510(k) SUBSTANTIAL EQUIVALENCE DETERMINATION
DECISION SUMMARY

A. 510(k) Number:
k043341

B. Purpose for Submission:
This is a new device.

C. Manufacturer and Instrument Name:
Bio-Rad Laboratories
BioPlex 2200 Medical Decision Support Software (MDSS) on the BioPlex 2200
Multi-Analyte Detection System.

D. Type of Test or Tests Performed:
The BioPlex™ 2200 Medical Decision Support Software (MDSS) is a separate
informatics software module for use with the BioPlex™ 2200 ANA Screen on the
BioPlex 2200 Multi-Analyte Detection System

E. System Descriptions:
1. Device Description:
   The BioPlex 2200 Medical Decision Support Software (MDSS) is a pattern
   recognition algorithm that can enhance the performance of the ANA Screen by
   identifying associated diagnostic patterns among its multiple assay results. The
   MDSS can suggest one or more possible disease associations after identifying
   patterns from the eleven (11) individual antibody results. The MDSS is based on
   the principles of the "k-nearest neighbor" (kNN) statistical techniques. Each
   "unknown" is compared to a pre-established database that contains the results for
   over 1,400 characterized sera/plasma. Results of MDSS analysis fall into one of
   the following general outcomes; Negative, No Association, or Association with
   Disease. When the results of the MDSS analysis fall into the Association with
   Disease category, the MDSS software will propose a maximum of two disease
   classifications based upon the similarity of the current analysis to the stored
   results. The MDSS output can also aid in determining appropriate additional
   autoimmune serological testing. All possible MDSS disease associations with
   corresponding definitions are listed in the following table. Note: MDSS outputs 9
   through 15 were not observed in the clinical trial.

Table: MDSS Output

#	MDSS Text Output	Internal Output Abbreviations
1	All antibody levels for systemic autoimmune disease are below pre-established cutoffs. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	Negative
2	Antibody levels show no association with MDSS profiles for systemic autoimmune diseases. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	No Association (NA)
3	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider SLE. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	SLE
4	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider SLE or Sjogren's syndrome. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	SS / SLE
5	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider Polymyositis. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	Polymyositis
6	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider Scleroderma. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	Scleroderma
7	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider MCTD or SLE. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	MCTD / SLE
8	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider SLE or Scleroderma. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	SLE / Scleroderma

#	MDSS Text Output	Internal Output Abbreviations
9*	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider Polymyositis or SLE. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	Polymyositis / SLE
10*	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider Polymyositis or MCTD. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	Polymyositis / MCTD
11*	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider Polymyositis or Sjogren's syndrome. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	Polymyositis / SS
12*	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider Polymyositis or Scleroderma. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	Polymyositis / Scleroderma
13*	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider MCTD or Sjogren's syndrome. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	MCTD / SS
14*	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider MCTD or Scleroderma. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	MCTD / Scleroderma
15*	Antibody levels show association with MDSS profiles for systemic autoimmune disease. Consider Scleroderma or Sjogren's syndrome. MDSS outputs of "Negative" or "No Association" do not rule out autoimmune disease. Patients with Rheumatoid Arthritis may result in an SLE association from MDSS, thus MDSS associations from patients with RA should be interpreted with caution.	Scleroderma / SS

*Note: these MDSS outputs were not observed in the clinical trial

The MDSS is not, in and of itself, diagnostic for the targeted diseases associations and must be considered in conjunction with other laboratory test results and the clinical presentation of the patient.

2. Principles of Operation:
When the MDSS module is activated, the autoantibody results are compared to the MDSS database that contain results for over 1,400 sera/plasma, representing test results from patients with systemic autoimmune diseases and from healthy individuals. If one or more results are obtained from a serum or plasma sample, the results are associated with the most appropriate MDSS profiles.

When the MDSS result is positive, the MDSS produces two outputs that BioPlex 2200 can display in its User Interface. The first output is a text result containing the specific disease association(s) results. The second output is a graph of the specific disease association(s) and the patient's analyte results.

