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ESTIMATION OF GAS-PHASE THERMOKINETIC
PARAMETERS. VOLUME I. A FORTRAN PROGRAM
FOR COMPUTING THE THERMOCHEMICAL
PROPERTIES OF COMPLEX GAS MOLECULES
BY THE METHOD OF GROUP ADDITIVITY. BOOK
2-APPENDIXES

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McDonnell Douglas Astronautics Company

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VOLUME I

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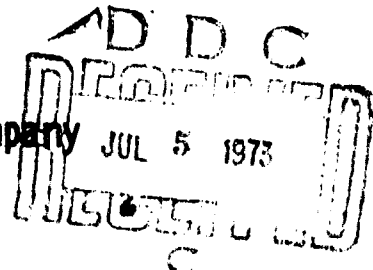
BOOK 2 - APPENDICES

Prepared by

McDonnell Douglas Astronautics Company
Huntington Beach, California

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CONTRACT REPORT NO. 107

REPORT NO. MDC G4388

ESTIMATION OF GAS-PHASE THERMOKINETIC PARAMETERS

VOLUME I

A FORTRAN PROGRAM FOR COMPUTING THE THERMOCHEMICAL PROPERTIES
OF COMPLEX GAS MOLECULES BY THE METHOD OF GROUP ADDITIVITY

BOOK 2 - APPENDIXES

APRIL 1973

BY

DR. MARIA RAMOS MARTINEZ
ADVANCE AERO/THERMODYNAMICS AND NUCLEAR EFFECTS

FOR

BALLISTIC RESEARCH LABORATORIES

PREPARED BY

MCDONNELL DOUGLAS ASTRONAUTICS COMPANY
HUNTINGTON BEACH, CALIFORNIA

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13. ABSTRACT A FORTRAN program for calculating the thermodynamic properties of complex gas molecules by the method of group additivity is documented herein. Included are descriptions of the computational method, characteristics, functions, input/output formats, and logic structure of the program. Seventeen case calculations for diversely structured molecules are presented. Also depicted are a listing of the program, a complete glossary of the program variables and the tables of data comprising the data library input.			

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Chemical Kinetics						

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Appendix A
TGAP GROUP ADDITIVITY DATA LIBRARY

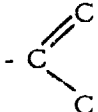
The Group Additivity Data Library is the permanent source of thermochemical data of the TGAP program. These data were derived from Benson's book (1). The data are listed below in three separate tables. A few revisions are included in the tables. These were obtained directly through the courtesy of Dr. Sidney Benson, via telephone communication.

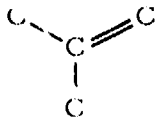
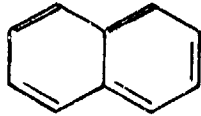
The heat capacity data of Benson has been curve fitted to the equation $C_p = c_0 + c_1 T + c_2 T^2 + c_3 T^4$. The program makes use of these coefficients instead of the tabular heat capacity data to compute the various thermodynamic properties of the molecule. The values of the coefficients are listed in the tables together with the corresponding value for the heat of formation and entropy at 298 K.

A.1 THERMOCHEMICAL GROUP CONTRIBUTIONS

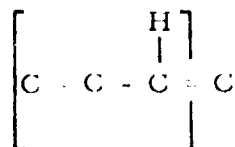
Table A-1 contains the Thermochemical group contributions for hydrocarbons and for oxygen- and nitrogen-containing compounds. The table constitutes a listing of a printout option of the program (See Section 3.1.1).

In the table, the composition of the groups is defined by specific symbols. In addition to the symbols C, H, O and N which have their usual chemical significance other symbols are also used. These are defined below:

<u>Symbol</u>	<u>Definition</u>
D	-C = C
T	-C ≡ C
Z	 (in benzene)

<u>Symbol</u>	<u>Definition</u>	
Z1		central carbon group in fused aromatic rings
		e.g. 
A	C = C = C	
N1	-N = C	
N2	-N = N	

The core atom of the group is always listed first followed by the symbols for the group ligands. For example, DDH represents the group



The thermochemical group values for Z1 were computed by the author. The results were derived by subtracting the sum of eight Z groups from the corresponding thermodynamic property value for gaseous naphthalene and dividing the result by two. The data for naphthalene were obtained from Reference 4 (Book 1).

