Caris Abstracts and Presentation Schedule

ESMO 2022

CARIS® LIFE SCIENCES

Where Molecular Science Meets Artificial Intelligence.

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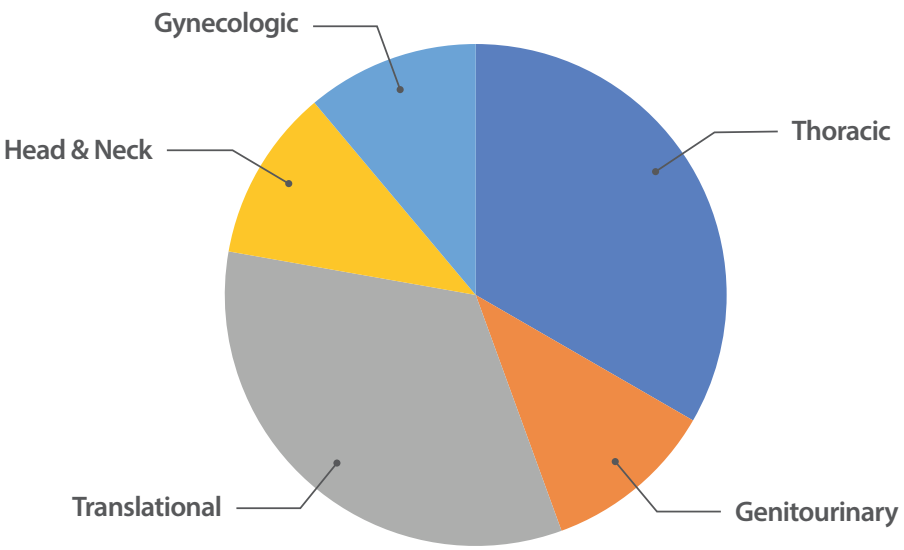
Caris Life Sciences® comprehensive molecular profiling provides the broadest and most comprehensive molecular analysis, leveraging whole exome sequencing to capture 22,000 genes, whole transcriptome sequencing to measure 61,000 transcripts, and immunohistochemistry to assess tumor-relevant protein biomarkers. Through this comprehensive approach, and in collaboration with our partners in the Caris Precision Oncology Alliance™ (POA), we are continually developing insights into a broad range of biomarkers and tumor types. As a result, this year's European Society for Medical Oncology (ESMO) posters cover an extensive set of insights across 17 tumor types. In total, Caris and our POA partners will present eight separate posters and one mini-oral presentation. These studies highlight the power of collaborative research and demonstrate that:

- Molecular profiling with a large dataset across more than 403,000 lifetime clinical cases allows the identification of rare biomarkers, and the implications for future research.
- Comprehensive analysis including whole exome sequencing, whole transcriptome sequencing, and immunohistochemistry drives the identification of new biomarkers and informs potential target identification for future treatment innovations.
- Caris supports the clinician across the full continuum to ensure the right diagnosis of the biopsy to the right treatment plan for each patient.

Accepted Caris POA Abstracts By POA Group



Mini-Oral Presentation

Differential Expression of Key Transcription Factors in Extra-Pulmonary Small Cell Carcinoma

Sonam Puri, Andrew Elliott, Heloisa Soares, Emil Lou, Balazs Halmos, Corey Langer, Dipesh Uprety, Sourat Darabi, Phillip Walker, Ari Vanderwalde, Wafik El-Deiry, Taofeek Owonikoko, Stephen Liu

Presentation Date and Time: Monday, September 12, 09:05-09:10 CEST

Location: 7.3.Q – Quimper Auditorium **Abstract:** 889MO

Key Findings:

The study showed different expression of key lineage-defining transcription factors in extra-pulmonary small cell carcinomas (EPSCC) from various anatomic sites were distinct from small cell lung cancer (SCLC). EPSCC and SCLC overall survival was similarly associated with transcription factor expression, suggesting the underlying biology of the EPSCC and SCLC subtypes might predict comparable therapeutic vulnerabilities.

Poster Presentations

Genomic Characteristics and Clinical Outcomes of *HRAS*-Mutated Urothelial Bladder Cancer

Jesus Antonio Ocejo Gallegos, Estelamari Rodriguez, Asaad Trabolsi, Samuel Kareff, Jun Yin, Phillip Walker, Wafik El-Deiry, Benedito Carneiro, Shuanzeng Wei, Chadi Nabhan, Gilberto Lopes, Jaime Merchan

Presentation Date and Time: Monday, September 12, 15:00-16:00 CEST

Location: Poster Area, Hall 4 **Abstract:** 1771P

Key Findings:

HRAS mutant tumors in urothelial bladder cancer show distinct differences to the general cohort. Of which, *HRAS*-Q61 point mutations, while rare, represent a clinically relevant mutation as evidenced by its association with worse clinical outcomes compared to *HRAS* wildtype tumors.

