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BARTLESVILLE, OKLAHOMA 74004 918 661-6600

HEALTH, ENVIRONMENT AND SAFETY

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(A)

August 24, 1992

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Gentlemen:

Phillips Petroleum Company is submitting the enclosed sixty (60) reports (two boxes, numbered 1 and 2) of toxicological studies pursuant to catagory II.B.2.b of the CAP Agreement 8ECAP-0075 Reports. Reports being submitted contain no confidential business information.

We are sending an additional five boxes (box numbers 3-7) of reports of studies that have, previously, been submitted to the FYI coordinator of the Office of Pollution Prevention and Toxics by the American Petroleum Institute (API). These are being provided solely for the Agency's convenience.

For questions concerning this correspondence, plese contact Fred Marashi at 918-661-8153.

Very truly yours,

Barbara J. Price
Vice President
Health, Environment & Safety

Enclosure (Seven Boxes)

4/21/95

FFM/dh:29

Phillips Petroleum Company

CAP Identification Number: 8ECAP-0075
Pursuant to Category: II.B.2.b

Contains No CBI

Title of Study: Mutagenicity Evaluation of R-01

Name of Chemical: R-01

CAS#: 64741-79-3

Summary: The test material, R-01, was clearly mutagenic for bacteria. Tests in cultured mouse cells for gene mutation, and in vivo cytogenetic analysis with rat bone marrow cells showed weak or marginal effects only at high dose levels. The biological significance of these increases is difficult to assess.

Fiche # 2381

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MUTAGENICITY EVALUATION

OF

[illegible]-01

FINAL REPORT

SUBMITTED TO

AMERICAN PETROLEUM INSTITUTE
2101 L STREET, N.W.
WASHINGTON, D.C. 20037

SUBMITTED BY

LITTON BIONETICS, INC.
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LBI PROJECT NO. 2725

MAY 1978

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1. INTRODUCTION AND BACKGROUND

The test chemical, R-01, was evaluated for its genetic properties in a battery of tests consisting of a test for mitotic gene conversion in yeast, gene mutation tests in bacteria, gene mutation tests in culture mammalian cells and in vivo chromosome analysis in rat bone marrow cells. This series of tests provides a sensitive screen for the detection of substances which produce mutagenic and/or clastogenic alterations. A high percentage of known mammalian mutagens and carcinogens demonstrate activity in one or more of the tests conducted in this evaluation, and positive results in one or more of these tests are an indication that the test substance has mutagenic and/or carcinogenic potential and that further analysis to define the limits of expression of this potential is warrented. Negative results in all of these tests suggest that the test material lacks genetic activity but are not sufficient for an unequivical determination of genetic safety.

The assumptions of mutagenic and carcinogenic potential or lack of potential are based on correlations between extensive data basis.

2. MICROBIAL ASSAYS

The test material, R-01, was found to be mutagenic in the Ames Salmonella/microsome assay. The indicator strains responding to the mutagen activity were TA-1537, TA-1538, and TA-98. These strains respond to various frameshift mutagens. Weak activity was observed under nonactivation test conditions, but the addition of rat liver S9 enhanced the overall activity. Strain TA-100 showed a weak response in the plate tests but the results were only marginal.

3. MOUSE LYMPHOMA ASSAY

The test material, R-01, was weakly mutagenic for mouse cells. Activity was observed in both nonactivation and activation assays with a significant effect seen only in the nonactivation series of tests. Due to toxicity, high concentrations could not be employed to develop a good dose response pattern.

4. RAT BONE MARROW CYTOGENETIC ANALYSIS

The test material, R-01, was not found to induce significant frequencies of chromosome aberrations in bone marrow cells from rats treated with 0.5 ml/kg, 1.7 ml/kg, and 5.0 ml/kg. The percent cells with aberrations was within the normal spontaneous range at all data points. The maximum aberration was to 3.2% at the high dose. The combined percent of cells with aberrations at the A and SC high dose level of 5.0 ml/kg was slightly higher than the negative control and all other dose levels but was not significant.

4. RAT BONE MARROW CYTOGENETIC ANALYSIS

Dose	Combined Percent Cells/Aberrations
Negative Control	1.3%
Low Dose	0.9%
Intermediate Dose	0.5%
High Dose	2.0%

5. CONCLUSIONS

The test material, R-01, was clearly mutagenic for bacteria. Tests in cultured mouse cells for gene mutation, and in vivo cytogenetic analysis with rat bone marrow cells showed weak or marginal effects only at high dose levels. The biological significance of these increases is difficult to assess. Using the microbial assays as a basis to demonstrate DNA and genotoxic potential, the weak activity of R-01 in the L5178Y mouse lymphoma cells and the elevated but not significant frequencies of chromosome aberrations in rat bone marrow cells must be viewed as suggestive of expression of biological activity in mammalian test systems.

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PART I

PLATE AND SUSPENSION ASSAYS

EVALUATION SUMMARY

The test material, R-01, was mutagenic in plate tests employing S. typhimurium strains TA-1537, TA-1538, TA-98, and appeared slightly mutagenic in strain TA-100. The positive results were primarily in activation assays although weak mutagenicity was also observed in nonactivation tests. Suspension tests with TA-1538, TA-98, and TA-100 were positive under S9 activation conditions.

SPONSOR: American Petroleum Institute

MATERIAL: R-01

SUBJECT: FINAL REPORT MUTAGENICITY PLATE ASSAY AND SUSPENSION ASSAY

1. OBJECTIVE

The objective of this study was to evaluate the test compound for genetic activity in microbial assays with and without the addition of mammalian metabolic activation preparations.

2. MATERIALS

A. Test Compound

1. Date Received: February 18, 1977

2. Description: Dark liquid

B. Indicator Microorganisms

The following strains of indicator microorgansims were used in the evaluation:

1. Yeast Strain: Saccharomyces cerevisiae, D4

2. Bacteria Strains: Salmonella typhimurium, strains
TA-1535
TA-1537
TA-1538
TA-98
TA-100

C. Reaction Mixture

The following reaction mixture was employed in the activation tests:

Component	Final Concentration/ml
1. TPN (sodium salt)	4 µmoles
2. Glucose-6-phosphate	5 µmoles
3. Sodium phosphate (dibasic)	100 µmoles
4. $MgCl_2$	8 µmoles
5. KCl	33 µmoles
6. Homogenate	0.1-0.15 ml 9,000 x g supernatant of rat liver

2. MATERIALS (Continued)

D. Tissue Homogenates and Supernatants

The tissue homogenates and 9,000 x g supernatants were prepared from Sprague-Dawley rats pretreated with Aroclor 1254.

E. Positive Control Chemicals

Table 1 below lists the chemicals used for positive controls in the nonactivation and activation assays.

TABLE 1

ASSAY	CHEMICAL[a]	SOLVENT	PROBABLE MUTAGENIC SPECIFICITY
Nonactivation	Ethylmethanesulfonate (EMS)	Water or Saline	BPS[b]
	Methylnitrosoguanidine (MNNG)	Water or Saline	BPS[b]
	2-Nitrofluorene (NF)	Dimethylsulfoxide[c]	FS[b]
	Quinacrine mustard (QM)	Water or saline	FS[b]
Activation	2-Anthramine (ANTH)	Dimethylsulfoxide[c]	BPS[b]
	2-Acetylaminofluorene (AAF)	Dimethylsulfoxide[c]	FS[b]
	8-Aminoquinoline (AMQ)	Dimethylsulfoxide[c]	FS[b]
	Dimethylnitrosamine (DMNA)	Water or Saline	BPS[b]

[a]Concentrations given in Results section

[b]BPS = Base-pair substitution

FS = Frameshift

[c]Previously shown to be nonmutagenic

F. Solvent

Either deionized water or Dimethylsulfoxide (DMSO) was used to prepare stock solutions of solid materials. All dilutions of test materials were made in the solvent vehicle. The specific solvent employed is recorded in the Results Section.

3. EXPERIMENTAL DESIGN

A. Toxicity

The solubility, toxicity, and dose levels for the test compound were determined prior to screening.

The test compound was assayed for toxicity against bacteria and yeast indicator strains over a wide range of doses to determine the 50% killing dose (LD50). Bacteria were tested in phosphate buffer, pH 7.4, for 1 hour at 37C in a shaker. Yeasts were tested in phosphate buffer, pH 7.4, for 4 hours at 30C in a shaker. The 50% killing dose and the 1/8, 1/4, and 1/2 50% killing doses were calculated from the toxicity assays. For most compounds, the toxicity test system employed a low amount of Dimethylsulfoxide (DMSO) to ensure solubility of the chemical at all screening levels.

If no toxicity was obtained for a chemical with indicator strains, a maximum dose of 5% was used as the high dose concentration.

The dose levels selected from preliminary toxicity tests were applied to both activation and nonactivation assays.

B. Plate Tests (Overlay Method)

Approximately 10^8 cells from an overnight culture of each indicator strain were added to test tubes containing 2.0 ml of molten agar supplemented with biotin and a trace of histidine. For nonactivation tests, a minimum of four dose levels of the test compound were added to the contents of the appropriate tubes and poured over the surfaces of selective agar plates. In activation tests, 0.5 ml of 9,000 x g tissue supernatant and required cofactors (core reaction mixture) were added to the overlay tubes. At least four dose levels of the test chemical were added to the appropriate tubes, which were then mixed and the contents poured over the surface of a minimal agar (selective medium) plate and allowed to solidify. The plates were incubated for approximately 48 hours at 37C and scored for the number of colonies growing on each plate. The concentrations of all chemicals are given in the Results section. Positive and solvent controls using both directly active mutagens and those that require metabolic activation were run with each assay.

3. EXPERIMENTAL DESIGN (Continued)

C. Suspension Tests

1. Nonactivation

Bacteria and yeast cultures were grown in complete broth, washed, and resuspended in 0.9% saline to densities of 1×10^{10} cells/ml and 5×10^{8} cells/ml, respectively. These constituted the working stocks for evaluation of the test compound and the respective controls. Tests were conducted in 24-well, sterile plastic tissue culture plates (Linbro Chemical Company). Cells plus appropriate volume(s) of the test compound were added to the wells to give a final volume of 1.5 ml. An equal volume of solvent replaced the test compound in the negative controls. Treatment was at 30C for 4 hours for yeast tests, and at 37C for 1 hour for bacterial tests. All flasks were shaken on a rotary shaker during treatment. Following treatment, the plates were set on ice. Aliquots of cells were removed, diluted in sterile saline (4C), and plated on the appropriate complete media. Undiluted samples from flasks containing the bacteria were plated on minimal selective medium in reversion experiments. Samples from a 10^{-1} dilution of treated cells were plated on the selected media for enumeration of gene conversion with strain D4. Bacterial plates were scored after incubation for approximately 48 hours at 37C. The yeast plates were incubated at 30C for 3 to 5 days before scoring.

2. Activation

Bacteria and yeast cells were grown and prepared as described in the nonactivation tests. Measured amounts of the test compound and the control chemicals plus 0.25 ml of the stock-cell suspension were added to wells of the Linbro plate containing the appropriate tissue fraction and reaction mixture (Section 2,C). All flasks (bacteria and yeast) were incubated at 37C with shaking. The treatment times as well as the dilutions, the plating procedures and the scoring of the plates were the same as described for nonactivation tests.

3. EXPERIMENTAL DESIGN (Continued)

D. Preparation of Tissue Homogenates and 9,000 x g Cell Fractions

Male animals (sufficient to provide the necessary quantities of tissues) were killed by cranial blow, decapitated, and bled. Organs were immediately dissected from the animal, using aseptic techniques, and placed in ice-cold 0.15M KCl. Upon collection of the desired quantity of organs, they were washed twice with fresh KCl and completely homogenized with a motor-driven homogenizing unit at 4C. The organ homogenate obtained from this step was centrifuged for 20 minutes at 9,000 x g in a refrigerated centrifuge. The supernatant from the centrifuged sample was retained and frozen at -80C.

E. Data Recording and Reporting

1. Plate Test Assays

The numbers of colonies on each plate were counted and recorded on printed forms. These raw data were transferred directly to the report form sheets and entered into a computer for analysis and printing.

2. Suspension Test Assays

Following the specified incubation periods, all population plates were scored by an automatic colony counter and the results from each plate of a set were recorded, in ink, on data processing forms. All minimal or other types of selective media plates were hand scored, and the results recorded along with the respective population data. Other relevant experimental data were recorded on experimental definition forms. For bacteria strains, the number of colonies recorded from either the population or the selective plates represents that number in 1 ml of test suspension plated. The numbers recorded for the yeast strain D4 represent the number in 0.3 ml of test suspension plated. The data were then processed and printed from a computer program.

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A. Solubility Properties of the Test Compound

1. Name or code designation of the test compound: R-01

2. Test solvent:* DMSO

3. Solubility of the test compound under treatment conditions: Soluble

4. Additional comments: Dark liquid

B. Toxicity and Dosage Determinations for the Test Compound

1. Test date for toxicity determination: Bacteria - March 10, 1977
Yeast - March 11, 1977

2. The 50% survival level was determined for bacteria and yeast indicator organisms by conducting survival curves with the test compound at the following concentrations:

Percent Concentration (w/v or v/v)

5.0
0.5
0.05
0.005
0.0005

3. Concentrations of the test compound used in the mutagenicity tests:

Test Doses	Percent Concentration	
	Bacteria	Yeast
1/8 50% Survival	0.0625	0.0825
1/4 50% Survival	0.1250	0.1650
1/2 50% Survival	0.2500	0.3300
50% Survival	0.5000	0.6600

*The concentration of solvent was equal to the highest volume of test material added.

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4. RESULTS (Continued)

C. Summary of Plate Assay Results

The plate test results are summarized in the first table. The values presented in this table are the number of revertants per plate.

D. Summary of Suspension Assay Results

The suspension assay results for the test compound are summarized in the two tables following the plate assay results. The values presented in these tables are the calculated mutation frequencies for each control and experimental test point. The first table presents the results for the nonactivation assays and the second table presents the results for the activation assays. A listing of computer codes and abbreviations is included for reference. Tabulation of all raw data is provided.

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SUMMARY OF PLATE TEST RESULTS [illegible] BIOMETICS, INC.

A. NAME OR CODE DESIGNATION OF THE TEST COMPOUND: [illegible]
B. SOLVENT: DMSO
C. TEST DATE: MARCH 14, 1977
NOTE: CONCENTRATIONS ARE GIVEN IN MICROLITERS (UL) OR MICROGRAMS (UG) PER PLATE.

TEST	SPECIES	TISSUE	REVERTANTS PER PLATE TA-1535 1	TA-1535 2	TA-1537 1	TA-1537 2	TA-1538 1	TA-1538 2	TA-98 1	TA-98 2	TA-100 1	TA-100 2	D4* 1	D4* 2
NONACTIVATION														
SOLVENT CONTROL	---	---	24		12	7	22		33		246		279	
POSITIVE CONTROL**	---	---	>1000		>1000		529		>1000		>1000		>1000	
TEST COMPOUND														
0.00100 UL	---	---	37		7	-	25		38		195		132	
0.01000 UL	---	---	32		15	-	18		36		323		149	
0.10000 UL	---	---	18		13	-	24		36		249		144	
1.00000 UL	---	---	28		17	31	36		42		327		121	
5.00000 UL	---	---	14		39	66	38		28		268		103	
10.00000 UL	---	---			-	40								
ACTIVATION														
SOLVENT CONTROL	RAT	LIVER	32		20	10	18	17	29	27	153		193	
POSITIVE CONTROL***	RAT	LIVER	254		262		605		473		370		345	
TEST COMPOUND														
0.00100 UL	RAT	LIVER	38		21	-	17	-	16	-	225		192	
0.01000 UL	RAT	LIVER	42		20	-	19	-	14	-	246		183	
0.10000 UL	RAT	LIVER	37		39	12	40	28	28	-	310		190	
1.00000 UL	RAT	LIVER	34		83	122	123	197	34	113	312		215	
5.00000 UL	RAT	LIVER	26		40	112	59	222	31	142	271		207	
10.00000 UL	RAT	LIVER			-	68	-	153	-	52				

* TRY: CONVERTANTS PER PLATE

** TA-1535 MNNG 10 UG/PLATE
TA-1537 QM 10 UG/PLATE
TA-1538 NF 100 UG/PLATE
TA-98 NF 100 UG/PLATE
TA-100 MNNG 10 UG/PLATE
D4 MNNG 10 UG/PLATE
SOLVENT DMSO 2.5 %/PLATE

*** TA-1535 ANTH 100 UG/PLATE
TA-1537 AMQ 100 UG/PLATE
TA-1538 AAF 100 UG/PLATE
TA-98 AAF 100 UG/PLATE
TA-100 ANTH 100 UG/PLATE
D4 DMNA 100 MICROMOLES/PLATE
SOLVENT DMSO 2.5 %/PLATE

\- INDICATES TEST WAS NOT DONE

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SUMMARY OF PLATE TEST RESULTS — LITTON BIONETICS, INC.

A. NAME OR CODE DESIGNATION OF THE TEST COMPOUND: P-01
B. SOLVENT: DMSO
C. TEST INITIATION DATE: JUNE 7, 1977
NOTE: CONCENTRATIONS ARE GIVEN IN MICROLITERS (UL) OR MICROGRAMS (UG) PER PLATE.

TEST	SPECIES	TISSUE	BEVERIDGE PELAIZ TA-1535 1	TA-1535 2	TA-1537 1	TA-1537 2	TA-1538 1	TA-1538 2	TA-98 1	TA-98 2	TA-100 1	TA-100 2	D4 1	D4 2
NONACTIVATION														
SOLVENT CONTROL	---	---	13	22	10	18	8	7	30	24	76	79	140	256
POSITIVE CONTROL**	---	---	>1000	>1000	225	200	>1000	>1000	>1000	>1000	536	661	690	807
TEST COMPOUND														
0.001000 UL	---	---	11	8	12	12	10	7	32	18	72	67	204	164
0.010000 UL	---	---	10	7	10	8	5	4	29	29	73	79	215	190
0.100000 UL	---	---	9	11	14	13	7	10	39	28	72	62	180	184
1.000000 UL	---	---	11	10	10	14	8	6	43	39	75	73	199	208
5.000000 UL	---	---	7	15	33	24	7	8	69	53	76	76	182	191
10.000000 UL	---	---							114	185				
ACTIVATION														
SOLVENT CONTROL	RAT	LIVER	12	14	25	32	11	20	28	34	96	85	214	231
POSITIVE CONTROL***	RAT	LIVER	96	159	537	635	>1000	>1000	874	>1000	204	199	480	480
TEST COMPOUND														
0.001000 UL	RAT	LIVER	10	16	25	17	11	15	33	27	95	88	220	194
0.010000 UL	RAT	LIVER	8	13	19	21	20	14	31	35	100	97	182	196
0.100000 UL	RAT	LIVER	11	12	23	25	72	71	64	83	94	77	142	165
1.000000 UL	RAT	LIVER	19	14	47	44	100	116	59	68	103	120	189	194
5.000000 UL	RAT	LIVER	10	12	78	75	154	154	154	79	123	103	147	197
10.000000 UL	RAT	LIVER			138	141	101	132	232	202				

* IBV* CONVERTANTS PER PLATE

** TA-1535 MNNG 10 UG/PLATE
TA-1537 9A 10 UG/PLATE
TA-1538 NF 100 UG/PLATE
TA-98 NF 100 UG/PLATE
TA-100 MNNG 10 UG/PLATE
D4 MNNG 10 UG/PLATE
SOLVENT DMSO 50 UL/PLATE

*** TA-1535 ANTH 100 UG/PLATE
TA-1537 AMQ 100 UG/PLATE
TA-1538 AAF 100 UG/PLATE
TA-98 AAF 100 UG/PLATE
TA-100 ANTH 100 UG/PLATE
D4 DMNA 100 MICROMOLES/PLATE
SOLVENT DMSO 50 UL/PLATE

LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
REPORT EX834

COMPOUND FREQUENCY SUMMARY REPORT 09/14/77

NONACTIVATION COMPOUND R-91

TEST	ORG	TA100 HIS EX-R	TA1535 HIS EX-R	TA1537 HIS EX-R	TA1538 HIS EX-R	TA98 HIS EX-R	000004 ADE EX-S	000004 TRY EX-S	
MAN		41.44	5.28	15.35	20.29	23.74	27.17	17.21	CONTROLS
NAP		526.60	667.05	960.61	89.05	109.67	180.45	124.68	
NA1		21.07	2.46	5.62	36.36	6.54	26.31	6.29	TEST DATA
NA2		21.07	1.93	10.37	10.83	20.88	27.37	12.91	
NA3		14.05	2.51	5.57	9.91	19.65	16.18	6.77	
NA4		34.19	2.50	5.63	18.06	21.44	18.26	8.11	

LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
REPORT EXR14

COMPOUND FREQUENCY SUMMARY REPORT 09/14/77

SPECIES SPRDAW/RAT COMPOUND R-01

TEST	ORG	TA100 HIS EX-R	TA1535 HIS EX-R	TA1537 HIS EX-R	TA1538 HIS EX-R	TA98 HIS EX-R	0000D4 ADE EX-S	0000D4 TRY EX-S	
ACT	A+C	60.67	3.17	4.32	117.78	10.70	12.95	1.50	NEGATIVE CONTROLS
ACT	A-C	47.96	1.98	3.15	4.44	13.81	10.60	1.31	
ACT	ALI	57.93	3.68	8.05	6.34	23.72	9.60	1.00	
ACT	PLI	349.02	74.39	41.15	335.01	533.71	55.24	50.83	POSITIVE CONTROLS
ACT	LI1	107.40	2.03	7.15	25.23		6.13	1.07	TEST COMPOUND
ACT	LI2	79.31	3.75	8.51	24.60	69.25	5.63	2.60	
ACT	LI3	71.04	4.04	8.98	24.75	68.08	9.27	2.06	
ACT	LI4	57.21	3.72	5.92	9.26	87.07	4.89	1.28	

DATA TABLE TERMS AND ABBREVIATIONS

ABBREVIATION OR TERM	DEFINITION OR EXPLANATION
COMPOUND	Client designated compound number appears in this column.
TEST CODES	NAN = Nonactivation: Solvent Control NAP = Nonactivation: Positive Control NA1 = Nonactivation: Test Compound Dose 1 NA2, etc. = Reflects the other dose level(s) A+C = Negative Chemical Control for ACP A-C = Activation: Solvent Control ALI or A+T = Activation: Homogenate Control (Liver) ALU = Activation: Homogenate Control (Lung) ACP = Activation: Positive Control ACT = Activation Test LI = Liver Tissue Activation Fraction LU = Lung Tissue Activation Fraction KI = Kidney Tissue Activation Fraction TE = Testes Tissue Activation Fraction 1,2, etc. = Dose Levels
CONCENTRATION	All test compound dose levels are expressed as a whole number followed by an exponent (negative) identified by the appropriate units. Example: 0025-2PCT = 0.25 percent concentration
POPU	Total number of viable cells in the plating sample raised to some exponent printed directly below the abbreviation (e.g., EP + 6 = x 10^6).
MUT 1	Total number of mutants or convertants obtained from the sample plated raised to some exponent printed directly below the abbreviation (e.g., EP + 0 = x 10^0). For strain D4, MUT 1 represents the number of ADE+ convertants.
MUT 2	Only used for strain D4 and represents the number of TRY+ convertants in the plated sample.
FREQ 1	The calculated mutation or gene conversion frequency times the negative exponent written directly below. For strain D4, FREQ 1 represents the ADE+ value.

