

ab326307 – Human PD-L1 [28-8] SimpleStep ELISA® Kit, Chemiluminescent

For the quantitative measurement of PD-L1 in human serum, plasma (heparin), plasma (EDTA), plasma (citrate), cell culture supernatant, urine, and cell extract.

For research use only - not intended for diagnostic use.

Patent pending.

For overview, typical data and additional information please visit: www.abcam.com/ab326307

Storage and Stability: Store kit at 2-8°C immediately upon receipt. Refer to list of materials supplied for storage conditions of individual components. Observe the storage conditions for individual prepared components in the Standard Preparation and Reagent preparation sections.

Limitations: All data, except typical standard curve and sensitivity were collected using the colorimetric version of this kit (ab277712).

Materials Supplied

Item	Quantity 1 x 96 tests	Storage Condition
Human PD-L1 Capture Antibody 10X	600 µL	+4°C
Human PD-L1 Detector Antibody 10X	600 µL	+4°C
Human PD-L1 Lyophilized Recombinant Protein	2 Vials	+4°C
Antibody Diluent CPI2	6 mL	+4°C
Cell Extraction Buffer PTR 5X	10 mL	+4°C
Sample Diluent NS	12 mL	+4°C
Wash Buffer PT 10X	20 mL	+4°C
ChemiHRP Reagent A	3 mL	+4°C
ChemiHRP Reagent B	3 mL	+4°C
SimpleStep Pre-Coated Black 96-Well Microplate	96 Wells	+4°C
Plate Seal	1	+4°C

Materials Required, Not Supplied

These materials are not included in the kit, but will be required to successfully utilize this assay:

Luminometer with the following settings: 0.5-1 second/well read time; summation mode (all wavelengths).

Method for determining protein concentration (BCA assay recommended).

Deionized water.

Multi- and single-channel pipettes.

Tubes for standard dilution.

Orbital microplate shaker for all incubation steps: capable of 750 rpm shaking speed.

Optional: Phenylmethylsulfonyl Fluoride (PMSF) (or other protease inhibitors).

Reagent Preparation

Equilibrate all reagents to room temperature (18-25°C) prior to use. The kit contains enough reagents for 96 wells. The sample volumes below are sufficient for 48 wells (6 x 8-well strips); adjust volumes as needed for the number of strips in your experiment.

Prepare only as much reagent as is needed on the day of the experiment. Capture and Detector Antibodies have only been tested for stability in the provided 10X formulations.

1X Wash Buffer PT: Prepare 1X Wash Buffer PT by diluting Wash Buffer PT 10X with deionized water. To make 50 mL 1X Wash Buffer PT combine 5 mL Wash Buffer PT 10X with 45 mL deionized water. Mix thoroughly and gently.

1X Cell Extraction Buffer PTR (For cell and tissue extracts only): Prepare 1X Cell Extraction Buffer PTR by diluting Cell Extraction Buffer PTR 5X to 1X with deionized water. To make 10 mL 1X Cell Extraction Buffer PTR combine 8 mL deionized water and 2 mL Cell Extraction Buffer PTR 5X. Mix thoroughly and gently. If required protease inhibitors can be added.

Antibody Cocktail: Prepare Antibody Cocktail by diluting the capture and detector antibodies in Antibody Diluent CPI2. To make 3 mL of the Antibody Cocktail combine 300 µL 10X Capture Antibody and 300 µL 10X Detector Antibody with 2.4 mL Antibody Diluent CPI2. Mix thoroughly and gently.

Lumi HRP Development Solution: Just prior to use, prepare Lumi HRP Development Solution by mixing equal volume of the ChemiHRP Reagent A and the ChemiHRP Reagent B. To make 3 mL of the Lumi HRP Development Solution combine 1.5 mL of ChemiHRP Reagent A and 1.5 mL of ChemiHRP Reagent B. Mix thoroughly and gently by inversion or slow pipetting (Avoid shaking or vortexing). Protect the prepared solution from light until use.

Standard Preparation

Always prepare a fresh set of standards for every use. Discard working standard dilutions after use as they do not store well. The following section describes the preparation of a standard curve for duplicate measurements (recommended).

