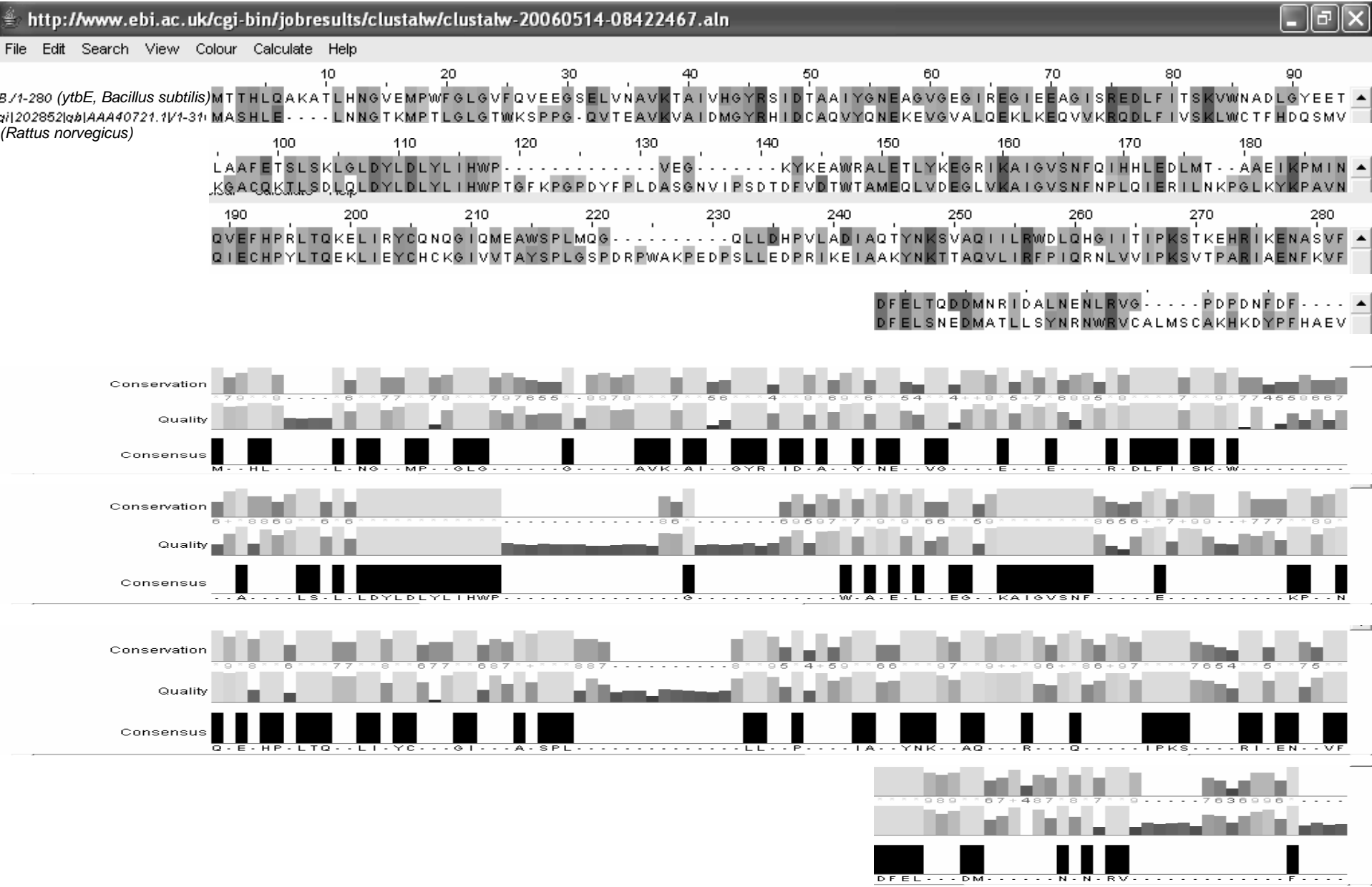
(*Pseudomonas putida*)



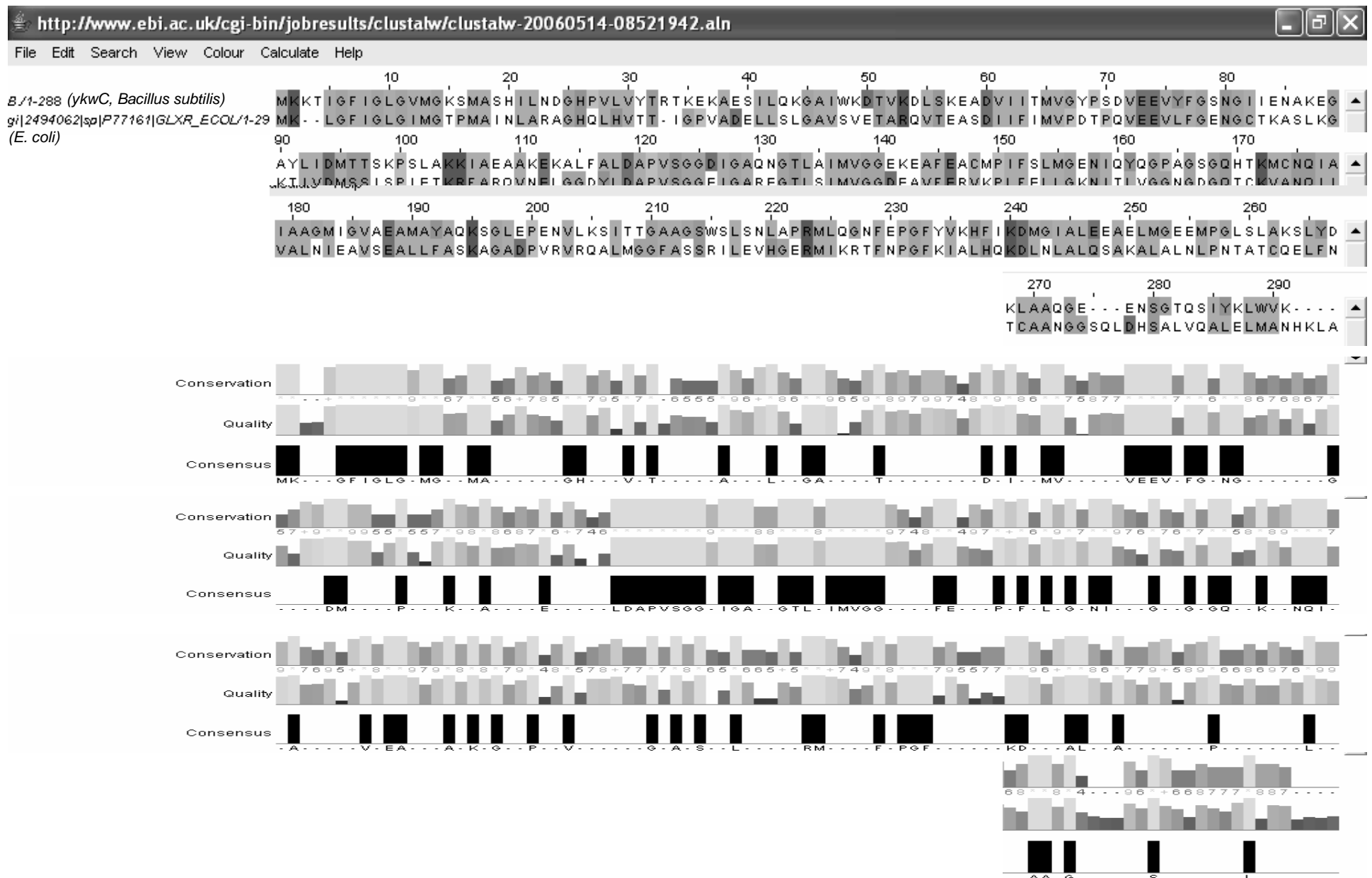