A. 2 CORRECTIONS FOR RING STRUCTURES

Table A-2 contains the nongroup ring corrections for a series of hydrocarbon, oxygen- and nitrogen-containing rings. Saturated and partially unsaturated as well as single and fused ring structures are included. These data are stored in the program per group function. Consequently, as missing data become available, they can be readily incorporated into the program.

A. 3 NEXT-NEAREST NEIGHBOR CORRECTIONS

The corrections for next-nearest neighbor interactions are given in Table A-3. The special molecular assignments for H_f^{298} and S_{298}° were described in Section 5.3.3.

Table A-1
 TABLES OF THERMOCHEMICAL GROUP CONTRIBUTIONS

GROUP	WEIGHT	HEAT OF FORMATION		ENTROPY		DATA FOR HYDROCARBONS		HEAT CAPACITY COEFFICIENTS	
		KCAL/MOLE 298 K	KCAL/DEG-MOLE 298 K	CAL/DEG-MOLE 298 K	CAL/DEG-MOLE 298 K	CAL/DEG-MOLE	CAL/DEG-MOLE	CAL/DEG-MOLE	CAL/DEG-MOLE
CH4C	296	-10.3800	30.4100	-1.679238340	.0248328426	.0000116714	.0000000022		
CH3CC	399	-4.5500	9.4200	-1.253911080	.0228786843	-.0900132553	.0000000030		
CH2CCC	502	-1.5000	-12.0700	-1.1723317900	.0265408883	.0000204192	.0000000056		
CHCCC	605	.5000	-35.1000	-4.1724432040	.0381256429	-.0000360168	.0000000107		
CH	1031	6.2000	27.6100	1.1557868560	.0194481085	.0000106666	.0000000023		
CHC	1134	8.5900	7.9700	1.8496673370	.0126226360	.00000063208	.0000000011		
CHC	1237	10.3400	-12.7000	2.1278483200	.0072124957	.00000049459	.0000000011		
CHC	2008	6.7000	6.3000	-1.10380755700	.0238648291	.0000196912	.0000000050		
CHC	2111	6.8800	-14.6000	1.3339654170	.0187546888	.0000182763	.0000000057		
CHC	2214	6.7000	6.3800	-1.1360755700	.0232648291	-.0000196512	.0000000058		
CHC	2314	6.6000	-14.6000	1.3339654170	.0187546888	.0000182763	.0000000057		
CHC	2409	6.7800	6.3800	-1.10380755700	.0238648291	.0000196512	.0000000058		
CHC	1273	-4.7600	9.8000	-1.1971603360	.0292631432	-.0000198328	.0000000051		
CHC	2147	-4.2900	10.2900	-3.17385440300	.0357678715	.0000269846	.0000000075		
CHC	2150	-4.2900	10.2900	-3.17385440300	.0357678715	.0000269846	.0000000075		
CHC	1274	-4.7300	10.3000	-1.13139338600	.0254749883	.0000156771	.0000000037		
CHC	1276	-4.8000	9.3400	-1.12931592600	.0300487840	.0000221458	.0000000059		
CHC	1376	-1.4800	-11.6900	-3.16040155200	.0337235204	.0000282179	.0000000082		
CHC	1377	-1.7200	-11.1500	-2.18399206600	.0291372022	.0000228410	.0000000064		
CHC	1379	-1.9800	-12.1900	-2.18910800400	.0341308621	.0000298252	.0000000097		
CHC	1470	1.6800	-34.7200	-5.16657888900	.0437931905	.0000417271	.0000000125		
CHC	1482	2.8100	-35.1600	-6.13231489100	.0499863257	.0000506946	.0000000154		
CH	1024	26.5300	24.7000	2.15622169400	.0115236646	.0000087032	.0000000025		
CH	1127	27.5500	6.3500	1.4668673070	.0069433901	.0000054627	.0000000020		
CH	2011	29.2000	6.4300	1.1143259500	.0154355057	.0000117472	.0000000030		
CH	2014	29.2000	6.4300	-1.1143259500	.0154355057	.0000117472	.0000000030		
CH	1016	3.3000	11.5300	-1.16891748400	.0201929000	.0000135394	.0000000034		
CH	1119	5.5000	-7.6500	1.7148216410	.007509018	.0000021992	.0000000001		
CH	1993	5.6800	7.8000	2.10392057700	.0057575321	.0000021371	.0000000000		
CH	1994	5.6800	-7.8000	-2.10392057700	.0057575321	.0000021371	.0000000000		
CH	1996	4.5600	8.6400	1.111683760	.0179264165	.0000159957	.0000000047		
CH	997	34.2000	6.0900	1.8886443180	.0087392859	.0000071663	.0000000020		
CH	999	4.8400	-4.6325	-1.0445622480	.0128993697	.0000102398	.0000000029		

