

IMMUNO-ONCOLOGY RESEARCH TOOLS

Cancer immunotherapy has emerged as an exciting new approach for cancer treatment, and immuno-oncology is one of the fastest growing fields in oncology. The development of immunomodulatory drugs and biologics dictate a clear need for human cell-based models to evaluate immune activation. To answer this need, ATCC provides a large collection of fully characterized and authenticated cell lines, human primary cells, and advanced cell models.

PRIMARY HUMAN IMMUNE CELLS

ATCC primary immune cells are able to support complex, physiologically relevant research projects, including:

- Cancer immunology studies
- Toxicity screening
- Transplantation and graft rejection

- Inflammation and allergy
- Vaccine and drug development

ATCC scientists have conducted in-depth authentication and quality control analyses on each of the primary immune cell types. In addition, the utility of these cells for scientific studies has been confirmed by ATCC R&D scientists. For example, the differentiation capacity of the bone marrow CD34+ cells and the peripheral blood CD14+ monocytes was characterized. Additionally, to confirm their immune activity the peripheral blood CD56+ natural killer cells were utilized as the effector cells in an NK activity assay.

CONTINUOUS CELL LINES

ATCC houses a vast collection of cell lines derived from various normal and diseased tissues from multiple species, representing a variety of immunological cells. ATCC routinely authenticates its cell lines using the following methods:

- Short tandem repeat (STR) profiling, to establish a DNA fingerprint
- Cellular morphology, which is monitored for consistency
- Cytochrome C Oxidase I (COI) Assay, for species determination
- PCR testing, for mycoplasma detection

ATCC offers many cells and other products for cancer immunology research. To see ATCC's complete cancer immunology offering, please visit www.atcc.org/cancerimmunology.

THP-1 REPORTER CELLS

ATCC introduced luciferase reporters containing the response element of immunologically important transcription factors into the THP-1 cell line. This advanced model provides a robust and highly sensitive means to measure immune activation through in vitro bioluminescence measurements.

To learn more about these advanced models please visit www.atcc.org/advancedimmunology.

CHECKPOINT MOLECULE PROFILING IN TUMOR AND IMMUNE CELLS AND APPLICATION FOR IMMUNO-ONCOLOGY DRUG SCREENING

Although immune checkpoint blockades have exhibited anti-tumor effects in multiple cancer types, there are still challenges to overcome such as resistance and low response rate. Thus, there is a need for comprehensive data on the expression levels of checkpoint molecules based on cancer type, which can be utilized to guide specific treatment plans and combinations.

ATCC has complied a comprehensive data set of checkpoint molecule expression levels on a variety of tumor and immune cell lines and primary T cells. The cells that were tested demonstrate high expression levels of both checkpoint inhibitory and co-stimulatory molecules. These established cell lines can be incorporated into simple blocking assays or be integrated into co-culture testing systems. Additionally, this information provides a relevant and accessible model system for studying checkpoint molecule interactions and screening biologics as cancer immunotherapy treatments.

Table 1: Checkpoint molecule expression levels of immune cell receptors

		Checkpoint inhibitory molecules										
		HLA ty	ping		Receptors (mainly expressed by T cells)							
Cell Lines	ATCC [®] No.	HLA-A, B, C	HLA-DP, DQ, DR	PD-1	CTLA4	LAG-3	TIM-3	BTLA	VISTA	TIGIT		
Jurkat	<u>TIB-152</u> ™	+	-	45		71	45		2406	17		
TALL-104	CRL-11386	+	-	78	2	158.5	1099	301	1051	0		
MOLT-3	CRL-1552	+	-	229	73	107	43	191	377	32		
НН	CRL-2105	-	+	239	42	1046	193	606	3878	1995		
Hut 78	<u>TIB-161</u>	-	+	182	17	416	312	1114	2884	88		
SUP-T1	CRL-1942	+	-	2098	220	81	12	487	1339	18		
HM2	HB-8587	+	-	354	0	119.5	0	464	4075	221		
MJ(G11)	CRL-8294	-	+	274	68	348	284	2740	1607	4727		
CCRF-CEM	CCL-119	+	-	112	5	81	115	222	119	53		
Primary CD8+ T cells	PCS-800-017	+	-	812	98	274	10745	623	1378	88		
Primary CD4+ T cells	<u>PCS-800-016</u> ™	+	-	921	106	35	1381	756	1029	32		

The expression levels of established and novel inhibitory check point molecule receptors were profiled on basal immune cell lines available at ATCC by FACS analysis. HLA typing is identified by low expression (-) and high expression (+). Conditional formatting is added to the table to compare the expression of checkpoint molecules between cell lines (compare within each column). The value is calculated by subtracting the median fluorescence intensity (MFI) of the sample by the MFI of the isotype control.

