

HCMI Searchable Catalog User Guide

What is the purpose of this document?

The purpose of this document is to provide users with a resource to effectively navigate the Human Cancer Models Initiative (HCMI) Searchable Catalog.

What is HCMI?

The Human Cancer Models Initiative (HCMI) is a collaboration between the US National Cancer Institute (NCI) – part of the National Institutes of Health (NIH), Cancer Research UK (CRUK), Wellcome Sanger Institute (WSI), and foundation Hubrecht Organoid Technology (HUB). The goal of HCMI is to create up to 1,000 next-generation cancer models from patient tumors that are clinically and molecularly characterized. For more information about the HCMI program, please visit: <https://www.cancer.gov/ccg/research/functional-genomics/hcmi>.

What is the HCMI Searchable Catalog?

The HCMI Searchable Catalog allows users to browse and identify next-generation cancer models generated by HCMI for use in research. Links to available associated molecular characterization data, clinical and biospecimen data at the National Cancer Institute’s (NCI) Genomic Data Commons (GDC), the European Genome-phenome Archive (EGA), and the 3rd party HCMI Model Distributor are available on each model page as data are processed and validated.

HCMI Searchable Catalog URL: <https://hcmi-searchable-catalog.nci.nih.gov/>

Supported browsers include Chrome, Firefox, and Edge.

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What is displayed on the landing page?

Human Cancer Models Initiative Searchable Catalog

Search By Model Name: e.g. HCM-BROD-0051-C64, ...

Search By Altered Gene(s): e.g. BRAF, EWSR, ...

Search By Research Somatic Variant: e.g. BRAF V600E, IDH1 R132H, ...

Primary Site

Research Somatic Variant Type

Consequence

Model Type

Has Multiple Models

Acquisition Site

Clinical Tumor Diagnosis

Clinical Stage Grouping

Tissue Status

Histological Subtype

Histological Grade

Age At Diagnosis (Years)

Gender

Available Molecular Characterizations

Neoadjuvant Therapy

Chemotherapeutic Drug List Available

Licensing Required For Commercial Use

Race

Models By Primary Site: 28 Total

Has Multiple Models

2D Versus 3D Growth

Most Frequently Mutated Genes: TP53, TNF, KRAS, MUC19, SYNE1, APC, PLO, CASP9, ZNF44, FLT3

Showing 1 - 20 of 316 models

Name	Primary Site	Clinical Tumor Diagnosis	Tissue Status	Age At Acquisition (Years)	Age At Diagnosis (Years)	Has Multiple Models	Expansion Status	# Mutated Genes	# Research Somatic Variants	# Clinical Variants	# Histo-Pathological Biomarkers
<input type="checkbox"/> HCM-BROD-0648-C71	Brain	Glioblastoma	Recurrent	68	63	No	EXPANDED	5326	7110	0	3
<input type="checkbox"/> HCM-BROD-0227-C43	Skin	Melanoma	Metastasis	40	40	No	EXPANDED	3075	4187	0	0
<input type="checkbox"/> HCM-SANG-0288-C18	Colon	Colorectal cancer	Primary	75	75	No	EXPANDED	3228	3908	0	0
<input type="checkbox"/> HCM-BROD-0569-C43	Skin	Melanoma	Metastasis	79	78	No	EXPANDED	2886	3802	0	1
<input type="checkbox"/> HCM-BROD-0594-C43	Skin	Melanoma	Metastasis	78	75	No	EXPANDED	2690	3555	0	0
<input type="checkbox"/> HCM-CSHL-0426-C18	Colon	Colorectal cancer	Primary	73	72	No	EXPANDED	2701	3183	0	0
<input type="checkbox"/> HCM-SANG-0273-C18	Colon	Colorectal cancer	Primary	78	78	No	EXPANDED	2597	2991	0	0
<input type="checkbox"/> HCM-BROD-0027-C34	Bronchus and lung	Lung cancer	Metastasis	66	65	No	EXPANDED	2313	2868	0	0
<input type="checkbox"/> HCM-CSHL-0459-C17	Small intestine	Rare cancers	Primary	57	57	No	EXPANDED	2426	2793	0	5
<input type="checkbox"/> HCM-BROD-0223-C43	Skin	Melanoma	Metastasis	74	73	No	EXPANDED	2187	2679	0	0
<input type="checkbox"/> HCM-SANG-0282-C18	Colon	Colorectal cancer	Primary	85	85	No	EXPANDED	2313	2636	0	0
<input type="checkbox"/> HCM-BROD-0724-C43	Skin	Melanoma	Metastasis	74	74	No	EXPANDED	2013	2530	1	0
<input type="checkbox"/> HCM-CSHL-0606-C17	Small intestine	Rare cancers	Metastasis	71	71	No	EXPANDED	2143	2383	0	3
<input type="checkbox"/> HCM-BROD-0106-C71	Brain	Glioblastoma	Recurrent	56	52	No	EXPANDED	2122	2333	0	3
<input type="checkbox"/> HCM-WCMC-0494-C16	Stomach	Stomach cancer	Primary	64	64	No	EXPANDED	1883	2107	0	2
<input type="checkbox"/> HCM-SANG-0276-C18	Colon	Colorectal cancer	Primary	78	78	No	EXPANDED	1768	1976	0	0
<input type="checkbox"/> HCM-BROD-0334-C43	Skin	Melanoma	Metastasis	72	70	No	EXPANDED	1619	1939	0	1
<input type="checkbox"/> HCM-CSHL-0174-C22	Intrahepatic bile duc	Intrahepatic bile duc	Primary	64	64	No	EXPANDED	1568	1713	0	0
<input type="checkbox"/> HCM-BROD-0702-C43	Skin	Melanoma	Metastasis	70	69	No	EXPANDED	1367	1658	0	1
<input type="checkbox"/> HCM-CSHL-0317-C18	Colon	Colorectal cancer	Primary	65	64	No	EXPANDED	1502	1639	0	0