Table A-1

TABLES OF THERMOCHEMICAL GROUP CONTRIBUTIONS (Continued)

DATA FOR OXYGEN-CONTAINING GROUPS

(CO)(CO)C	1502	-29,2000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2	1825	-33,5000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)OZ	1838	-46,0000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)OC	901	-33,4000	14,7800	3,1924243400	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)OH	878	-29,5000	34,9300	4,6330096300	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)ZH	1717	-31,7000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)ZC	2700	-39,1000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)ZC	1823	-37,6000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)ZC	1740	-31,7000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)CC	946	-31,5000	15,0300	3,1089144000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)CH	843	-29,6000	34,9300	4,6330096300	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)CH	750	-27,7000	53,6700	6,2663876200	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)(CO)C	1524	-50,5000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2	1073	-19,0000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2	1842	-41,3000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	968	-41,3000	8,3500	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	805	-61,3000	24,5200	-1,8852445700	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	447	-24,5000	5,4200	1,9937598500	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	482	19,0000	9,4000	3,9937598500	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	344	-16,2700	27,8500	2,4972053200	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	2160	-32,8000	8,1000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	1286	-31,3000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	2156	-19,3000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	1289	-22,6000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	1196	-37,9000	29,1000	4,8016326300	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	412	-23,7000	8,6800	3,7350787000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	319	-37,8800	26,0200	5,0581202900	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	1828	6,3000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2C	1793	9,4000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	1690	7,6800	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	2146	8,6000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	1272	10,3000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	1169	8,0000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	1675	9,7000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	1194	-1,8000	-10,2000	-4,4497723400	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	1511	-7,2000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	1028	-1,8000	-12,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	955	-5,0000	9,6000	1,3596201380	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	1161	-1,6000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	872	-10,0800	30,4100	-1,1679238340	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	675	-16,2000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	572	-17,2000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	469	-17,7000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	1311	-6,6000	9,7000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	1308	-6,6000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	640	-6,6000	-33,5600	-6,2146738100	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	537	-7,0000	-11,0000	-5,1897782000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	434	-8,5000	10,0800	-3,4611576000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
(CO)O2H	331	-10,0800	30,4100	-1,1758713840	0,0000000000	0,0000000000	0,0000000000	0,0000000000

Table A-1

TABLES OF THERMOCHEMICAL GROUP CONTRIBUTIONS (Continued)