3. Modes of Operation:
The MDSS module interacts with the BioPlex 2200 Instrument software (BPX), which runs on a PC running the Windows operating system. MDSS activates the kNN algorithm which runs queries on a database of serum and plasma results from over 1,000 previously-diagnosed systemic autoimmune patients. This database is stored within the BPX database. Using XML (Extensible Markup Language) strings, BPX sends patient analyte data to the MDSS module and retrieves resultant disease associations from the MDSS module.

4. Specimen Identification:
Refer to k041658 (BioPlex 2200 ANA Screen on the BioPlex 2200 Multi-Analyte Detection System)

5. Specimen Sampling and Handling:
Refer to k041658 (BioPlex 2200 ANA Screen on the BioPlex 2200 Multi-Analyte Detection System)

6. Calibration:
Refer to k041658 (BioPlex 2200 ANA Screen on the BioPlex 2200 Multi-Analyte Detection System)

7. Quality Control:
Refer to k041658 (BioPlex 2200 ANA Screen on the BioPlex 2200 Multi-Analyte Detection System)

8. Software:
FDA has reviewed applicant's Hazard Analysis and Software Development processes for this line of product types:
Yes__√_____ or No_____

F. **Regulatory Information**:
1. Regulation section:
21 CFR§ 862.3100 Amphetamine Test System

2. Classification:
   Class II
3. Product code:
   NVI, Diagnostic software, k-nearest neighbor algorithm, autoimmune disease
4. Panel:
   91 Clinical Toxicology

G. Intended Use:

1. Indication(s) for Use:
   The BioPlex 2200 Medical Decision Support Software (MDSS), used in conjunction with the ANA Screen, is an optional laboratory tool that associates patient antibody results with predefined MDSS profiles that have been correlated with the following systemic autoimmune diseases: Systemic Lupus Erythematosus (SLE), Mixed Connective Tissue Disease (MCTD), Sjögren's Syndrome (SS),Scleroderma (Systemic Sclerosis) and Polymyositis

2. Special Conditions for Use Statement(s):
   For use with the BioPlex 2200 ANA Screen Assay on the BioPlex 2200 Multi-Analyte Detection System. (k041658)

H. Substantial Equivalence Information:

1. Predicate Device Name(s) and 510(k) numbers:
   Remedi HS™ Drug Profiling System (k941596)

2. Comparison with Predicate Device:

Table 1 (a): Similarities between data processing modules

	BioPlex 2200 Medical Decision Support Software	**Remedi HS Drug Profiling System**
Input	Library or training set data on test results from 1,130 patients.	Library of known drug spectra stored in memory
Function	Data processing module for association of patient specific information with the current condition of patient	Same
Technology	Computer based, software driven, data driven algorithm.	Sophisticated computer algorithm.
	Test results as compared to training set	

Table 1 (b): Differences between data processing modules

	BioPlex 2200 Medical Decision	**Remedi HS Drug Profiling System**
Input	Results from serological analysis of patient serum or plasma for specific autoantibodies	Results from chromatographic analysis of patient urine or serum for drugs
Modules	Identification of possible disease associations	Identification of possible drugs in the biological specimen
Algorithm Technology	k-Nearest Neighbor data analysis algorithm and pre-established medical database.	Peak Identification for comparison of unknown to spectral library of drugs.
Output	List of test results in IU/ml and AI (antibody index).	List of test results in the form of a Chromatogram.

I. Special Control/Guidance Document Referenced (if applicable):
None referenced.

J. Performance Characteristics*:*
1. <u>Analytical Performance</u>:
Performance testing in this section is limited to additional clinical concordance and MDSS related claims. Clinical performance testing relating to BioPlex ANA Screen on the BioPlex 2200 ANA Screen was presented on prior (k041658) application.

   a. Accuracy:
   The following table presents %disease agreement of the MDSS output with the diagnosis provided by a physician. Data is presented as % disease agreement for patients with one or more positive antibodies and for patients with a targeted connective tissue disease (TCTD) classification, regardless of antibody response. The difference between disease agreements is the inclusion of negative results for all antibodies in the TCTD patients. MDSS does not provide an association with a patient with negative test results for all antibodies.