(B1) Aldose reductase (1.1.1.21)



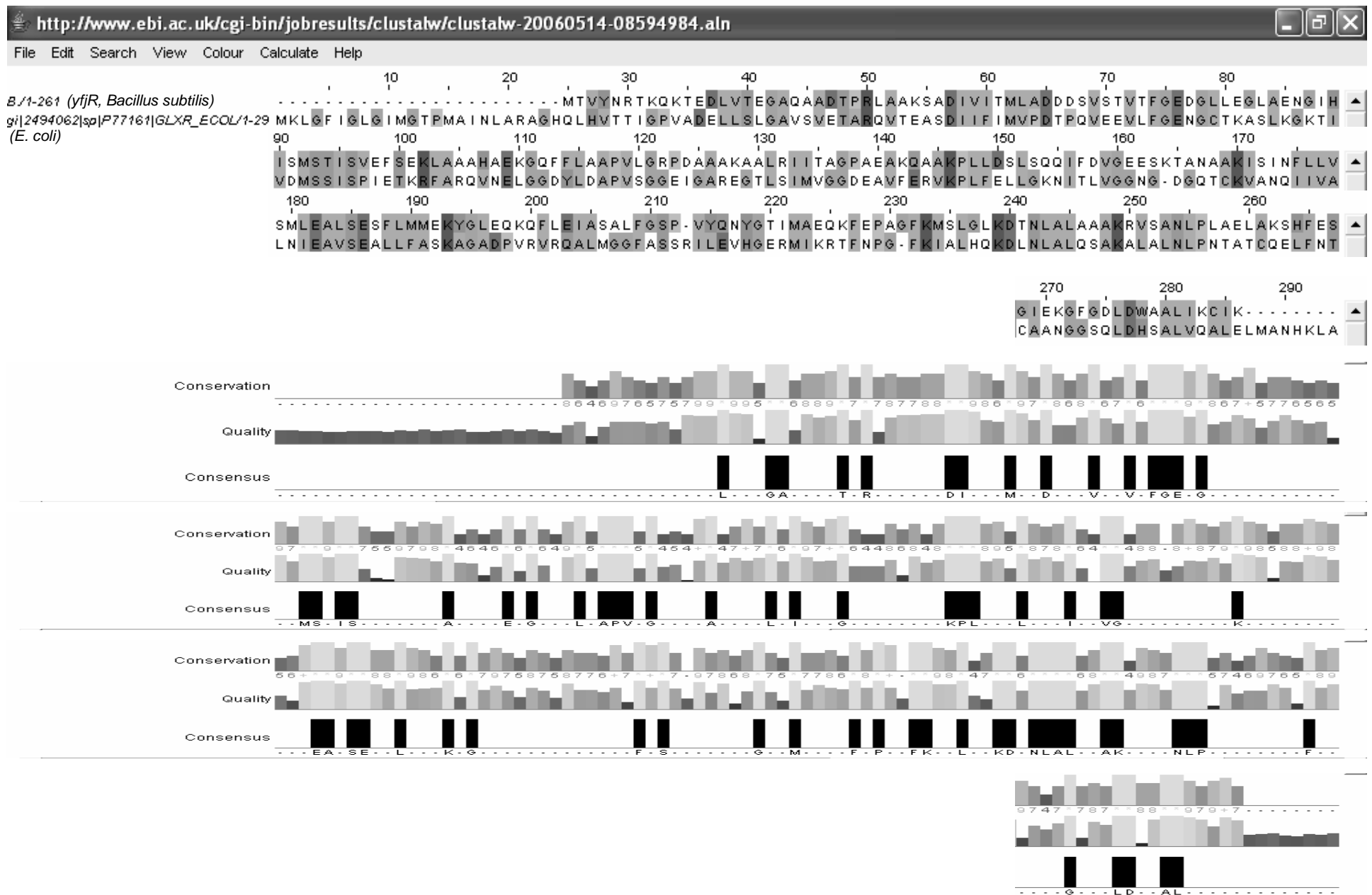
(B2) Aldose reductase (1.1.1.21)



