

Bromochloromethane (ブロモクロロメタン)

<u>Chemical Name:</u>	Bromochloromethane
<u>Synonym</u>	Methane, bromochloro-
<u>Molecular weight:</u>	129.4
<u>Melting point:</u>	- 88 °C
<u>Boiling point:</u>	67.8-68°C
<u>Chemical Structure</u>	
	C l C H ₂ B r
<u>CAS No :</u>	74-97-5
<u>MITI No :</u>	(2)-58
<u>Source of Substance:</u>	Tokyo Kasei Kogyo Co., Ltd.
<u>Lot. No. :</u>	FA001
<u>Purity:</u>	%
<u>Vehicle:</u>	1%CMC

Judgement for Chromosomal Aberration in CHL: Positive

IARC Evaluation : not yet cited

Experimental Data

		(Petri dish)												
Treated Time (Hr)	Concentration (mg/ml)	No. of Meta-phase	Poly-ploid (%)	Judge	Cell with Structural Chromosome Aberration (%)							Total		Judge
					Gap	CTB	CTE	CSB	CSE	-G	+G			
CMC	24	200	0	—	0	0	0	0	0	0	0	0	0	—
	48	200	0	—	0	0	0	0	0	0	0	0	0	—
Test Chemical														
	24	1.0	200	0.5	—	0	0	1.0	0	0	1.0	1.0	—	
		2.0	200	0.5	—	0	0	0.5	0	0	0.5	0.5	—	
		3.0	200	0	—	0.5	0	0	0	0	0	0.5	—	
		4.0	200	0	—	0.5	0	0	0	0	0	0.5	—	
		5.0	200	1.5	—	0	0.5	0	0	0	0.5	0.5	—	
	48	1.0	200	0.5	—	0	0.5	0.5	0	0	1.0	1.0	—	
		2.0	200	0	—	0.5	0	0	0	0	0	0.5	—	
		3.0	200	1.0	—	0	0	0.5	0	0	0.5	0.5	—	
		4.0	200	0	—	1.0	0	0	0	0	0	1.0	—	
		5.0	200	1.0	—	0	0	0.5	0	0	0.5	0.5	—	
Positive Control														
(MMC)	24	0.00008	200	0	—	2.0	6.5	30.0	0	0	33.0	33.5	+	
	48	0.00008	200	0.5	—	2.0	8.0	49.5	0	0.5	53.0	53.5	+	

<u>Experimental Data</u>													
(Square glass bottle, sealed)													
Treated Time (Hr)	Concentration (mg/ml)	No. of Meta-phase	Poly-ploid (%)	Judge	Cell with Structural Chromosome Aberration (%)							Judge	
					Gap	CTB	CTE	CSB	CSE	Total			
										-G	+G		
CMC	24		200	0.5	—	1.0	0	0	0	0	0	1.0	—
Test Chemical	24	3.0	200	0.5	—	0	0	2.5	0	0	2.5	2.5	—
		4.0	200	2.5	—	0	1.0	2.5	0	0	3.5	3.5	—
		5.0	200	1.5	—	1.0	1.5	9.5	0	0	11.0	11.5	+
		6.0	200	0	—	1.0	1.5	19.5	0	0	23.0	23.5	+
		7.0	200			No observation for metaphase							
Positive Control (MMC)	24	0.00008	200	0.5	—	4.5	7.5	48.0	0	0	50.0	50.0	+

Experimental Data

(Petri dish)

S 9 with or without	Concent- ration (mg/ml)	No. of Meta- phase	Poly- ploid (%)	Judge	Cell with Structural Chromosome Aberration (%)								
					Gap	CTB	CTE	CSB	CSE	Total		Judge	
										-G	+G		
CMC	-	200	0	-	0	1.0	0	0	0	0	1.0	1.0	-
	+	200	0	-	0	0	0	0	0	0	0	0	-
Test Chemical													
-	1.3	200	0	-	0	0.5	0.5	0	0	0	1.0	1.0	-
	2.5	200	0	-	0.5	0	0	0	0	0	0	0.5	-
	5.0	200	2.5	-	0	0.5	0	0	0	0	0.5	0.5	-
	7.5	200	1.0	-	0	0	0	0	0	0	0	0	-
	10.0					No observation for metaphase							
+	1.3	200	0	-	0.5	0	0.5	0	0	0	0.5	1.0	-
	2.5	200	0	-	0.5	0	0	0	0	0	0	0.5	-
	5.0	200	1.0	-	0.5	0.5	0	0	0	0	0.5	1.0	-
	7.5	200	0.5	-	0	1.0	0	0	0	0	1.0	1.0	-
	10.0					No observation for metaphase							
Positive Control													
(B(a)P)	-	200	0.5	-	0	0	0	0	0	0	0	0	-
	+	200	0	-	4.0	7.0	26.0	0	0	0	29.5	32.0	+