MDSS vs. Disease Classification (n = 1130)

Disease Classification By Criteria**	(N)	MDSS Output								% Disease Agreement	
		Negative for all antibodies	Positive for one or more antibody (P)	No Association	Any SLE Association	Any Sjogren;s syndrome Association	Any SclCR Association	Any MCTD Association	Any Polymyositis Association	Patients with Positive Antibody Only	Patients with TCTD Classification
*Systemic Lupus Erythematosus (SLE)	16	1	15	0	15	13	0	0	0	86.7% 13/15	81.3% 13/16
*Primary Sjogren's Syndrome	16	1	15	0	15	13	0	0	0	86.7% 13/15	81.3% 13/16
* Scleroderma	44	13	31	3	19	1	16	3	0	51.6% 16/31	36.4% 16/44
*MCTD	16	0	16	0	15	0	1	13	0	81.3% 13/16	81.3% 13/16
*Polymyositis	12	6	6	0	4	0	0	1	2**	33.3% 2/6	16.7% 2/12

 * Targeted Connective Tissue Disease (TCTD)

** For these patients, the MDSS outputs suggesting Polymyositis referenced the disorder alone and not in combination with another TCTD

The table below presents the % agreement of the MDSS output when a specific positive antibody result is present and the diagnosis provided by the physician is consistent with the presence of that antibody.

MDSS Assignments in Patients with TCTD and a Positive Antibody Result

Positive Antibody Test Results	Disease by Established Medical Criteria*	MDSS Output**	% Agreement	95% Confidence Interval
dsDNA (N = 119)	SLE (N = 92)	Any SLE (N = 87)	87/92 or 95%	89-100%
Chromatin (N = 168)	SLE (N = 122)	Any SLE (N = 112)	112/122 or 92%	86-97%
Ribosomal Protein (N = 37)	SLE (N = 30)	Any SLE (N = 29)	29/30 or 97%	83-99%
SSA (N = 173)	SS (N = 15)	SS or SLE (N = 13)	13/15 or 87%	62-96%
	SLE (N = 111)	Any SLE (N = 106)	106/111 or 96%	91-100%
SSB (N = 76)	SS (N = 13)	SS or SLE (N = 13)	13/13 or 100%	83-100%
Sm (N = 60)	SLE (N = 49)	Any SLE (N = 49)	49/49 or 100%	99-100%
SmRNP (N = 103)	MCTD (N = 15)	MCTD or SLE (N = 13)	13/15 or 87%	62-96%
RNP (N = 112)	MCTD (N = 15)	MCTD or SLE (N = 13)	13/15 or 87%	62-96%

Scl-70 (N = 23)	Scleroderma (N = 7)	Scleroderma; SLE or Scleroderma (N = 5)	5/7 or 71%	36-92%
Jo-1 (N = 6)***	Polymyositis (N = 2)	Polymyositis (N = 2)	2/2 or 100%	43-100%
Centromere (N = 38)	Scleroderma (N = 12)	Scleroderma; SLE or Scleroderma (N = 11)	11/12 or 92%	65-99%
	SLE (N = 11)	Any SLE (N = 9)	9/11 or 82%	52-95%

* Targeted diseases presented include all patients with each disease classification, and patients may have multiple disease classifications. Established medical criteria used in this study include criteria established by the American College of Rheumatology (ACR), American-European Consensus Group, Alarcon-Segovia or Kahn, as well as literature criteria for Polymyositis.
***Note: The presence of antibodies to Jo-1 in patients diagnosed with Polymyositis has been well documented

Since some MDSS outputs contain more disease associations with other diseases than the disease association under consideration, the results in the first table were calculated by excluding patients with other diseases listed in the output. The second table presents results where these patients were not excluded. Not all patients with a targeted connective tissue disease produce antibodies that may be detected with the BioPlex 2200 ANA Screen

MDSS Agreement with Disease Classification (excluding patients with other MDSS associations)

