3,3'-Dimethyl-4,4'-biphenylene diisocyanate (3,3'-ｼﾞﾒﾁﾙ-4,4'-ﾋﾞﾌｪﾆﾚﾝｼﾞｲｿｼｱﾅｰﾄ)

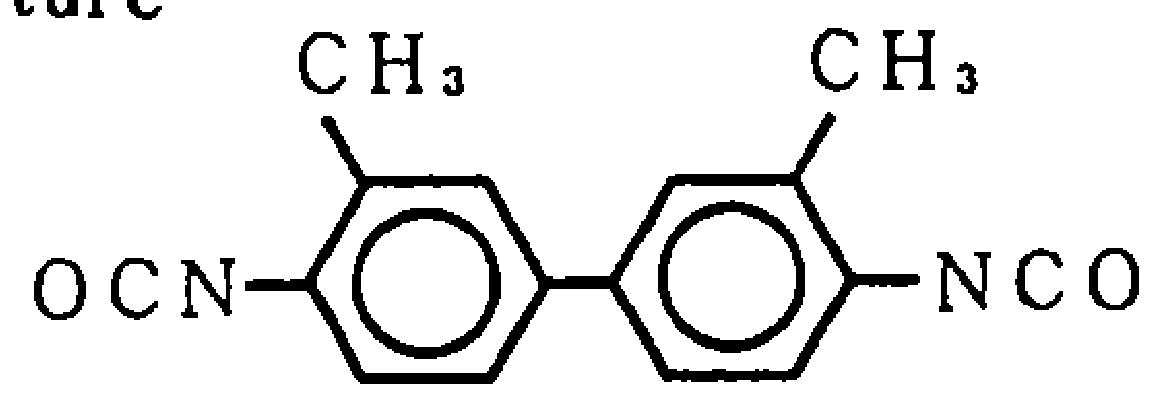
Experimental Data

Chemical Name: 3,3'-Dimethyl-4,4'-biphenylene diisocyanate

Synonym: 4,4'-Diisocyanate-3,3'-dimethyl-1,1'-biphenyl
Isocyanic acid, 3,3'-dimethyl 4,4'-biphenylene ester
o-Tolidine diisocyanate

Molecular weight: 264.29
Melting point: 19.6 ℃
Boiling point: 195-197℃

Chemical Structure



CAS No : 91-97-4
MITI No : (4)-33

Source of Substance: Nippon Soda Co., Ltd.
Lot.No.:
Purity: %
Vehicle: DMSO

	Treated Time (Hr)	Concentration (mg/ml)	No. of Metaphase	Polyploid (%)	Judge	Cell with Structural Chromosome Aberration (%)							
											Total		
						Gap	CTB	CTE	CSB	CSE	-G	+G	Judge
DMSO	24		200	0	−	0	0.5	0	0	0	0.5	0.5	−
	48		200	0	−	0.5	0	0.5	0	0	0.5	1.0	−
Test Chemical													
	24	0.1	200	1.0	−	0	0	0	0	0	0	0	−
		0.2	200	0	−	0	0	0.5	0	0	0.5	0.5	−
		0.3	200	1.5	−	1.5	0	1.0	0	0	1.0	2.5	−
		0.4	200	1.5	−	2.5	2.5	1.5	0	0	3.0	5.0	±
		0.5				No observation for metaphase							
	48	0.1	200	0	−	0.5	0	0	0	0	0	0.5	−
		0.2	200	0	−	0	0	1.5	0	0	1.5	1.5	−
		0.3	200	2.0	−	0	0	1.0	0	0.5	1.5	2.0	−
		0.4	200	2.0	−	0.5	0.5	1.0	0	1.0	2.5	2.5	−
		0.5				No observation for metaphase							
Positive Control													
(MMC)	24	0.00008	200	0	−	2.5	6.0	34.0	0	0	38.5	39.0	+
	48	0.00008	200	1.5	−	2.0	9.0	44.5	0	0.5	49.0	50.0	+

Judgement for
Chromosomal Aberration in CHL: Positive

IARC Evaluation : not yet cited

Experimental Data

	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 -G	Total +G	Judge
DMSO	−		200	0	−	0.5	0	0.5	0	0	0.5	1.0	−
	+		200	0.5	−	1.5	0	0	0	0	0	1.5	−
Test Chemical													
	−	0.2	200	0	−	0.5	0	0	0	0	0	0.5	−
		0.3	200	0	−	0	0	0.5	0	0	0.5	0.5	−
		0.4	200	0.5	−	0	0	0	0	0	0	0	−
		0.5	200	6.0	±	1.5	0.5	3.5	0	0	3.5	4.5	−
		0.6				No observation for metaphase							
	+	0.2	200	0	−	0.5	0.5	0	0	0	0.5	1.0	−
		0.3	200	1.0	−	1.0	0	0	0	0	0	1.0	−
		0.4	200	0.5	−	1.0	0	0.5	0	0	0.5	1.5	−
		0.5	200	1.5	−	2.0	1.5	1.5	0	0	2.5	4.0	−
		0.6	177	2.8	−	5.1	2.3	6.2	0	0	7.9	11.3	+
Positive Control (B(a)P)	−		200	1.0	−	1.0	0	0	0	0	0	1.0	−
	+		200	0.5	−	5.5	4.0	27.5	0	0	29.0	31.0	+