1. Reconstitute the **PD-L1** protein standard by adding the volume indicated on the protein vial label. For **serum, plasma, cell culture supernatant, and urine samples measurements**, use Sample Diluent NS. For **cell extract samples measurements**, use 1X Cell Extraction Buffer PTR. Hold at room temperature for 10 minutes and mix thoroughly and gently. This is the 10,000 pg/mL **Stock Standard** Solution.
2. Label nine tubes, Standards 1–9.
3. Use the same Sample Diluent as used to resuspend the Stock Standard to prepare the standard curve. Add 208 µL of Sample Diluent into tube number 1 and 150 µL of Sample Diluent into numbers 2-9.
4. Use the **Stock Standard** to prepare the following dilution series. Standard #9 contains no protein and is the Blank control:

Standard #	Dilution Sample	Volume to Dilute (µL)	Volume of Diluent (µL)	Starting Conc. (pg/mL)	Final Conc. (pg/mL)
1	Stock Standard	192	208	10,000	4,800
2	Standard#1	75	150	4,800	1,600
3	Standard#2	75	150	1,600	533.3
4	Standard#3	75	150	533.3	177.8
5	Standard#4	75	150	177.8	59.3
6	Standard#5	75	150	59.3	19.8
7	Standard#6	75	150	19.8	6.58
8	Standard#7	75	150	6.58	2.19
9	Blank Control	0	150	0	0

Sample Preparation

Typical Sample Dynamic Range	
Sample Type	Range
Serum	12 – 95%
Plasma – Citrate*	≤ 95%
Plasma – EDTA*	≤ 95%
Plasma – Heparin*	≤ 50%
Stimulated PBMC Cell Culture Supernatant	3.13 – 100%
Urine*	≤ 25%
HDLM-2 Cell Extract	0.31 – 10 µg/mL

*Based on spiked sample.

Serum Samples should be collected into a serum separator tube. After clot formation, centrifuge samples at 2,000 x g for 10 minutes and collect serum. Assay, or dilute samples into Sample Diluent NS and assay. Store un-diluted serum at -20°C or below. Avoid repeated freeze-thaw cycles.

Plasma Collect plasma using citrate, EDTA or heparin. Centrifuge samples at 2,000 x g for 10 minutes. Assay plasma (citrate or EDTA), or dilute samples into Sample Diluent NS and assay. Dilute plasma (heparin) samples at least 1:2 into Sample Diluent NS and assay. Store un-diluted plasma samples at -20°C or below for up to 3 months. Avoid repeated freeze-thaw cycles.

Cell Culture Supernatants Centrifuge cell culture media at 2,000 x g for 10 minutes to remove debris. Collect supernatants. Assay, or dilute samples into Sample Diluent NS and assay. Store un-diluted samples at -20°C or below. Avoid repeated freeze-thaw cycles.

Urine Centrifuge urine at 2,000 x g for 10 minutes to remove debris. Dilute samples at least 1:4 into Sample Diluent NS and assay. Store un-diluted urine samples at -20°C or below. Avoid repeated freeze-thaw cycles.

Preparation of extracts from cell pellets Collect non-adherent cells by centrifugation or scrape to collect adherent cells from the culture flask. Typical centrifugation conditions for cells are 500 x g for 5 minutes at 4°C. Rinse cells twice with PBS. Solubilize pellet at 2x10⁷ cell/mL in chilled 1X Cell Extraction Buffer PTR. Incubate on ice for 20 minutes. Centrifuge at 18,000 x g for 20 minutes at 4°C. Transfer the supernatants into clean tubes and discard the pellets. Assay samples immediately or aliquot and store at -80°C. The sample protein concentration in the extract may be quantified using a protein assay. Dilute samples to desired concentration in 1X Cell Extraction Buffer PTR.

Preparation of extracts from adherent cells by direct lysis (alternative protocol) Remove growth media and rinse adherent cells 2 times in PBS. Solubilize the cells by addition of chilled 1X Cell Extraction Buffer PTR directly to the plate (use 750 µL - 1.5 mL 1X Cell Extraction Buffer PTR per confluent 15 cm diameter plate). Scrape the cells into a microfuge tube and incubate the lysate on ice for 15 minutes. Centrifuge at 18,000 x g for 20 minutes at 4°C. Transfer the supernatants into clean tubes and discard the pellets. Assay samples immediately or aliquot and store at -80°C. The sample protein concentration in the extract may be quantified using a protein assay. Dilute samples to desired concentration in 1X Cell Extraction Buffer PTR.

Plate Preparation

The 96 well plate strips included with this kit are supplied ready to use. It is not necessary to rinse the plate prior to adding reagents.

Unused plate strips should be immediately returned to the foil pouch containing the desiccant pack, resealed and stored at 4°C.

For each assay performed, a minimum of two wells must be used as the zero control.

For statistical reasons, we recommend each sample should be assayed with a minimum of two replicates (duplicates).

Differences in well absorbance or "edge effects" have not been observed with this assay.

Assay Procedure

Equilibrate all materials and prepared reagents to room temperature prior to use.

We recommend that you assay all standards, controls and samples in duplicate.