DATA TABLE TERMS AND ABBREVIATIONS (Continued)

ABBREVIATION OR TERM	DEFINITION OF EXPLANATION
FREQ 2	Only used for strain D4 and represents the TRY+ conversion frequency.
CONTAM	Presence of contamination on any plates.
AAF	2-Acetylaminofluorene
AMQ	8-Aminoquinoline
DMSO	Dimethylsulfoxide
DMNA	Dimethylnitrosamine
EMS	Ethylmethanesulfonate
QM	Quinacrine Mustard
NF	Nitrofluorene
SPECIES	Animal Strains
SPRDAW	Sprague-Dawley Rats
ICRFLO	Flow ICR Random Bred Mice
RHESUS	Rhesus Monkey (Macaca mulatta)
MIXEDB	Dog, Mixed Breed
NEWZEA	New Zealand White Rabbit
UG	Microgram
UM	Micromole
ADE	Adenine
TRY	Tryptophan

6. EXPLANATION OF EVALUATION PROCEDURES FOR PLATE ASSAYS

Plate test data consist of direct revertant colony counts obtained from a set of selective agar plates seeded with populations of mutant cells suspended in a semisolid overlay. Because the test chemical and the cells are incubated in the overlay for 2 to 3 days, and a few cell divisions occur during the incubation period, the test is semi-quantitative in nature. Although these features of the assay reduce the quantitation of results, they provide certain advantages not contained in a quantitative suspension test:

- The small number of cell divisions permits potential mutagens to act on replicating DNA, which is often more sensitive than nonreplicating DNA.
- The combined incubation of the compound and the cells in the overlay permits constant exposure of the indicator cells for 2 to 3 days.

A. Surviving Populations

Plate test procedures do not permit exact quantitation of the number of cells surviving chemical treatment. At low concentrations of the test chemical, the surviving population on the treatment plates is essentially the same as that on the negative control plate. At high concentrations, the surviving population is usually reduced by some fraction. Our protocol normally employs several doses ranging over two or three log concentrations, the highest of these doses being selected to show slight toxicity as determined by subjective criteria.

B. Dose Response Phenomena

The demonstration of dose-related increases in mutant counts is an important criterion in establishing mutagenicity. A factor that might modify dose-response results for a mutagen would be the selection of doses that are too low (usually mutagenicity and toxicity are related). If the highest dose is far lower than a toxic concentration, no increases may be observed over the dose range selected. Conversely, if the lowest dose employed is highly cytotoxic, the test chemical may kill any mutants that are induced, and the compound will not appear to be mutagenic.

6. EXPLANATION OF EVALUATION PROCEDURES FOR PLATE ASSAYS (Continued)

C. Control Tests

Positive and negative control assays are conducted with each experiment and consist of direct-acting mutagens for nonactivation assays and mutagens that require metabolic biotransformation in activation assays. Negative controls consist of the test compound solvent in the overlay agar together with the other essential components. The negative control plate for each strain gives a reference point to which the test data are compared. The positive control assay is conducted to demonstrate that the test systems are functional with known mutagens.

D. Evaluation Criteria for Ames Assay

Because the procedures used to evaluate the mutagenicity of the test chemical are semiquantitative, the criteria used to determine positive effects are inherently subjective and are based primarily on a historical data base. Most data sets are evaluated using the following criteria:

1. Strains TA-1535, TA-1537 and TA-1538

If the solvent control value is within the normal range, a chemical that produces a positive dose response over three concentrations with the lowest increase equal to twice the solvent control value is considered to be mutagenic.

2. Strains TA-98, TA-100 and D4

If the solvent control value is within the normal range, a chemical that produces a positive dose response over three concentrations with the highest increase equal to twice the solvent control value for TA-100 and two to three times the solvent control value for strains TA-98 and D4 is considered to be mutagenic. For these strains, the dose response increase should start at approximately the solvent control value.

3. Pattern

Because TA-1535 and TA-100 were both derived from the same parental strain (G-46) and because TA-1538 and TA-98 were both derived from the same parental strain (D3052), there is a built-in redundancy in the microbial assay. In general the two strains of a set respond to the same mutagen and such a pattern is sought. It is also anticipated that if a

6. EVALUATION OF EVALUATION PROCEDURES FOR PLATE ASSAYS (Continued)

D. Evaluation Criteria for Ames Assay

3. Pattern

given strain, e.g., TA-1537, responds to a mutagen in nonactivation tests, it will generally do so in activation tests. (The converse of this relationship is not expected.) While similar response patterns are not required for all mutagens, they can be used to enhance the reliability of an evaluation decision.

4. Reproducibility

If a chemical produces a response in a single test that cannot be reproduced in one or more additional runs, the initial positive test data loses significance.

The preceding criteria are not absolute and other extenuating factors may enter into a final evaluation decision. However, these criteria are applied to the majority of situations and are presented to aid those individuals not familiar with this procedure. As the data base is increased, the criteria for evaluation can be more firmly established.

E. Relationship Between Mutagenicity and Carcinogenicity

It must be emphasized that the Ames Salmonella/microsome test is not a definitive test for chemical carcinogens. It is recognized, however, that correlative and functional relationships have been demonstrated between these two end points. The results of comparative tests on 300 chemicals by McCann et al. (Proc. Nat. Acad. Sci. USA, 72:5135-5139, 1975) show an extremely good correlation between results of microbial mutagenesis tests and in vivo rodent carcinogenesis assays.

All evaluation and interpretation of the data presented in this report are based only on the demonstration of or lack of mutagenic activity.

7. EXPLANATION OF EVALUATION PROCEDURES FOR SUSPENSION ASSAYS

Data obtained from mutagenicity tests are evaluated on a test by test basis followed by an examination of the total response pattern using all the data. To facilitate this type of evaluation, we have prepared two separate formats in which data are processed. The first is the Compound Summary Backup Detail Sheet, which details the essential raw data from each experiment showing surviving population counts, total mutant or convertant counts, as well as calculated mutation frequencies. This format permits close examination of each set of test data. The following considerations are part of any assessment:

A. Surviving Population Counts

A certain level of chemically-induced toxicity is anticipated, but occasionally isolated tests or groups of tests show very low (< 25%) survival compared to the tissue controls. Such isolated decreases may result from improper dilution procedures or defective growth media and decrease confidence in the calculated mutation frequencies, especially if the total mutant counts appear unaffected. Data of this type are generally unacceptable and these experiments are routinely repeated at a lower dose level to reduce killing and to increase confidence in the nature of the response.

B. Total Mutant Counts

For nonmutagens, the mutant/surviving population ratio should be roughly equivalent for each test point in a given experiment. If the cell number drops in response to killing, the mutant number should decrease proportionately. A mutagenic chemical, however, will produce an altered mutant/surviving population ratio. Mutant numbers as well as calculated frequencies are compared to the negative control data. In certain instances, the mutant frequencies will increase with little or no change in the absolute number of mutants, especially where the test chemical is toxic. Data of this type, although not necessarily aberrant, or even rare, must be viewed with special care to ensure that the increased frequencies were not the result of selective toxicity of the test chemical for the his⁻ cells. This phenomenon, referred to as selection, can lead to erroneous conclusions. Thus we attempt to keep the surviving population of cells high and look for positive responses that show increases in both numbers of mutants and mutation frequencies. Again, occasional isolated fluctuations in mutant counts are found that can be attributed to improper pipetting or media contamination. These fluctuations are usually easy to identify by inspection of the other data points in the experiment that will be negative.

7. EXPLANATION OF EVALUATION PROCEDURES FOR SUSPENSION ASSAYS (Continued)

C. Dose-Response Phenomena

Dose-related increases in mutants and mutation frequencies are the most convincing data to have in assessing mutagenic activity of chemicals. In some cases, however, dose-related increases are not observed for mutagens. This depends considerably on the dose levels selected. The figure on the following page illustrates how one might obtain various types of dose-related responses by a mutagen based solely on dose selection. It also emphasizes the need to keep dose levels within a relatively low range of toxicity so that data are consistently on the uphill side of the hypothetical curve.

D. Control Tests

Positive and negative control tests are conducted with each experiment and consist of direct-acting positive agents for nonactivation assays and chemicals that require metabolic transformation for activation assays. In nonactivation assays, the NAN control contains the test chemical solvent plus cells, but no chemical, and is used as a reference to assess the level of response obtained in the various tests. It is not possible at this time to put precise cutoff points where negative responses become positive responses. A statistical component for our computer program is under development and will be included when available. Positive controls are only used as relative reference points and to demonstrate that the system is functioning with known mutagens. In activation assays, three types of negative controls are run:

1. A solvent control minus the chemical and minus the activation system (A-C)

2. A control plus the positive control chemical minus the activation system (A+C), and

3. A control containing the activation system and the test chemical solvent (ALI or ALU).

All three controls are used collectively to assess the level of response in the various activation tests. A chemical may appear positive when compared to an A-C control, but not when compared to an A+T control. The value of each of the above controls with respect to their weight in evaluation is ALI or ALU > A-C > A+C.

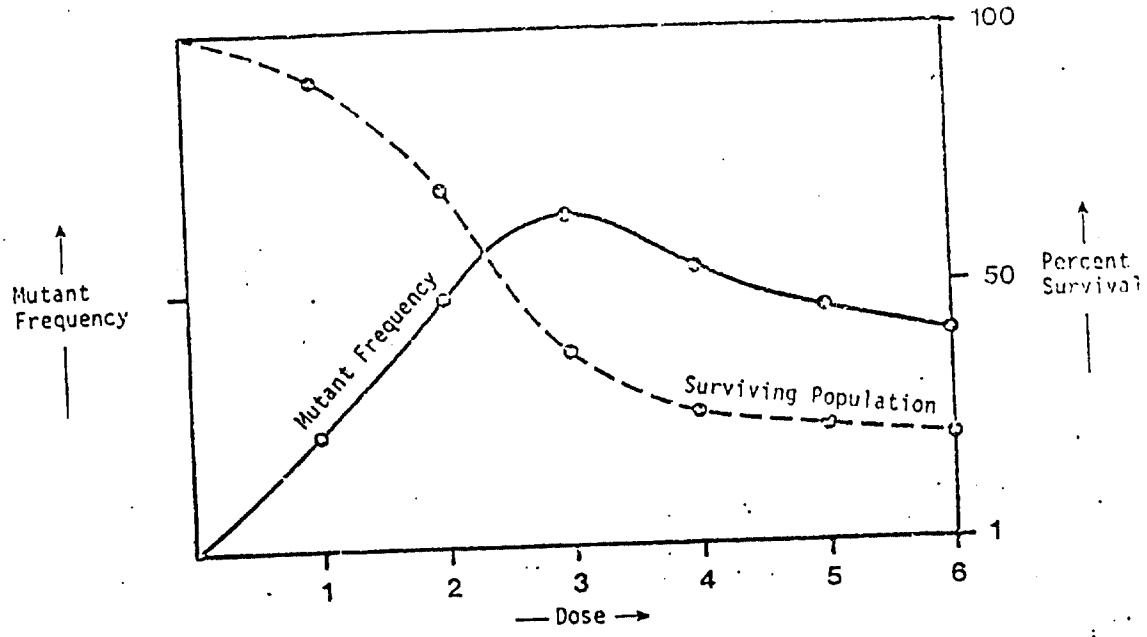
7. EXPLANATION OF EVALUATION PROCEDURES FOR SUSPENSION ASSAYS (Continued)

D. Control Tests

The other data format is the Compound Frequency Summary Report sheet in which all the calculated frequencies obtained for a given compound are displayed in a table. This format permits an overview of all data. The points form a matrix of information that should present a consistent pattern. Nonmutagens should produce a matrix with data frequencies clustered around the negative control values. Occasional random high or low fluctuations are not uncommon and seldom indicate true genetic activity. Mutagenic chemicals should, on the other hand, produce a set of consistent responses that demonstrate a logical pattern. The patterns depend on the mutagenic specificity of the chemical, but can be easily recognized in the Compound Frequency Summary Report format.

These mutagenicity assays are designed to optimize the probability of recognizing mutagens from nonmutagens, and, in most cases, they work well. Occasionally, the data points are such that a definitive conclusion cannot be made without additional data.

HYPOTHETICAL MUTATION AND TOXICITY KINETICS



HYPOTHETICAL EXPERIMENT

(1) Dose levels 1,2 & 3 were used

(2) Dose levels 2, 3 & 4 were used

(3) Dose levels 3, 4 & 5 were used

OBSERVED DOSE RESPONSE

A typical positive dose response set of data would be obtained.

The intermediate dose level shows a higher mutation frequency than both the low dose and the high dose.

Here an inverted dose response would be observed with the highest dose level showing the lowest response.

TABULATION OF DATA

REPORT EXR33 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

PROJECT 2525 / DATE - 09/14/77

EXPERIMENT 709104 CONTRACT AMPETRINST DETECTOR TA100 SPECIES

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+6	MUTI EP+0	FREQI EP-8	CONTAM
	NAN		SOLVENT	0900	0391	43.44	0
	NAP		EMS 0.066%	0703	3702	526.60	0
R-01	NA1		0005-1 PCT.	0707	0149	21.07	0
R-01	NA2		0025-2 PCT.	0788	0166	21.07	0
R-01	NA3		0125-3 PCT.	0833	0117	14.05	0
R-01	NA4		0675-4 PCT.	0974	0333	34.19	0

REPORT EXR33 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

EXPERIMENT 709401 CONTRACT AMPETRINST DETECTOR TA1535 SPECIES PROJECT 2525 / DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+6	MUTI EP+0	FREQ1 EP-8	CONTAM
	NAN		SOLVENT	0492	0026	5.28	0
	NAP		EMS 0.2%	0868	5790	667.05	0
R-01	NA1		0005-1 PCT.	0285	0007	2.46	0
R-01	NA2		0025-2 PCT.	0519	0010	1.93	0
R-01	NA3		0125-3 PCT.	0676	0017	2.51	0
R-01	NA4		0625-4 PCT.	0801	0020	2.50	0

REPORT EXP33 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

CONTRACT AMPETRINST PROJECT 2525
EXPERIMENT 707582 DETECTOR TA1537 SPECIES / DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+6	MUTI EP+0	FREQ1 EP-8	CONTAM
	NAN		SOLVENT	1029	0158	15.35	0
	NAP		QM 13 UG/ML	0033	0317	960.61	0
R-01	NA1		0005-1 PCT.	0516	0029	5.62	0
R-01	NA2		0025-2 PCT.	0482	0050	10.37	0
R-01	NA3		0125-3 PCT.	0610	0034	5.57	0
R-01	NA4		0625-4 PCT.	0480	0027	5.63	0

REPORT EXR33 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

EXPERIMENT 709102 CONTRACT AMPETRINST DETECTOR TA1538 SPECIES / PROJECT 2525 DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+6	MUTI EP+0	FREQ1 EP-8	CONTAM
	N&N		SOLVENT	0069	0014	20.29	1
	NAP		NF 667 UG/ML	0137	0122	89.05	0
R-01	NA1		0005-1 PCT.	0033	0012	36.36	1
R-01	NA2		0025-2 PCT.	0120	0013	10.83	0
R-01	NA3		0125-3 PCT.	0222	0022	9.91	0
R-01	NA4		0675-4 PCT.	0144	0026	18.06	0

REPORT EXR13 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

EXPERIMENT CONTRACT 709163 AMPETRINST DETECTOR TA98 SPECIES PROJECT 2525 / DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+6	MUTI EP+0	FREQ1 EP-8	CONTAM
	NAN		SOLVENT	0973	0231	23.74	0
	NAP		NF 667 UG/ML	1214	1329	109.47	1
R-01	NA1		0005-1 PCT.	1131	0074	6.54	2
R-01	NA2		0025-2 PCT.	1269	0265	20.88	0
R-01	NA3		0125-3 PCT.	0982	0193	19.65	0
R-01	NA4		0675-4 PCT.	1208	0259	21.44	0

REPORT EXR33 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

EXPERIMENT 714301 CONTRACT AMPETRINST DETECTOR 000004 SPECIES PROJECT 2525 / DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+4	MUT1 EP+1	MUT2 EP+1	FREQ1 EP-5	FREQ2 EP-5	CONTAM
	NAN		SOLVENT	1104	0300	0190	27.17	17.21	0
	NAP		EMS 1.0 %	0624	1126	0778	180.45	124.68	0
R-01	NA1		0066-2 PCT.	0954	0251	0060	26.31	6.29	0
R-01	NA2		0033-2 PCT.	1162	0318	0150	27.37	12.91	0
R-01	NA3		0165-3 PCT.	1255	0203	0085	16.18	6.77	0
R-01	NA4		0825-4 PCT.	1331	0243	0108	18.26	8.11	0

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REPORT EX833 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

EXPERIMENT T13601 CONTRACT AMPETRINST DETECTOR TA100 PROJECT 2525 SPECIES SPRDAW/RAT DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+6	MUTI EP+0	FREQ1 EP-8	CONTAM
	A+C		DMN 90 UM/ML	1442	0887	60.67	0
	A-C		SOLVENT	1055	0506	47.96	0
	ALI		TISSUE	1160	0672	57.93	0
	ACP	LI	DMN 90 UM/ML	1379	4813	349.02	0
R-01	ACT	LI1	0005-1 PCT.	0932	1001	107.40	0
R-01	ACT	LI2	0025-2 PCT.	1503	1192	79.31	0
R-01	ACT	LI3	0125-3 PCT.	1640	1165	71.04	0
R-01	ACT	LI4	0625-4 PCT.	1603	0917	57.21	0

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REPORT EX333 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