Updated: November 12, 2024

20 rows

3

The landing page features a dynamic view, enabling users to filter the models by several elements, and easily download saved results.

Box (1) shows the main viewing pane of the HCMI models. Users can sort the models in ascending or descending alphabetical or numerical order by clicking on the column headers (1a) such as “NAME”, “PRIMARY SITE”, etc.

Box (2) shows the number of models that users can choose to view.

Box (3) shows additional pages, if any, of available models.

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Querying the Searchable Data Elements

Human Cancer Models Initiative Searchable Catalog

Search By Model Name **4**
 Search By Altered Gene(s)
 Search By Research Somatic Variant
 Primary Site: Pancreas, Colon, Brain, Esophagus
 Research Somatic Variant Type: Missense Variant, Synonymous Variant, Frameshift Variant, Stop Gained
 Consequence: Missense Variant, Synonymous Variant, Frameshift Variant, Stop Gained
 Model Type
 Acquisition Site
 Clinical Tumor Diagnosis
 Clinical Stage Grouping
 Tissue Status
 Histological Subtype
 Histological Grade
 Age At Diagnosis (Years)

CLEAR CONSEQUENCE is Missense Variant and AVAILABLE MOLECULAR CHARACTERIZATIONS in WGS of model, WGS of parent tumor and PRIMARY SITE is Colon **4a**

Models by Primary Site: 1 Total
 Has Multiple Models
 2D Versus 3D Growth
 Most Frequently Mutated Genes: APC, TTN, TP53, FAT2, SYNE1, CSM2B3, MUC16, CTNNA4, HNF1B