Disease Classification by Criteria	Systemic Lupus Erythematosus (SLE) (N = 332)	Primary Sjögren's Syndrome (N = 16)	Scleroderma (N = 44)	Mixed Connective Tissue Disease (N = 16)	Polymyositis (N = 12)
Positive Antibody Test(s)	218	15	31	16	6
MDSS Associations	186	13	16	13	2
Odds Ratio (OR)	12.8	479.8	22.1	481	223.4
OR 95% Confidence Interval	9.1 -17.8	111.4 -2065.6	10.3 -47.5	111.7 -2071.9	11.9 -2667.6
Positive Likelihood Ratio (PLR)	6.17	90.8	14.4	91.0	186.3
(PLR) 95% Confidence Interval	4.8 -7.9	41.8 -196.9	7.9 -26.1	41.95 -197.35	18.1 -1919.2
Negative Likelihood Ratio (NLR)	0.48	0.19	0.65	0.19	0.83
NLR 95% Confidence Interval	0.43 -0.54	0.07 -0.52	0.52 -0.81	0.07 -0.52	0.65 -1.07
Total N after exclusions	1059	798	798	800	1130

MDSS Agreement with Disease Classification (including patients with multiple MDSS associations)

Disease Classification by Criteria	Systemic Lupus Erythematosus (SLE) (N = 332)	Primary Sjögren's Syndrome (N = 16)	Scleroderma (N = 44)	Mixed Connective Tissue Disease (N = 16)	Polymyositis (N = 12)
Positive Antibody Test(s)	218	15	31	16	6
MDSS Associations	186	13	16	13	2
Odds Ratio (OR)	7.9	162.1	23.3	196.8	223.4
OR 95% Confidence Interval	5.9 -10.6	43.8 -599.6	11.3 -48.2	52.6 -735.4	11.9 -2667.6
Positive Likelihood Ratio (PLR)	4.03	31.21	15.19	37.71	186.3
(PLR) 95% Confidence Interval	3.3 -4.9	20.3 -47.9	8.8 -26.2	23.8 -59.8	18.1 -1919.2
Negative Likelihood Ratio (NLR)	0.51	0.19	0.65	0.19	0.83
NLR 95% Confidence Interval	0.45 -0.57	0.07 -0.53	0.52 -0.81	0.07 -0.53	0.65 -1.07
Total N	1130	1130	1130	1130	1130

Some of the Clinical Disease Classifications encountered do not have an associated MDSS output. These non-targeted connective tissue diseases should be classified as either Negative or No Association by MDSS. The table below presents MDSS results incorrectly associated with a targeted connective tissue disease (% Incorrect Association).

MDSS vs.Non-targeted Connective Tissue Diseases

Clinical Disease Classification		(N)	Negative or No MDSS Associations	Incorrect MDSS Associations	% Incorrect Association
Non TCTD	Dermatomyositis-only	15	12	3	20% (3/15)
	Rheumatoid Arthritis-only	341	310	31*	9% (31/341)
	Other CTD-only	45	36	9	20% (9/45)
No CTD		77	77	61	16
Blood Donor Samples		222	222	214	8**

* Of the 31 patients with only rheumatoid arthritis, 27 were associated with SLE by MDSS.
Patients with Rheumatoid Arthritis may result in an SLE association from MDSS. Additionally, patients with Rheumatoid Arthritis who are receiving anti-TNF α blockers as part of their therapy have been reported to produce antibodies against both dsDNA and Chromatin. For these reasons, MDSS associations from patients with Rheumatoid Arthritis should be interpreted with caution.