CONTRACT AMPETRINST PROJECT 2525
EXPERIMENT 713201 DETECTOR TA1535 SPECIES SPRDAW/RAT DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP-6	MUTI EP-0	FREQ1 EP-8	CONTAM
	A+C		DMN 90 UM/ML	1073	0034	3.17	0
	A-C		SOLVENT	0962	0019	1.98	0
	ALI		TISSUE	0815	0030	3.68	0
	ACP	LI	DMN 90 UM/ML	0652	0485	74.39	0
R-01	ACT	LI1	0005-1 PCT.	0739	0015	2.03	0
R-01	ACT	LI2	0025-2 PCT.	0827	0031	3.75	0
R-01	ACT	LI3	0125-3 PCT.	0867	0042	4.84	0
R-01	ACT	LI4	0625-4 PCT.	0907	0030	3.72	0

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REPORT EXP11 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

CONTRACT ANPETRINST PROJECT 2525
EXPERIMENT 713202 DETECTOR TA1537 SPECIES SPRAGUE/RAT DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+6	MUTI EP+0	FREQ1 EP-6	CONTAM
	A+C		AMO 333 UG/ML	2546	0110	4.32	0
	A-C		SOLVENT	2730	0006	3.15	0
	ALI		TISSUE	1243	0100	8.05	0
	ACP	LI	AMO 333 UG/ML	1633	0672	41.15	0
R-01	ACT	LI1	0005-1 PCT.	2015	0144	7.15	0
R-01	ACT	LI2	0025-2 PCT.	1622	0138	8.51	0
R-01	ACT	LI3	0125-3 PCT.	1447	0130	8.98	0
R-01	ACT	LI4	0625-4 PCT.	1858	0110	5.92	0

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REPORT EA-33 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

CONTRACT ANPETRINST PROJECT 2525
EXPERIMENT 715201 DETECTOR TA1538 SPECIES SPRDAW/RAT DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+6	MUTI EP+0	FREQI EP-8	CONTAM
	A+C		ANTH 67 UG/ML	0703	0934	117.78	2
	A-C		SOLVENT	1486	0066	4.44	2
	ALI		TISSUE	1072	0068	6.34	2
	ACP	LI	ANTH 67 UG/ML	0697	2335	335.01	0
R-01	ACT	LI1	0005-1 PCT.	0646	0163	25.23	2
R-01	ACT	LI2	0025-2 PCT.	0630	0155	24.60	2
R-01	ACT	LI3	0125-3 PCT.	0590	0146	24.75	2
R-01	ACT	LI4	0A25-4 PCT.	1296	0120	9.26	2

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REPORT EXP33 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

EXPERIMENT 711399 CONTRACT ANPETRINST PROJECT 2525
DETECTOR TA98 SPECIES S.TYPHIMUR/RAT DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+6	MUTI EP+0	FREQ1 EP-8	CONTAM
	A+C		ANTH 67 UG/ML	1533	0164	10.70	0
	A-C		SOLVENT	1144	0150	13.81	0
	ALI		TISSUE	0624	0140	23.72	0
	ACP	LI	ANTH 67 UG/ML	0531	2834	533.71	0
R-01	ACT	LI1	0005-1 PCT.	0536	0483	90.11	0
R-01	ACT	LI2	0025-2 PCT.	0521	0465	89.25	0
R-01	ACT	LI3	0125-3 PCT.	0509	0401	68.08	0
R-01	ACT	LI4	0625-4 PCT.	0526	0458	87.07	0

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REPORT EXR33 LITTON BIONETICS MUTAGENIC ACTIVITY SYSTEM
COMPOUND SUMMARY BACKUP DETAIL

EXPERIMENT 719501 CONTRACT AMPETRINST DETECTOR 000004 PROJECT 2525 SPECIES SPRDAW/RAT DATE - 09/14/77

COMPOUND	TEST	ORG ID	CONCENTRATION	POPU EP+4	MUT1 EP+1	MUT2 EP+1	FREQ1 EP-5	FREQ2 EP-5	CONTAM
	4+C		DMN 90 UM/ML	0865	0112	0011	12.95	1.50	0
	4-C		SOLVENT	0840	0089	0011	10.60	1.31	0
	ALI		TISSUE	0802	0077	0008	9.60	1.00	0
	ACP	LI	DMN 90 UM/ML	1021	0564	0519	55.24	50.83	0
R-01	ACT	LI1	0066-2 PCT.	1175	0072	0022	6.13	1.87	0
R-01	ACT	LI2	0033-2 PCT.	1421	0080	0037	5.63	2.60	0
R-01	ACT	LI3	0165-3 PCT.	0874	0081	0018	9.27	2.06	0
R-01	ACT	LI4	0825-4 PCT.	0941	0046	0012	4.89	1.28	0

PART II

MOUSE LYMPHOMA ASSAY

EVALUATION SUMMARY

The test substance, R-01, produced increases in the mutant frequencies at the high concentrations in both the nonactivation and activation tests, the only significant evidence of mutagenicity in this test was the data from the nonactivation high concentration.

SPONSOR: American Petroleum Institute

MATERIAL: R-01

SUBJECT: FINAL REPORT L5178Y MOUSE LYMPHOMA MUTAGENICITY ASSAY

1. OBJECTIVE

The objective of this study was to evaluate R-01 for specific locus forward mutation induction in the L5178Y Thymidine Kinase (TK) mouse lymphoma cell assay.

2. MATERIALS

A. Test Compound

1. Date Received: February 18, 1977

2. Description: Dark liquid

B. Indicator Cells

The Fischer mouse lymphoma cell line used in this study was derived from L5178Y. The cells are heterozygous for a specific autosomal mutation at the TK locus and are bromodeoxyuridine (BUdR) sensitive. Scoring for mutation was based on selecting cells that have undergone forward mutation from a TK+/- to a TK-/- genotype by cloning them in soft agar with BUdR.

C. Media

The cells were maintained in Fischer's Medium for Leukemic Cells of Mice with 10% horse serum and sodium pyruvate. Cloning medium consisted of Fischer's medium with 20% horse serum, sodium pyruvate, and 0.37% agar. Selection medium was made from cloning medium by the addition of 5.0 mg of BUdR to 100 ml of cloning medium.

D. Control Compounds

1. Negative Control

The solvent in which the test compound was dissolved was used as a negative control and is designated as solvent control in the data table. The actual solvent is listed in the Results Section.

2. MATERIALS (Continued)

D. Control Compounds

2. Positive Controls

Ethylmethanesulfonate (EMS), which induces mutation by base-pair substitution, was dissolved in culture medium and used as a positive control for the nonactivation studies at a final concentration of 0.3 µl/ml.

Dimethylnitrosamine (DMN), which requires metabolic biotransformation by microsomal enzymes, was used as a positive control substance for the activation studies at a final concentration of 0.5 µl/ml.

3. EXPERIMENTAL DESIGN

A. Toxicity

The solubility, toxicity, and doses for all chemicals were determined prior to screening. The effect of each chemical on the survival of the indicator cells was determined by exposing the cells to a wide range of chemical concentrations in complete growth medium. Toxicity was measured as loss in growth potential of the cells induced by a five-hour exposure to the chemical followed by a 24-hour expression period in growth medium. A minimum of four doses was selected from the range of concentration by using the highest dose that showed no loss in growth potential as the penultimate dose and by bracketing this with one higher dose and at least two lower doses. Toxicity produced by chemical treatment was monitored during the experiment.

B. Assays

1. Nonactivation Assay

The procedure used is a modification of that reported by Clive and Spector (Mutation Research, 31:17-29, 1975). Prior to each treatment, cells were cleansed of spontaneous TK-/- by growing them in a medium containing thymidine, hypoxanthine, methotrexate, and glycine (THMG). This medium permits the survival of only those cells that produce the enzyme thymidine kinase, and can therefore utilize the exogenous thymidine from the medium. The test compound was added to the cleansed cells in growth medium at the predetermined doses for five hours. The mutagenized cells were washed, fed, and allowed to express in growth medium for three days. At the end of this expression period, TK-/- mutants were detected by cloning the cells in the selection medium for ten days. Surviving cell populations were determined by plating diluted aliquots in nonselective growth medium.

3. EXPERIMENTAL DESIGN (Continued)

B. Assays

2. Activation Assay

The activation assay differs from the nonactivation assay in the following manner only. Two milliliters of the reaction mixture were added to 10 ml of growth medium. The desired number of cleansed cells was added to this mixture, and the flask was incubated on a rotary shaker for five hours. The incubation period was terminated by washing the cells twice with growth medium. The washed mutagenized cells were then allowed to express for three days and were cloned as indicated for the nonactivated cells.

C. Preparation of 9,000 x g Supernatant

Male random bred mice were killed by cranial blow, decapitated, and bled. The liver was immediately dissected from the animal using aseptic technique and placed in ice-cold 0.25M sucrose buffered with Tris buffer at a pH of 7.4. When an adequate number of livers had been collected, they were washed twice with fresh buffered sucrose and completely homogenized. The homogenate was centrifuged for 20 minutes at 9,000 x g in a refrigerated centrifuge. The supernatant from this centrifuged sample was retained and frozen at -80C until used in the activation system. This microsome preparation was added to a "core" reaction mixture to form the activation system described below:

Component	Final Concentration/ml
1. TPN (sodium salt)	6 µmoles
2. Isocitric acid	35 µmoles
3. Tris buffer, pH 7.4	28 µmoles
4. $MgCl_2$	2 µmoles
5. Homogenate fraction equivalent to 25 mg of wet tissue	

D. Screening

A mutation index was derived by dividing the number of clones formed in the BUdR-containing selection medium by the number found in the same medium without BUdR. The ratio was then compared to that obtained from other dose levels and from positive and negative controls. Colonies were counted on an electronic colony counter that resolves all colonies greater than 200 microns in diameter.

4. RESULTS

The data presented in the following table show the concentrations of the test compound employed, the number of mutant clones obtained, the surviving populations after the expression period, and the calculated mutation frequencies.

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A. NAME OR CODE DESIGNATION OF THE TEST COMPOUND: B-01

B. SOLVENT: DMSO
C. TEST DATE: APRIL 12, 1977
NOTE: CONCENTRATIONS ARE GIVEN IN MICROLITERS (UL) OR MICROGRAMS (UG) OR NANOLITERS (NL) PER MILLILITER.

TEST	S-9 TISSUE	S-9 SOURCE	DAILY COUNTS (CELLS/PLATE X 10E5) 1	2	3	RELATIVE SUSPENSION GROWTH (% OF CONTROL)	MUTANT COLONIES	VIABLE COLONIES	RELATIVE CLONING EFFICIENCY (% OF CONTROL)	PERCENT RELATIVE GROWTH*	MUTANT FREQUENCY** IN 10E-5
NONACTIVATION											
SOLVENT CONTROL	---	---	16.8	12.0	10.0	100.0	59.0	310.0	100.0	100.0	0.1903
NEGATIVE CONTROL	---	---	18.6	11.5	12.3	130.5	67.0	205.0	66.1	86.3	0.3268
EMS .03 UL/ML	---	---	5.4	14.4	10.8	41.7	113.0	114.0	36.8	15.3	0.9912
TEST COMPOUND											
0.02000 UL/ML	---	---	17.4	9.0	17.0	132.1	124.0	208.0	67.1	88.6	0.5962
0.04000 UL/ML	---	---	8.6	15.6	15.2	103.5	65.0	523.0	168.7	174.6	0.1243
0.08000 UL/ML	---	---	17.0	8.8	13.8	102.4	95.0	204.0	65.8	67.4	0.4657
0.16000 UL/ML	---	---	7.0	13.2	12.6	57.7	60.0	252.0	81.3	46.9	0.2381
0.32000 UL/ML	---	---	3.2	5.0	7.0	5.6	233.0	168.0	54.2	3.0	1.3869
ACTIVATION											
SOLVENT CONTROL	MOUSE	LIVER	17.6	9.4	14.0	100.0	91.0	327.0	100.0	100.0	0.2783
DMN .5 UL/ML	MOUSE	LIVER	9.3	6.3	6.5	16.4	102.0	25.0	7.6	1.3	4.0800
TEST COMPOUND											
0.02000 UL/ML	MOUSE	LIVER	17.0	11.6	12.0	109.0	85.0	265.0	81.0	88.3	0.3208
0.04000 UL/ML	MOUSE	LIVER	11.8	12.4	13.0	82.1	57.0	414.0	126.6	104.0	0.1377
0.08000 UL/ML	MOUSE	LIVER	11.2	16.6	9.6	77.1	143.0	266.0	81.3	62.7	0.5376
0.16000 UL/ML	MOUSE	LIVER	13.4	7.2	13.0	54.2	62.0	454.0	138.8	75.2	0.1366
0.32000 UL/ML	MOUSE	LIVER	5.6	13.2	11.6	37.0	102.0	212.0	64.8	24.0	0.4811

* (RELATIVE SUSPENSION GROWTH X RELATIVE CLONING EFFICIENCY) / 100
** (MUTANT CLONES / VIABLE CLONES) X 10E-4

6. CRITERIA USED IN THE EVALUATION

Several criteria have been established which, if met, provide a basis for declaring a material genetically active in the Mouse Lymphoma Assay. These criteria are derived from a historical data base and are helpful in maintaining uniformity in evaluations from material to material and run to run. While these criteria are reasonably objective, a certain amount of flexibility may be required in making the final evaluation since absolute criteria may not be applicable to all biological data.

A compound is considered mutagenic in the Mouse Lymphoma Assay if:

a. A dose response relationship is observed over three of the four dose levels employed.

b. The minimum increase at the high level of the dose response curve is at least 2.5 times greater than the solvent control value.

c. The solvent control data are within the normal range of the spontaneous background for the TK locus.

All evaluations of mutagenic activity are based on the concurrent solvent control value run with the experiment in question. Positive control values are not used as reference points, but are included to ensure the current cell population responds to direct and promutagens under the appropriate treatment conditions.

Occasionally, a single point within a concentration range will show an increase 2.5 times greater than the spontaneous background. If the increase is at the high dose, is reproducible, and if an additional higher dose level is not feasible because of toxicity, the chemical can be considered mutagenic. If the increase is internal within the dose range and is not reproducible, the increase will normally be considered aberrant. If the internal increase is reproducible, several doses clustered around the positive concentration will be examined to either confirm or reject the reliability of the effect.

As the data base on the assay increases, the evaluation criteria can be expected to become more firmly established.

PART III

RAT BONE MARROW CYTOGENETIC ANALYSIS

EVALUATION SUMMARY

The test material, R-10, did not produce significant clastogenic activity in rat bone marrow cells. The rats were exposed by acute and subchronic administration of the test material.

BIONETICS

SPONSOR. American Petroleum Institute

MATERIAL: R-01

SUBJECT: FINAL REPORT
Rat Bone Marrow Cytogenetic Analysis

1. OBJECTIVE

The purpose of this study was to evaluate the chromosomes of bone marrow cells from R-01 treated rats for genetic aberrations.

2. MATERIALS

A. Test Compound

1. Date Received: February 18, 1977

2. Description: Dark liquid

3. OVERVIEW AND RATIONALE

One means of detecting chemically-induced in vivo genetic activity is to examine mitotically active cells that have been arrested at metaphase for structural changes and rearrangements of their chromosomes. The occurrence of such chromosome aberrations correlates well with the administration of known chemical mutagens to the animals, and thus can serve as an indicator for possible mutational events and the compounds that induce them. Rats were treated with one of three dosage levels of the test compound or a positive or negative control substance both on an acute and a subchronic schedule. Acute study rats were killed 6, 24, and 48 hours after treatment, and bone marrow spreads prepared. Subchronic study rats were killed six hours after the last dose was administered and the bone marrow removed and processed like the acute dose.

4. EXPERIMENTAL DESIGN

A. Animal Husbandry

Male rats, ages 10 to 12 weeks old, from a random bred closed colony were purchased from Charles River Laboratories and used in the cytogenetic experiments. These rats were housed five to a cage and offered a commercial laboratory chow (pellet) diet (Purina) and water ad libitum. These animals were quarantined and observed for 10 days prior to being used in the experiments.

Personnel handling the animals or working within the animal facility wear suitable protective clothing, gloves, and face masks. When appropriate, individuals with respiratory or other overt infections were excluded from the animal facilities.

B. Acute Studies

Figure 1 shows the design of the test. Fourty-five animals were dosed acutely with the three levels of the compound. The remaining 14 animals were used as controls.

Two hours prior to being killed, the animals were injected with 4 mg/kg of colchicine to arrest dividing cells in metaphase. These animals were killed with CO_2 6, 24, and 48 hours after the compound was administered and the bone marrow aspirated from the canals of the femurs and tibias of the lower limbs. The marrow plug was transferred to Hank's balanced salt solution and the cells pelleted by centrifugation. The marrow button was resuspended in 0.075 M KCl by repeated pipetting during a 10-minute incubation at 37C. Centrifugation was repeated and the marrow button resuspended in Carnoy's fixative. Fixative was changed after one-half hour, and the cells were left in fixative overnight at 4C.

Slides were prepared by dropping cells from the fixative onto a glass slide and air drying the slide. Spreads were stained with 5% Giemsa at pH 6.8.

Slides were coded and searched for metaphases according to a standardized pattern. Fifty spreads were located for each animal and when of suitable quality, the chromosomes were counted and evaluated for the presence of abnormalities.

FIGURE 1

RAT BONE MARROW CYTOGENETIC ANALYSIS

NUMBER OF ANIMALS USED

LITTON BIONETICS

ACUTE STUDY

TREATMENT	NUMBER OF ANIMALS KILLED 6, 24, AND 48 HOURS AFTER DOSING		
	6 Hours	24 Hours	48 Hours
High Level	5	5	5
Intermediate Level	5	5	5
Usage Level	5	5	5
Positive Controls	-	5	-
Negative Controls	5	5	5

SUBCHRONIC STUDIES

5 EXPOSURES - 24 HOURS APART

ANIMALS KILLED 6 HOURS AFTER LAST EXPOSURE

TREATMENT	NUMBER OF ANIMALS KILLED AT TERMINATION
High Level	5
Intermediate Level	5
Usage Level	5
*Positive Controls	5
Negative Controls	5

* Positive controls will not be utilized in subchronic studies if acute studies are conducted since the positive controls are administered on an acute one-time dosage basis only. TEM (0.3 mg/kg) is used as a positive control substance.

4. EXPERIMENTAL DESIGN (Continued)

C. Subchronic Studies

Figure 1 also shows the overall scheme of the subchronic studies. Eighteen animals were used in this study. They were dosed with the three levels of the test compound and the control compounds as indicated, once each day for five days. All animals were killed six hours after administration of the last dose. Two hours prior to being killed, the animals were injected with 4 mg/kg of colchicine to arrest dividing cells in metaphase.

The bone marrow was removed from the animals and processed exactly as indicated for the acute study.

D. Control Compounds

The negative control compound consisted of the solvent vehicle for the test compound. It was administered to the animals in doses which were equivalent to the maximum amount given the experimental animals.

Triethylene melamine (TEM) at 0.3 mg/kg was used as the positive control substance. It was given in an acute dosage for 24 hours prior to killing the animals.

E. Dosage Levels

Based on a preliminary dose range study, a series of doses were selected. The material was administered by oral gavage at 0.5 ml/kg, 1.7 ml/kg, and 5.0 ml/kg. Corn oil alone was administered to the negative control animals at 5.0 ml/kg. No significant toxicity was observed except at the high dose level of the subchronic administration.

5. DATA COLLECTION

The test compound was evaluated in the rat bone marrow cytogenetic assay under both acute and subchronic schedules. Bone marrow cells from animals treated with the test and control substances were evaluated for the presence of chromosome aberrations. Breaks, gaps, fragments, and chromosome rearrangement figures were all recorded on the standard record sheet along with the number of centromeres scored in each spread and the coordinates of the microscope stage which identify the position of the aberration. These records are attached in the Appendix. Fifty cells were located and scored with a 100X objective for each dose level. In the event that 50 suitable spreads could not be found on one slide then additional slides labeled B, C, D, etc. were prepared from the original fixed marrow material and these were searched. In some cases, the material dosed to the animals appeared sufficiently toxic to the cells to prevent scoring 250 cells per animal and in other cases the colchicine appeared to be ineffective in arresting the cells. These slides/animals are identified in the slide code/animals list and on the raw data sheets appended.

6. RESULTS

The data have been collected from the raw data sheets and tabulated in summary form in Table 1.