1. Prepare all reagents, working standards, and samples as directed in the previous sections.
2. Remove excess microplate strips from the plate frame, return them to the foil pouch containing the desiccant pack, reseal and return to 4°C storage.
3. Add 50 µL of all sample or standard to appropriate wells.
4. Add 50 µL of the Antibody Cocktail to each well.
5. Seal the plate and incubate for 30 minutes at room temperature on a plate shaker set to 750 rpm.
6. Wash each well with 3 x 350 µL 1X Wash Buffer PT. Wash by aspirating or decanting from wells then dispensing 350 µL 1X Wash Buffer PT into each well. Wash Buffer PT should remain in wells for at least 30 seconds. Complete removal of liquid at each step is essential for good performance. After the last wash invert the plate and tap gently against clean paper towels to remove excess liquid.
7. Add 50 µL of prepared Lumi HRP Development Solution to each well and incubate for 1 minute in the dark on a plate shaker set to 750 rpm. Further optimization of incubation time vs signal strength can be performed if needed. Avoid introducing bubbles into the wells.
8. Measure the produced light of each well using a microplate luminometer with the following settings: 0.5-1 second/well read time in summation mode (all wavelengths). Relative light unit (RLU) readings may vary between luminometer models. It is recommended to configure instrument settings according to the manufacturer's specifications. Note: Relative light unit (RLU) values may change over the course of the 15-minute reading window.
9. Analyze the data as described below.

Mode:	Luminescence
Instrument settings:	Endpoint
Detection Mode:	All wavelengths
Read Time:	0.5-1 sec
Read:	Top

Note For microplate readers with Pre-Read Optimization option, the Read Height as well as Microplate Optimization is recommended before the first read.

Download our ELISA guide for technical hints, results, calculation, and troubleshooting tips:

<https://www.abcam.com/en-us/technical-resources/guides/elisa-guide>

Technical Support

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Additional information

ASSAY SPECIFICITY

This kit is designed for the quantification of human PD-L1.

The standard protein in this kit is the extracellular domain of human PD-L1.

Native signal was detected in serum, cell culture supernatant, and cell extract sample types.

Spiked protein experiments were used to validate serum, plasma (citrate), plasma (EDTA), plasma (heparin), cell culture supernatant, and urine sample types.

Saliva, milk, CSF, and tissue extract samples have not been tested with this kit.

CROSS REACTIVITY

Recombinant human PD-L2, human PD-1, and mouse PD-L1 were each prepared at 50 ng/mL and 500 pg/mL and assayed for cross reactivity. No cross-reactivity was observed.

INTERFERENCE

Recombinant human PD-L2 and human PD-1 were each prepared at 50 ng/mL and 500 pg/mL and tested for interference. No interference with was observed.

SPECIES REACTIVITY

Other species reactivity was determined by measuring 50% serum samples of various species, interpolating the protein concentrations from the human standard curve, and expressing the interpolated concentrations as a percentage of the protein concentration in human serum assayed at the same dilution.

Reactivity < 3% was determined for the following species: Mouse, Rat, Cow

50% Rhesus macaque serum interpolated as 134.95 pg/ml on the human standard curve.

Other species reactivity not determined.

CALCULATION

- Preconfigured protocols are available when using SoftMax Pro software from Molecular Devices.
- Calculate the average chemiluminescence value for the blank control (zero) standards. Subtract the average blank control standard chemiluminescence value from all other chemiluminescence values.
- Create a standard curve by plotting the average blank control subtracted chemiluminescence value for each standard concentration (y-axis) against the target protein concentration (x-axis) of the standard. Use graphing software to draw the best smooth curve through these points to construct the standard curve.
- Note: Most chemiluminescence reader software or graphing software will plot these values and fit a curve to the data. A four-parameter curve fit (4PL) is often the best

choice; however, other algorithms (e.g. linear, semi-log, log/log, 4-parameter logistic) can also be tested to determine if it provides a better curve fit to the standard values.

- Determine the concentration of the target protein in the sample by interpolating the blank control subtracted chemiluminescence values against the standard curve. Multiply the resulting value by the appropriate sample dilution factor, if used, to obtain the concentration of target protein in the sample.
- Samples generating chemiluminescence values greater than that of the highest standard should be further diluted and reanalyzed. Similarly, samples which measure at chemiluminescence values less than that of the lowest standard should be retested in a less dilute form.

TYPICAL DATA

Typical standard curve – data provided for demonstration purposes only. A new standard curve must be generated for each assay performed.