Name	Primary Site	Clinical Tumor Diagnosis	Tissue Status	Age At Acquisition (Years)	Age At Diagnosis (Years)	Has Multiple Models	Expansion Status	# Mutated Genes	# Research Somatic Variants	# Clinical Variants	# Histo-Pathological Biomarkers
HCM-SANG-0288-C18	Colon	Colorectal cancer	Primary	75		No	EXPANDED	3228	3908	0	0
HCM-CSHL-0426-C18	Colon	Colorectal cancer	Primary	73	72	No	EXPANDED	2701	3183	0	0
HCM-SANG-0273-C18	Colon	Colorectal cancer	Primary	78		No	EXPANDED	2597	2991	0	0
HCM-SANG-0282-C18	Colon	Colorectal cancer	Primary	85		No	EXPANDED	2313	2636	0	0
HCM-SANG-0276-C18	Colon	Colorectal cancer	Primary	78		No	EXPANDED	1768	1976	0	0
HCM-CSHL-0317-C18	Colon	Colorectal cancer	Primary	65	64	No	EXPANDED	1502	1639	0	0
HCM-SANG-0729-C18	Colon	Colorectal cancer	Primary	60	60	No	EXPANDED	1433	1572	0	6
HCM-WCMC-0504-C18	Colon	Colorectal cancer	Recurrent	58	58	No	EXPANDED	1354	1462	0	8
HCM-CSHL-0064-C18	Colon	Colorectal cancer	Primary	75	75	No	EXPANDED	342	350	0	5
HCM-SANG-0285-C18	Colon	Colorectal cancer	Primary	71		No	EXPANDED	323	333	0	0
HCM-SANG-0277-C18	Colon	Colorectal cancer	Primary	78		No	EXPANDED	306	319	0	6
HCM-SANG-0268-C18	Colon	Colorectal cancer	Primary	80		No	EXPANDED	223	233	0	0
HCM-SANG-0281-C18	Colon	Colorectal cancer	Primary	44		No	EXPANDED	222	226	0	0
HCM-CSHL-0245-C18-A	Colon	Colorectal cancer	Primary	73	72	Yes (2)	EXPANDED	218	226	0	9
HCM-SANG-0265-C18	Colon	Colorectal cancer	Metastasis	51		No	EXPANDED	208	219	0	0
HCM-CSHL-0247-C18-B	Colon	Colorectal cancer	Metastasis	76	76	Yes (2)	EXPANDED	209	216	1	5
HCM-CSHL-0245-C18-B	Colon	Colorectal cancer	Metastasis	73	73	Yes (2)	EXPANDED	211	215	0	7
HCM-SANG-0267-D12	Colon	Other	Primary	63		No	EXPANDED	196	203	0	0
HCM-CSHL-0056-C18	Colon	Colorectal cancer	Primary	75	75	No	EXPANDED	188	193	0	6
HCM-SANG-0283-C18	Colon	Colorectal cancer	Primary	58		No	EXPANDED	191	191	0	0

How do I filter data elements to query the available models?

Users may filter the models using the data types displayed in Box (4) by checking or unchecking boxes to select or deselect data elements of interest. The list of models displayed in the main viewing pane and graphs will dynamically change as data elements in box (4) are selected or deselected.

Box (4a) at the top of the viewing pane shows the selected filtered data elements. Users may deselect a searchable data element by clicking the 'X' next to the name of the filtered element. To reset all selections, utilize the "CLEAR" button at the top of the pane.

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Human Cancer Models Initiative Searchable Catalog

← Use the filter panel on the left to customize your model search. SHARE VIEW LIST

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a Models By Primary Site

b Has Multiple Models

c 2D Versus 3D Growth

d Most Frequently Mutated Genes

Showing 1 - 20 of 316 models Include 272 unexpanded models COLUMNS EXPORT

Name	Primary Site	Clinical Tumor Diagnosis	Tissue Status	Age At Acquisition (Years)	Age At Diagnosis (Years)	Has Multiple Models	Expansion Status	# Mutated Genes	# Research Somatic Variants	# Clinical Variants	# Histo-Pathological Biomarkers
<input type="checkbox"/> HCM-BROD-0648-C71	Brain	Glioblastoma	Recurrent	68	63	No	EXPANDED	5326	7110	0	3
<input type="checkbox"/> HCM-BROD-0227-C43	Skin	Melanoma	Metastasis	40	40	No	EXPANDED	3075	4187	0	0
<input type="checkbox"/> HCM-SANG-0288-C18	Colon	Colorectal cancer	Primary	75		No	EXPANDED	3228	3908	0	0
<input type="checkbox"/> HCM-BROD-0569-C43	Skin	Melanoma	Metastasis	79	78	No	EXPANDED	2886	3802	0	1
<input type="checkbox"/> HCM-BROD-0594-C43	Skin	Melanoma	Metastasis	78	75	No	EXPANDED	2690	3555	0	0
<input type="checkbox"/> HCM-CSHL-0426-C18	Colon	Colorectal cancer	Primary	73	72	No	EXPANDED	2701	3183	0	0
<input type="checkbox"/> HCM-SANG-0273-C18	Colon	Colorectal cancer	Primary	78		No	EXPANDED	2597	2991	0	0
<input type="checkbox"/> HCM-BROD-0027-C34	Bronchus and lung	Lung cancer	Metastasis	66	65	No	EXPANDED	2313	2868	0	0
<input type="checkbox"/> HCM-CSHL-0459-C17	Small intestine	Rare cancers	Primary	57	57	No	EXPANDED	2426	2793	0	5
<input type="checkbox"/> HCM-BROD-0223-C43	Skin	Melanoma	Metastasis	74	73	No	EXPANDED	2187	2679	0	0
<input type="checkbox"/> HCM-SANG-0282-C18	Colon	Colorectal cancer	Primary	85		No	EXPANDED	2313	2636	0	0
<input type="checkbox"/> HCM-BROD-0724-C43	Skin	Melanoma	Metastasis	74	74	No	EXPANDED	2013	2530	1	0
<input type="checkbox"/> HCM-CSHL-0606-C17	Small intestine	Rare cancers	Metastasis	71	71	No	EXPANDED	2143	2383	0	3
<input type="checkbox"/> HCM-BROD-0106-C71	Brain	Glioblastoma	Recurrent	56	52	No	EXPANDED	2122	2333	0	3
<input type="checkbox"/> HCM-WCMC-0494-C16	Stomach	Stomach cancer	Primary	64	64	No	EXPANDED	1883	2107	0	2
<input type="checkbox"/> HCM-SANG-0276-C18	Colon	Colorectal cancer	Primary	78		No	EXPANDED	1768	1976	0	0
<input type="checkbox"/> HCM-BROD-0334-C43	Skin	Melanoma	Metastasis	72	70	No	EXPANDED	1619	1939	0	1
<input type="checkbox"/> HCM-CSHL-0174-C22	Intrahepatic bile duc	Intrahepatic bile duc	Primary	64	64	No	EXPANDED	1568	1713	0	0
<input type="checkbox"/> HCM-BROD-0702-C43	Skin	Melanoma	Metastasis	70	69	No	EXPANDED	1367	1658	0	1
<input type="checkbox"/> HCM-CSHL-0317-C18	Colon	Colorectal cancer	Primary	65	64	No	EXPANDED	1502	1639	0	0