** The clinical status of blood donors tested in this study was not known.

The following tables present % correctness in conjunction with the following prevalence of diseases: study: SLE 29% (332/1130), Sjögren's Syndrome 1.4% (16/1130), Scleroderma 3.9% (44/1130), Mixed Connective Tissue Disease 1.4% (16/1130), Polymyositis 1.1% (12/1130), Other Connective Tissue Disease 36.9% (417/1130), and
No Connective Tissue Disease 6.8% (77/1130). Note: the Correct Association values presented in the following tables may change in different patient populations. The % correctness is defined as the number of patients with given MDSS association who also have that disease by ACR, literature, or established medical criteria

Correct Association without any Targeted Disease Classification

MDSS Output	# by MDSS	# Without any Targeted Disease	Correct Association	95% Confidence Interval
Negative	719	585	81.4% (585/719)	78.4 -84.3%
No Association	89	57	64% (57/89)	53.3 -74.8

Correct Association with Targeted Disease Classification

MDSS Output	# by MDSS	# by Clinical Diagnosis	Correct Association	95% Confidence Interval
SLE only	198	142	71.7% (142/198)	65.1 -78.3%
SLE or SS	42	35	83.3% (35/42)	70.2 -96.5%
MCTD or SLE	37	30	81.1% (30/37)	66.3 -95.9%
Scleroderma	22	9	40.9% (9/22)	23.3 -61.3%
SLE or Scleroderma	20	11	55% (11/20)	34.2 -74.2%
Polymyositis only	3*	2	66.7% (2/3)	20.8 -93.9%

One of these 3 patients was diagnosed with Dermatomyositis.

b. *Precision/Reproducibility:*
Reproducibility testing was performed at three (3) US testing facilities on a total of three (3) lots of the ANA Screen. Each testing facility evaluated reproducibility using one (1) kit lot of the ANA Screen. The eleven (11) panel members consisted of ten (10) positive panel members prepared by combining one (1) or more antibody positive patient samples for one (1) or more of the 13 analytes contained in the ANA Screen (dsDNA, Chromatin, SS-A 52, SS-A 60, SS-B, Sm, RNP 68, RNP A, Sm/RNP, Centromere, Ribosomal Protein, Scl-70,and Jo-1. Five of the 10 members had higher levels of the antibodies and five had antibody levels near the cut-off. One panel member was negative for all 13 analytes. In addition, three lots of the ANA Screen Control set positive control (antibody positive for all 13 analytes), 1 diluted positive control and a negative control (negative for all 13 analytes) were also tested.

Each of the eleven (11) panel members and the Autoimmune Control Set was tested in duplicate (x2) on two (2) runs per day (morning and afternoon) for ten (10) days using one (1) lot of ANA Screen Reagent Pack and one (1) lot of ANA Screen. Calibrator Set at each of three (3) sites. [2 times x 2 runs x 10 days = 40 replicates per panel member per site. Total replicates at 3 sites = 120 replicates per panel member.] The data were then analyzed for intra-assay and inter-assay reproducibility according to the National Committee for Clinical Laboratory Standards (NCCLS EP5-A, Vol. 19, No. 2, p7, Eq. (1) and p8 Eq. (4)). The mean Antibody Index (AI), standard deviation (SD), and percent coefficient of variation (%CV) for each panel member is presented. For dsDNA, the mean International Units per ml (IU/mL), standard deviation (SD), and percent coefficient of variation (%CV) for each panel member is presented. Results for Positive Control, High Positive Panel, and Low Positive Panel can be found in the following tables.

Intra-assay- Site 1

Clinical Site 1, Lot 1		dsDNA (IU/mL)	Chromatin (AI)	RibosomalProtein (AI)	SS-A 52 (AI)	SS-A 60 (AI)	SS-B (AI)	Sm (AI)	SmRNP (AI)	RNP A (AI)	RNP 68 (AI)	Scl-70 (AI)	Jo-1 (AI)	Centromere B (AI)
													ANA Screen - Intra-assay	
High Positive Panel	Mean	45.6	2.7	2.4	4.1	3.4	3.6	3.3	4.0	4.1	3.8	3.3	3.9	3.7
	SD*	0.89	0.08	0.07	0.19	0.07	0.07	0.09	0.08	0.10	0.13	0.08	0.10	0.08
	% CV	2.0%	2.9%	2.7%	4.6%	1.9%	2.0%	2.9%	2.0%	2.4%	3.5%	2.4%	2.5%	2.2%
	N=	40	40	40	36	36	36	40	40	40	40	40	40	40
Low Positive Panel	Mean	17.0	1.3	1.2	2.2	1.8	1.7	1.5	2.2	1.9	1.8	1.9	1.9	2.0
	SD*	0.05	0.06	0.04	0.17	0.07	0.05	0.05	0.06	0.05	0.09	0.06	0.09	0.05
	% CV	2.9%	4.4%	3.9%	7.9%	3.9%	3.1%	3.2%	2.6%	2.6%	4.9%	2.9%	5.0%	2.7%
	N=	40	40	40	40	40	40	40	40	40	40	36	40	40
Positive Control	Mean	23.2	2.5	1.7	3.1	2.5	2.7	2.8	3.0	2.7	2.5	2.7	2.7	2.8
	SD*	0.62	0.10	0.04	0.16	0.04	0.07	0.07	0.07	0.08	0.16	0.06	0.08	0.05
	% CV	2.7%	4.0%	2.6%	5.1%	1.7%	2.6%	2.4%	2.2%	3.0%	6.6%	2.0%	2.9%	1.9%
	N=	36	36	40	36	36	36	36	40	36	36	36	36	36