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Table 2: Checkpoint molecule expression levels of immune cell receptors

			Checkpoint co-stimulatory molecules ILA typing Receptors (mainly expressed by T cells)										
	-	HLA ty	ping		Rec	marker							
Cell Lines	ATCC [®] No.	HLA-A, B, C	HLA-DP, DQ, DR	4-1BB	SOOI	CD30	CD28	0X40	GITR	CD226	CD4	CD8	
Jurkat	<u>TIB-152</u> ™	+	-		77	3442	0		156	11054	280	12	
TALL-104	CRL-11386	+	-	32	503	39	14507	319	243			86882	
MOLT-3	CRL-1552	+	-		921	663	4353	273	303	149	0	617	
НН	CRL-2105	-	+	100	0	2E+05	512	1368	610	26814	30399		
Hut 78	<u>TIB-161</u>	-	+	229	1049	2E+05	431	3661	9674	901	7974	362	
SUP-T1	CRL-1942	+	-		48	3	15430	876	32	656	29346	81828	
HM2	HB-8587	+	-		510	529	56	854	322	736	203	5490	
MJ(G11)	CRL-8294	-	+	505	9215	52406	0	15528	37952	2987	21202	101	
CCRF-CEM	CCL-119	+	-	9	355	592	5884	163	479	342	9904	6301	
Primary CD8+ T cells	PCS-800-017	+	-	57	1567	71	607	119	720	4268	0	223247	
Primary CD4+ T cells	PCS-800-016 [™]	+	-	43	2252	862	6477	380	1040	5041	7916	21	
Median		Max											

The expression levels of established and novel co-stimulatory check point molecule receptors were profiled on basal immune cell lines available at ATCC by FACS analysis. HLA typing is identified by low expression (-) and high expression (+). Conditional formatting is added to the table to compare the expression of checkpoint molecules between cell lines (compare within each column). The value is calculated by subtracting the median fluorescence intensity (MFI) of the sample by the MFI of the isotype control.