Showing 20 rows Updated: November 12, 2024

What do the graphs on the main viewing page indicate?

Users may filter the models by clicking on various colors within the interactive graphs shown in (5). Hovering over different colors in a graph will reveal relevant information.

Box (5a) shows that users can click on different colors within the circle graph and filter the models by primary sites of the available models.

Box (5b) shows that users can select the models by whether the cases have multiple models derived from independent tumors from the same donor (e.g. primary and metastatic, primary and pre-malignant tissues, etc.) or not.

Box (5c) shows that users can query the models by the growth type: 2-D, 3-D, or other.

Box (5d) shows that users can query the models within the main viewing table by selecting the most frequently mutated gene(s). Users may select more than one gene at a time.

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Showing 1 - 20 of 47 models

<input type="checkbox"/>	Name	Primary Site	Clinical Tumor Diagnosis	Tissue Status	Age At Acquisition (Years)	Age At Diagnosis (Years)	Has Multiple Models
<input type="checkbox"/>	HCM-SANG-0288-C18	Colon	Colorectal cancer	Primary	75		No
<input type="checkbox"/>	HCM-CSHL-0426-C18	Colon	Colorectal cancer	Primary	73	72	No
<input type="checkbox"/>	HCM-SANG-0273-C18	Colon	Colorectal cancer	Primary	78		No
<input type="checkbox"/>	HCM-SANG-0282-C18	Colon	Colorectal cancer	Primary	85		No
<input type="checkbox"/>	HCM-SANG-0276-C18	Colon	Colorectal cancer	Primary	78		No
<input type="checkbox"/>	HCM-CSHL-0317-C18	Colon	Colorectal cancer	Primary	65	64	No
<input type="checkbox"/>	HCM-CSHL-0729-C18	Colon	Colorectal cancer	Primary	60	60	No
<input checked="" type="checkbox"/>	HCM-WCMC-0504-C18	Colon	Colorectal cancer	Recurrent	58	58	No
<input type="checkbox"/>	HCM-CSHL-0064-C18	Colon	Colorectal cancer	Primary	75	75	No
<input type="checkbox"/>	HCM-SANG-0285-C18	Colon	Colorectal cancer	Primary	71		No
<input type="checkbox"/>	HCM-SANG-0277-C18	Colon	Colorectal cancer	Primary	78		No
<input type="checkbox"/>	HCM-SANG-0268-C18	Colon	Colorectal cancer	Primary	80		No
<input checked="" type="checkbox"/>	HCM-SANG-0281-C18	Colon	Colorectal cancer	Primary	44		No
<input type="checkbox"/>	HCM-CSHL-0245-C18-A	Colon	Colorectal cancer	Primary	73	72	Yes (2)
<input type="checkbox"/>	HCM-SANG-0265-C18	Colon	Colorectal cancer	Metastasis	51		No
<input checked="" type="checkbox"/>	HCM-CSHL-0247-C18-B	Colon	Colorectal cancer	Metastasis	76	76	Yes (2)
<input checked="" type="checkbox"/>	HCM-CSHL-0245-C18-B	Colon	Colorectal cancer	Metastasis	73	73	Yes (2)
<input type="checkbox"/>	HCM-SANG-0267-D12	Colon	Other	Primary	63		No

