ASSIGN™ ATF

proven *software*

MUTATION DETECTION

High throughput, automated DNA sequence mutation/variant detection analysis software

Improve testing accuracy and save time by tracking sequence quality

CONEXIO

Mutation detection software that improves testing accuracy and saves time

Assign™ ATF is a high throughput, automated DNA sequence mutation/variant detection sequence analysis software product that produces graphed quality control information in a unique and informative manner. Laboratories are able to *track sequence quality over time to improve testing accuracy and save time*.

Sequencing applications for Assign™ ATF are extensive and range from testing for genetic mutations associated with a particular disease to viral genotyping. Importantly, the technology was originally developed from a user's perspective by Clinical Laboratory Scientists and computer programmers, with expertise in DNA sequencing and quality assurance.

Enhanced quality of data - Base Call Score

Users are able to experience enhanced base call accuracy since the software has the ability to distinguish background noise from real data and accurately monitor sequence quality through Assign™ ATF's unique Base Call Score (BCS) system.

The system provides real time evaluation of :

- *Peak shape*
- *Background noise*
- *Lateral peak resolution*

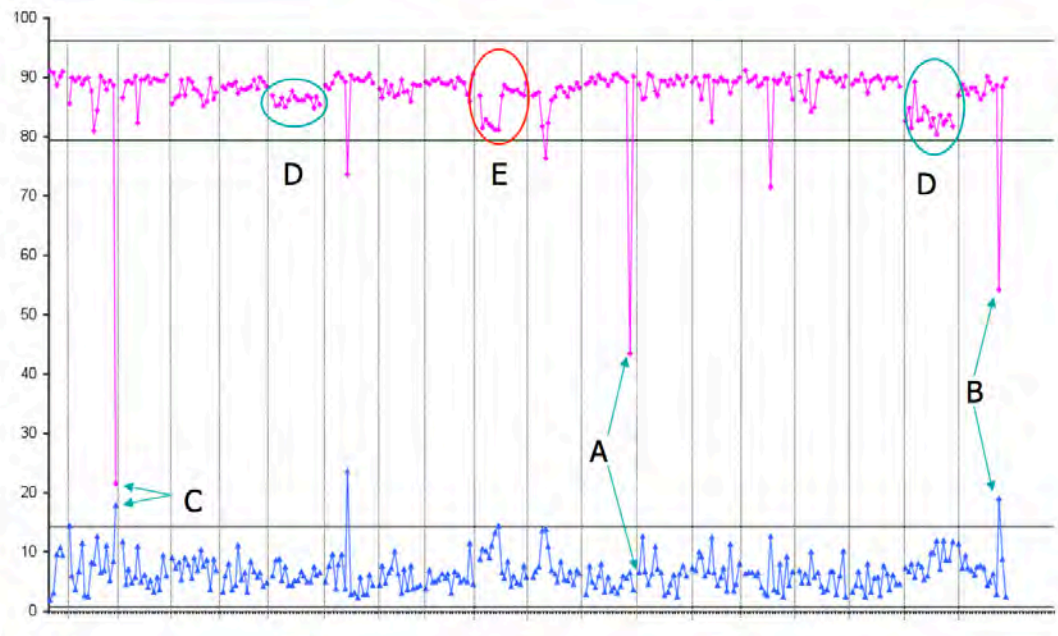
Base Call Score (Ideal Data BCS=50)
Quantitative Assessment of Peak Quality

Consensus sequence BCS is calculated from base calls contributing to the consensus and is a score out of 100. *Note: BCS does not discriminate against heterozygous base calls*.

Sequencing Quality Control
Sample to Sample and Run to Run Quality Analysis

This graph is a quality report generated by Assign™ ATF. The graph demonstrates how the BCS system is used to monitor sequence quality. A BCS is assigned to each base call. The mean and standard deviation (SD) of BCS for base calls spanning a region of sequence provide a quantitative quality score for the region of sequence. This can then be compared between samples and also PCR and sequencing "runs". This graph contains the mean BCS (pink) and SD (blue) of the consensus sequence of a single amplicon sequenced bi-directionally. Each section of BCS data is from different sequencing runs, allowing sample to sample and run to run comparisons.