TABLE 1

A SUMMARY OF THE CYTOGENETIC ANALYSIS OF R-01 IN RAT BONE MARROW

Treatment	Dose (mg/kg)	Kill Time (hrs)[a]	No. of Animals	Unique Animal No.[b]	Total No. of Cells	Type and Frequency of Aberrations Structural	Numerical	No. of Cells With One or More Aberrations	No. of Animals Without Aberrations	Mitotic[c] Index
Negative Control	Corn Oil	A 6 hr	5(0)	16-20	250	1tb,1sb	-	2 (0.8%)	4	4.5
		A 24 hr	5(0)	36-40	212	1tb	4pp	5 (2.4%)	2	5.0
		A 48 hr	4(1)	61-65	134	1f,1tb	1pp	3 (1.9%)	2	6.2
		SC 6 hr	5(0)	81-85	223	-	-	0 (0.0%)	5	5.0
Triethyl Melamine	0.5 mg/kg	A 24 hr	5(0)	41-45	182	15tb,1sb, 11f,9af,4t, 5r,2qr,2pv, 4td,1dicentric	-	54 (29.7%)	1	1.5
R-01	0.5 ml/kg	A 6 hr	4(1)	11-15	155	2f	-	2 (1.3%)	3	2.7
		A 24 hr	4(1)	31-35	200	-	-	0 (0.0%)	4	6.3
		A 48 hr	5(0)	56-60	183	1tb	1pp	2 (1.1%)	4	5.0
		SC 6 hr	5(0)	76-80	250	2tb	-	3 (1.2%)	3	5.4
R-01	1.7 ml/kg	A 6 hr	5(0)	6-10	250	1f,1tb	-	2 (0.8%)	3	6.5
		A 24 hr	5(0)	26-30	250	-	-	0 (0.0%)	5	7.5
		A 48 hr	5(0)	51-55	250	2tb	-	2 (0.8%)	3	8.4
		SC 6 hr	5(0)	71-75	250	1af	-	1 (0.4%)	4	4.2
R-01	5.0 ml/kg	A 6 hr	4(1)	1-5	157	4f,1af	-	5 (3.2%)	1	4.6
		A 24 hr	4(1)	21-25	200	1tb,1f	1pp	3 (1.5%)	2	7.2
		A 48 hr	5(0)	46-50	250	1tb	1pp	2 (0.8%)	3	7.8
		SC 6 hr	2(3)	66-70	75	1f,1td	-	2 (2.6%)	0	2.9

FOOTNOTES AND SYMBOLS FOR TABLE I

[a]Time of death after dosing.

[b]Refers to the 1, 2, or 3 digits following the hyphen in the Cytogenetics Exp. No. on the raw data sheets in the Appendix

[c]Based on a count of at least 500 cells per animal.

[d]Numbers in ( ) are animals for which less than 5 metaphase spreads were found.

Any of the following abbreviations may be used in the summary tables:

f = fragments
af = acentric fragment (2 tid)
lm = large metacentric
pp = polyploid
tb = chromatid break
sb = chromosome break
d = dicentric
r = ring
t = translocation
qr = quadriradial
pu = pulverized chromosome
cr = complex rearrangement
> = greater than 10 aberrations
tr = triradial
td = chromatid deletion
sd = chromosome deletion
cf = centric fusion
sl = slide lost or broken
min= minute chromosome

SC = subchronic
A = acute

TABLE 2

RAT-[illegible]
CYTOGENETIC
HISTORIC NEGATIVE CONTROL DATA[a]

TYPE OF ABBERATION	ACUTE 6 HR. KILL No.	%	24 HR. KILL No.	%	48 HR. KILL No.	%	SUBACUTE 6 HR. KILL No.	%
Chromatid Gaps	53	0.92	13	0.22	33	0.50	53	0.82
Chromatid Breaks	31	0.54	45	0.75	47	0.75	61	0.95
Chromosome Gaps	4	0.07	3	0.05	3	0.05	5	0.08
Chromosome Breaks	0	0.0	1	0.02	4	0.06	2	0.03
Fragments	4	0.07	1	0.02	2	0.03	4	0.06
Acentric Fragments	1	0.02	4	0.07	1	0.02	0	0.00
Other Aberrations	1	0.02	6	0.10	1	0.02	4	0.06
Percent Cells With Aberrations	94	1.62	73	1.21	91	1.46	129	2.00
	37	0.64	57	0.95	55	0.88	71	1.10
Total Cells Scored	5785		6010		6227		6436	
Approximate Number of Animals Scored	122		122		130		131	

[a]Compiled from several studies using Sprague-Dawley Rats with various solvents. No significant difference was noted among solvents and the data were pooled. These data were collected over the period 1972 - 1977.

[b]Gaps included.

[c]Gaps excluded. This is the value normally employed in evaluation decisions. Gaps are not considered as hard evidence of clastogenic effects unless found in extremely high percentages.

8. GUIDELINES USED IN EVALUATING CYTOGENETIC DATA

A number of general guidelines has been established to serve as an aid in determining the meaning of bone marrow chromosomal aberrations.

A. General

Basically, we were trying to establish whether a substance or its metabolites can interact with chromosomes to produce gross lesions or changes in chromosome numbers, and whether these were of a type which can survive more than one mitotic cycle of the cell. The assay design was such that bone marrow samples were taken at 6, 24, and 48 hours after an acute administration of the compound. Since the cell transit time for bone marrow was 20 to 24 hours, one can, based on the time of kill obtain an indication of when in the cell cycle a compound may be active.

One would anticipate that many of the cells bearing breaks or reunion figures would be eliminated during their first mitotic division, and as a corollary, that those cells which survived the first anaphase would primarily bear balanced lesions. The detection of these lesions; and hence, a complete risk evaluation must usually rely on additional testing, but in general a cell bearing configurations such as small deletions or translocations not involving duplication of the centromere may be perpetuated and, therefore, constitute a greater risk to the individual than simple breaks.

B. Aberrations/Records

All aberration figures detected by this assay result from breaks in the chromatin which have either failed to repair or have repaired in atypical combinations. We scored and recorded on standard forms gaps, breaks, fragments, and reunion figures which involved a single chromatid or both chromatids of a single chromosome. The number and type of aberration for each cell was recorded as was the number of chromosomes for every cell located and scored. Up to 50 cells were scored on each slide. Depending upon the suitability of the material, it could have been necessary to prepare additional slides from the original fixed material. The location of cells bearing aberrations was identified by the use of coordinates on the mechanical stage. A mitotic index based on at least 500 cells counted was also recorded.

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C. Data Interpretation

Data were summarized in tabular form and evaluated. Gaps were not counted as significant aberrations unless they were presnt in a higher than usual frequency. Open breaks were considered as indicators of genetic damage as were configurations resulting from the repair of breaks. The latter would include deletions, translocations, multiradials, rings, multicentrics, etc. Reunion figures such as these were weighted slightly higher than one break and may lead to stable configurations.

The number of aberrations per cell was also considered to be significant and frequent; cells with more than one aberration would be considered to indicate more genetic damage than those containing evidence of single events. Consistent variations from the euploid number was also considered in the evaluation of mutagenic potential.

Frequently, one was unable to locate 50 suitable metaphase spreads for each animal even after preparing additional material. Possible causes for this appear to relate to colchicine failure or to cytotoxic effects which altered the duration of the cell cycle, killed the cell or caused clumping of the chromosomes. Additional information can be gained from the mitotic index which also appeared to reflect cytotoxic effects. The type and extent of this damage must be evaluated in terms of dose response, the ability to determine anything about the integrity of the chromatin and the ability of the cell to recover and divide.

Comparison with a concurrent negative control which lacks aberrations can suggest statistical significance; therefore, treatment data were also considered against historical control data. In either event, the type of aberration, its frequency, and its correlation to dose trends within a given time period, were all considered in evaluating a compound as being mutagenically positive or negative.

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APPENDIX

CYTOGENETICS [illegible]

Cytogenetics Exp. No. 5167, 1-A Date: [illegible]
Scope No. 8947 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	• Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
A 1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
B 7			42						
8									
9									
10									
11									
12									
13									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
31									
32									
33									
34									
35									
36									
37									
38									
39									
40									
41									
42									
43									
44									
45									
46									
47									
48									
49									
50									
Mitotic Index: 0%			TOTALS:						

BIONETICS
Litton

$A = \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} = \frac{0}{500} = \frac{0}{1000}$ $B = \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} = \frac{0}{500} = \frac{0}{100}$

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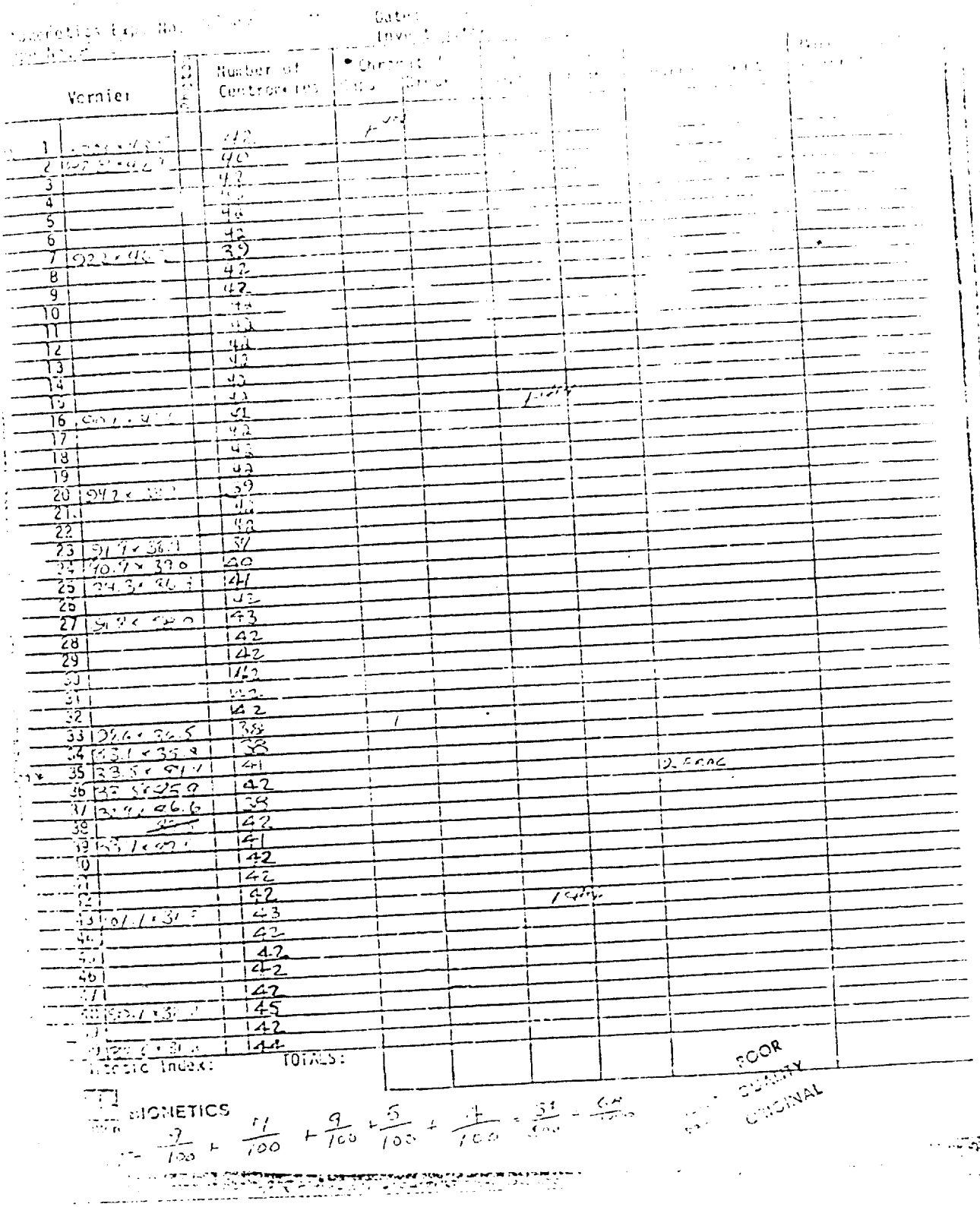

Cri[illegible]

[illegible]netics Exp. No. [illegible] Date: [illegible]
[illegible] Inve[illegible]

	Vernier	[illegible]	Number of Centromeres	Chromat[illegible] Gaps	Chromat[illegible] Breaks	[illegible]	[illegible]	[illegible]	[illegible]
1	[illegible]		42	[illegible]					
2	[illegible]		40						
3			42						
4			[illegible]						
5			42						
6			42						
7	92.2 × 46.[illegible]		39						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42			[illegible]			
16	[illegible]		41						
17			42						
18			42						
19			42						
20	94.2 × [illegible]		39						
21			42						
22			42						
23	91.9 × 36.[illegible]		37						
24	90.9 × 39.0		40						
25	94.3 × 36.[illegible]		41						
26			42						
27	91.9 × [illegible]		43						
28			42						
29			42						
30			42						
31			42						
32			42						
33	92.6 × 36.5		38						
34	83.1 × 35.8		38						
35	83.5 × 91.[illegible]		41					2 FRAG	
36	83.5 × 95.9		42						
37	32.9 × 46.6		38						
38	~~[illegible]~~		42						
39	83.1 × [illegible]		41						
40			42						
41			42						
42			42			[illegible]			
43	101.1 × 31.[illegible]		43						
44			42						
45			42						
46			42						
47			42						
48	90.1 × 3[illegible]		45						
49			42						
50	[illegible] × 31.[illegible]		44						
	[illegible]tatic Index:		TOTALS:						

POOR QUALITY ORIGINAL

BIONETICS

$$= \frac{7}{100} + \frac{11}{100} + \frac{9}{100} + \frac{5}{100} + \frac{4}{100} = \frac{34}{100} = \frac{68}{100}$$

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Stamp Series No. 51c 7 3 A

	Vernier		Number of Centromeres	•Chromatid Gaps	Breaks				
1			42						
2			42						
3			42						
4	150.5, 49		42						
5			42						
6			42						
7			42						
8			42						
9	145.9, 46.3		42	1				IRC	
10	146.5, 45.3		42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21	147.4, 39.5		38						
22	147.1, 34.7		41						
23			42						
24	147, 40.3		41						
25	132.9, 37.5		39						
26			42						
27			42						
28			42						
29			42						
30	144.9, 37.7		41						
31			42						
32	148.1, 35.3		41						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40	139.2, 35.9		41						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
	Mitotic Index: 6.8%		TOTALS:	1					

BIONETICS

$$A = \frac{7}{100} + \frac{8}{100} + \frac{8}{100} + \frac{4}{100} + \frac{7}{100} = \frac{34}{500} = \frac{68}{1000}$$

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CYTOGENETIC [illegible]

Biogenetics Exp. No. [illegible]
Type No. = 3

Date:
Investigator:

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	[illegible]	[illegible]	[illegible]	[illegible]
1	96.1 x 46.9		41						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9	94.1 x 37.7		42	1 [illegible]					
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24	101.8 x 37.4		37						
25	102.9 x 34.6		40						
26			42						
27			42						
28	34.5 x [illegible]		42	1 [illegible]				[illegible]	
29			42						
30	95.1 x 37.4		41						
31			42						
32			42						
33			42						
34			42						
35	33.5 x 40.8		43						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47	92.0 x [illegible]		38						
48			42						
49	31.6 x 93.3		41						
50			42						
			TOTALS:						

Mitotic Index: 4.6%

BIONETICS

$$\frac{4}{100} + \frac{4}{100} + \frac{7}{100} + \frac{2}{100} + \frac{6}{100} = \frac{23}{300} \quad \frac{40}{1000}$$

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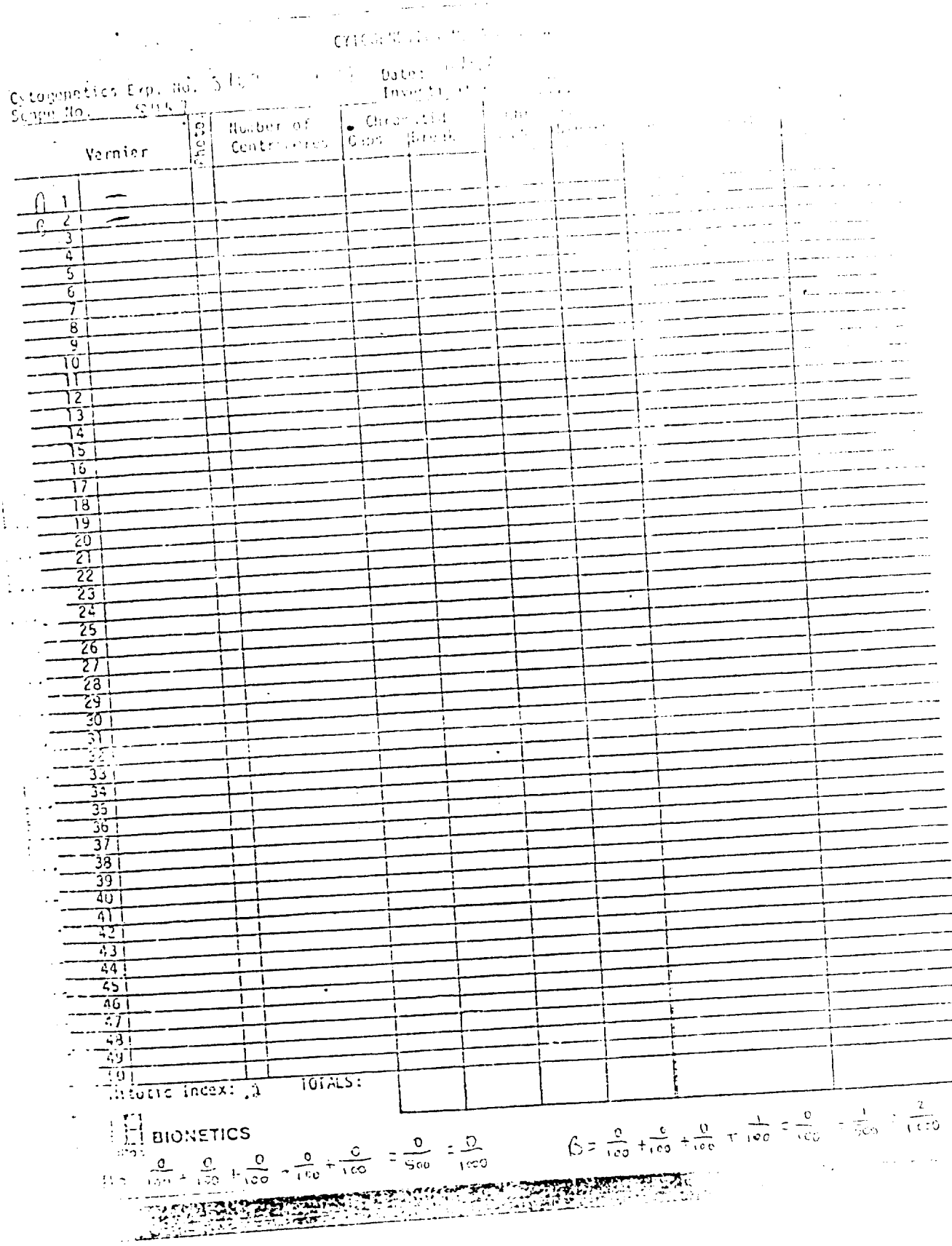

CYTOGENETICS [illegible]

Cytogenetics Exp. No. [illegible] Date: [illegible]

Scope No. [illegible] Investigator [illegible]

	Vernier	Photo	Number of Centrifuges	Chromatid Gaps	Chromatid Break	[illegible]	[illegible]	[illegible]	[illegible]
A 1	—								
B 2	—								
3									
4									
5									
6									
7									
8									
9									
10									
11									
12									
13									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
31									
32									
33									
34									
35									
36									
37									
38									
39									
40									
41									
42									
43									
44									
45									
46									
47									
48									
49									
50									
Mitotic Index:			TOTALS:						

BIONETICS

$\beta = \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} = \frac{0}{500} = \frac{0}{1000}$

$\beta = \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{1}{100} = \frac{0}{100} = \frac{1}{500} = \frac{2}{1000}$

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CYTOGENETICS METAPHASE WORKSHEET

Cytogenetics Exp. No. [illegible] Date: [illegible]
No. 8412 Investigators: [illegible]

	Vernier	Photo	Number of Centromeres	• Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 1 Abnormality
A 1			42						
2			42						
3			42						
4			42						
5			42					[illegible]	
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12	42.7, 41.3		40						
13	42.6, 25.3		36						
14			42						
15			42						
16			42						
17	44.7, 39.3		42						
18			42						
19	43.4, 26.5		41						
			42						
B 21	44.1, 33.0		38						
22			42						
23			42						
24	45.7, 24.3		39						
25			45						
26			42						
27			42						
28			42						
29			42						
30	[illegible]		22					[illegible]	
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			43						
[illegible]			42						
[illegible]			42						
[illegible]			41						
[illegible]			42						
Mitotic Index:	15		TOTALS:						