Include 0 unexpanded models **6 COLUMNS** ^

EXPORT 7

✓ Select All ↺ Reset to Defaults

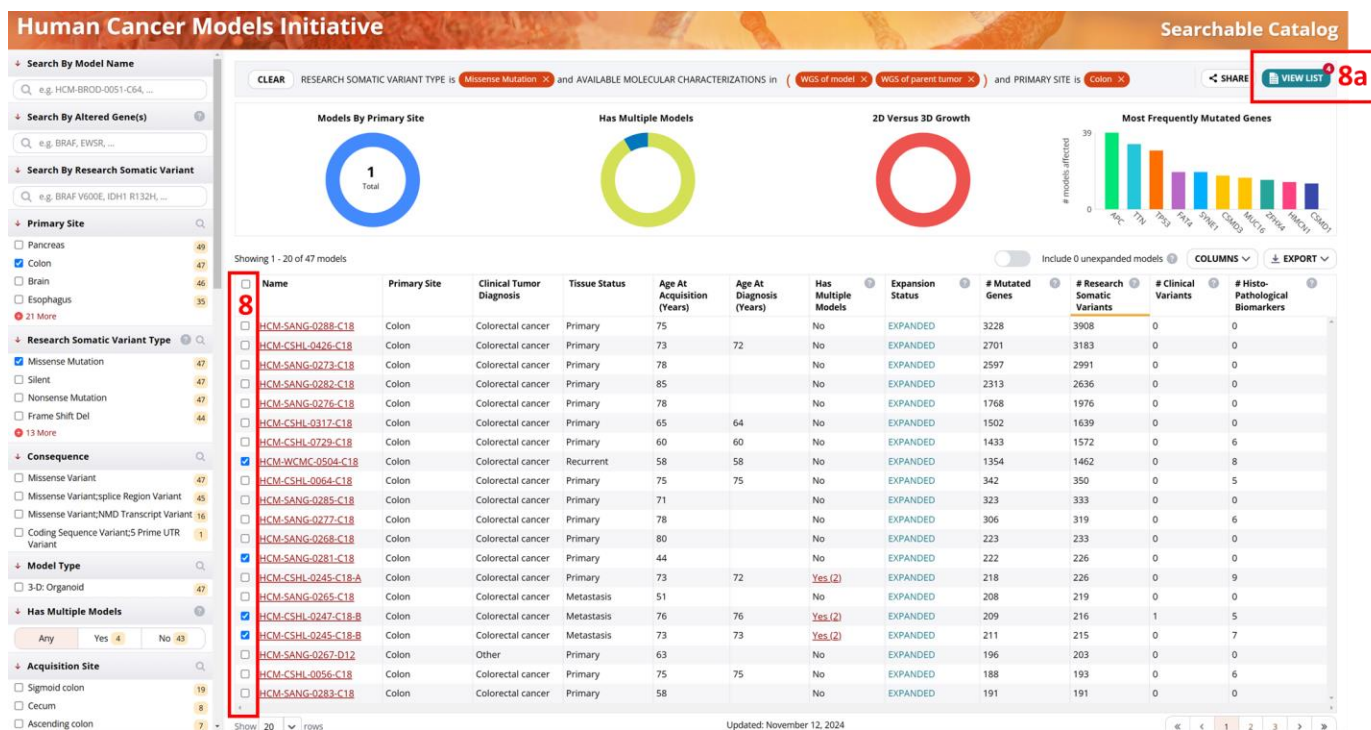
- Primary Site
- Clinical Tumor Diagnosis
- Histological Subtype
- Tissue Status
- Acquisition Site
- Gender
- Race
- Age At Acquisition (Years)
- Age At Diagnosis (Years)
- Disease Status
- Vital Status

How can I download information regarding selected models?

The default columns shown in the main viewing pane can be customized based on information of interest. Users can select the data elements under the “**COLUMNS**” button shown in Box (6) to view in the main viewing pane.




Once users have selected the data elements to be shown in the viewing pane, these data can be exported using the “**EXPORT (current columns)**” function in box (7) and saved as a .tsv file. Additionally, users can download all associated data by using the “**EXPORT (all columns)**” function in box (7). To view the .tsv file in a tabular format, users may open the saved file in Excel or similar program.