Sample A has a BCS <50 and a low standard deviation (SD) indicating good quality sequence from a single direction only. Sample B has a low mean (but >50) and high SD indicating that both strands have been sequenced but at least one strand is of poor quality. Sample C also has a low mean and high SD indicating poor quality of one (probably both) strands.



The D group of samples are from the same sequencing run and have a similar BCS to each other but slightly lower than the BCS of neighbouring runs indicating a reduction in quality that results either from the PCR or the sequencing run itself.

The E group of samples have scores from the same sequencing run but from different PCR runs demonstrating the effect of the PCR on the quality of the sequence.

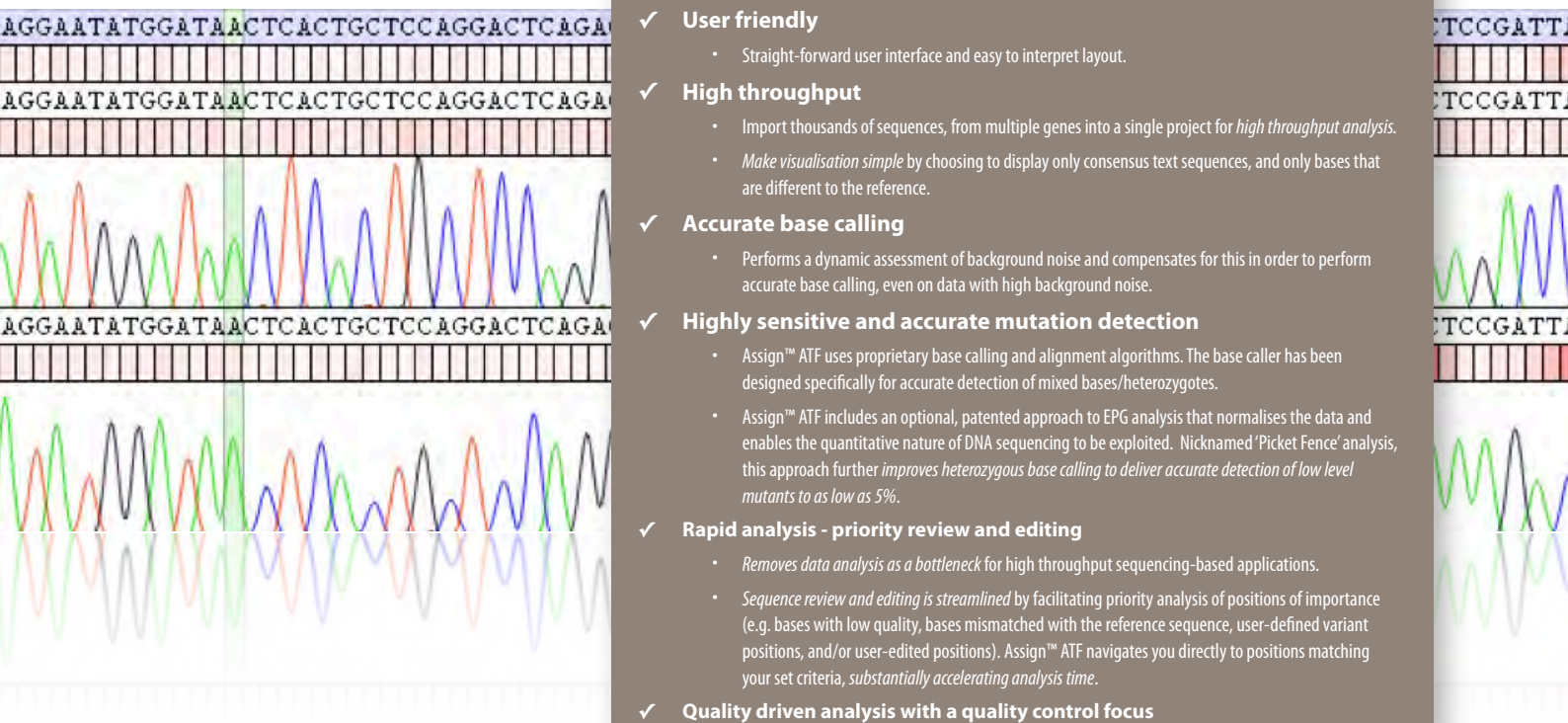
The Quality reports in Assign™ ATF allow the setting of quality targets and also assists in effective trouble shooting.