Intra-assay Site 2

Clinical Site 2, Lot 2		ANA Screen - Intra-assay												
		dsDNA (IU/mL)	Chromatin (AI)	RibosomalProtein (AI)	SS-A 52 (AI)	SS-A 60 (AI)	SS-B (AI)	Sm (AI)	SmRNP (AI)	RNP A (AI)	RNP 68 (AI)	Scl-70 (AI)	Jo-1 (AI)	Centromere B (AI)
High Positive Panel	Mean	44.9	2.9	2.7	3.8	3.6	3.5	3.9	3.4	3.8	3.9	3.2	3.1	2.9
	SD*	1.06	0.09	0.07	0.09	0.09	0.07	0.11	0.12	0.10	0.16	0.10	0.12	0.10
	% CV	2.4%	3.2%	2.8%	2.4%	2.6%	2.1%	2.9%	3.4%	2.7%	4.2%	3.3%	4.0%	3.3%
	N=	40	40	40	40	40	40	40	40	40	40	40	40	40
Low Positive Panel	Mean	18.2	1.5	1.6	2.2	1.9	1.6	1.7	1.9	1.8	1.8	1.8	1.4	1.6
	SD*	0.52	0.09	0.07	0.09	0.07	0.05	0.15	0.07	0.08	0.09	0.13	0.07	0.08
	% CV	2.9%	5.5%	4.4%	4.3%	3.9%	3.1%	8.6%	3.5%	4.3%	5.2%	7.1%	5.1%	5.2%
	N=	40	40	40	40	40	40	40	40	40	40	40	40	40
Positive Control	Mean	24.7	2.3	2.7	2.8	2.8	3.8	3.0	2.7	2.9	3.4	2.4	3.6	2.4
	SD*	0.72	0.09	0.07	0.13	0.10	0.12	0.09	0.07	0.11	0.14	0.08	0.14	0.09
	% CV	2.9%	4.1%	2.5%	4.7%	3.5%	3.1%	3.0%	2.5%	3.8%	4.2%	3.2%	3.8%	3.7%
	N=	40	40	40	40	40	40	40	40	40	40	40	40	40