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How can I save models from multiple searches for later use?

In box (8), users can select the models of interest by clicking on the checkboxes next to the model name. In the example shown, the “Primary Site” of “Colon” is selected. Users can further sort and select models that meet certain characteristics, for example, “# of Research Somatic Variants”. Selecting models adds them to the “VIEW LIST” box (8a), which functions as a ‘saved list’ so that users can refer back to specific models of interest. This feature may be helpful to users if multiple searches are conducted within a session. For example, if the user is also interested in models from the “Primary Site” of “Pancreas”, an additional search may be conducted, and further models may be added to “My Model List”.

Clicking on the  icon in box (8a) allows users to view the models that have been saved to “My Model List”. Users may download the list of saved models and their Catalog data by clicking the  icon, individually delete the selected models by clicking the corresponding trash symbol, , or clear all selected models from the list by clicking “CLEAR”.

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V3.0 Last updated December 10, 2024
How do I find unexpanded models?

The screenshot shows the 'Human Cancer Models Initiative Searchable Catalog' interface. On the left, there are search filters for Model Name, Altered Genes, Research Somatic Variant, Primary Site, Research Somatic Variant Type, Consequence, and Model Type. The main area displays a table of models with columns: Name, Primary Site, Clinical Tumor Diagnosis, Tissue Status, Age At Acquisition (Years), Age At Diagnosis (Years), Has Multiple Models, Expansion Status, # Mutated Genes, Somatic Variants, Variants, and Histo-Pathological Biomarkers. A red box (9) highlights the 'Exclude 272 unexpanded models' toggle, which is currently turned off. Another red box (10) highlights the first two rows of the model list, which are unexpanded models.

The default model view shows the models that are expanded and available at the HCMI model distributor. To view the models that are not yet expanded, users can toggle on the “Include ## unexpanded models” in box (9). To view a specific unexpanded model, users can select one of the model names within the main viewing pane (10).

The screenshot shows the individual model page for 'Model: HCM-WCMC-0751-C54 (UNEXPANDED)'. The page is divided into several sections: MODEL DETAILS, MULTIPLE MODELS FROM THIS PATIENT (0), AVAILABLE MOLECULAR CHARACTERIZATIONS (0), PATIENT DETAILS, VARIANTS, and REPOSITORY STATUS. A red box (11) highlights the model name and its 'UNEXPANDED' status. Another red box (12) highlights the 'VISIT ATCC TO EXPRESS INTEREST' button, which is part of a message from ATCC stating that this is an unexpanded model and is not yet available for purchase.

When viewing an individual model page of an unexpanded model, the expansion status is marked next to the model name as in box (11). If you are interested in a particular unexpanded model, users can click on the “VISIT ATCC TO EXPRESS INTEREST” button (12).

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Human Cancer Models Initiative Searchable Catalog

Model: **HCM-CSHL-0247-C18-B** EXPANDED

1 < Previous Model 16 of 47 Next >
2 < BACK TO SEARCH ✓ SELECTED FOR DOWNLOAD 📄 VIEW LIST

MODEL DETAILS

Model Type: 3-D: Organoid
 Split Ratio: N/A
 Time to Split: N/A
 Doubling Time: N/A
 Tissue Status: Metastasis

MULTIPLE MODELS FROM THIS PATIENT (1)

HCM-CSHL-0247-C18-A
 Tissue Status: Primary

AVAILABLE MOLECULAR CHARACTERIZATIONS (10)

	Model	Tumor	Normal
WGS	✓	✓	✓
WXS	✓	✓	✓
RNA-seq	✓	✓	✗
DNA Methylation	✓	✓	✗

PATIENT DETAILS

Tissue Status: **Metastasis**
 Gender: **Female**
 Race: **White**
 Age At Diagnosis (Years): **76**
 Age At Acquisition (Years): **76**
 Disease Status: **Stable disease**
 Vital Status: **Alive**
 Neoadjuvant Therapy: **No**
 Therapy: **Surgery**
Cytotoxic chemotherapy
Targeted therapy (small molecule inhibitors and targeted antibodies)
 Chemotherapeutic Drug List Available: **Yes**
 Clinical Tumor Diagnosis: **Colorectal cancer**
 Histological Subtype: **Adenocarcinoma**
 Primary Site: **Colon**
 Acquisition Site: **Lymph node(s)**
 TNM Stage: **T3N2aM1a**
 Clinical Stage Grouping: **Stage IVA**
 Histological Grade: **G2**