ASSIGN™ ATF

Key features

- ✓ **Tailored to an extensive range of sequencing applications**
  - Variant / Mutation detection
  - Quality Control
  - Sequence Alignment
  - Genotyping
- ✓ **Efficient and rapid setup**
  - *Create reference sequences directly from GenBank* and be ready for analysis in just a few minutes.
  - *Improve analysis speed and quality* by tailoring analysis according to your PCR strategy to remove poor quality and unwanted sequence.
- ✓ **User friendly**
  - Straight-forward user interface and easy to interpret layout.
- ✓ **High throughput**
  - Import thousands of sequences, from multiple genes into a single project for *high throughput analysis.*
  - *Make visualisation simple* by choosing to display only consensus text sequences, and only bases that are different to the reference.
- ✓ **Accurate base calling**
  - Performs a dynamic assessment of background noise and compensates for this in order to perform accurate base calling, even on data with high background noise.
- ✓ **Highly sensitive and accurate mutation detection**
  - Assign™ ATF uses proprietary base calling and alignment algorithms. The base caller has been designed specifically for accurate detection of mixed bases/heterozygotes.
  - Assign™ ATF includes an optional, patented approach to EPG analysis that normalises the data and enables the quantitative nature of DNA sequencing to be exploited. Nicknamed 'Picket Fence' analysis, this approach further *improves heterozygous base calling to deliver accurate detection of low level mutants to as low as 5%*.
- ✓ **Rapid analysis - priority review and editing**
  - *Removes data analysis as a bottleneck* for high throughput sequencing-based applications.
  - *Sequence review and editing is streamlined* by facilitating priority analysis of positions of importance (e.g. bases with low quality, bases mismatched with the reference sequence, user-defined variant positions, and/or user-edited positions). Assign™ ATF navigates you directly to positions matching your set criteria, *substantially accelerating analysis time*.
- ✓ **Quality driven analysis with a quality control focus**
  - *Strong focus on data quality* - generates visible quality indicators based on critical quality parameters such as peak quality and signal intensities.
  - *Allows performance criteria establishment* for the acceptance or rejection of base calls, entire EPGs and/or entire samples.
  - *Enables automatic generation of longitudinal quality control reports*, allowing for run to run analysis of quality. This facilitates the assessment of the effect of changes (such as reagent changes) on sequence data quality.
  - *Different levels of user access are available* to allow only selected users to perform final reviews (Quality Control Checks), prior to result release.
- ✓ **Audit trail**
  - *An analysis audit trail is recorded and can be reported.* This allows reference to, and reporting of, which user has performed which steps. This feature further improves quality control.
- ✓ **Distinctive features**
  - *Enables analysis of heterozygous insertions and deletions*. Calculates the inserted or deleted bases for reporting, enabling all sequence variants to be reported.
  - *Allows the ability to include overlapping genes and coding sequences in a single project, maximising analysis of the impact of sequence variants.*