Intra-Assay Site-3

Clinical Site 3, Lot 3		ANA Screen - Intra-assay												
		dsDNA (IU/mL)	Chromatin (AI)	RibosomalProtein (AI)	SS-A 52 (AI)	SS-A 60 (AI)	SS-B (AI)	Sm (AI)	SmRNP (AI)	RNP A (AI)	RNP 68 (AI)	Scl-70 (AI)	Jo-1 (AI)	Centromere B (AI)
High Positive Panel	Mean	52.8	2.8	2.6	4.7	4.2	4.0	3.7	3.7	4.7	4.3	3.8	3.9	4.2
	SD*	1.16	0.11	0.07	0.41	0.11	0.10	0.09	0.11	0.13	0.16	0.09	0.13	0.09
	% CV	2.2%	3.9%	2.9%	8.7%	2.6%	2.4%	2.3%	3.0%	2.7%	3.8%	2.5%	3.4%	2.1%
	N=	40	40	40	40	40	40	40	40	40	40	40	40	40
Low Positive Panel	Mean	19.9	1.4	1.3	2.8	2.2	2.1	1.8	1.9	2.2	2.3	2.3	2.0	2.5
	SD*	0.72	0.07	0.05	0.25	0.10	0.08	0.05	0.05	0.07	0.10	0.06	0.10	0.08
	% CV	3.6%	4.7%	3.5%	9.1%	4.4%	3.7%	3.0%	2.8%	3.1%	4.5%	2.7%	4.8%	3.0%
	N=	40	40	40	40	40	40	40	40	40	40	40	40	40
Positive Control	Mean	26.1	2.7	2.5	3.4	3.1	3.1	2.7	3.4	3.5	2.8	2.9	3.1	2.9
	SD*	0.60	0.07	0.08	0.38	0.08	0.08	0.07	0.07	0.10	0.09	0.07	0.11	0.09
	% CV	2.3%	2.7%	3.1%	11.1%	2.8%	2.5%	2.5%	2.2%	3.0%	3.4%	2.5%	3.6%	3.1%
	N=	36	36	40	36	36	36	36	40	36	36	36	36	36

Inter-Assay Site 1

Clinical Site 1, Lot 1		**ANA Screen - Inter-assay**												
		dsDNA (IU/mL)	**Chromatin (AI)**	**RibosomalProtein (AI)**	**SS-A 52 (AI)**	**SS-A 60 (AI)**	**SS-B (AI)**	**Sm (AI)**	**SmRNP (AI)**	**RNP A (AI)**	**RNP 68 (AI)**	**Scl-70 (AI)**	**Jo-1 (AI)**	**Centromere B (AI)**
High Positive Panel	Mean	45.6	2.7	2.4	4.1	3.4	3.6	3.3	4.0	4.1	3.8	3.3	3.9	3.7
	SD*	1.82	0.13	0.16	0.28	0.20	0.21	0.10	0.14	0.14	0.20	0.12	0.20	0.10
	% CV	4.0%	4.8%	6.7%	6.8%	5.8%	5.8%	3.2%	3.5%	3.5%	5.4%	3.7%	5.0%	2.8%
	N=	40	40	40	36	36	36	40	40	40	40	40	40	40
Low Positive Panel	Mean	17.0	1.3	1.2	2.2	1.8	1.7	1.5	2.2	1.9	1.8	1.9	1.9	2.0
	SD*	0.60	0.08	0.06	0.21	0.08	0.08	0.07	0.09	0.08	0.12	0.12	0.12	0.11
	% CV	3.5%	6.1%	5.6%	9.7%	4.6%	5.0%	5.0%	4.0%	4.0%	6.3%	6.3%	6.2%	5.3%
	N=	40	40	40	40	40	40	40	40	40	40	36	40	40
Positive Control	Mean	23.2	2.5	1.7	3.1	2.5	2.7	2.8	3.0	2.7	2.5	2.7	2.7	2.8
	SD*	2.09	0.29	0.10	0.39	0.25	0.29	0.26	0.10	0.26	0.29	0.28	0.27	0.27
	% CV	9.0%	11.7%	5.8%	12.8%	10.0%	10.7%	9.5%	3.2%	9.7%	11.6%	10.5%	10.1%	9.8%
	N=	36	36	40	36	36	36	36	40	36	36	36	36	36