MODEL IMAGES (2)

Scale-bar length: 1000 µm | Magnification: 4 x

REPOSITORY STATUS

Date Updated: **July 23, 2024**
 Date Of Availability: **June 30, 2021**
 Licensing Required For Commercial Use: **Yes**
 Date Created: **July 06, 2021**

EXTERNAL RESOURCES

[SEQUENCING FILES](#) [CASE METADATA](#) [MASKED SOMATIC MAF](#)

[VISIT PDM-277 TO PURCHASE](#)

VARIANTS

Research Somatic Variants Research Somatic Variants are imported from GDC and are identified from filtered, open-access MAFs. Controlled-access data at GDC requires dbGaP approval; [see GDC](#) for details.

Variant	Gene	AA Change	Transcript	Consequence	Class	Type
chr1.g.21701545T>C	USP48	K894E	ENST00000308271	Missense Variant	SNV	SNP
chr1.g.40091396C>T	PPT1	R121=	ENST00000433473	Synonymous Variant	SNV	SNP
chr1.g.111456731C>A	ATP5B	R163=	ENST00000369722	Synonymous Variant	SNV	SNP
chr1.g.121177307T>C	FAM72B	I86V	ENST00000369390	Missense Variant	SNV	SNP
chr1.g.152353150G>T	ELG2	Q1546K	ENST00000388718	Missense Variant	SNV	SNP
chr1.g.158843353C>T	MNDA	P114S	ENST00000368141	Missense Variant	SNV	SNP
chr1.g.170726226T>A	PRRX1	F142I	ENST00000239461	Missense Variant	SNV	SNP
chr1.g.182814818C>T	NPL	I108=	ENST00000258317	Synonymous Variant	SNV	SNP
chr1.g.185100278G>A	RNF2	A330T	ENST00000367510	Missense Variant	SNV	SNP
chr2.g.1922953G>A	MYT1L	H272=	ENST00000399161	Synonymous Variant	SNV	SNP
chr2.g.10419783G>A	HPCAL1	R9Q	ENST00000307845	Missense Variant	SNV	SNP
chr2.g.21006080C>A	APDB	M3596I	ENST00000233242	Missense Variant	SNV	SNP
chr2.g.28778850G>T	PPP1CB	E76*	ENST00000296122	Stop Gained	SNV	SNP
chr2.g.30910973G>A	GALNT14	N529=	ENST00000349752	Synonymous Variant	SNV	SNP
chr2.g.61853952G>A	FAM161A	Y30=	ENST00000405894	Synonymous Variant	SNV	SNP
chr2.g.72957033G>A	SEK3	S117=	ENST00000272433	Intron Variant	SNV	SNP
chr2.g.73229502G>A	PRADC1	N79=	ENST00000258083	Synonymous Variant	SNV	SNP
chr2.g.79858065G>A	CTNNA2	S117=	ENST00000402739	Synonymous Variant	SNV	SNP
chr2.g.90154355T>C	IGKV1D-13	T44=	ENST00000611391	Synonymous Variant	SNV	SNP
chr2.g.96284397G>A	SNRNP200	F1451=	ENST00000323853	Synonymous Variant	SNV	SNP

Showing 1 - 20 of 216 Variants

1 < Previous Model 16 of 47 Next >

How do I navigate from one individual model page to the next?

To view an individual model page, users can select one of the models listed within the main viewing table by clicking on the model's name. In box (1), users can navigate to the previous or next individual model pages within the filtered list by clicking on the left/right arrows at the top or bottom of the page.

To return to the search results, users can select the "Back to Search" button located at the top of the page (2).

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Viewing Individual Model Data

Human Cancer Models Initiative
Searchable Catalog

Model: **HCM-BROD-0011-C71** EXPANDED

[← BACK TO SEARCH](#)

 + ADD MODEL TO MY LIST
3

3a

[← Previous](#)
Model 1 of 1
[Next >](#)

MODEL DETAILS

Type	3-D: Other (e.g. neurosphere, air-liquid interface, etc.)
Split Ratio	1:2
Time to Split	N/A
Doubling Time	N/A
Tissue Status	Primary

MULTIPLE MODELS FROM THIS PATIENT (0) 4

There are no other models from this patient.