Table 3: Checkpoint molecule expression levels of tumor cell ligands

				LA oing			Ligano		ooint inhib expresse	itory molo d by tumo		\PCs)		
Туре	Cell Lines	ATCC [®] No.	HLA-A, B, C	HLA-DP, DQ, DR	PD-L1-	PD-L1+	PD-L2-	PD-L2+	В7-Н3-	B7-H3+	В7-Н4-	B7-H4+	HVEM -	HVEM +
31	A375 wt	CRL-1619	+	_	1,255	27,782	0	433	52,580	40,341	0	0	566	1,127
	A375 KRAS	CRL-1619IG-1	+	_	40,740	45,361	1,368	6,892	21,853	16,451			1,785	2,838
Melanoma	SH-4	CRL-7724	+	_	1,291	12,124	0	0	54,016	44,759		68	2,556	3,350
	SK-MEL-24	HTB-71	_	+	400	17,538	1,001	750	26,932	17,137	27	60	236	1,187
	RPMI-7951	HTB-66	+	_	10,229	26,724	2,662	8,763	65,180	80,081	0	0	523	1,646
	A549	CCL-185	+	_	1,512	9,611	0	2,476	34,719	33,139			764	752
	NCI-H1299	CRL-5803	+	_	278	3,437		92	37,817	36,030			0	0
Lung	NCI-H596	HTB-178	+	_	2,483	23,447	490	4,677	70,851	62,007			368	1,729
Cancer	NCI-H1975	CRL-5908	+	-	18,669	40,780	1,275	3,245	84,320	77,592			0	275
	H1650	CRL-5883	+	-	3,491	15,369	0	0	127,539	134,041	1,738	1,422	263	476
	HCC827	CRL-2868	+	_	9,795	60,468			41,249	47,178	1,817	1,721	879	0
Bladder Cancer	HT-1197	CRL-1473	+	-	36,857	61,670			361,220	350,756	0	88	1,424	3,429
	HT-1376	CRL-1472	+	-	27,135	51,493	1,692	8,578	74,668	66,185		0	365	1,790
	RT4	HTB-2	+	-	0	5,054	52	518	143,148	139,442		42	717	1,602
Head and	A-253	<u>HTB-41</u>	+	-	2,070	16,019	123	3,176	43,926	41,341	18	0	45	477
Neck Cancer	FaDu	HTB-43	+	-	2,733	37,007	205	13,372	39,475	31,090			138	855
	BT20	HTB-19	+	-	6,082	17,072	565	2,691	44,830	44,507	711	761	0	
	DU4475	HTB-123	+	-	1,912	3,232	0	0	59,238	54,996	1,941	1,317	4,014	4,293
Breast	MDA-MB-231	<u>HTB-26</u>	+	-	11,359	20,492	986	1,880	12,979	11,668	149	125	456	1,033
Cancer	MDA-MB-468	HTB-132	+	-	221	5,046	115	380	16,180	16,342	806	575	140	438
	MCF7	<u>HTB-22</u>	+	-	1576	17877	445	563	436501	387743	4940	4041	5878	6456
	AU565	CRL-2351	+	-	2428	11013	0		9476		3514	2925	307	831
Liver Cancer	Sk-Hep-1	HTB-52	+	-	657	8,371	1,201	8,770	13,236	13,610	283	599	642	1,096
Liver Cancer	C3A	CRL-10741	+	-	0	2,114		2,698	18,098	16,938	441	453	1,362	2,682
Colon Cancer	LoVo	CCL-229	-	+	468	17,697			20,338	19,572	347	346	975	2,483
Skin Cancer	A431	CRL-1555	+	-	13020	37809	1660	6635	64875	61082	996	1792	2656	5120
Brain Cancer	U87-MG	<u>HTB-14</u>	+	-	321	2990	249	246	73474	72722	338	263	4718	3312

The expression levels of established and novel checkpoint inhibitory molecule ligands were profiled on basal (-) and 100 ng/mL IFNy-stimulated (+) tumor cell lines available at ATCC were profiled by FACS analysis. HLA typing is identified by low expression (-) and high expression (+). Conditional formatting is added to the table to compare the expression of checkpoint molecules between cell lines (compare within each column). The value is calculated by subtracting the median fluorescence intensity (MFI) of the sample by the MFI of the control isotype.

Median

Max

Table 4: Checkpoint molecule expression levels of tumor cell ligands.