Standard Curve Measurements			
Concentration (pg/mL)	RLU		Mean RLU
	1	2	
0	3,015	3,015	3,015
2.19	4,798	5,212	5,005
6.58	11,156	9,013	10,085
19.8	24,920	25,905	25,413
59.3	67,528	69,698	68,613
177.8	215,910	225,370	220,640
533.3	715,820	682,380	699,100
1,600	1,907,100	1,899,700	1,903,400
4,800	6,289,800	6,399,000	6,344,400

Table 1. Example of human PD-L1 standard curve in Sample Diluent NS. The PD-L1 standard curve was prepared as described in the Standard Preparation section. The table shows raw data values.

Standard Curve Measurements			
Concentration (pg/mL)	RLU		Mean RLU
	1	2	
0	2,777	2,777	2,777
2.19	4,869	5,142	5,006
6.58	10,152	10,709	10,431
19.8	26,099	26,749	26,424
59.3	73,340	76,389	74,865
177.8	225,780	242,040	233,910
533.3	640,190	756,770	698,480
1,600	1,980,000	2,044,100	2,012,050
4,800	7,066,300	6,950,200	7,008,250

Table 2. Example of human PD-L1 standard curve in 1X Cell Extraction Buffer PTR. The PD-L1 standard curve was prepared as described in the Standard Preparation section. The table shows raw data values.

TYPICAL SAMPLE VALUES

Sensitivity:

The minimal detectable dose (MDD) was determined by calculating the mean of zero standard replicates and adding 2 standard deviations then extrapolating the corresponding concentration.

Sample Diluent Buffer	N=	Minimal Detectable Dose
Sample Diluent NS	16	0.66 pg/mL
1X Cell Extraction Buffer PTR	16	0.57 pg/mL

Recovery

Three concentrations of PD-L1 were spiked in duplicate to the indicated biological matrix to evaluate signal recovery in the working range of the assay.

Sample Type	Average % Recovery	Range (%)
95% Serum	96	94 - 97
95% Plasma – Citrate	90	87 - 95
95% Plasma – EDTA	90	89 - 92
50% Plasma – Heparin	101	90 - 111
12.5% Stimulated PBMC Cell Culture Supernatant	93	82 - 100
25% Pooled Gender Urine	93	86 - 97
1 µg/mL HDLM-2 Cell Extract	102	99 - 106

Linearity of Dilution

Linearity of dilution is determined based on interpolated values from the standard curve. Linearity of dilution defines a sample concentration interval in which interpolated target concentrations are directly proportional to sample dilution.

Native PD-L1 was measured in the following biological samples in a 2-fold dilution series. Sample dilutions are made in Sample Diluent NS.

Dilution Factor	Interpolated Value	95% Human Serum	100% Stimulated PBMC Supernatant
Undiluted	pg/mL	109	393
	% Expected value	100	100
2	pg/mL	55	192
	% Expected value	101	97
4	pg/mL	26	90
	% Expected value	95	91
8	pg/mL	13	45
	% Expected value	95	91
16	pg/mL	NL	21
	% Expected value	NL	86

NL – Nonlinear

Recombinant PD-L1 was spiked into the following biological samples in a 2-fold dilution series. Sample dilutions are made in Sample Diluent NS.

Dilution Factor	Interpolated Value	95% Human Serum	95% Human Plasma (Citrate)	50% Human Plasma (Heparin)	95% Human Plasma (EDTA)	25% Human Urine
Undiluted	pg/mL	359	283	334	324	262
	% Expected value	100	100	100	100	100
2	pg/mL	183	145	169	167	137
	% Expected value	102	102	101	103	104
4	pg/mL	90	75	83	83	70
	% Expected value	100	106	99	103	107
8	pg/mL	57	41	50	42	35
	% Expected value	108	116	119	103	108
16	pg/mL	23	19	20	20	17
	% Expected value	104	109	98	100	104

Native PD-L1 was measured in the following biological samples in a 2-fold dilution series. Sample dilutions are made in 1X Cell Extraction PTR.

Dilution Factor	Interpolated Value	10 µg/mL HDLM-2 Cell Extract
Undiluted	pg/mL	412
	% Expected value	100
2	pg/mL	196
	% Expected value	95
4	pg/mL	96
	% Expected value	94
8	pg/mL	48
	% Expected value	93
16	pg/mL	24
	% Expected value	94

Precision

Mean coefficient of variations of interpolated values of PD-L1 from two concentrations of PBMC stimulated with 1.5% PHA-M within the working range of the assay.

	Intra-assay	Inter-assay
N=	8	3
CV (%)	2.7	4.3

Download our ELISA guide for technical hints, results, calculation, and troubleshooting tips:

<https://www.abcam.com/en-us/technical-resources/guides/elisa-guide>

Technical Support

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