BIONETICS

A: $\frac{1}{100} + \frac{0}{100} + \frac{1}{100} + \frac{0}{100} + \frac{1}{100} = \frac{3}{500} =$ [illegible]

B: $\frac{2}{100} + \frac{3}{100} + \frac{1}{100} + \frac{4}{100} + \frac{2}{100} = \frac{12}{500} =$ [illegible]

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CYTOGENETICS [illegible]

Cytogenetics Exp. No. 5167-74 Date: 31 Oct [illegible]
Scope No. 7-3 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2	93.2 × 44.0		38						
3			42						
4			42						
5			42						
6			42						
7			42						
8	83.1 × 42.5		40						
9			42						
10			42						
11	86.7 × 38.7		40						
12	86.9 × 38.6		41						
13	87.2 × 38.7		38						
14	93.3 × 38.2		36						
15	90.7 × [illegible]		41						
16			42						
17			42						
18	[illegible] × 35.2		43						
19			42						
20			42						
21			42						
22	96.2 × 30.9		36						
23	93.9 × 30.3		41						
24	[illegible]		42						
25	99.5 × 24.4		40						
26	90.7 × 24.3		41						
27			42						
28			42						
29	[illegible]		39						
30			42						
31			42						
32	22.2 × 84.3		42						
33			42						
34	22.4 × 81.1		40						
35	20.3 × 80.0		41						
36	20.0 × 80.5		41						
37			42						
38			42						
39			42						
40	85.0 × 18.3		43						
41			42						
42			42						
43	18.4 × 87.7		40						
44	18.7 × 87.6		41						
45	18.9 × 72.0		41						
46			42						
47	84.4 × 14.9		41						
48			42						
49			42						
50			42						
Mitotic Index: 7.4			TOTALS:						

BIONETICS

$$A = \frac{7}{100} + \frac{7}{100} + \frac{8}{100} + \frac{6}{100} + \frac{9}{100} = \frac{37}{500} = \frac{74}{1000}$$

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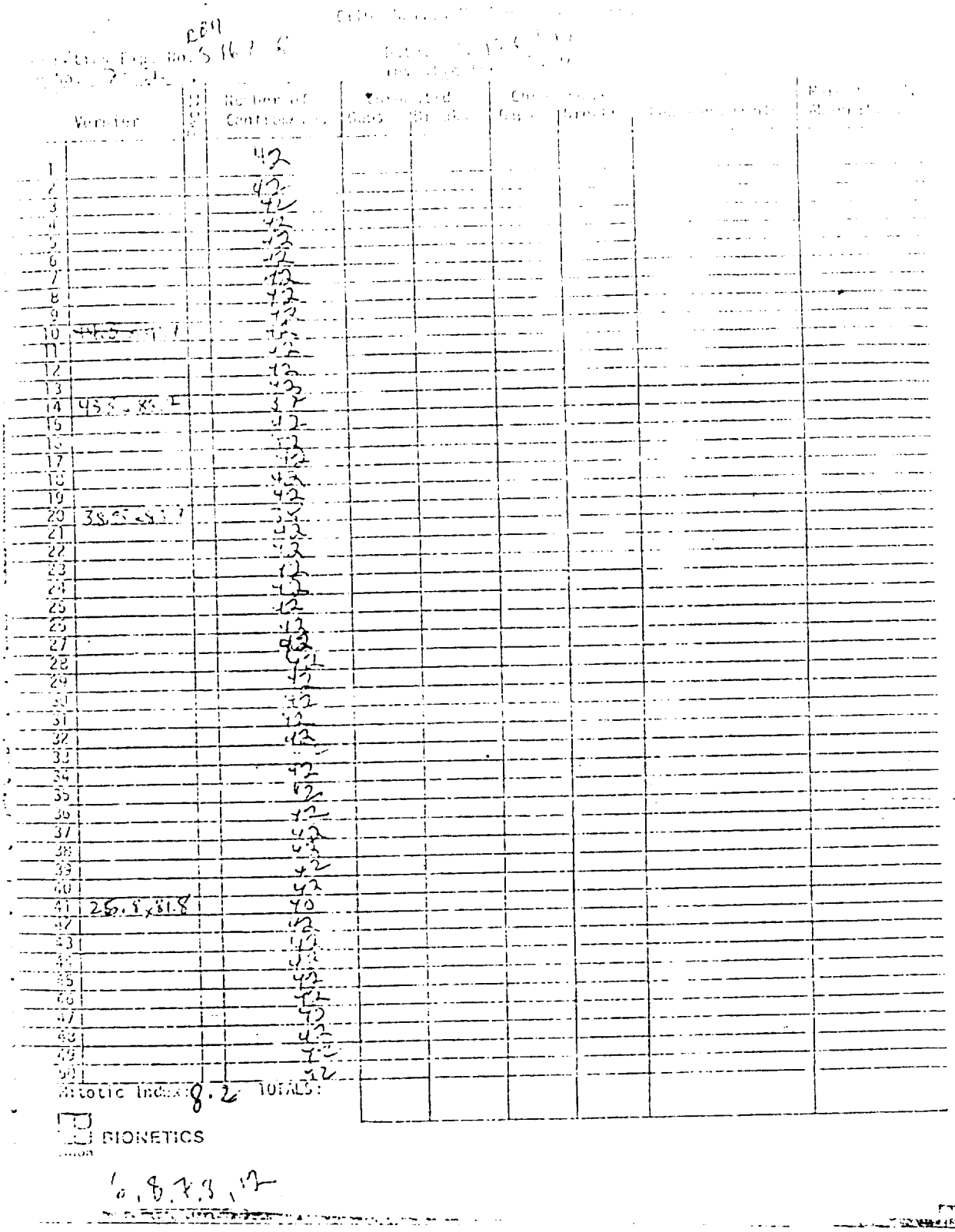

Cells [illegible]

[illegible] Exp. No. 5167 [illegible]

[illegible]

	Vernier	[illegible]	Number of Contractions	Corrected Gaps	Corrected Breaks	Corrected Gaps	Corrected Breaks	[illegible]	[illegible]
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10	~~[illegible]~~		42						
11			42						
12			42						
13			42						
14	43.5 x 85.2		37						
15			42						
16			42						
17			42						
18			42						
19			42						
20	38.5 x 83.7		38						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41	25.8 x 81.8		40						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						

Mitotic Index: 8.2 TOTALS:

BIONETICS

6, 8, 7, 3, 12

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[illegible]

[illegible]etics Exp. No. 5167-9 RBM

No. 2-1

Date: 5/[illegible]/[illegible]

Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromatid Gaps	Chromatid Breaks	[illegible]	[illegible]
1			42						
2	44.5×80.4		38						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18	45.8×91.5		41						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34	44.3×96.5		41						
35			42						
36	44.6×97.0		41						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46	43.2×86.2		36						
47			42						
48			42						
49			42						
50			42						

Mitotic Index: 5 TOTALS:

BIONETICS

7+4+4+3+7 = 25/500

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CYTOGEN[illegible]

...netics Exp. No. 5167 10 A Date: [illegible]
No. 5792 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chrom. Gaps	Chrom. Breaks	Rearrangements	Normal or Abnormal
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14	146.4, 41.7		43						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29	130.2, 39.0		42	1					
30			42						
31			42						
32	134.9, 40.1		38						
33			42						
34			42						
35	137.1, 39.3		41						
36			42						
37			42						
38	145.12, 40.5		41						
39	148.2, 38.1		42		1				
40	142.4, 38.2		40						
41			42						
42	140.1, 37.5		42	1		1			
43			42						
44			42						
45			42						
46	139, 31.9		41						
47			42						
48			42						
49			42						
50			42						

Mitotic Index: 10.6% TOTALS: 2 1 1

GENETICS

$$\frac{12}{100} + \frac{7}{100} + \frac{13}{100} + \frac{11}{100} + \frac{10}{100} = \frac{53}{500} = \frac{106}{1000}$$

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CYTOGENETICS LABORATORY

Cytogenetics Exp. No. 5161, 11-A Date: 10/6/11

Type No. 8947 Investig. Init: C.P.S.

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	Miscellaneous Abnormalities
A 1	—								
B 2	44.4, 82.0		38						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23	40.0, 91.1		36 37 [2]						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33	35.3, 90.7		42	1					
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42	21.0, 81.8		42					REARRANGEMENT C#5	
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50	8.5, 90.0		40						
Mitotic Index: .9			TOTALS:						

BIONETICS

$= \frac{0}{100} + \frac{1}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} = \frac{1}{500}$

$R = \frac{3}{100} + \frac{0}{100} + \frac{2}{100} + \frac{3}{100} + \frac{0}{100} = \frac{8}{500}$

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CYTOGENETICS METAPHASE NUMBERS

Cytogenetics Exp. No. 5167 12 A Date: [illegible]
Type No. 2-3 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
A B1									
2									
3									
4									
5									
6									
7									
8									
9									
10									
11									
12									
13									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
31									
32									
33									
34									
35									
36									
37									
38									
39									
40									
41									
42									
43									
44									
45									
46									
47									
48									
49									
50									
Mitotic Index: 0.5			TOTALS:						

BIONETICS $= \frac{5}{1000}$

$A = \frac{2}{100} + \frac{0}{100} + \frac{0}{100} + \frac{1}{100} + \frac{0}{100}$ // $B = \frac{0}{100} + \frac{0}{100} + \frac{1}{100} + \frac{0}{100} + \frac{1}{100}$

BEST COPY AVAILABL

	Vernier		Number of Centrosomes
1			42
2			42
3			42
4			42
5			42
6			42
7			42
8			42
9			42
10			42
11			42
12			42
13			42
14			42
15			42
16			42
17			42
18			42
19			42
20	40.8 × 84.6		32
21			42
22			42
23			42
24			42
25			42
26			42
27			42
28			42
29			42
30			42
31			42
32	41.5 × 91.2		40
33	40.9 × 91.6		39
34			42
35			42
36			42
37	40.7 × 95.4		34
38			42
39			42
40			42
41			42
42			42
43			42
44			42
45			42
46			42
47			42
48			42
49			42
50			42

Mitotic Index: 3.8 TOTALS:

DIONETICS

1 + 3 + 7 + 6 + 1 = 19/500 38/1000

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CYTOGENETICS METAPHASE WORKSHEET

Genetics Exp. No. 54, 2 Date: 1/8/
Investigator: [illegible]

	Vernier	Number of Centromeres	• Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Other Comments	Mitotic Index
1	[illegible]	42						
2		42						
3		42						
4		42						
5		42						
6	[illegible]	42						
7		42						
8		42						
9		42						
10		42						
11		42						
12		42						
13	[illegible]	42						
14		42						
15		42						
16		42						
17		42						
18		42						
19		42					2 TDG	
20	[illegible]	42						
21	[illegible]	41	I					
22		43						
23		42						
24		42						
25		42						
26		42						
27		42						
28		42						
29		42						
30		42						
31		42						
32	[illegible]	42						
33		42						
34		42						
35		42						
36		42						
37		42						
38		42						
39	[illegible]	41						
40		42						
41		42						
42		42						
43		42						
44		42						
45		42						
46		42						
47	[illegible]	41						
48		42						
49		42						
50		42						
	TOTALS:							

Mitotic Index: 5.8%

DIONETICS

$= \frac{2}{100} + \frac{6}{100} + \frac{3}{100} + \frac{4}{100} + \frac{9}{100} = \frac{23}{500} = \frac{5^2}{1000}$

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...genetics Exp. No. 5[illegible] Date: [illegible]
...e No. [illegible] Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	• Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangement	More than [illegible]
1			42						
2			42						
3			42						
4			42						
5			42						
6									
7									
8									
9									
10									
11									
12									
13									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
31									
32									
33									
34									
35									
36									
37									
38									
39									
40									
41									
42									
43									
44									
45									
46									
47									
48									
49									
50									
Mitotic Index: 2.7%			TOTALS:						

BIONETICS

$= \frac{27}{1000}$

$\frac{3}{100} + \frac{3}{100} + \frac{2}{100} + \frac{4}{100} + \frac{1}{100}$ A. $\frac{6}{100} + \frac{6}{100} + \frac{0}{100} + \frac{2}{100} + \frac{0}{100}$

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CYTOGENETICS LABORATORY MANUAL

Genetics Exp. No. 5161, 11-21 Date: 11/4/92
Slide No. 5011 Investigator: C.P.S.

	Vernier		Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Remarks	Slide Number
1	42.0, 80.3		42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8	43.4, 81.8		40						
9			41						
10			42						
11			42						
12			42						
13			43						
14			42						
15			42						
16	34.0, 83.9		42					[illegible] C.P.S.	
17	35.8, 79.1		42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42					[illegible] C.P.S.	
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			43						
34			42						
35			42						
36			43						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45	30.3, 83.7		39						
46			42						
47			42						
48			42						
49			42						
50			42						
	Mitotic Index: 5.0		TOTALS:						

DIONETICS

$$\frac{6}{100} + \frac{9}{100} + \frac{6}{100} + \frac{9}{100} = \frac{25}{500} = \frac{50}{1000}$$

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	Vernier		Number of Contacts
1			42
2			42
3			42
4	[illegible]		41
5			42
6			42
7			42
8			42
9			42
10			42
11			42
12			42
13			42
14			42
15			42
16			42
17			42
18			42
19			42
20			42
21			42
22			42
23			42
24			42
25	146.1, 36.2		42
26			42
27			42
28			42
29	146, 33.4		41
30			42
31			42
32			42
33			42
34			42
35			42
36			42
37			42
38			42
39			42
40			42
41			42
42			42
43			42
44			42
45			42
45	146.9, 26.21		41
47			42
48			42
49			42
50			42

[illegible] Index: 5 % TOTALS:

BIONETICS

$$A = \frac{3}{100} + \frac{6}{100} + \frac{7}{100} + \frac{3}{100} + \frac{6}{100} = \frac{25}{500} = \frac{50}{1000}$$

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CYTOGENETICS [illegible]

Cytogenetics Exp. No. [illegible] Date: [illegible]
ope No. [illegible] Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	• Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	[illegible]	[illegible]
A 1			42						
2	91.5×46.3		42	[illegible]				[illegible]	
3	100×48.1		42						
4	89.9×43.1		38						
5			42						
6			42						
7			42						
8			42						
9	89.4×42.2		41						
10			42						
11			42						
12			42						
13			42						
14			42						
15	88.8×37.0		34						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23	91.4×85.7		41						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30	92.5×29.0		41						
31			42						
32			42						
33			42						
34			42						
35			40						
36			42						
37			42						
38			42						
39	30.3×85.1		41						
40			42						
41			42						
42			42						
43			42						
44			42						
45	96.4×36.0		41						
46			42						
47			42						
48			42						
49			42						
50			42						
Mitotic Index: 5.6%			TOTALS:						

BIONETICS

$\frac{3}{100} + \frac{4}{100} + \frac{7}{100} + \frac{16}{100} + \frac{22}{100} = \frac{22}{500} = \frac{56}{1000}$

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CYTOGENETICS RECORD SHEET

Cytogenetics Exp. No. 5161, Pl. 6 Date: 11/21/77
Spec No. 9917 Investigator: C. L.

	Vernier		Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Isochromatid Gaps	Isochromatid Breaks	Rcpl. Components	Mean Cell Number
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10	42.1, 44.2		41						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25	25.8, 79.8		36						
26			42						
27			42						
28	18.1, 80.5		42	1					
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
Mitotic Index: 2.0			TOTALS:						

BIONETICS

$$A = \frac{3}{100} + \frac{3}{100} + \frac{1}{100} + \frac{1}{100} + \frac{2}{100} = \frac{10}{500} = \frac{20}{1000}$$

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CYTOGENETICS METAPHASE [illegible]

Cytogenetics Exp. No. [illegible]
Scope No. [illegible]

Date: [illegible]
Investigator: [illegible]

		Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	[illegible]	[illegible]
A	1	93.5×48.1		42		/		/	[illegible]	
	2	100.8×48.5		42			/			
	3	[illegible]		42						
	4			42						
	5	82.8×40.7		41						
	6	36.5×[illegible]		41						
	7			42						
	8			42						
	9	95.4×22.2		41						
	10			41						
	11	28.9×21.2		36						
	12			42						
B	13			42						
	14	95.1×46.4		41						
	15			42						
	16			42						
	17			42						
	18			42						
	19			42						
	20			42						
	21			42						
	22			42						
	23			42						
	24			42						
	25			42						
	26			42						
	27			42						
	28			42						
	29			42						
	30			42						
	31			42						
	32	[illegible]		41						
	33			42						
	34			42						
	35			42						
	36			42						
	37			42						
	38			42						
	39			42						
	40			42						
	41			42						
	42			42						
	43			42						
	44	86.5×27.2		41						
	45	90.1×27.2		37						
	46			42						
	47			42						
	48			42						
	49			42						
	50			42						
				TOTALS:						

Aneuploid Index: 5.1%

BIONETICS

$\frac{3}{100} + \frac{4}{100} + \frac{4}{100} + \frac{6}{100}$ $B = \frac{6}{100} + \frac{8}{100} + \frac{5}{100} + \frac{9}{100} + \frac{2}{100} = \frac{5}{1000}$

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CYTOGENETICS DATA SHEET

Genetics Exp. No. 5167, 21 A Date: 3/2/11
No. 8417 Investigator: [illegible]

	Vernier	Cells	Number of Centromeres	Uncounted Gaps	Uncounted Breaks	Questionable Gaps	Questionable Breaks	Rearrangements	Misc. Observations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20	43.9, 86.8		40 41 (?)						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30	44.3, 46.7		40						
31			42						
32			42						
33			42						
34			42						
35			42						
36	37.0, 86.5		c.f.s. 3 340					PP, FRAGMENT	
37			42						
38			42						
39			42						
40			42						
41	37.0, 81.1		39						
42			42						
43			42						
44	22.7, 82.7		40						
45			42						
46			42						
47			42						
48			42						
49			42						
	Mitotic Index: 6.2		TOTALS:						

CYTOGENETICS

$$\frac{4}{100} + \frac{3}{100} + \frac{9}{100} + \frac{7}{100} + \frac{8}{100} = \frac{31}{500} = \frac{62}{1000}$$

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CYTOGENETICS

Genetics Exp. No. 5167 22 A Date: Nov 9/94
Investigator: [illegible]
ID. 9732

	Vernier	Slide	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Interpretation	Para Chromosomal
1			42						
2			42						
3	146.2, 46.1		41						
4			42						
5	140.6, 45		38						
6	140.5, 45.1		41						
7			42						
8			42						
9	135.4, 43.3		39						
10			42						
11			42						
12			42						
13			42						
14			42						
15	141.2, 46.4		40						
16			42						
17	140, 42.4		41						
18			42						
19			42						
20			42						
21	141.3, 39.1		39						
22			42						
23			42						
24			42						
25			42						
26			43						
27			42						
28			42						
29			42						
30			42						
31	142.9, 35.5		40						
32	143, 35.1		41						
33	134.4, 34.1		42	1					
34			42						
35			42						
36			42						
37			42						
38			42						
39	145.7, 31.5		41						
40			42						
41			42						
42			42						
43	33.2, 32.3		41						
44			42						
45			42						
46			42						
47			42						
48	151.4, 27.6		40						
49			42						
50			42						

Mitotic Index: 10.8% 10.4%:

XNH

CYTOGENETICS

$\frac{6}{100} + \frac{9}{100} + \frac{10}{100} + \frac{12}{100} + \frac{15}{100} + \frac{54}{500} = \frac{105}{1000}$

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CYTOGENETICS METAPHASE WORKSHEET

...genetics Exp. No. 5167, 95 A, B. Date: 11/3/77
...No. 8947 Investigator: C.P.S.

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26	39.5, 91.0		35						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42					~~[illegible]~~ C.P.S.	
34	31.5, 85.7		42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
51			42						
			TOTALS:						

...ubain Index: 2.4

...ONETICS

$\frac{3}{100} + \frac{1}{100} + \frac{1}{100} = \frac{10}{500}$

$B = \frac{1}{100} + \frac{1}{100} + \frac{6}{100} + \frac{2}{100} + \frac{4}{100} = \frac{14}{500}$

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CYTOGENETICS METAPHASE WORKSHEET

Cytogenetics Exp. No. 5161 24-A Date: Nov. 3, 1977
Tape No. 8742. Investigator: K. M. G.