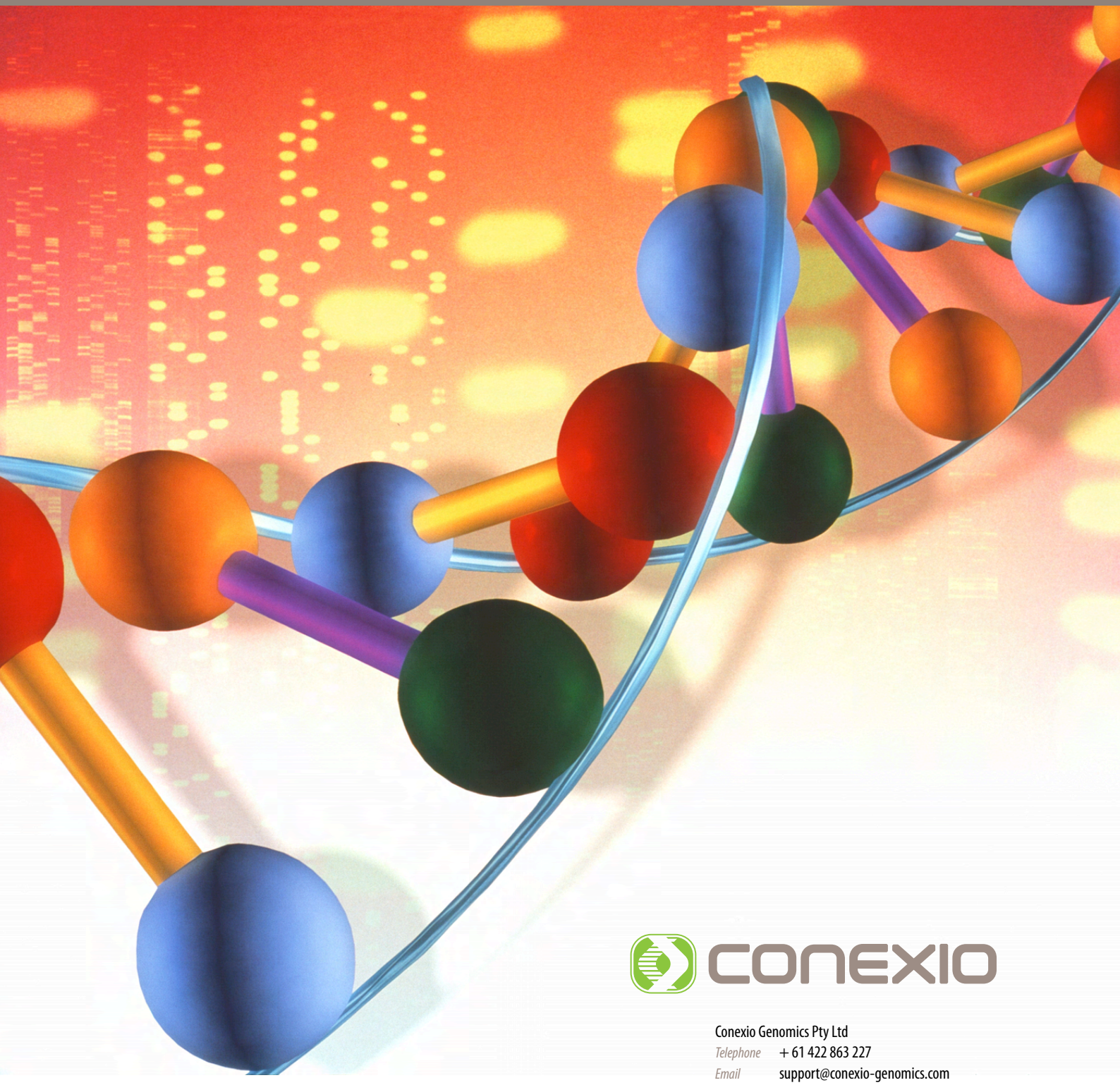
Quality Is Assured with ISO 13485
Conexio Genomics is an ISO 13485 certified company.



Conexio Genomics

Conexio Genomics is a privately operating life sciences company located in Fremantle, Western Australia. The company has developed and supplied a wide range of novel genetic sequencing and mutation detection products and services for more than 10 years and has established itself as a world leader with over 200 laboratories using its technologies.

Assign™ ATF is for Research Use Only. Not for use in diagnostic procedures. No claim or representation is intended to provide information for the diagnosis, prevention, or treatment of a disease.



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