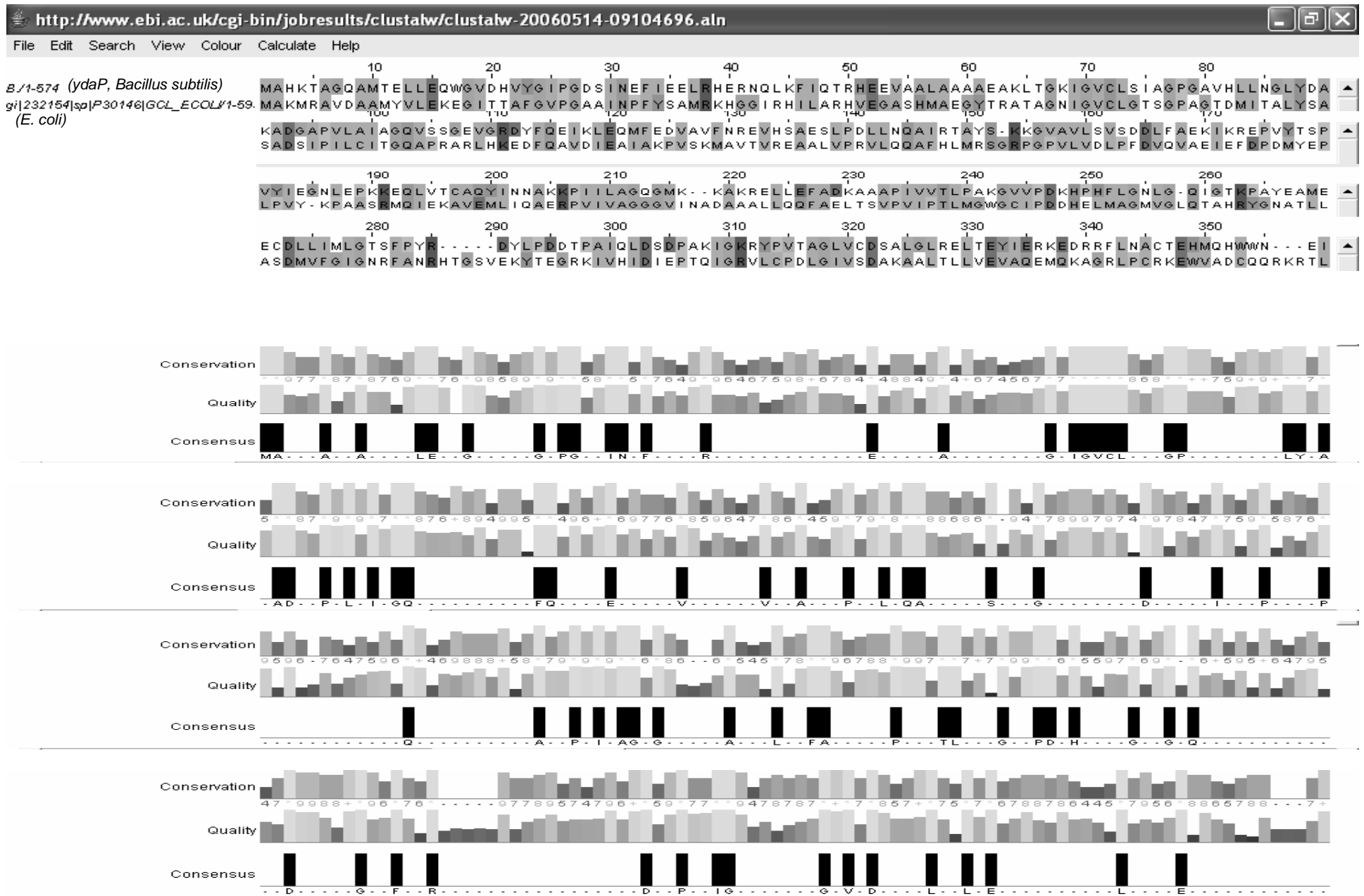
(C1) Tartronate semialdehyde reductase (EC1.1.1.60)



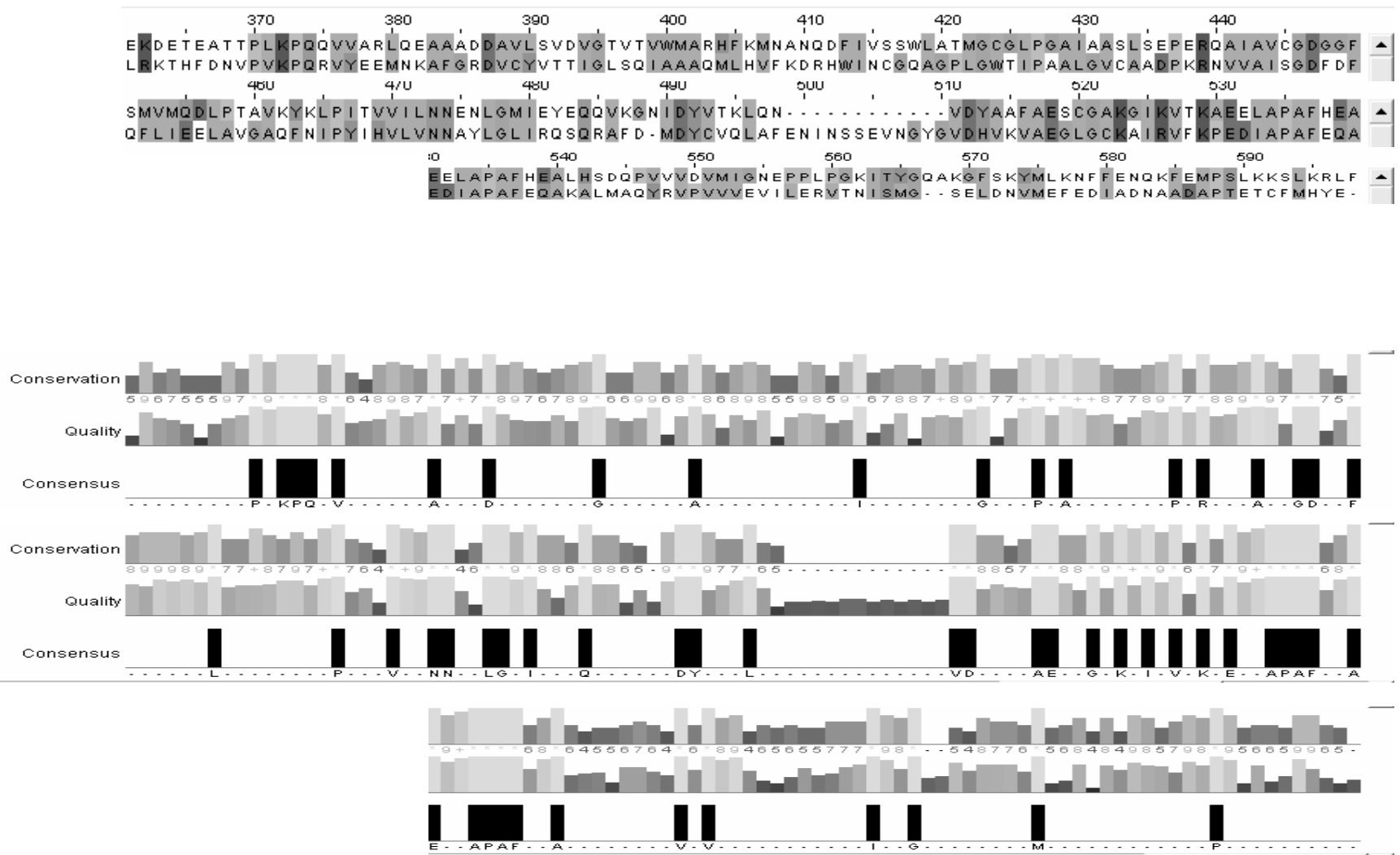
(C2) Tartronate semialdehyde reductase (EC1.1.1.60)



(D-1) Tartronate semialdehyde synthase (EC4.1.1.47)



(D-2) Tartronate semialdehyde synthase (EC4.1.1.47)



(E) Galactitol 1-phosphate 5-dehydrogenase (EC1.1.1.251)