DATA FOR ALIPHATIC-CONTAINING GROUPS

CAHMH	712	-10,0800	39,4100	-1479238340	0244328424	-50000116714	00000000622
CAHMM	815	-6,6000	9,8000	-1,8919676100	0301279382	00000233047	00000000074
CAHCC	918	-5,2000	-11,7000	-3,7379120600	0382564597	00000362709	00000000140
CAHCC	1024	-3,2000	-34,1000	-5,4117685700	0475192184	00000538081	00000000291
CAHCH	699	4,8000	29,7100	2,8959473800	0100598751	0000023272	00000000001
CAHCH	802	15,4000	6,9400	1,0095954513	0170255903	00000109772	00000000026
CAHCC	905	24,4000	-13,4600	-1,8410294200	0233777734	00000208419	00000000060
CAHCH	1115	11,4000	29,1300	1,9759068520	0211752446	00000146100	00000000039
CAHCH	1218	20,5000	9,5100	1,9568461210	0164283897	00000126832	00000000035
CAHCC	1321	29,2000	-13,8000	0,0000000000	00000000000	00000000000	00000000000
CAHCH	2099	22,1000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	479	0,0000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	583	21,3000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	1429	16,7000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	527	25,1000	26,8000	2,419114000	0071523525	00000022180	00000000000
CAHCH	630	32,5000	-8,0400	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	1376	4,8000	29,7100	2,8959473800	0100598751	0000023272	00000000001
CAHCH	1479	16,9000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	1782	26,2000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	2356	16,2000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	3335	-1,5000	-9,6900	-3,3715753900	00369462129	00000046672	000000000181
CAHCH	1044	23,0000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	1259	-29,6000	34,9300	4,6330796330	0065844185	00000060340	00000000051
CAHCH	1362	-32,6000	16,2300	3,6876785500	0038940571	00000370014	00000000034
CAHCH	1625	-14,9000	24,6900	-3,2529295200	0389737873	00000242737	00000000078
CAHCH	1356	-4,4000	3,9300	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	1461	0,0000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	2235	4,8000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	1914	-18,5000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	2017	-5,9000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	2874	2,3000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	679	22,5000	40,2000	1,5936711300	0380737392	00000228626	00000000045
CAHCH	782	25,8000	19,8000	4,4547547800	029552780	00000149811	00000000020
CAHCH	865	0,0000	-2,8000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	1165	0,0000	28,4500	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	1414	37,4000	36,5800	1,6278912400	0341575604	00000250052	00000000065
CAHCH	1717	84,1000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	1247	0,0000	44,4000	1,9059065240	0524768384	00000376314	00000000102
CAHCH	1399	35,8000	20,5000	3,1311565000	0294963575	00000270021	00000000095
CAHCH	1392	63,2000	35,4000	4,3238018900	0346234963	00000186637	00000000032
CAHCH	512	-15,1000	48,4900	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	615	-15,8000	26,9000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	718	0,0000	3,9800	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	728	-14,9000	0,0000	0,0000000000	0,0000000000	0,0000000000	0,0000000000
CAHCH	518	-5,9000	41,9300	4,1979442100	0191590634	00000122788	00000000027
CAHCH	525	-19,4000	48,5000	0,0000000000	0,0000000000	0,0000000000	0,0000000000

Table A-2
CORRECTIONS FOR RING STRUCTURES




Ring	ΔH_f° keal/mole	S_{298}° cal/deg-mole	C_P° cal/deg-mole	Coefficients		
				cal/deg ² -mole	cal/deg ³ -mole	cal/deg ⁴ -mole
Cyclopropane	27.6	32.1	-5.5952	1.1577×10^{-2}	-1.115×10^{-5}	3.50×10^{-9}
Cyclopropene	53.7	33.6	-			
Cyclobutane	26.2	29.8	-7.9609	1.3812×10^{-2}	-9.772×10^{-6}	2.54×10^{-9}
Cyclobutene	29.8	29.0	-4.1570	7.0499×10^{-3}	-5.930×10^{-6}	1.69×10^{-9}
Cyclopentane	6.3	27.3	-1.2010	1.7322×10^{-2}	-8.845×10^{-6}	1.65×10^{-9}
Cyclopentene	5.9	25.8	-7.9649	6.4757×10^{-3}	4.718×10^{-7}	-1.15×10^{-9}
Cyclopentadiene	6.0					
Cyclohexane	0	18.8				
Cyclohexene	1.4	21.5				
1,3 Cyclohexadiene	4.8					
1,4 Cyclohexadiene	0.5					
Cycloheptane	6.4	15.9				
Cycloheptene	5.4					
1,3 Cycloheptadiene	6.6					
1,3,5 Cycloheptatriene	4.7	23.7				
Cyclooctane	9.9	16.5				
Cis-cyclooctene	9.0					
Trans-cyclooctene	15.3					
1,3,5 Cyclooctatriene	8.9					
Cyclooctatetraene	17.1					
Cyclononane	12.8					
Cis-cyclononene	9.9					
Trans-cyclononene	12.8					
Spiropentane	63.5	67.6				
Bicyclo-(1,1,0)-butane	68.4	69.2				
Bicyclo-(2,1,0)-pentane	55.3					
Bicyclo-(3,1,0)-hexane	32.7					
Bicyclo-(4,1,0)-heptane	28.9					
Bicyclo-(5,1,0)-octane	29.6					
Bicyclo-(6,1,0)-nonane	31.1					
	27.6	31.4	4.5377	-3.6617×10^{-2}	5.709×10^{-5}	-2.73×10^{-8}
	26.4	27.7	-5.3154	2.4626×10^{-3}	-4.325×10^{-6}	7.39×10^{-9}
	6.7					

