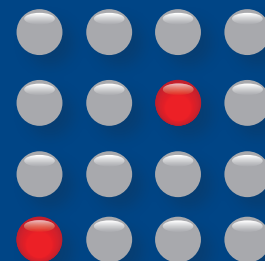


# Colorectal Cancer DSA™ Technical Note



The Almac Diagnostics Colorectal Cancer DSA™ research tool offers the most comprehensive platform available for the study of Colorectal Cancer.

The Almac Diagnostics **Colorectal Cancer DSA™** research tool offers the most comprehensive gene expression analysis platform for the study of colorectal cancer with over 50,000 biologically relevant transcripts available for interrogation, tens of thousands of which are unavailable on leading generic arrays.



Based upon the Affymetrix GeneChip® technology, the **Colorectal Cancer DSA™** research tool provides multiple independent measurements for each transcript.

| COLORECTAL CANCER DSA™<br>Technical Specifications |           |
|--|-----------|
| Total Probesets on Array                           | ~61,528   |
| Control Probesets                                  | 162       |
| Number of Transcripts                              | ~52,000   |
| Feature Size                                       | 11 Micron |
| Probe Length                                       | 25-MER    |
| Probe Pairs / Probeset                             | 100       |

The end result is a tailored research solution providing accurate and reproducible expression data for the transcripts that really matter to your research setting.

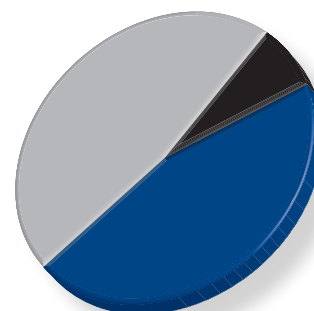
## ARRAY CONTENT

The Almac Diagnostics **Colorectal Cancer DSA™** research tool was compared to the NCBI's Reference Sequence (RefSeq) database and over 50% of the Almac Diagnostics **Colorectal Cancer DSA™** research tool content is not present in the RefSeq database and 8% of this content represents potential antisense transcripts to annotated genes.

The transcriptome based design enables expression analysis of over 2,000 endogenous antisense transcripts, of which more than 1,600 have been detected, in both orientations, in in-house experiments.

## COLORECTAL CANCER DSA™ RESEARCH TOOL COMPARED WITH REFSEQ

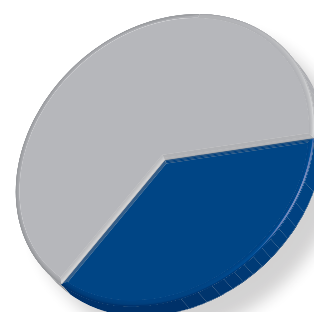
- 47% Similar
- 45% Unique
- 8% Reverse Orientation



Sequence analysis comparing the **Colorectal Cancer DSA™** research tool with a leading commercially available microarray clearly highlights the extent of its unique content (see figure below).

## COLORECTAL CANCER DSA™ RESEARCH TOOL COMPARED WITH A LEADING GENERIC ARRAY

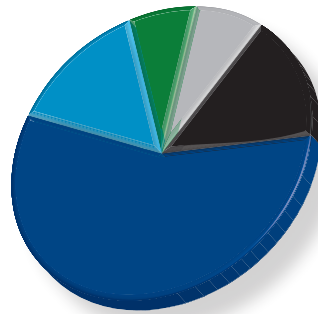
- 64% Similar
- 36% Unique



## UNIQUE CONTENT ANALYSIS

Analysis of the unique content of the **Colorectal Cancer DSA™** research tool (see figure below) demonstrates that 23% corresponds to RefSeq transcripts in both sense and anti-sense orientation.

- 8% RefSeq
- 15% RefSeq Antisense
- 56% Colorectal Ests
- 14% dbEst
- 7% Genome

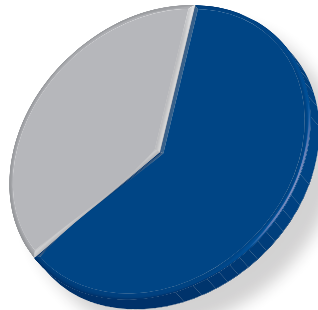


## COMPARISONS OF DISEASE TRANSCRIPTOMES

Comparison of the content of the **Colorectal Cancer DSA™** research tool with the **Ovarian Cancer DSA™**, research tool demonstrates unequivocally the differences between disease transcriptomes.

## COLORECTAL CANCER DSA™ RESEARCH TOOL COMPARED WITH OVARIAN CANCER DSA™ RESEARCH TOOL

- 62% Similar
- 38% Unique



## PROTEIN HOMOLOGY ANALYSIS

Protein homology analysis as shown in the table, reveals that a large proportion of the unique transcripts are likely to be protein coding and are involved in processes closely related to cancer initiation and development. A similar proportion are transcripts with antisense homology to these cancer-related proteins and represent sequences with important regulatory potential.

| PROTEIN HOMOLOGY ANALYSIS  | SENSE       | ANTISENSE  |
|--|-------------|------------|
| Uncharacterised protein count  | 270         | 216        |
| Hypothetical protein count   | 68          | 27         |
| Cell-cycle-related protein count                                       | 11          | 6          |
| Intercellular signaling-related protein count                          | 58          | 7          |
| Metabolism-related protein count                                       | 160         | 68         |
| Cytoskeleton, motility and spindle assembly-related protein count      | 48          | 29         |
| Proteasome-related protein count                                       | 17          | 12         |
| DNA damage/repair-related protein count                                | 57          | 17         |
| Cellular signalling-related protein count                              | 108         | 38         |
| Apoptosis-related protein count  | 5           | 4          |
| Chromatin remodelling-related protein count                            | 5           | 1          |
| Kinase of unknown function count                                       | 24          | 6          |
| Cell surface and intracellular receptors/channel-related protein count | 83          | 23         |
| Transcription-related protein count                                    | 45          | 124        |
| Cancer-related proteins of unknown function count                      | 21          | 9          |
| Immunoglobulin-related protein count                                   | 15          | 5          |
| Translation-related protein count                                      | 13          | 25         |
| Cellular stress response-related protein count                         | 2           | 1          |
| Cell-adhesion & extracellular matrix-related protein count             | 19          | 10         |
| DNA replication-related protein count                                  | 11          | 1          |
| Other proteins of known function                                       | 376         | 154        |
|  | <b>1416</b> | <b>783</b> |

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