AVAILABLE MOLECULAR CHARACTERIZATIONS (8)

	Model	Tumor	Normal
WGS	✓	✓	✓
WXS	✓	✓	✓
Targeted-seq	✗	✗	✗
RNA-seq	✓	✓	✗

PATIENT DETAILS

Tissue Status	Primary
Gender	Male
Race	White
Age At Diagnosis (Years)	54
Age At Acquisition (Years)	54
Disease Status	Progressive disease
Vital Status	Dead
Neoadjuvant Therapy	No
Therapy	<ul style="list-style-type: none"> • Surgery • Cytotoxic chemotherapy • Targeted therapy (small molecule inhibitors and targeted antibodies) • Radiation therapy

Chemotherapeutic Drug List Available	Yes
Clinical Tumor Diagnosis	Glioblastoma
Histological Subtype	NOS
Primary Site	Brain
Acquisition Site	Brain
TNM Stage	N/A
Clinical Stage Grouping	N/A
Histological Grade	N/A

MODEL IMAGES (2)

Scale-bar length: 1000 μm | Magnification: 4 x

REPOSITORY STATUS

Date Updated	October 05, 2020
Date Of Availability	February 28, 2019
Licensing Required For Commercial Use	Yes
Date Created	December 03, 2018

EXTERNAL RESOURCES 5

🔗 SEQUENCING FILES
🔗 MODEL SOURCE

🔗 MASKED SOMATIC MAF
🛒 VISIT PDM-18 TO PURCHASE

How do I save models of interest?

While viewing individual model pages, models can be saved under “My Model List” by clicking + ADD MODEL TO MY LIST (3). To view and download the saved models and their Catalog data, click the “My Model List” icon (3a) and click ↓ TSV (ALL COLUMNS).

What information are available on individual model pages?

On each individual model page, all available data elements such as “MODEL DETAILS”, “PATIENT DETAILS”, and “MODEL IMAGES” are described.

What information do additional categories include?

“MULTIPLE MODELS FROM THIS PATIENT” (4) indicates whether there are other models derived from independent tumors from the same patient (e.g. primary and metastasis, primary and pre-malignant, primary and recurrent, etc.).

“EXTERNAL RESOURCES” (5) contains links to available sequencing data at the GDC, corresponding model page at the GDC, models’ masked somatic MAF data page, and the model distributor’s page.

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VARIANTS

6 Research Somatic Variants

Showing 1 - 10 of 59 Variants

9

10 ↓ TSV

Variant	Gene	AA Change	Transcript	Consequence	Class	Type
chr1:g.2605576G>A	MMEL1	N266N	ENST00000378412	Synonymous Varian	SNV	SNP
chr1:g.117075643C>	TFE2	D353D	ENST00000369466	Synonymous Varian	SNV	SNP

7 Clinical Variants

8 Histopathological Biomarkers

What information does the “VARIANTS” section contain?


The “**VARIANTS**” section contains available “Research Somatic Variants”, “Clinical Variants”, and “Histopathological Biomarkers” data tabs. The data columns within each tab can be sorted either in ascending or descending order by clicking on the column header of interest.

“Research Somatic Variants” tab (6) shows available [open-access masked somatic MAF variant](#) data at the GDC. As part of GDC’s harmonization process, potential germline mutations are filtered from the variants identified by DNA sequencing of the model and normal tissues. These highly-filtered lists of somatic mutations without the germline variants are called “masked somatic mutations”. The masked somatic mutations generated at GDC for each model are shown as “Research Somatic Variants” on the Searchable Catalog. Users may search the available models for gene mutations of interest. If omission of true-positive somatic mutations is a concern, it is recommended that users access the [controlled-access MAF files](#) housed at the GDC. Access to controlled-access data is granted through dbGaP. Visit the “[Accessing HCI Data](#)” page for more information.

The “Clinical Variants” tab (7) shows available clinical variants reported from clinical sequencing of the tumor collected from the clinical record.

The “Histopathological Biomarkers” tab (8) shows the results of reported clinical histopathological biomarkers collected from the clinical record.

Can the “VARIANTS” data be queried or downloaded?

In box (9), users may filter the “**VARIANTS**” information on each tab by entering querying text (e.g. MSH6, TP53, etc.). Users may download the variant information by clicking the  icon (10).

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Who do I contact if I have questions?

For questions, users may visit the HCMI FAQs page by clicking the “[Help](#)” button at the bottom of the webpage.

How do I report a bug?

Users may provide feedback or report bugs directly to the Office of Cancer Genomics by emailing: ncicccgenomics@mail.nih.gov or by clicking “[Contact Us](#)” at the bottom of the Catalog webpage.

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