Table A-2
CORRECTIONS FOR RING STRUCTURES (Continued)














Ring	ΔH_f° kcal/mole	S_{298}° cal/deg-mole	C_p° cal/deg-mole	Coefficients		
				cal/deg ² -mole	cal/deg ³ -mole	cal/deg ⁴ -mole
	2.2					
	3.5					
	5.4					
	3.4					
	-6.2					
	2.5					
	6.0					
	3.4					
	1.1					
	1.4					
	4.6					
	27.7	31.6				
	26.2	29.3				

Table A-2
CORRECTIONS FOR RING STRUCTURES (Continued)





Ring	ΔH_f°	S_{298}°	C_p°	Coefficients		
	kcal/mole	cal/deg-mole	cal/deg-mole	cal/deg ² -mole	cal/deg ³ -mole	cal/deg ⁴ -mole
	6.8	26.7	-7.4924	1.4742×10^{-3}	1.186×10^{-5}	-8.02×10^{-9}
	1.0					
	3.4					
	8.5					

Table A-3
NEXT-NEAREST NEIGHBOR CORRECTIONS

Interaction	H_f°	S_{298}°	C_p°	Coefficients		
	kcal/mole	cal/deg-mole	cal/deg-mole	cal/deg ² -mole	cal/deg ³ -mole	cal/deg ⁴ -mole
Alkane gauche	0.80					
Alkene gauche	0.50					
Ether oxygen gauche	0.3					
Di-tertiary ethers	8.4					
Cis	1.00 (a)	0 (a)	-2.7198	5.8531×10^{-3}	-4.785×10^{-6}	1.39×10^{-9}
Ortho (benzene)	0.57	-1.61	3.6765×10^{-1}	4.4047×10^{-3}	-6.267×10^{-6}	2.10×10^{-9}
Ortho/para(pyridine)	-1.5					

(a) See Table 5-4 for exceptions.

Appendix B
FLOW LIST OF TGAP PROGRAM

The flow list of the TGAP program and the program glossary presented in the following section were generated by the McDonnell Douglas JOYCE Automated Documentation System. The flow list comprises a listing of the source program bounded by brackets or arrows on the left and right margins. The brackets on the left margin delineate the cycles or DO loops of the program. The brackets on the right margin delineate all transfers, both conditional and unconditional. The numbers of the statements to which the transfers are made are also depicted. The flow list of the main routine, TGAP, is presented first followed by the flowlists of the 54 subroutines of the program listed in alphabetical order. The names of the routines and their respection locations in the text are presented below.

	<u>Routine</u>	<u>Page</u>
1	TGAP	12
2	ASSIGN	16
3	ASYMC	18
4	BOND	19
5	CHAINM	20
6	CHANGE	22
7	CIS	23
8	CISCOR	25
9	CORCIG	28
10	CRINGS	34
11	CTWO	36
12	CYCORR	38
13	DATA1	45
14	DELETE	50
15	DELTA1	51
16	DELTA2	52
17	DITERE	53
18	ENTSYM	54
19	EQUAL	56
20	EQUALR	60
21	EXTROT	65