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 1 Aberrations
1	134.6, 45.6		42	1 42					
2			42						
3			42						
4			42						
5			42						
6			42						
7	143.9, 42.5		42	1					
8	145.9, 41.1		42	1 42					
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23	141.7, 42.5		41	1	1	1 41	1		
24			42						
25			42						
26			42						
27	140.7, 39.2		39						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36	145, 35.3		34						
37			42						
38			42						
39	132.3, 35.2		42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
	Mitotic Index: 0.290		TOTALS:	31 42	1	1 42			

CYTOGENETICS $\frac{7}{100} + \frac{13}{100} + \frac{8}{100} + \frac{10}{100} + \frac{8}{100} = \frac{46}{500} = \frac{92}{1000}$

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CYTOGENETICS METAPHASE WORKSHEET

Cytogenetics Exp. No. 5167, 25 A Date: 11/5/[illegible]
Scope No. 8947 Investigator: C. P. S.

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
A 1	48.6, 91.2		42			1			
2			42						
3			42						
4	49.0, 99.2		42			1			
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17	42.0, 82.6		41						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42	30.5, 89.0		39						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
Mitotic Index: 5.4			TOTALS:						

CIONETICS

$$\frac{5}{100} + \frac{6}{100} + \frac{5}{100} + \frac{6}{100} + \frac{5}{100} = \frac{27}{500} = \frac{54}{1000}$$

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Cytogenetics Lab No. [illegible] Date: [illegible]
Case No. [illegible] Investigator: [illegible]

	Vernier	Sex	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than one Abnormality
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18	9S [illegible]		41						
19			42						
20			42						
21			42						
22			42						
23	41.7+9S-1		40						
24			42						
25			42						
26			42						
27	9S-2+42-2		41						
28			42						
29			42						
30	9S-3+41-3		38						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43	9S-8+9S-8		41						
44	42-4+9S-5		39						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
	Mitotic Index: 11.4		TOTALS:						

GENETICS 2: 11 . 7 . 5 . 12 . 22 . 57 114

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CYTO[illegible] METAPHA[illegible] SHEET

[illegible]netics Exp. No. 51[illegible] Date: [illegible]
[illegible] No. 8947 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than [illegible] Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
[illegible]			42						
[illegible]			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38	15.5, 81.6		43						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible] Index:	10.4		TOTALS:						

[illegible]IOMETICS

$$\frac{[illegible]}{[illegible]} + \frac{9}{100} + \frac{8}{100} + \frac{13}{100} = \frac{52}{500} = \frac{104}{100}$$

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CYTOGENETICS METAPHASE WORKSHEET

...netics Exp. No. 5162 "A" Date: Nov 5, 1991
No. 8273 Investigators: D. Mc...

	Vernier	Diploid	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosomal Gaps	Chromosomal Breaks	Rearrangements	More than 1 Aberrations
1			42						
2	139.9, 46.5		41						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10	135.1, 43		39						
11			42						
12			42						
13			42						
14	135.3, 28.7		37						
15			42						
16			42						
17			42						
18			42						
19	139.9, 35.1		41						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29	148, 32.4		41						
30	141.3, 32.4		42	2					
31			42						
32	145.4, 35.3		40						
33			42						
34			42						
35			42						
36			42						
37	134.5, 33.4		41						
38			42						
39			42						
40			42						
41			42						
42			42						
43	132.3, 26.8		41						
44	140.3, 27.6		40						
45			42						
46	142.1, 29.1		44						
47			42						
48	132.2, 35.1		41						
49			42						
50			42						
	Mitotic Index: 3.6%		TOTALS:	2					

CYTOGENETICS

$$\frac{4}{100} + \frac{4}{100} + \frac{3}{100} + \frac{3}{100} + \frac{4}{100} = \frac{18}{500} = \frac{36}{1000}$$

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CYTOGENETICS MET PHASE WORKSHEET

togenetics Exp. No. 5767-3[illegible]
ope No. 2-3

Date: [illegible]
Investigator:

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than Aberrations
1			42						
2			42						
3	103.8 × 46.4		42						
4			42						
5			42						
6			42						
7			42						
8			42						
9	41.7 × 83.8		40						
10	41.0 × 84.2		37						
11			42						
12	90.3 × 39.9		38						
13	91.6 × 40.3		41						
14	92.7 × 39.9		41						
15			42						
16			42						
17			42						
18			42						
19	35.8 × 95.9		41						
20			42						
21			42						
22			42						
23	90.3 × 37.3		37						
24	85.9 × 37.2		41						
25			42						
26			42						
27			42						
28			42						
29			42						
30	35.5 × [illegible]		39						
31			42						
32			42						
33			42						
34	93.4 × 33.5		38						
35	93.8 × 32.9		39						
36	95.1 × 33.2		40						
37			42						
38			42						
39			42						
40	32.4 × 95.2		37						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49	82.8 × 27.8		42	1					
50			42						
Mitotic Index:		6.8	TOTALS:						

[illegible]IONETICS

$$[illegible] = \frac{[illegible]}{100} + \frac{6}{100} + \frac{5}{100} + \frac{5}{100} + \frac{11}{100} = \frac{34}{[illegible]} = \frac{68}{1000}$$

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CYTOGENETICS METAPHASE [illegible]

netics Exp. No. 5187, 31-A Date: 11/7/77
No. [illegible] Investigator: C.P.S.

	Vernier	[illegible]	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More Than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
[illegible]			42						
[illegible]			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
[illegible]	[illegible]		41						
32			42						
33			42						
34	98.4, 93.3		44						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
			TOTALS:						

[illegible]tic Index: 6.0

[illegible]BIONETICS

$$\frac{9}{100} + \frac{8}{100} + \frac{4}{100} + \frac{5}{100} = \frac{30}{500} = \frac{60}{1000}$$

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CYTOGENETICS [illegible]

Cytogenetics Exp. No. 54 [illegible] Date: [illegible]
Type No. 42 3 Inject[illegible]

	Vernier	Rod	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Comments	Mono-Acentrics
1			42						
2			42						
3	43.4×[illegible]		40						
4			42						
5	100.8×40.2		39						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15	31.4×[illegible]		41						
16	34.6×27.3		41						
17	39.8×[illegible]		40						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31	[illegible]		40						
32			42						
33	27.3×24.6		41						
34	27.4×83.2		41						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47	12.7×86.9		41						
48			42						
49	19.6×83.5		39						
50			42						
	Mitotic Index: 10.2		TOTALS:						

CYTOGENETICS $\frac{9}{100} + \frac{10}{100} + \frac{9}{100} + \frac{10}{100} + \frac{13}{100} = \frac{57}{500} = \frac{102}{1000}$

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CYTOGENETICS [illegible]

Cytogenetics Exp. No. 5167, 33-A Date: [illegible]
Scope No. 8447 Investigator [illegible]

	Vernier	Pos.	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	[illegible]	[illegible] Breaks	Rearrangements	More than 10 Aberrations
A 1			42						
2			42						
3			42						
4			42						
5	43.4, 97.8		41						
6	43.5, 88.1		41						
7			42						
8			42						
9			42						
10			42						
11			42						
12	39.5, 87.8		40						
13			42						
14			42						
15			42						
16			42						
17	38.0, 98.2		38						
18			42						
19			42						
20	~~38.2~~		~~42~~ 42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27	36.3, 94.1		41						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						

Mitotic Index: 9.8 TOTALS:

BIONETICS
Litton

$$A = \frac{9}{100} + \frac{7}{100} + \frac{11}{100} + \frac{11}{100} + \frac{11}{100} = \frac{49}{500} = \frac{98}{1000}$$

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CYTOGENETICS LABORATORY

Genetics Exp. No. 516 / 591 A1 Date: Nov 1 1991
Investigator: [illegible]
No. 3792-

	Vernier	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chr. Gaps	Chr. Breaks	Rearrangements	Other Abnormalities
1	145.2, 417.3	41						
2	142.0, 414.6	40						
3		42						
4		42						
5		42						
6		42						
7		42						
8		42						
9		42						
10		43						
11		42						
12		42						
13		42						
14		42						
15		42						
16		42						
17		42						
18		42						
19		42						
20	128.4, 316.3	42 41	1					
21		42						
22	129.5, 32.1	41						
23		42						
24	130.1, 21.7	41	1		1			
25		42						
26		42						
27	149.1, 32.7	41						
28		42						
29		42						
30		42						
31		42						
32	134.7, 33.9	41						
33	133.4, 22.3	39						
34		42						
35		42						
36	133.0, 31.9	41						
37		42						
38		42						
39		42						
40	145.5, 21.5	41						
41		42						
42		42						
43	135.3, 19.7	42	1					
44	133.7, 29.9	39						
45		42						
46		42						
47		42						
48		42						
49		42						
50		42						
	Mitotic Index: 1.8%	TOTALS:	3	1				

BIONETICS

$$\frac{1}{50} + \frac{3}{100} + \frac{3}{100} + \frac{0}{100} + \frac{2}{100} = \frac{9}{500} = \frac{18}{1000}$$

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CYTOGENETICS [illegible]

...netics Exp. No. 5160 ... Date: Nov ...
...No. 87[illegible] Investigator ...

	Vernier	Ref. Cell	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than [illegible] Aberrations
1	145.2, 47.3		41						
2	142.0, 41.6		42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20	123.4, 16.5		42 41	1					
21			42						
22	129.5, 32.1		41						
23			42						
24	130.1, 21.7		41	1		1			
25			42						
26			42						
27	149.1, 22.7		41						
28			42						
29			42						
30			42						
31			42						
32	131.1, 22.4		41						
33	132.4, 22.3		39						
34			42						
35			42						
36	133.0, 21.9		41						
37			42						
38			42						
39			42						
40	135.2, 21.5		41						
41			42						
42			42						
43	[illegible], 19.7		42	1					
44	[illegible], 19.1		39						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
	Mitotic Index: 1.6%		TOTALS:	3	1				

CYTOGENETICS

$$\frac{3}{100} + \frac{3}{100} + \frac{0}{100} + \frac{2}{100} = \frac{9}{500} = \frac{18}{1000}$$

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CYTOGENETICS METAPHASE WORKSHEET

togenetics Exp. No. 5167-35 Date: Nov 7 [illegible]

ope No. 2-3 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than [illegible] Aberrations
B1									
2									
3									
4									
5									
6									
7									
8									
9									
10									
11									
12									
13									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
31									
32									
33									
34									
35									
36									
37									
38									
39									
40									
41									
42									
43									
44									
45									
46									
47									
48									
49									
50									

Mitotic Index: 3.6 TOTALS:

BIONETICS

[illegible] B= 2/100 + 3 + 1 + 0 + 6 = 36/100

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CYTOGENETICS METAPHASE WORKSHEET

Slide Exp. No. 516-1, 5C A Date: 11/21/11
Investigator:

Number	Number of Centromeres	Acentric Fragments Caps	Acentric Fragments Pieces	Gaps	Breaks	Exchanges	Other Abnormalities
1	42						
2	42						
3	42						
4	42						
5	42						
6	40						
7	42						
8	42						
9	42						
10	42						
11	42						
12	42						
13	45,2,3,x,x						
14	37						
15	42						
16	42						
17	42						
18	42						
19	42						
20	42						
21	42						
22	42						
23	42						
24	42						
25	42						
26	42						
27	42						
28	42						
29	42						
30	42						
31	37,1,4,3,5						pp
32	35,2,4,x,5						dp
33							
34	37,6,7,8,9						
35	36						
36	42						
37	42						
38	35,5,8,6,4						
39	43						
40	43						
41	42						
42	42						
43	42						
44	42						
45	42						
46	42						
47	42						
48	42						
49	42						
50	42						
Mitotic Index:	4.2	TOTALS:					

BIONETICS

$$\frac{2}{100} + \frac{3}{100} + \frac{4}{100} + \frac{9}{100} = \frac{21}{500} = \frac{42}{1000}$$

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CYTOGENETICS — ECHINOIDEA E. MORPHO

Genetics Exp. No. 5167 -A Date 11/8/77

Case No. 9447 Investigator

	Vernier		Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Remarks	Other Chromosome Aberrations
1			42						
2	45.8 x 82.6		85					PP	
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			41						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24	31.6 x 79.9		≈ 262					PP	
25			42						
26			42						
27			42						
28	30.0 x 92.6		41						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			43						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			41						
Mitotic Index: 6.0			TOTALS:						

BIONETICS

$$\frac{6}{100} + \frac{6}{100} + \frac{7}{100} + \frac{9}{100} = \frac{30}{500} = \frac{60}{1000}$$

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CYTOGENETICS [illegible]

[illegible]tics Exp. No: [illegible] Date: [illegible]

No. [illegible] Investigat[illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 1 Aberration
1	83.3 • 46.7		40		1/[illegible]	1/[illegible]			
2	85.6 • 46.7		40						
3			42						
4	43.6 • [illegible]		41						
5	43.1 • [illegible]		40						
6	[illegible]		40						
7			42						
8	85.2 • 13.7		41						
9	[illegible] • 10.[illegible]		39						
10	[illegible] • [illegible]		39						
11			42						
12			42						
13									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
31									
32									
33									
34									
35									
36									
37									
38									
39									
40									
41									
42									
43									
44									
45									
46									
47									
48									
49									
50									
	[illegible] Index: 1.5	TOTALS:							

[illegible]IOGENETICS

$\frac{5}{[illegible]} + \frac{2}{[illegible]} + \frac{1}{100} + \frac{1}{[illegible]}$ $A = \frac{2}{100} + \frac{1}{100} + \frac{0}{100} + \frac{0}{100} + \frac{1}{100} = \frac{15}{100}$

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CYTOGENETICS [illegible] WORKSHEET

netics Exp. No 5167, 31-A Date: 11/1/91
No. 83127 Investigator: C.S.

	Vernier	Ind	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 1 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43	36.7, 90.8		41						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
Mitotic Index:			8.6	TOTALS:					

PIONETICS

$$\frac{12}{100} + \frac{11}{100} + \frac{10}{100} + \frac{3}{100} = \frac{43}{500} = \frac{86}{1000}$$

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CYTOGENETICS METAPHASE WORKSHEET

...etics Exp. No. 3467-40 Date: 5/6/87
...0.2-3 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6	431×483		40						
7			42						
8			42						
9	484×525		41						
10			42						
11			42						
12			42						
13	470×481		42	1	1 gap				
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28	445×1071		41						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35	495.3×433		43						
36	446×43.2		42	1	1 gap				
37	44.2×43.5		41						
38			42						
39			42						
40	418×43.6		42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49	497×490		41						
50			42						

...atic Index: 4.8 TOTALS:

BIONETICS

$\frac{3}{100} + \frac{5}{100} + \frac{5}{100} + \frac{5}{100} = \frac{24}{500} = \frac{48}{1000}$

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CYTOGENETICS METAPHASE [illegible]

[illegible]etics Exp. No. 516 / 41A Date: Nov 9, 1977
No. 8772 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1	50, 139.7		42	~~2~~ 1					
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8	47.5, 146.3		42	2					
9			42						
10			42						
11			42						
12	48.7, 141.5		45						
13			42						
14			42						
15			42						
16			42						
17			42						
18	45.8, 134.7		40	1					
19			42						
20			42						
21			42						
22			42						
23	46.3, 140.4		41						
24			42						
25			42						
26			42						
27			42						
28	44.1, 140.1		42	~~1~~ 2					
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			41						
40	42.1, 136.4		41						
41	41.5, 135.6		39						
42			42						
43			42						
44	42.3, 124.7		42	1					
45			42						
46			42						
47	39.4, 131.7		42		1				
48			42						
49			42						
50			42						

[illegible]tatic Index: 5.6% TOTALS: [illegible]

[illegible]IONETICS $\frac{6}{100} + \frac{1}{100} + \frac{5}{100} + \frac{5}{100} + \frac{5}{100} = \frac{29}{500} = \frac{56}{1000}$

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CYTOGENETICS [illegible]

[illegible]tics Exp. No. [illegible] Date: [illegible]

Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	[illegible]
	27.4×47.2		42	1					
			42						
			42						
			42						
	90.0×35.0		43					1 [illegible] frag	
	32.2×30.9		42						
			42					[illegible]	✓
	27.1×95.1		42						
			42						
			42					[illegible]	✓
	84.5×26.6		41						
			42						
	26.4×82.5		42	1					
			42					[illegible]	✓
15	81.4×26.5		42						
16			42						
17	21.5×[illegible]		42						
18	21.8×[illegible]		42	1				[illegible]	
19	19.8×97.2		42	1					
20	20.2×92.1		43					[illegible]	✓
21	19.5×99.0		39						
22			42					1 [illegible] frag	
23	95.2×14.3		~~43~~ 42	1	1 [illegible]			[illegible] 1 frag	
24	95.0×14.5		43		1			1 frag	
25	81.0×14.3		41		~~2~~				
26	83.4×11.1		37						
27			42						
28			42						
29	10.8×45.[illegible]		41		1			[illegible] frag	
30	11.2×96.[illegible]		42						
31	07.5×[illegible]		42	1					
32	08.2×86.9		40						
33	08.1×85.3		42	1					
34	46.4×28.2		43						
35			42						
36			42						
37			42						
38	43.9×33.9		43						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42		3		1		
45	20.0×91.[illegible]		41						
46			42						
47			42						
48	91.3×17.4		37						
49	80.6×14.0		42		2				
50	82.5×14.0		41						

Mitotic Index: .7 TOTALS:

[illegible]BIONETICS

$$\frac{0}{100} + \frac{1}{100} + \frac{2}{100} + \frac{1}{100} \qquad \beta = \frac{0}{100} + \frac{1}{100} + \frac{0}{100} + \frac{0}{100} + \frac{2}{100} = \frac{7}{100}$$

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CYTOGENETICS METAPHASE WORKSHEET

genetics Exp. No. 5161,43-A Date: 11/10/77
No. 8947 Investigator: C. S.

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11									
12									
13									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
31									
32									
33									
34									
35									
36									
37									
38									
39									
40									
41									
42									
43									
44									
45									
46									
47									
48									
49									
50									
Mitotic Index:			TOTALS:						

BIONETICS

$$\frac{0}{100} + \frac{0}{100} + \frac{1}{100} + \frac{0}{100} + \frac{0}{100} = \frac{1}{500}$$

$$B = \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} = \frac{0}{500}$$

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CYTOGENETICS METAPHASE WORKSHEET

...etics Exp. No. 5167, 44-A Date: 11/10/77

No. 8947 Investigator: C.S.

	Vernier	Photo.	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			[illegible]						
18			42						
19	17.9 x 97.1		36					2 Q-Radial, 0 3 Frag. 4	Pulv. chrom.
20			42						
21			42						
22			42						

...totic Index: .6 TOTALS:

...NETICS

$\frac{[illegible]}{[illegible]} + \frac{0}{100} + \frac{1}{100} + \frac{0}{100} = \frac{3}{500}$ $B = \frac{1}{100} + \frac{2}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} = \frac{3}{500}$

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CYTOGENETICS METAPHASE WORKSHEET

...netics Exp. No. 5167 ... Date: ...
No. 8792 Investigator: ...

