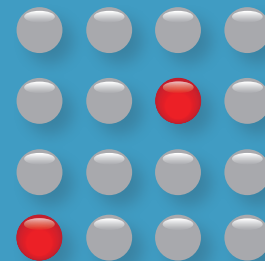


# Prostate Cancer DSA™ Technical Note



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

The Almac Diagnostics **Prostate Cancer DSA™** research tool offers the most comprehensive gene expression analysis platform for the study of prostate cancer with over 90,000 biologically relevant transcripts available for interrogation, tens of thousands of which are unavailable on leading generic arrays.



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

PROSTATE CANCER DSA™ Technical Specifications	
Total Probesets on Array	~121,563
Control Probesets	2,567
Number of Transcripts	~93,000
Feature Size	11 Micron
Probe Length	25-MER
Probe Pairs / Probeset	11

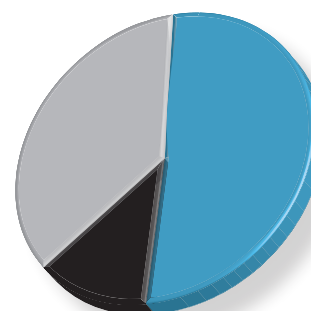
The end result is a tailored research solution providing accurate and reproducible expression data for the transcripts that really matter to your research setting.

## ARRAY CONTENT

The **Prostate Cancer DSA™** research tool was compared to the NCBI's Reference Sequence (RefSeq) database and it was determined that 62% of the **Prostate Cancer DSA™** research tool content is not present in the RefSeq database and 14% of the content represents antisense sequences to annotated transcripts.

## PROSTATE CANCER DSA™ RESEARCH TOOL COMPARED WITH REFSEQ

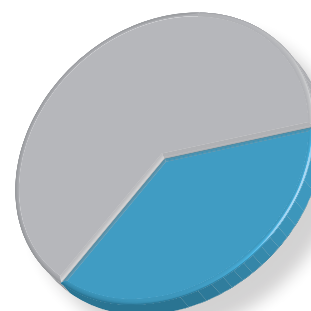
- 38% Similar
- 48% Unique
- 14% Reverse Orientation



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

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

- 63% Similar
- 37% Unique

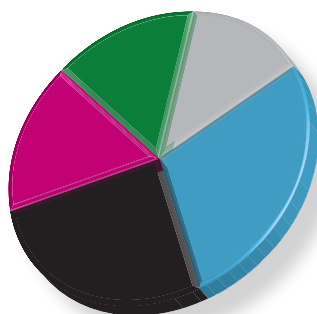


## UNIQUE CONTENT ANALYSIS

Analysis of the unique content of the **Prostate Cancer DSA™** research tool (see figure below) demonstrates that 42% corresponds to RefSeq transcripts in both sense and anti-sense orientation.

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

- 14% RefSeq
- 28% RefSeq Antisense
- 27% Prostate Ests
- 16% dbEst
- 15% Genome

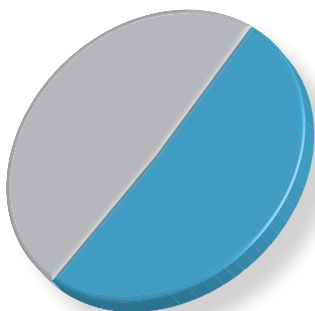


## COMPARISONS OF DISEASE TRANSCRIPTOMES

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

### PROSTATE CANCER DSA™ RESEARCH TOOL COMPARED TO LUNG CANCER DSA™ RESEARCH TOOL

- 49% Similar
- 51% 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	1773	2118
Hypothetical protein count	213	475
Cell-cycle-related protein count	40	4
Intercellular signalling-related protein count	303	48
Metabolism-related protein count	645	77
Cytoskeleton, motility and spindle assembly-related protein count	453	113
Proteasome-related protein count	131	16
DNA damage/repair-related protein count	181	23
Cellular signalling-related protein count	378	81
Apoptosis-related protein count	21	15
Chromatin remodelling-related protein count	39	0
Kinase of unknown function count	43	6
Cell surface and intracellular receptors/channel-related protein count	211	42
Transcription-related protein count	295	153
Cancer-related proteins of unknown function count	81	36
Immunoglobulin-related protein count	30	16
Translation-related protein count	390	76
Cellular stress response-related protein count	29	8
Cell-adhesion & extracellular matrix-related protein count	51	14
DNA replication-related protein count	17	2
Other proteins of known function	1399	491
	<b>6723</b>	<b>3814</b>

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