Pan-Tumor Survey of *RET* Fusions as Detected by Next-Generation RNA Sequencing Identified *RET*+ Colorectal Carcinoma as a Unique Molecular Subset of CRC

Misako Nagasaka, Danielle Brazel, Yasmine Baca, Joanne Xiu, Jorge Nieva, Chul Kim, Qing Zhang, Jeffrey Swensen, David Spetzler, W. Michael Korn, Mark Socinski, Balazs Halmos, Sai-Hong Ignatius Ou

Presentation Date and Time: Saturday, September 10, 10:00 - 11:00 CEST

Location: Poster Area, Hall 4 **Abstract:** 72P

Key Findings:

Outside of the approved indications of NSCLC and thyroid cancers, *RET* fusions were identified in multiple tumor types such as colorectal, breast, cancer of unknown primary, and pancreatic cancer.

The Molecular and Immune Landscape of Recurrent Head and Neck Squamous Cell Carcinoma (HNSCC) in Patients Undergoing Definitive Therapy

A. Alloghbi, J. McGrath, I. Aijazuddin, T. Wise-Draper, J. Leddon, P. Walker, M. Oberley, A. Sukari

Presentation Date and Time: Sunday, September 11, 14:00-15:00 CEST

Location: Poster Area, Hall 4 **Abstract:** 699P

Key Findings:

Recurrent HNSCC cancers manifest heterogenous molecular and immune profiles on subgroups analysis with no clear marker to predict response to nivolumab.

Tumor Microenvironment (TME) of *HRAS* Mutated Non-Small Cell Lung Cancer (NSCLC)

Asaad Trabolsi, Estelamari Rodriguez, Samuel Kareff, Jesus Antonio Ocejo Gallegos, Jun Yin, Phillip Walker, Patrick Ma, Hirva Mamdani, Jorge Nieva, Hossein Borghaei, Chadi Nabhan, Misako Nagasaka, Sonam Puri, Stephen Liu, Balazs Halmos, Gilberto Lopes

Presentation Date and Time: Monday, September 12, 12:00-13:00 CEST

Location: Poster Area, Hall 4 **Abstract:** 1066P

Key Findings:

HRAS mutant NSCLC displayed a relatively immune-cold pattern with less CD4+ and CD8+T cells infiltrates compared with general cohort with a trend towards inferior overall survival for patients treated with pembrolizumab.

Comprehensive Molecular Profiling of Squamous Non-Small Cell Lung Cancer by Smoking Status

Joshua Reuss, Nishant Gandhi, Phillip Walker, Balazs Halmos, Charu Aggarwal, Joanne Xiu, Sandip Patel, Ari Vanderwalde, Suresh Ramalingam, Stephen Liu

Presentation Date and Time: Monday, September 12, 12:00-13:00 CEST

Location: Poster Area, Hall 4 **Abstract:** 1052P

Key Findings:

Differences in the molecular and immunologic composition of squamous NSCLC by smoking status were observed, though clinically actionable mutations were seen in both groups. Relevant information can be gleaned from next-generation sequencing (NGS) to guide decision-making in squamous NSCLC regardless of smoking status.

CLEC3B mRNA Expression Levels Are Linked to Distinct Genetic Backgrounds, Transcriptomic Signatures, and Survival in NSCLC

Andreas Seeber, Yasmine Baca, Joanne Xiu, Sonam Puri, Taofeek Owonikoko, Trudy Oliver, Katie Kerrigan, Shiven Patel, Dipesh Uprety, Hirva Mamdani, Amit Kulkarni, Gilberto Lopes, Balazs Halmos, Hossein Borghaei, Wallace Akerley, Stephen Liu, W. Michael Korn, Andreas Pircher, Dominik Wolf, Florian Kocher

Presentation Date and Time: Sunday, September 11, 16:00-17:00 CEST

Location: Poster Area, Hall 4 **Abstract:** 1723P

Key Findings:

This study represents the largest analysis of *CLEC3B* mRNA expression in NSCLC. Patients with high *CLEC3B* mRNA expression showed an improved overall survival when compared to *CLEC3B* low expression; a similar observation was made in patients treated with checkpoint inhibitors.colorectal, breast, cancer of unknown primary, and pancreatic cancer.

The Heterogeneic Molecular Landscape of Ovarian Cancer Metastases (OCM)

Matthew Hadfield, Sharon Wu, Premal Thaker, Alex Farrell, Matthew Oberley, Nathaniel Jones, Thomas Herzog, Don Dizon

Presentation Date and Time: Sunday, September 11, 13:00-14:00 CEST

Location: Poster Area, Hall 4 **Abstract:** 594P

Key Findings:

OCM to liver and brain have a unique molecular alteration pattern, while OCM to genitourinary organs were more immune hot than primary lesions. The observed differences may be secondary to evolving genomics in metastatic sites. Better understanding of the varying genomic landscape can help guide future treatment options.

Pan-Tumor Survey of *ROS1* Fusions Detected by Next-Generation RNA Sequencing

Shannon Zhang, Misako Nagasaka, Yasmine Baca, Joanne Xiu, Jorge Nieva, Ari Vanderwalde, Qing Zhang, Jeffrey Swensen, David Spetzler, W. Michael Korn, Stephen Liu, Sai-Hong Ignatius Ou

Presentation Date and Time: Saturday, September 10, 10:00-11:00 CEST

Location: Poster Area, Hall 4 **Abstract:** 105P

Key Findings:

ROS1 fusions occurred at a low frequency among a diverse range of tumors.

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