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5	39.4, 145.1		42	1					
6	39.0, 136.2		39	1					
7	37.4, 133.6		42	1					
8	33.2, 138.4		42			1			
9			42						
10	32.6, 133		42	2					
11			42						
12			42						
13	27.8, 135.6			~~3~~ KZ				~~1 QR, 1 FR~~ KZ	✓
14	26.3, 130.8		41	1		1		1 dicentric	
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21	20.1, 135.4		42	3	1 ~~3~~ KZ			2 deleted, 1 trans, 6 AK	
22	20.1, 131.3		41						
23			42						
24	17.7, 136.8		42	2					
25			42						
26			42						
27	15.6, 142.9		41						
28	17.4, 142.9		43	2					
29			42						
30			42						
31	13.3, 141.[illegible]		42	5 ~~3~~ KZ	2			1 [illegible], 3 [illegible]	
32			42						
33			42						
34			42						
35	8.0, 140.6		42	1					
36			42						
37			42						
38			42						
39	139.9, 36.1		41						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47	[illegible] 22.3		42			1			
48	[illegible] 22.4		42		~~1~~			~~[illegible]~~	
49			42						
50	[illegible] 19.5		42		1				
	...ic Index: .6% .8%		TOTALS: 0.7%	~~1~~ AK	~~1~~ AK	~~3~~ AK			

...IONETICS

$= \frac{1}{100} + \frac{1}{100} + \frac{1}{100} + \frac{0}{100} = \frac{3}{500} = \frac{6}{1000}$ $B: \frac{1}{100} + \frac{1}{100} + \frac{0}{100} + \frac{0}{100} + \frac{2}{100} = \frac{4}{500} = \frac{8}{1000}$

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CYTOGENETICS METAPHASE [illegible]

[illegible] Exp. No. 576 [illegible] Date: [illegible]

[illegible] Investigator: [illegible]

Vernier	Photo	Number of Centromeres	•Chromatid Gaps	•Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
		42						
		42						
		42						
319 x 484		41						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
499.7 x 584		41						
		42						
		42						
483.4 / 100.2		42	1					
		42						
		42						
103.1 x 47.9		42	1					
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		41						
[illegible] Index: 8.8		TOTALS:						

[illegible] CYTOGENETICS

$\frac{9}{100} + \frac{8}{100} + \frac{9}{100} + \frac{9}{100} = \frac{44}{500} = \frac{88}{1000}$

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CYTOGENETICS METAPHASE WORKSHEET

tics Exp. No. 5167 47 Date:
Investigator:

Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More Complex Aberrations
		42						
42.1×63.2		42	2		1			
		42						
		42						
		42						
32.3×46.7		41						
		42						
		42						
		42						
35.4×53.8		41						
41.9×54.0		40						
		42						
34.0×41.3		43						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
94.3×46.0		40						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
72.2×100.1		41						
		42						
		42						
		42						
		42						
37.7×47.1		41						
		42						
tic Index: 6.6		TOTALS:						

POOR QUALITY ORIGINAL

CYTOGENETICS

$$\frac{1}{100} \cdot \frac{50}{100} \cdot \frac{7}{100} \cdot \frac{7}{100} \cdot \frac{33}{500} = \frac{66}{1000}$$

17

BEST COPY AVAILABLE

CYTOGENETICS METAPHASE WORKSHEET

...tics Exp. No. 5167, 48-A Date: 11/13/77

... 8947 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
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...Index: 9.6 TOTALS:

POOR QUALITY ORIGINAL

...ONETICS

$\frac{13}{[illegible]} + \frac{7}{[illegible]} + \frac{10}{[illegible]} + \frac{8}{100} = \frac{48}{560} = \frac{96}{1000}$

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CYTOGENETICS METAPHASE WORKSHEET

...netics Exp. No. 5767 '77 | Date: ... 1977
...e No. 2 3 | Investigator: ...

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4	45.7 x 84.4		39						
5			42						
6			42						
7			42						
8			42						
9	35.7 x 43.7		41						
10			42						
11			42						
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16			42						
17			42						
18			42						
19			42						
20			42						
21	46.3 x 53.1		41						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30	29.0 x 46.4		42					~~1 Deletion~~ [illegible]	
31			42						
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...Index: 7.0			TOTALS:	ORIG.NAL					

...NETICS

$$\frac{4}{100} + \frac{7}{100} + \frac{4}{100} + \frac{6}{100} = \frac{35}{500} = \frac{70}{1000}$$

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CYTOGENETICS METAPHASE WORKSHEET

...etics Exp. No: 5167, 50 Date: 11/26/97
No. 5167 Investigator:

	Vernier	Sex	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 1 Aberration
1			42						
2			42						
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15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22	42,1x,-Dic		42		1				
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
				2005					
				20					
				ORIG					

...ic Index: 6.8 TOTALS:

...ETICS

$$\frac{2}{100} + \frac{5}{100} + \frac{4}{100} + \frac{8}{100} = \frac{34}{500} = \frac{68}{1000}$$

BEST COPY AVAILABL

CYTOGENETICS LABORATORY WORKSHEET

Exp. No: 67C1 92 Date:

Investigator:

	Vernier	2n=40	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 1 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8	45.5×85.1		40						
9			42						
10			42						
11			42						
12			42						
13	35.7×40.5		41						
14			42						
15	47.4×85.0		41						
16			42						
17			42						
18	35.2×49.7		42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27	47.7×95.1		41						
28			42						
29			42						
30			42						
31			42						
32	9.14×47.01		40						
33	48.2×48.2		41						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46	78.6×46.2		41						
47			42						
48			42						
49			42						
50			42						

Mitotic Index: 11.0 TOTALS: P

QUALITY

ORIGI

KINETICS

$$\frac{17}{100} + \frac{9}{100} + \frac{10}{100} + \frac{6}{100} = \frac{55}{500} = \frac{110}{1000}$$

BEST COPY AVAILABLE

CYTOGENETICS METAPHASE [illegible]

[illegible]netics Exp. No: 516752-A Date: N[illegible]
[illegible] No. [illegible] Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More [illegible] Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14	500, 145.5		42	2					
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36	147.5, 141.4		42	1					
37	146.5, 141.9		42	12	1				
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
	[illegible]tic Index: 9.0%		TOTALS:	[illegible]					

[illegible]IONETICS $\frac{12}{100} + \frac{9}{100} + \frac{7}{100} + \frac{5}{100} + \frac{12}{100} = \frac{45}{500} = \frac{90}{1000}$

BEST COPY AVAILABLE

CYTOGENETICS METAPHASE [illegible]

...netics Exp. No. 5167,53 Date: 11/14/77

...No. 8947 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6	44.1x81.4		41						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14	48.0x84.2		37						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21	~~[illegible]~~ 41x76.5		41						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
	...Index: 6.4		TOTALS:						

...ETICS

$\frac{5}{100} + \frac{5}{100} + \frac{6}{100} + \frac{10}{100} = \frac{32}{500} = \frac{64}{1000}$

ORIGINAL

BEST COPY AVAILABLE

CYTOGENETICS METAPHASE WORKSHEET

...netics Exp. No: 5167 [illegible]
No. 2-3

Date: [illegible]
Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	[illegible]
1			42						
2			42						
3			42						
4			42						
5			42						
6	85.9 x 45.2		42	X [illegible]					
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13	45.5 x 42.2		40						
14			42						
15			42						
16			42						
17	45.3 x 46.2		43						
18	45.5 x [illegible]		42	/					
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26	44.0 x 101.6		41						
27	43.9 x 101.8		41						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35	100.3 x 42.2		41						
36			42						
37			42						
38	40.4 x 40.3		42		/				
39			42						
40			42						
41	93.0 x 40.9		41						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						

...otic Index: 6.2 TOTALS:

POOR QUALITY ORIGINAL

BIONETICS

$$\frac{5}{100} + \frac{4}{100} + \frac{8}{100} + \frac{7}{100} = \frac{31}{500} = \frac{62}{1000}$$

BEST COPY AVAILABLE

CYTOGENETICS [illegible]

[illegible]netics Exp. No: 5167 55 A　　　Date: N 19 [illegible]

[illegible] No. [illegible]　　　Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
			42						
			42						
			42						
			42						
			42						
			42 →						
			42						
			42						
			42						
			41						
			42						
	107.3 104		42	1					
			42						
			42						
			42						
			42						
			42						
			42						
			42						
			42						
			42						
Mitotic Index: 9.0%			TOTALS:	1	ORIGINAL				

CYTOGENETICS

$$\frac{12}{100} + \frac{8}{100} + \frac{9}{100} + \frac{11}{100} = \frac{47}{500} \simeq \frac{94}{[illegible]}$$

BEST COPY AVAILABLE

CYTOGENETICS [illegible]

enetics Exp. No. 5167, 56 Date: 11/14/77
No. 8947 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	•Chromatid Gaps	•Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9	14.7 x 95.5		c.s. 4	3 c.s.					
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18	3.7 x 97.3		42	F c.s.					
19			42						
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
31									
32									
33									
34									
35									
36									
37									
38									
39									
40									
41									
42									
43									
44									
45									
46									
47									
48									
49									
50									

[illegible] Index: .3 TOTALS:

QUALITY ORIGINAL

[illegible]ONETICS

$$\frac{0}{[illegible]} + \frac{1}{100} + \frac{0}{100} = \frac{3}{500} \qquad B = \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} = \frac{0}{500}$$

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CYTOGENETICS METAPHASE WORKSHEET

netics Exp. No: 3467-3 Date: 11/3/77
No. 223 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2	140.9×30.4		40						
3	132.4×26.9		43						
4			42						
5			42						
6			42						
7			42						
8			42						
9	132.3×42.0		41						
10	132.2×42.5		42						
11	132.3×42.8		41						
12			42						
13			42						
14			42						
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
31									
32									
33									
34									
35									
36									
37									
38									
39									
40									
41									
42									
43									
44									
45									
46									
47									
48									
49									
50									

Mitotic Index: 1.7 TOTALS:

POOR QUALITY ORIGINAL

GENETICS

$\frac{2}{100} + \frac{1}{100} + \frac{0}{100} + \frac{2}{100}$ $\beta = \frac{2}{100} + \frac{2}{100} + \frac{1}{100} + \frac{1}{100} + \frac{3}{100} = \frac{17}{1000}$

BEST COPY AVAILABLE

CYTOGENETICS METAPHASE WORKSHEET

...atics Exp. No. 5161 ,53 Date: ../../..

No. ..... Investigator ...

	Vernier	Stage	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						

...otic index: 3.0 TOTALS:

...IONETICS

C.P.S. ~~60 — 300 — 500~~

$A = \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} = \frac{0}{500}$ $B = \frac{0}{100} + \frac{0}{100} + \frac{4}{100} + \frac{12}{100} + \frac{14}{100} = \frac{30}{500}$

BEST COPY AVAILABL...

CYTOGENETICS METAPHASE WORKSHEET /

...etics Exp. No: [illegible] Date: [illegible] 1977

No. [illegible] Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7	50.0,121.4		42	2					
8	50.3,120.0		42	~~42~~ 1		1			
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49	[illegible]3.4,135.2		42	1					
50			42						
TOTALS:				4		1			

Mitotic Index: 11.2%

BIONETICS

$$\frac{12}{100} + \frac{13}{100} + \frac{11}{100} + \frac{11}{100} + \frac{9}{100} = \frac{56}{500} = \frac{112}{1000}$$

BEST COPY AVAILABLE

CYTOGENETICS METAPHASE WORKSHEET

tics Exp. No. 5167-60 Date: 14 Nov 77
Investigator: [illegible]

Vernier	Photo	Number of Centromeres	•Chromatid Gaps	•Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
		42						
		42						
		42						
		42						
		42						
27.7×49.0		42		1				
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
41.0×41.0		42		1			[illegible]	1
		42						
		42						
41.8×46.4		43						
		42						
		42						
		42						
		42						
		42						
46.5×44.6		41						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
42.6×42.1		84					Polyploid	
		42						
		42						
42.2×42.2		84				1	Dicentric/Frag	
		42						
Index: 88		TOTALS:	POOR QUALITY ORIGINAL					

CYTOGENETICS

$\frac{1}{100} + \frac{11}{100} + \frac{8}{100} \cdot \frac{9}{100} = \frac{44}{5000} = \frac{88}{10000}$

BEST COPY AVAILABLE

CYTOGENETICS METAPHASE WORKSHEET

...netics Exp. No. 5167, 61 Date: 11/14/77

No. 8447 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17	24.4 x 83.2		332					PP	
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42					Fragment	
32	14.1 x 82.5		42	1					
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
			TOTALS:						

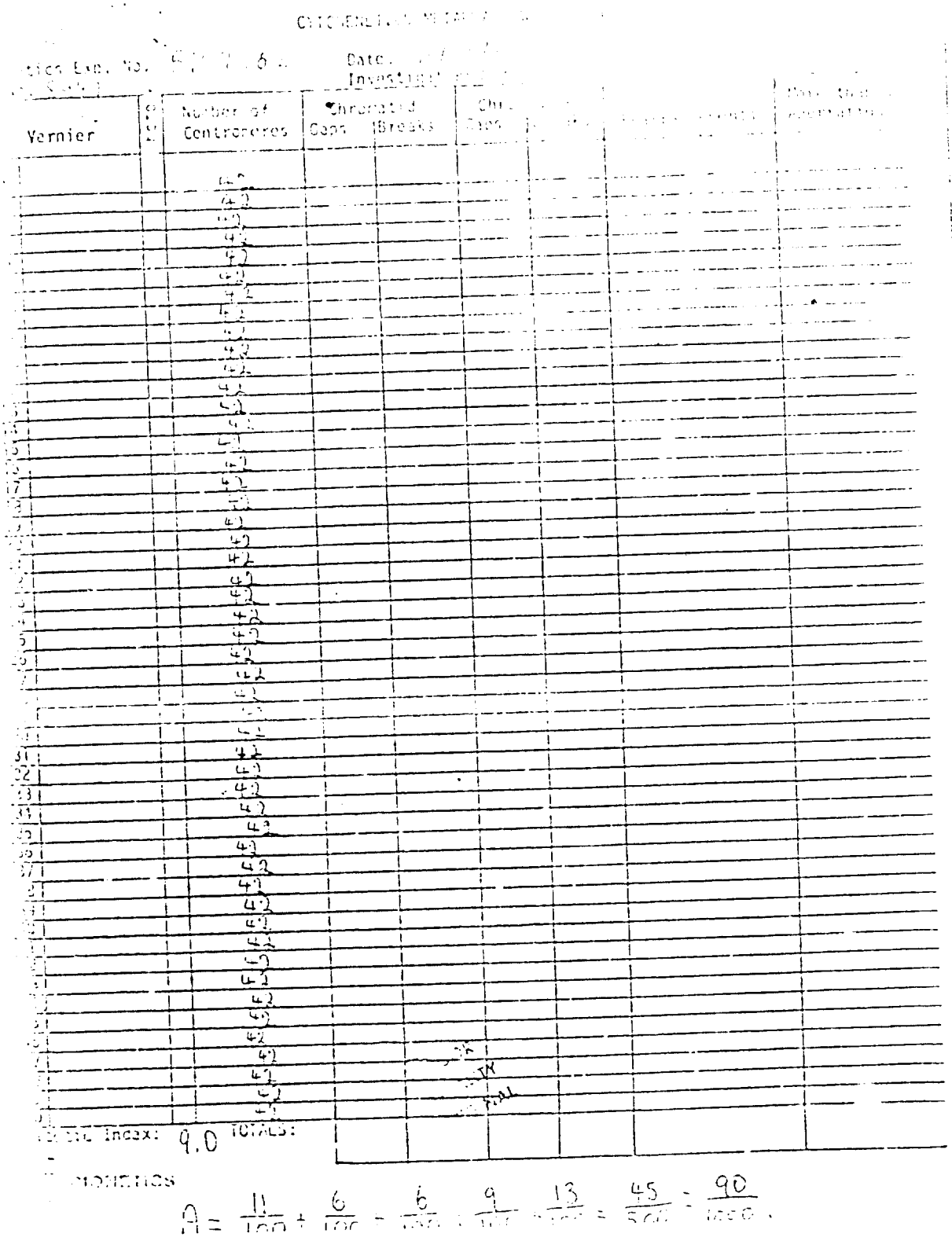
...ic Index: 6.2

...ONETICS

$$\frac{7}{100} + \frac{5}{100} + \frac{6}{100} + \frac{9}{100} = \frac{31}{500} = \frac{62}{1000}$$

FSC
QUA...
ORIGI...

BEST COPY AVAILABLE



$$A = \frac{11}{100} + \frac{6}{100} = \frac{6}{100} \quad \frac{9}{100} \quad \frac{13}{100} = \frac{45}{500} = \frac{90}{1000}$$

BEST COPY AVAILABLE

	Vernier	Number of Centimeters	Chromosome Index Males	Chromosome Index Females
1		42		
2		42		
3		42		
4		42		
5		42		
6		42		
7		42		
8		42		
9		42		
10		41		
11		42		
12		42		
13		42		
14		42		
15		42		
16		42		
17		41		
18		41		
19		41		
20		42		
21		42		
22		42		
23		42		
24		42		
25		42		
26		42		
27		42		
28		42		
29		42		
30		42		
31		42		
32		41		
33		42		
34		43		
35		42		
36		42		
37		42		
38		42		
39		42		
40		42		
41		42		
42		42		
43		42		
44		42		
45		42		
46		42		
47		42		
48		42		
49		42		
50		42		
51		42		
52		42		
53		42		
54		42		
55		42		
56		42		
57		42		
58		42		
59		42		
60		42		
61		42		
62		42		
63		42		
64		42		
65		42		
66		42		
67		42		
68		42		
69		42		
70		42		
71		42		
72		42		
73		42		
74		42		
75		42		
76		42		
77		42		
78		42		
79		42		
80		42		
81		42		
82		42		
83		42		
84		42		
85		42		
86		42		
87		42		
88		42		
89		42		
90		42		
91		42		
92		42		
93		42		
94		42		
95		42		
96		42		
97		42		
98		42		
99		42		
100		42		
	Index:	12.6	TOTALS:	

GENETICS

$$\frac{6}{100} + \frac{15}{100} + \frac{12}{100} + \frac{12}{100} = \frac{63}{500} = \frac{126}{1000}$$

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CYTOGENETICS METAPHASE [illegible]

[illegible] Exp. No. [illegible] Date: [illegible]

Investigator: [illegible]

Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Fourmilements	More than [illegible] Aberrations
[illegible]								
[illegible]								

[illegible] Index: .4%, 0%

TOTALS:

POOR QUALITY ORIGINAL

[illegible]NETICS

$$\frac{0}{100} + \frac{1}{100} + \frac{0}{100} + \frac{0}{100} = \frac{0}{500} = \frac{0}{1000} = .4\% \quad B = \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{0}{100} = \frac{0}{500} \quad \frac{0}{1000} = 0\%$$

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CYTOGENETICS [illegible]

...etics Exp. No. 576-69 Date: [illegible]
No. 2-3 Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than [illegible] Aberrations
1	415×845		41						
2			41						
3	1032.4[illegible]		42	3		[illegible]			
4	815×[illegible]		43						

... Index: 2.7 TOTALS:

POOR QUALITY ORIGINAL

...GENETICS

$\frac{2}{100} + \frac{3}{100} + \frac{1}{100} + \frac{4}{100}$ $\quad$ $2 = \frac{2}{100} + \frac{4}{100} + \frac{3}{100} + \frac{2}{100} + \frac{2}{100} = \frac{13}{100}$

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CYTOGENETICS METAPHASE WORKSHEET

...etics Exp. No. 5167, 66 Date: 11/15/...
... 8147 Investigator: C.S.

