

Validation Report #029581

Summary

Antigen	Human Chromosome 19 Open Reading Frame 80 (C19ORF80)
Catalog number	<u>ABIN1136417</u>
Supplier	EIAab
Supplier catalog number	<u>E11644h</u>
Lot number	3L306L
Method validated	Enzyme-linked immunosorbent assay
Laboratory	Shakti Bioresearch
Validation number	<u>29581</u>
Positive Control	Human serum
Negative Control	Mouse serum
Notes	Matrix interference indicates that serum must be diluted >10 fold for accurate measurement. Kit returned minor signal for negative control sample.

Validation Date: 01/26/14



Full Methods

Primary Antibody

- Antigen: Human Chromosome 19 Open Reading Frame 80 (C19ORF80)
- Catalog number: E11644h
- Supplier: EIAAB Science Co.
- Lot number: 3L306L

Controls

- Positive control: normal human serum
- Negative control: mouse serum

• Standard curve: serial two-fold dilutions from 5000 pg/ml (5000, 2500, 1250, 625, 312.5, 156.25, 78.125, 0) were generated from the standard provided in the kit using sample diluent buffer.

• Spike control: standard diluted in human or mouse serum (500 pg/mL).

Protocol

• All reagents in the ELISA kit were brought up to room temperature (RT) before use.

• 100 μ l of each sample was added per well to the micro ELISA plate well. All samples and standards were assayed in triplicate.

- The plate was covered with sealer (provided in kit) and incubated for 120 mins at 37°C.
- Liquid was removed from each well by pipette.

• Detection Reagent A was diluted 100 fold in Assay Diluent A. 100 µl of diluted detection reagent A was added to each well and the plate was sealed. The plate was tapped to ensure mixing and incubated for 60 mins at 37°C.

• Wells were washed with 300 µl wash buffer three times. Each wash involved fully aspirating the liquid from each well by pipette. After the last wash the plate was inverted against clean absorbent paper to remove any remaining liquid.

• Detection Reagent B was diluted 100 fold in Assay Diluent B. 100 µl of diluted detection reagent B was added to each well and the plate was sealed. The plate was tapped to ensure mixing and incubated for 60 mins at 37°C.

• Wells were washed with 300 µl wash buffer five times. Each wash involved fully aspirating the liquid from each well by pipette. After the last wash the plate was inverted against clean absorbent paper to remove any remaining liquid.

• 90 μ l of Substrate Solution was added to each well and the plate was covered with a new plate sealer. The plate was tapped to ensure mixing and incubated at room temperature in the dark.

• After about 10 mins, when an apparent gradient appeared in the standard wells, the reaction was terminated by adding 50 μ l of Stop Solution to each well.

- The optical density (OD value) of each well was read using a micro-plate reader set to 450 nm.
- The triplicate readings for each sample were averaged and the average zero standard optical density subtracted.

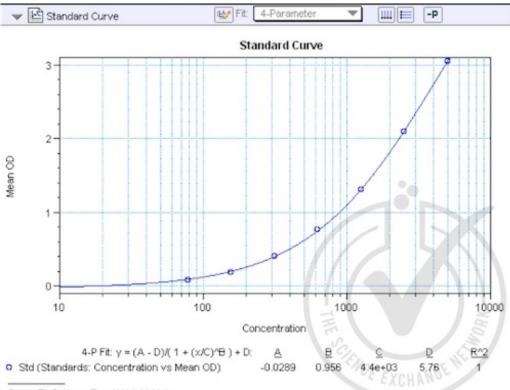
A standard curve was generated by plotting the mean OD value for each standard on the y-axis against the concentration on the x-axis using Softmax Pro softare.

• The equation $y = (A-D)/(1 + (x/C)^B) + D$ was used to calculate IL-6 concentrations of the samples based on their average OD values.

Experimental Notes

Percent recovery of the spiked samples shows that there is matrix interference. Dilution of >10 fold is required for accurate measurement of the analyte in human serum samples.

Figures



Curve Fit Option - Fixed Weight Value

Figure 1:	Graph of	corrected-average	absorbance (OI	D 450 nm)	readings	plotted for	standard curve san	nples.
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Sample Description	OD 450nm	Conc (pg/mL)	Mean Conc (pg/mL)	Std. Dev.	CV%	Dilution Factor	Conc (pg/mL) in neat serum	% Recovery
Human serum	0.744	622.01	644.52	27.26	4.2	-		
	0.759	636.73					644.52	
	0.798	674.82						
500 pg/mL of	0.652	534.74		152.32	24.2			
TD26 spiked	0.666	547.25	628.86					54.9
into human serum	0.924	804.60						
	0.084	73.02		67.90	52.7	10	1287.75	
Human serum diluted 10 fold	0.135	108.91	128.78					
	0.263	204.39						
500 pg/mL of	0.541	434.37		28.70	7.2			
TD26 spiked into diluted human serum	0.487	387.10	401.33					63.8
	0.482	382.54						
	-0.008	12.16	11.17	1.35	12.1			
Mouse serum	-0.009	11.73					11.17	
	-0.012	9.64						
	-0.021	4.64	5.17	0.57	THE			X
Mouse serum diluted 10 fold	-0.020	5.11				10	51.72	
diluted 10 told	-0.019	5.77						3
500 pg/mL of	0.550	442.33	355.25	101.26		ENO		14
TD26 spiked	0.478	379.28			28.5		XCHANGY	70.3
into diluted mouse serum	0.314	244.14						

Table 1: ELISA. C19ORF80 could be detected in human serum (positive control). Spike controls indicate that there is interference from the human serum matrix and a dilution of >10 fold is required. Mouse serum was used as negative control, there were residual levels of C19ORF80.

Sample	Concentration (pg/mL)	BackCalcConc (pg/mL)	Wells	OD 450nm	Mean OD	Std.Dev.	CV%	%Accuracy
St01	5000	4979.52	A1	3.038	3.047	0.009	0.3	99.6
		5041.28	A2	3.055				100.8
		5013.93	A3	3.048				100.3
St02	2500	2293.61	B1	1.993	2.094	0.132	6.3	91.7
		2784.55	B2	2.243				111.4
		2390.16	B3	2.045				95.6
	1250	1318.03	C1	1.361	1.31	0.068	5.2	105.4
St03		1284.59	C2	1.335				102.8
		1156.21	C3	1.233				92.5
	625	684.81	D1	0.808	0.76	0.041	5.4	109.6
St04		613.97	D2	0.736				98.2
		615.52	D3	0.737				98.5
	312.5	353.49	E1	0.448	0.402	0.04	10	113.1
St05		300.25	E2	0.384				96.1
		291.75	E3	0.373				93.4
	156.25	135.41	F1	0.171	0.186	0.019	10.3	86,7
St06		162.34	F2	0.208				103.9
		141.20	F3	0.179				90.4
St07	78.125	73.51	G1	0.085	0.08	0.005	6.8	.94.1
		71.92	G2	0.082				92.1
		66.35	G3	0.074				84.9
St08	0	12.72	H1	-0.007	-0.017	7 0.008	CH48.1	NA
		3.87	H2	-0.022				NA
		4.93	H3	-0.020				NA

Table 2: Table of absorbance readings (OD 450 nm) for standard curve. Value for Average Reading is derived from the average of three readings (OD 450nm). The Average Reading for BLANK (0 pg/ml) was subtracted from all Average Readings to yield Average Absorbance values for Standards. Standard deviation is included for all samples. An equation (see Figure 1) was generated from the standard curve and used to calculate C19ORF80 concentrations shown in Table 1.