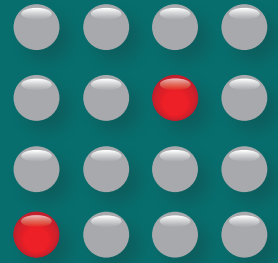
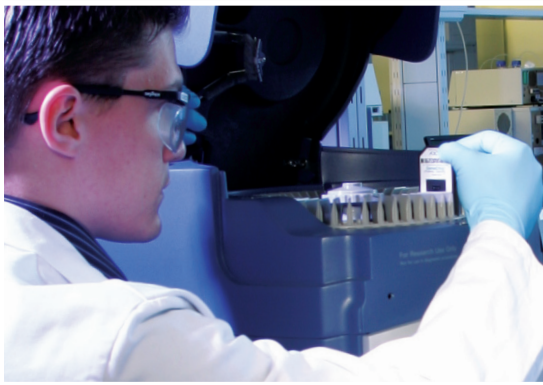


# Ovarian Cancer DSA™ Technical Note



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

The Almac Diagnostics **Ovarian Cancer DSA™** research tool offers the most comprehensive gene expression analysis platform for the study of ovarian cancer with over 100,000 biologically relevant transcripts available for interrogation, tens of thousands of which are unavailable on leading generic arrays.



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

OVARIAN CANCER DSA™ Technical Specifications	
Total Probesets on Array	~120,373
Control Probesets	2,596
Number of Transcripts	~100,000
Feature Size	11 Micron
Probe Length	25-MER
Probe Pairs / Probeset	11

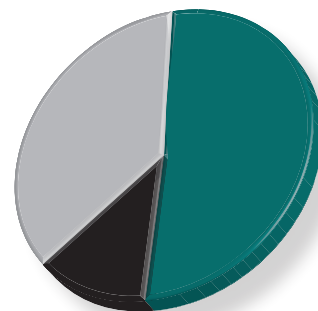
The end result is a tailored research solution providing accurate and reproducible expression data for the transcripts that really matter to your research setting.

## ARRAY CONTENT

The **Ovarian Cancer DSA™** research tool was compared to the NCBI's Reference Sequence (RefSeq) database and it was determined that 64% of the **Ovarian Cancer DSA™** research tool content is not present in the RefSeq database and 13% of the content represents antisense sequences to annotated transcripts.

## OVARIAN CANCER DSA™ RESEARCH TOOL COMPARED WITH REFSEQ

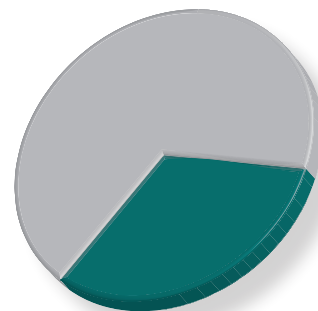
- 36% Similar
- 51% Unique
- 13% Reverse Orientation



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

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

- 68% Similar
- 32% Unique

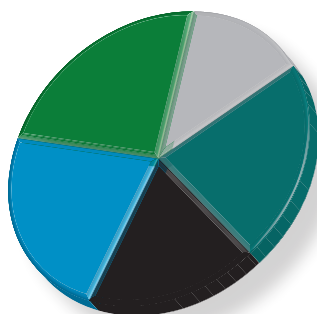


## UNIQUE CONTENT ANALYSIS

Analysis of the unique content of the **Ovarian Cancer DSA™** research tool (see figure below) demonstrates that 36% corresponds to RefSeq transcripts in both sense and anti-sense orientation.

### OVARIAN CANCER DSA™ RESEARCH TOOL UNIQUE CONTENT ANALYSIS

- 14% RefSeq
- 22% RefSeq Antisense
- 18% Ovarian Ests
- 23% dbEst
- 23% Genome

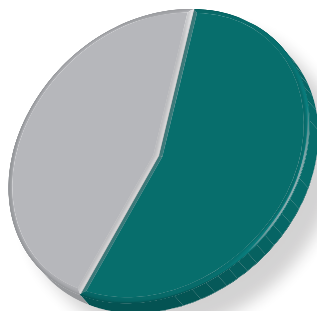


## COMPARISONS OF DISEASE TRANSCRIPTOMES

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

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

- 45% Similar
- 55% 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	3141	4026
Hypothetical protein count	375	989
Cell-cycle-related protein count	33	10
Intercellular signalling-related protein count	243	42
Metabolism-related protein count	487	118
Cytoskeleton, motility and spindle assembly-related protein count	574	174
Proteasome-related protein count	50	17
DNA damage/repair-related protein count	161	29
Cellular signalling-related protein count	342	110
Apoptosis-related protein count	18	33
Chromatin remodelling-related protein count	39	5
Kinase of unknown function count	36	5
Cell surface and intracellular receptors/channel-related protein count	194	63
Transcription-related protein count	440	174
Cancer-related proteins of unknown function count	99	92
Immunoglobulin-related protein count	25	11
Translation-related protein count	188	31
Cellular stress response-related protein count	19	12
Cell-adhesion & extracellular matrix-related protein count	67	16
DNA replication-related protein count	11	2
Other proteins of known function	1177	756
	<b>7719</b>	<b>6715</b>

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