Vernier		Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More Than Aberrations
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
27.5 x 44.9		42					F	
		42						
		42						
		42						
		42						
...ic Index:		.9 TOTALS:						

...IONETICS

$\frac{0}{0} + \frac{0}{100} + \frac{3}{100} + \frac{1}{100} = \frac{6}{500}$ $\beta = \frac{0}{100} + \frac{0}{100} + \frac{1}{100} + \frac{2}{100} + \frac{0}{100} = \frac{3}{500}$

POOR QUALITY ORIGINAL

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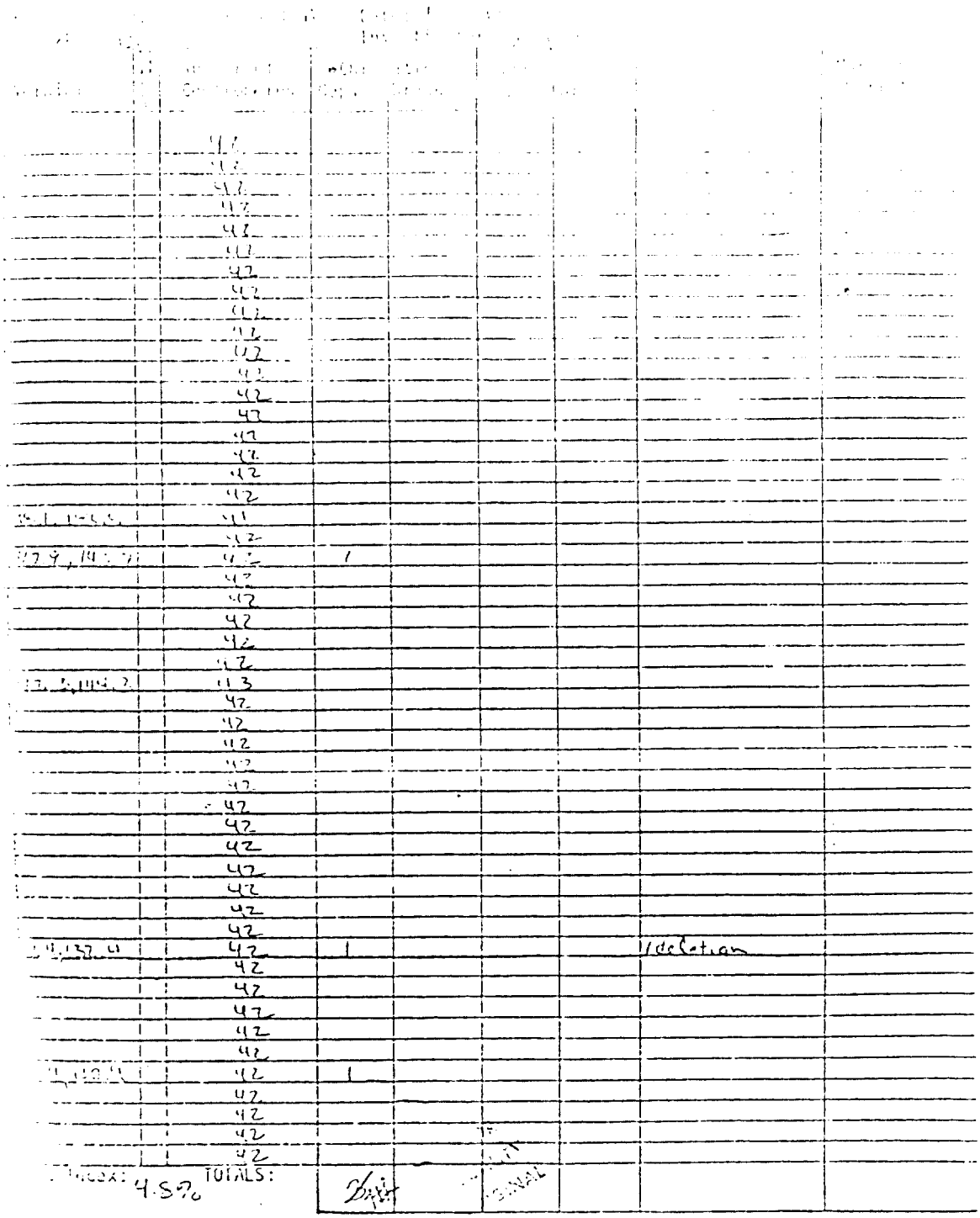

$$\frac{6}{100} + \frac{4}{100} + \frac{2}{100} + \frac{7}{100} = \frac{24}{500} = \frac{43}{1000}$$

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	Vernier	Rack	Rack or Centicharres	Observed Bases	Observed Breaths	Observed Bases	Observed Breaths	Observer Comments	Corrections Made
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8	116.4 × 46.8		41		JATP				
9			42						
10			42						
11	47.6 × 10.7		41						
12			42						
13			42						
14			42						
15			42						
16			42						
17	82.3 × 43.7		43						
18			42						
19			42						
20			42						
21			42						
22			42						
23	40.3 × 92.4		45						
24			42						
25			42						
26	100.8 × 38.7		46					1 Accent. Fact.	
27			42						
28			42						
29			42						
30	101.5 × 33.0		40						
31			42						
32			42						
33	32.7 × 40.5		41						
34			42						
35			42						
36			42						
37			42						
38			42						
39	34.5 × 21.8		40						
40			42						
41			42						
42			42						
43	19.5 × 22.0		41						
44			42						
45			42						
46	6.4 × 100.1		40						
47			42						
48			42						
49			42						
50	23.2 × 23.0		41						

Index: 3.8 TOTALS:

POOR QUALITY ORIGINAL

PHONETICS

$$\frac{}{} + \frac{17}{100} + \frac{2}{100} + \frac{5}{100} + \frac{1}{100} = \frac{19}{500} = \frac{38}{1000}$$

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CYTOGENETICS [illegible]

[illegible]etics Exp. No. [illegible]
No. [illegible]

Date: [illegible]
Investigat[illegible]

	Vernier	Phot	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
[illegible]			42						
[illegible]			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						
[illegible]			42						

[illegible]tatic Index: 3.6 TOTALS:

POOR QUALITY ORIGINAL

[illegible]IONETICS

$$\frac{7}{100} + \frac{1}{100} + \frac{2}{100} + \frac{5}{100} = \frac{18}{500} = \frac{36}{1000}$$

BEST COPY AVAILABLE

CYTOGENETICS METAPHASE

...netics Exp. No. 516 / 5 A Date: N...
...No. 5/... Investigator: ...

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2	44.2, 138.7		41						
3			42						
4			42						
5			42						
6	49.5, 127.2		40						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19	45.5, 125.7		39						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35	45.7, 126.1		40						
36	50.1, 149.9		42	1					
37			42						
38			42						
39	43.5, 141.5		39						
40			42						
41			42						
42	43.9, 132.0		42					HH K7	
43			42						
44			42						
45			42						
46			42						
47			42						
48			42			POOR QUALITY ORIGINAL			
49			42						
50	Centric Index: 5.29%		TOTALS:	X					

...NETICS

$$\frac{5}{100} + \frac{7}{100} + \frac{7}{100} + \frac{5}{100} = \frac{26}{500} = \frac{52}{1000}$$

BEST COPY AVAILABLE

CITOGENETICS [illegible]

tics Exp. No. [illegible] Date: [illegible]
Investigator: [illegible]

Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chr[illegible] Gaps	[illegible]	[illegible]	[illegible] Aberrations
		42						
		42						
		42						
		42						
		42						
		42						
		42						
31.7 x 40.3		40						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
37.7 x [illegible]		40						
		42						
		42						
		42						
		42						
41.7 x 34.9		37						
		42						
		42						
		42						
27.2 x 37.1		40						
27.0 x 41.4		39						
27.2 x 45.4		40						
		42						
[illegible]		41						
[illegible]		43						
		42						
		42						
		42						
		42						
41.1 x 45.9		41						
		42						
		42						
34.1 x 41.3		40						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
[illegible] Index: 34		TOTALS:						

POOR QUALITY ORIGINAL

[illegible]NETICS

$\frac{[illegible]}{100} + \frac{1}{100} + \frac{6}{100} + \frac{4}{100}$ $\beta = \frac{3}{100} + \frac{2}{100} + \frac{5}{100} + \frac{6}{100} + \frac{2}{100} = \frac{39}{[illegible]}$

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CYTOGENETICS [illegible]

...tics Exp. No. 516 [illegible] Date. [illegible]

Investigator [illegible]

Vernier	Poly.	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	[illegible]	[illegible]
		42						
		42						
		42						
		42						
		42						
		42						
41.1x 38.1		41						
		42						
		42						
		[illegible]						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
42.0x 88.7		41						
		42						
		42						
		42						
42.7x 88.5		36						
		42						
		42						
43.3x 81.8		41						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
Index:	5.2	TOTALS:						

POOR QUALITY ORIGINAL

...METICS

$$\frac{3}{100} + \frac{10}{100} + \frac{5}{100} + \frac{5}{100} = \frac{26}{500} = \frac{52}{1000}$$

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Cytogenetics Laboratory

Slide Exp. No. 516 - 76 A Cytogenetics Laboratory

ST 20 AG-55 Investigator: [illegible]

Vernier	Number of Centromeres	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Remarks	Poor Chromosome Morphology
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
45.9, 134.7	42	1				
	42					
	42					
	42					
43.9, 141.6	45					
	42					
44.2, 144	42	1				
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
	42					
103.3, 146.4	42	2				
	42					
	42					
	42					
	42					
	42					
	42				POOR QUALITY ORIGINAL	
	42					
	42					
6.2%	TOTALS:	4				

METICS

$$\frac{2}{100} + \frac{3}{100} + \frac{9}{100} + \frac{7}{100} + \frac{7}{100} = \frac{31}{500} = \frac{62}{1000}$$

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CYTOGENETICS METAPHASE [illegible]

[illegible]etics Exp. No. 5[illegible] Date: [illegible]
No. [illegible] Investigator [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than [illegible] Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16	38.9 x 91.1		42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38	21.6 x 38.9		40						
39			42						
40	18.3 x 42.6		38						
41			42						
42			42						
43			42						
44	13.4 x 81.0		42	1					
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
	[illegible] Index: 2.4		TOTALS:						

POOR QUALITY ORIGINAL

[illegible]GNETICS

$\frac{3}{100} + \frac{2}{100} + \frac{3}{100} + \frac{1}{100} = \frac{12}{500} \quad \frac{24}{1000}$

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CYTOGENETICS [illegible]

[illegible] Exp. No. [illegible] Date: [illegible]
No. of [illegible] Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Exchanges	More than 1 Aberrations
1	[illegible]		42	3	1	1			
2			42						
3			42						
4	[illegible]		41						
5			42						
6			42						
7	[illegible]		41						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			43						
15			40						
16	[illegible]		42	2					
17			42						
18			42						
19			42						
20			42						
21			42						
22	[illegible]		42	1					
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40			42						
41			42						
42	[illegible]		41						
43	[illegible]		40						
44			42						
45			42						
46			42						
47			42						
48			42						
49	[illegible]		40						
50			42						
	Index:		3.6	TOTALS:					

POOR QUALITY ORIGINAL

[illegible]ETICS

$\frac{4}{100} + \frac{4}{100} - \frac{4}{100}$ $B = \frac{6}{100} + \frac{1}{100} + \frac{4}{100} + \frac{1}{100} + \frac{1}{100} = \frac{36}{1000}$

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CYTOGENETICS [illegible]

[illegible]etics Exp. No. 5[illegible]7, [illegible] Date: [illegible]
[illegible]o. 5947 Investigat[illegible] [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than [illegible] Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20	44.5x 92.3		37						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38	33.0x 48.7		40						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						

[illegible]ic Index: 10.8 TOTALS:

POOR QUALITY ORIGINAL

[illegible]IONETICS

$$[illegible] + \frac{10}{100} + \frac{13}{100} + \frac{10}{100} + \frac{12}{100} = \frac{54}{500} = \frac{108}{1000}$$

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CYTOGENETICS [illegible]

[illegible]tics Exp. No. [illegible] Date: [illegible]

[illegible] Investigator: [illegible]

Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than [illegible] Aberration
		42						
		42						
		42						
		42						
		42						
		42						
48.4, 105.1		40						
		42						
		42						
		42						
		42						
		42						
		42						
46.4, 124.3		42	42					
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
40.3, 134.5		42	42					
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
		42						
35.6, 105.5		36						
		42						
		42						
		41						
		42						
		42						
[illegible]tic Index: 3.8%		TOTALS:						

POOR QUALITY ORIGINAL

[illegible]IONETICS

$$\frac{4}{100} + \frac{5}{100} + \frac{1}{100} + \frac{6}{100} + \frac{3}{100} = \frac{19}{500} = \frac{38}{1000}$$

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CYTOGENETICS METAPHASE WORKSHEET

...etics Exp. No. [illegible] Date: [illegible]
No. [illegible] Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10	87.1 × 42.5		40						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24	33.3 × 82.2		43						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35	86.3 × 21.[illegible]		37						
36			42						
37	81.2 × 20.9		40						
38			42						
39	86.8 × 17.5		41						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49	[illegible] × 15.3		58						
50			42						
	... Index:		6.4 TOTALS:						

POOR QUALITY ORIGINAL

...ETICS

$$\frac{6}{50} + \frac{6}{100} + \frac{8}{100} + \frac{7}{100} = \frac{32}{500} = \frac{64}{1000}$$

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CYTOGENETICS METAPHASE

Cytogenetics Exp. No. 5167, x2 Date: 11/17/
Case No. 5247 Investigator: C.

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than one Aberration
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			40						
8			42						
9			40						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33			42						
34			42						
35	32.9 x 84.5		40						
36			42						
37			42						
38			42						
39	37.4 x 82.7		41						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
	Index: 4.3		TOTALS:						

POOR QUALITY ORIGINAL

GENETICS

$\frac{}{100} + \frac{7}{100} + \frac{3}{100} + \frac{6}{100} + \frac{4}{100} = \frac{24}{500} = \frac{48}{1000}$

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CYTOGENETICS METAPHASE WORKSHEET

...etics Exp. No. 5747 5A1 Date: Nov 19 ...
No. 8792 Investigator: ...

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1	50.5, 121.5		45						
2			42						
3	50.4, 131.4		39						
4			42						
5			42						
6			42						
7			42						
8			42						
9	50.3, 135.3		41						
10			42						
11			42						
12			42						
13			42						
14			42						
15			42						
16			42						
17	48.7, 138.3		39						
18			42						
19			42						
20			42						
21			42						
22	46.2, 139.8		36						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29	43.6, 144		42	1			X 42		
30			42						
31			41						
32			42						
33			42						
34			42						
35			42						
36			42						
37			42						
38			42						
39			42						
40	43.3, 145.5		41						
41			42						
42			42						
43	43.3, 146.8		41						
44			42						
45			42						
46			42						
47	45.7, 138		35						
48			42						
49			42						
50			42						
	...tic Index: 6.09%		TOTALS:	1			1		

...TOGENETICS

$$\frac{5}{...} + \frac{7}{100} + \frac{7}{100} + \frac{4}{100} + \frac{7}{100} = \frac{30}{500} = \frac{60}{1000}$$

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CYTOGENETICS METAPHASE [illegible]

netics Exp. No. 5167, [illegible] Date: [illegible]
No. [illegible] Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than Aberrations
1			42						
2			42						
3			42						
4			42						
5			42						
6			42						
7			42						
8			42						
9			42						
10			42						
11			42						
12			42						
13	44.3 x 92.5		41						
14			42						
15			42						
16			42						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24			42						
25			42						
26			42						
27			42						
28			42						
29			42						
30			42						
31			42						
32			42						
33	28.3 x 91.1		42					~~[illegible]~~ C.S.	
34			42						
35			42						
36	25.8 x 92.8		41						
37			42						
38			42						
39			42						
40			42						
41			42						
42			42						
43			42						
44			42						
45			42						
46			42						
47			42						
48			42						
49			42						
50			42						
	Mitotic Index: 6.6		TOTALS:						

[illegible]IONETICS

$$\frac{5}{100} + \frac{9}{100} + \frac{7}{100} + \frac{5}{100} + \frac{7}{100} = \frac{33}{500} = \frac{66}{1000}$$

BEST COPY AVAILABLE

CYTOGENETICS METAPHASE [illegible]

...netics Exp. No. [illegible] Date: [illegible]
No. [illegible] Investigator: [illegible]

	Vernier	Photo	Number of Centromeres	Chromatid Gaps	Chromatid Breaks	Chromosome Gaps	Chromosome Breaks	Rearrangements	More than 10 Aberrations
1	35.2 x 42.4		43						
2			42						
3	38.6 x 44.6		39	8					
4			42						
5	83.0 x 31.3		43						
6	94.7 x 31.2		40						
7	100.2 x 32.1		40						
8			42						
9	24.7 x 100.8		41						
10	21.2 x 83.8		39						
11	12.6 x 86.8		41						
12			42						
13			42						
14			42						
15	92.5 x 06.?		41						
16	89.2 x 03.3		41						
17			42						
18			42						
19			42						
20			42						
21			42						
22			42						
23			42						
24									
25									
26									
27									
28									
[illegible] index: 1.1			TOTALS:						

POOR QUALITY ORIGINAL

[illegible] $\frac{[illegible]}{[illegible]} + \frac{0}{100} + \frac{1}{100} + \frac{2}{100}$

$B = \frac{0}{100} + \frac{0}{100} + \frac{0}{100} + \frac{1}{100} + \frac{4}{100} = \frac{11}{1000}$

BEST COPY AVAILABLE

Triage of 8(e) Submissions

Date sent to triage: 2/5/96

NON-CAP (CAP)

Submission number: 12567A

TSCA Inventory: (Y) N D

Study type (circle appropriate):

Group 1 - Dick Clements (1 copy total)

ECO AQUATO

Group 2 - Ernie Falke (1 copy total)

ATOX SBTOX SEN w/NEUR

Group 3 - Elizabeth Margosches (1 copy each)

STOX CTOX EPI RTOX (GTOX)

STOX/ONCO CTOX/ONCO IMMUNO CYTO NEUR

Other (FATE, EXPO, MET, etc.): _____

Notes:

THIS IS THE ORIGINAL 8(e) SUBMISSION; PLEASE REFILE AFTER TRIAGE DATABASE ENTRY

For Contractor Use Only

entire document: (0) 1 2 **pages** 1,2 **pages** [redacted]

Notes:

Contractor reviewer : LPS **Date:** 12/6/95

CECATS\TRIAGE TRACKING DBASE ENTRY FORM

CECATS DATA:
Submission # 8EHQ- 0992-12567 SEQ. A

TYPE: (INT) SUPP FLWP

SUBMITTER NAME: Phillips Petroleum Company

INFORMATION REQUESTED: FLWP DATE:
0501 NO INFO REQUESTED
0502 INFO REQUESTED (TECH)
0503 INFO REQUESTED (VOL ACTIONS)
0504 INFO REQUESTED (REPORTING RATIONALE)

DISPOSITION:
(0639) REFER TO CHEMICAL SCREENING
(0678) CAP NOTICE

VOLUNTARY ACTIONS:
(0401) NO ACTION REPORTED
0402 STUDIES PLANNED/UNDERWAY
0403 NOTIFICATION OF WORKER PROTECTION
0404 LABEL/MSDS CHANGES
0405 PROCESS/HANDLING CHANGES
0406 APP/USE DISCONTINUED
0407 PRODUCTION DISCONTINUED
0408 CONFIDENTIAL

SUB. DATE: 08/24/92 OTS DATE: 09/02/92 CSRAD DATE: 05/21/95

CHEMICAL NAME: CAS#

64741-79-3

INFORMATION TYPE:		P	F	C
0201	ONCO (HUMAN)	01	02	04
0202	ONCO (ANIMAL)	01	02	04
0203	CELL TRANS (IN VITRO)	01	02	04
(0204)	MUTA (IN VITRO)	01	02	04
0205	MUTA (IN VIVO)	01	02	04
0206	REPRO/TERATO (HUMAN)	01	02	04
0207	REPRO/TERATO (ANIMAL)	01	02	04
0208	NEURO (HUMAN)	01	02	04
0209	NEURO (ANIMAL)	01	02	04
0210	ACUTE TOX. (HUMAN)	01	02	04
0211	CHR. TOX. (HUMAN)	01	02	04
0212	ACUTE TOX. (ANIMAL)	01	02	04
0213	SUB ACUTE TOX (ANIMAL)	01	02	04
0214	SUB CHRONIC TOX (ANIMAL)	01	02	04
0215	CHRONIC TOX (ANIMAL)	01	02	04

INFORMATION TYPE:		P	F	C
0216	EPI/CLIN	01	02	04
0217	HUMAN EXPOS (PROD CONTAM)	01	02	04
0218	HUMAN EXPOS (ACCIDENTAL)	01	02	04
0219	HUMAN EXPOS (MONITORING)	01	02	04
0220	ECO/AQUA TOX	01	02	04
0221	ENV. OCCC/REL/FATE	01	02	04
0222	EMER INCI OF ENV CONTAM	01	02	04
0223	RESPONSE REQEST DELAY	01	02	04
0224	PROD/COMP/CHEM ID	01	02	04
0225	REPORTING RATIONALE	01	02	04
0226	CONFIDENTIAL	01	02	04
0227	ALLERG (HUMAN)	01	02	04
0228	ALLERG (ANIMAL)	01	02	04
0239	METAB/PHARMACO (ANIMAL)	01	02	04
0240	METAB/PHARMACO (HUMAN)	01	02	04

INFORMATION TYPE:		P	F	C
0241	IMMUNO (ANIMAL)	01	02	04
0242	IMMUNO (HUMAN)	01	02	04
(0243)	CHEM/PHYS PROP	01	02	04
0244	CLASTO (IN VITRO)	01	02	04
(0245)	CLASTO (ANIMAL)	01	02	04
0246	CLASTO (HUMAN)	01	02	04
0247	DNA DAM/REPAIR	01	02	04
0248	PROD/USE/PROC	01	02	04
0251	MSDS	01	02	04
0299	OTHER	01	02	04

TRIAGE DATA: NON-CBI INVENTORY

(YES)

CAS SR NO

IN TRANSIT

COMPLETE

ONGOING REVIEW

YES (DROP/REFER)

NO (CONTINUE)

REJECT

SPECIES
In vitro
Rat

TOXICOLOGICAL CONCERN:

LOW

(MED)

HIGH

USE:

PRODUCTION:

10) ✓ 8EHQ-92-12567: Rank - medium.

Chemical: R-01 (CAS# 64741-79-3).

Mutagenicity evaluation of R-01, Litton Bionetics, Inc., Kensington MD, dated May 1978: Positive for gene mutations in Salmonella typhimurium in strains TA98, TA1535, TA1537 and TA1538 both without (weakly) and with metabolic activation, weakly positive in TA100 both without and with activation.

Negative for DNA effects (gene conversion) in Saccharomyces cerevisiae strain D4 both without and with metabolic activation.

Weakly positive for gene mutations in L5178Y $TK^{+/-}$ mouse lymphoma gene mutation assay in vitro both without and with metabolic activation.

Negative for chromosome mutations (aberrations) in rats exposed in vivo.