Max

Median

			HLA Checkpoing co-stimulatory molecules typing Ligands (mainly expressed by tumor cells or APCs)											
Туре	Cell Lines	ATCC [®] No.	HLA-A, B, C	HLA-DP, DQ, DR	4-1BBL-	4-1BBL+	-1 SOOI	+ 1 5001	CD155-	CD155+	-080	+ 080	-980-	CD86+
	A375 wt	CRL-1619	+	-			755	544	30,126	37,903	3,133	2,863	1,237	1,077
	A375 KRAS	CRL-1619IG-1	+	-		1,852	1,682	1,837	105,114	127,213	4,220	6,126	2,120	2,878
Melanoma	SH-4	CRL-7724	+	-	108	2,006	1,142	760	66,235	65,168	3,429	4,481	932	1,507
	SK-MEL-24	HTB-71	-	+	2,903	3,177	6,613	5,316	45,197	75,332	888	826	2,945	2,605
	RPMI-7951	HTB-66	+	-	0	0	1,930	1,297	66,083	91,229	883	1,097	1,482	1,954
	A549	CCL-185	+	-	943	1,345	2,547	3,209	87,047	88,786		1,227	810	1,078
	NCI-H1299	CRL-5803	+	-	2,768	3,391	2,961	4,373	196,936	184,904	3,765	3,790	909	662
Lung	NCI-H596	HTB-178	+	-	227	208	535	1,455	168,919	175,547	3,665	4,409	1,160	1,412
Cancer	NCI-H1975	CRL-5908	+	-			3,411	3,890	255,616	311,989	5,243	2,880	1,349	1,078
	H1650	CRL-5883	+	-	8,605	9,501	0		353,964	391,949	9,642	7,584	1,455	916
	HCC827	CRL-2868	+	-	3,726	3,399	162		58,497	105,562	5,176	7,123	2,222	1,917
Bladder	HT-1197	CRL-1473	+	-	1,001	1,598	1,731	2,259	30,961	34,790	6,962	6,269	5,420	14,57
	HT-1376	CRL-1472	+	-		0	3,440	6,322	36,478	44,828	4,293	4,179	1,233	1,707
Cancer	RT4	HTB-2	+	-	2,395	2,962	5,676	7,754	40,953	48,452	883	1,097	1,482	1,954
Head and	A-253	HTB-41	+	-	1,431	2,558	3,380	3,887	67,935	83,057	3,303	3,051	731	985
Neck Cancer	FaDu	HTB-43	+	-	1,640	0	3,643	4,161	60,462	62,858	2,728	2,720	1,904	1,951
	BT20	HTB-19	+	-	7,297	8,831	300	136	203,815	235,198	8,916	9,398	1,172	1,244
	DU4475	HTB-123	+	-	8,298	6,525			36,382	32,343	8,865	6,426	2,523	1,278
Breast	MDA-MB-231	HTB-26	+	-	531	777	14	37	38,583	53,188	563	428	346	234
Cancer	MDA-MB-468	HTB-132	+	-	740	769	401	747	36,560	43,422	475	464	308	290
	MCF7	HTB-22	+	-	7609	6437	7465	9125	144033	136643	12176	7719	2803	2684
	AU565	CRL-2351	+	-	1289	841	633	856	37017	35953	983	1027	433	454
Liver	Sk-Hep-1	HTB-52	+	-	3,066	2,824	156	271	61,906	75,802	449	3,240	383	1,339
Cancer	C3A	CRL-10741	+	-	1,243	2,171	394	511	54,751	59,271	1,729	1,914	1,136	1,100
Colon Cancer	LoVo	CCL-229	-	+	1,581	1,647	775	1,080	24,870	36,144	903	1,271	1,044	1,010
Skin Cancer	A431	CRL-1555	+	-	2623	4203	1369	1757	130495	152286	2297	2824	1078	893
Brain Cancer	U87-MG	<u>HTB-14</u>	+	-	2804	3010	339	454	30877	33809	2926	2597	2080	1968

The expression levels of established and novel co-stimulatory checkpoint molecule ligands were profiled on basal (-) and 100 ng/mL IFNy-stimulated (+) tumor cell lines available at ATCC were profiled by FACS analysis. HLA typing is identified by low expression (-) and high expression (+). Conditional formatting is added to the table to compare the expression of checkpoint molecules between cell lines (compare within each column). The value is calculated by subtracting the median fluorescence intensity (MFI) of the sample by the MFI of the control isotype.

ADDITIONAL IMMUNO-ONCOLOGY RESOURCES

- Ap Note: A Simple and Rapid Alternative to 51Chromium or Fluorescent Dye Loading for Quantification of Natural Killer Cell Activity:
 ATCC® K-562-GFP™ Cells
- Ap Note: Differentiation and Expansion of Hematopoietic Precursor Cells from Bone Marrow-Derived CD34+ Progenitors
- Ap note: In Vitro Differentiation of Macrophages and Dendritic Cells from Primary Human CD14+ Monocytes
- Webinar: Discovering ATCC Hematopoietic Progenitor Cells Model Systems to Study the Immune and Cardiovascular Systems
- Webinar: Illuminate Immuno-oncology Research with THP-1 Luciferase Reporter Cell Lines
- Poster: Checkpoint Molecule Profiling in Tumor Cell Lines and Immune Cell Lines for Applications in Immuno-oncology Drug Screening
- Poster: Primary NK Cells and Luciferase Expressing Reporter Cell Lines for Use in Developing ADCC Assays for Immuno-oncology Drug
- Cancer Immunology Brochure

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