Inter-Assay Site 2

Clinical Site 2, Lot 2		**ANA Screen - Inter-assay**												
		dsDNA (IU/mL)	**Chromatin (AI)**	**RibosomalProtein (AI)**	**SS-A 52 (AI)**	**SS-A 60 (AI)**	**SS-B (AI)**	**Sm (AI)**	**SmRNP (AI)**	**RNP A (AI)**	**RNP 68 (AI)**	**Scl-70 (AI)**	**Jo-1 (AI)**	**Centromere B (AI)**
High Positive Panel	Mean	44.9	2.9	2.7	3.8	3.6	3.5	3.9	3.4	3.8	3.9	3.2	3.1	2.9
	SD*	3.40	0.25	0.19	0.28	0.24	0.30	0.22	0.25	0.24	0.28	0.21	0.28	0.18
	% CV	7.6%	8.8%	7.2%	7.4%	6.8%	8.4%	5.8%	7.2%	6.3%	7.2%	6.5%	9.0%	6.2%
	N=	40	40	40	40	40	40	40	40	40	40	40	40	40
Low Positive Panel	Mean	18.2	1.5	1.6	2.2	1.9	1.6	1.7	1.9	1.8	1.8	1.8	1.4	1.6
	SD*	1.15	0.16	0.10	0.19	0.15	0.14	0.20	0.13	0.15	0.18	0.17	0.12	0.17
	% CV	6.3%	10.2%	6.6%	8.4%	8.1%	8.8%	11.9%	6.8%	8.7%	10.2%	9.5%	9.0%	10.6%
	N=	40	40	40	40	40	40	40	40	40	40	40	40	40
Positive Control	Mean	24.7	2.3	2.7	2.8	2.8	3.8	3.0	2.7	2.9	3.4	2.4	3.6	2.4
	SD*	1.71	0.19	0.19	0.24	0.21	0.32	0.23	0.18	0.24	0.29	0.18	0.30	0.20
	% CV	7.0%	8.3%	7.1%	8.6%	7.3%	8.4%	7.8%	6.8%	8.4%	8.6%	7.3%	8.2%	8.6%
	N=	40	40	40	40	40	40	40	40	40	40	40	40	40

Inter-Assay Site 3

Clinical Site 3, Lot 3		ANA Screen - Inter-assay												
		dsDNA (IU/mL)	Chromatin (AI)	RibosomalProtein (AI)	SS-A 52 (AI)	SS-A 60 (AI)	SS-B (AI)	Sm (AI)	SmRNP (AI)	RNP A (AI)	RNP 68 (AI)	Scl-70 (AI)	Jo-1 (AI)	Centromere B (AI)
High Positive Panel	Mean	52.8	2.8	2.6	4.7	4.2	4.0	3.7	3.7	4.7	4.3	3.8	3.9	4.2
	SD*	2.05	0.16	0.15	0.47	0.21	0.20	0.17	0.18	0.20	0.23	0.16	0.24	0.15
	% CV	3.9%	5.6%	5.9%	9.8%	5.1%	5.0%	4.5%	5.1%	4.2%	5.5%	4.3%	6.0%	3.6%
	N=	40	40	40	40	40	40	40	40	40	40	40	40	40
Low Positive Panel	Mean	19.9	1.4	1.3	2.8	2.2	2.1	1.8	1.9	2.2	2.3	2.3	2.0	2.5
	SD*	1.29	0.11	0.09	0.28	0.15	0.15	0.10	0.11	0.13	0.13	0.13	0.15	0.14
	% CV	6.5%	7.9%	7.0%	10.0%	6.8%	7.2%	5.5%	5.8%	5.6%	5.9%	5.7%	7.2%	5.5%
	N=	40	40	40	40	40	40	40	40	40	40	40	40	40
Positive Control	Mean	26.1	2.7	2.5	3.4	3.1	3.1	2.7	3.4	3.5	2.8	2.9	3.1	2.9
	SD*	1.06	0.15	0.23	0.41	0.15	0.14	0.12	0.25	0.16	0.18	0.13	0.19	0.14
	% CV	4.1%	5.6%	9.5%	12.0%	5.0%	4.5%	4.5%	7.5%	4.6%	6.4%	4.4%	6.0%	4.8%
	N=	36	36	40	36	36	36	36	40	36	36	36	36	36

    c. *Linearity*:
       Refer to k041658
    d. *Carryover*:
       Refer to k041658
    e. *Interfering Substances*:
       Refer to k041658
2. <u>Other Supportive Instrument Performance Data Not Covered Above:</u>
None

K. Proposed Labeling:
The labeling is sufficient and it satisfies the requirements of 21 CFR Part 809.10.

L. Conclusion:
The submitted information in this premarket notification is complete and supports a substantial equivalence determination.