<u>Routine</u>	<u>Page</u>
22 FIND	70
23 FIRSTR	71
24 FUSION	73
25 GADATA	76
26 GAUCHE	77
27 HEXGON	80
28 IDENT	85
29 INTROT	88
30 LESSEN	89
31 LINEAR	92
32 MAXCHN	93
33 MULTI	95
34 NEWCOL	96
35 NEWKC	97
36 NRINGS	98
37 NUMBER	99
38 ORDER	100
39 OXYATM	101
40 PRINT1	102
41 PRINT2	103
42 RESETR	104
43 RING	105
44 SAME	106
45 SCAN	107
46 SCANBR	109
47 SCANCH	110
48 SEARCH	111
49 SETUP	112
50 SHIFT	114
51 SORNGI	115
52 STAND	117
53 SUMATM	121
54 SYMRNG	122
55 SYMTRY	127

TGAP

```

1. PROGRAM TGAP(INPUT,OUTPUT,TAPE5=INPUT,TAPE6=OUTPUT) TGAP
2. C THIS IS THE MAIN OR CONTROL UNIT OF THE THERMOCHEMICAL GROUP TGAP
3. C ADDITIVITY PROGRAM (TGAP). IT PRINTS OUT THE DATA LIBRARY TGAP
4. C (OPTIONAL), READS AND PRINTS OUT INPUT DATA, TRANSFERS CONTROL TGAP
5. C TO THREE MAIN SECTIONS OF THE PROGRAM, AND COMPUTES AND PRINTS TGAP
6. C THE THERMOCHEMICAL PROPERTIES OF THE MOLECULE. TGAP
7. INTEGER ENDCS1,ENDCS2,ENDCS3,ENDRUN,CASE,BLANK,ALTER(20,2), TGAP
8. IORDSUM(100),SEARCH TGAP
9. INTEGER SYM(4),SYMBOL(9),GRID(50,80) TGAP
10. INTEGER WRIGHT(9) TGAP
11. INTEGER SUM(100) TGAP
12. DIMENSION TARRAY(14),CPT(14),ST(14),HST(14),FT(14),HSOT(14), TGAP
13. INTT(14),CPI(4),CPSYM(4),KGRID(103),LABEL(50) TGAP
14. COMMON/BLK1/NO,NOS,SYMR,SYMBOL,NOVAL(9),GRID TGAP
15. COMMON/BLK2/WEIGHT,MWGT(9),MOLWT(100),IX(100,5,6),NC(100),KCC TGAP
16. COMMON/BLK3/IRING(40,30),IMATX(50,80),NW(100),IBC(100),KON(100), TGAP
17. IIOBR(100),IB(100,8),IRO,NOBR TGAP
18. COMMON/BLK4/NBC(60,50),NBS(60,2),NBX(60,20),IRC,NONFUS,INCTOT TGAP
19. COMMON/BLK5/NDATM,NUMATM(5),MBC(50),MBS(2),JM,JV,LFLAGS,LFLAGB TGAP
20. COMMON/BLK6/NUMFRO(24) TGAP
21. COMMON/BLK7/SUM,MP298(100),S298(100),CPX(100,4) TGAP
22. EQUIVALENCE (CPT(1),IMATX(5,1)),(ST(1),IMATX(19,1)),(HST(1), TGAP
23. IMATX(33,1)),(FT(1),IMATX(47,1)),(HSOT(1),IMATX(11,2)),(HTT(1), TGAP
24. IMATX(25,2)),(KGRID(1),NBC(1,7)),(LABEL(1),NBC(1,4)) TGAP
25. DATA (SYM(1),1=1,4)/1H-1H-1H-1H / TGAP
26. DATA NDATM/ 5/,NOS/ 9/,(SYMBOL(1),WEIGHT(1),1=1,9) /1HH. 10, TGAP
27. 11HC, 121,1HO, 156,1HN, 537,1HE, 498,2HCO, 677,2HCN, 401, TGAP
28. 22HNO, 217,3HNO2, 234/ TGAP
29. DATA (MST(1),1=1, 9)/0,0,14,5,0,27,0,0,0/ TGAP
30. DATA (NUMFRO(1),1=1,24)/2,1,3,1,1,0,2,1,4,1,1,0,4,1,3,1,1,0, TGAP
31. 14,1,3,2,1,0/ TGAP
32. DATA NOVAL/1,4,2,3,1,2,1,1,1/ TGAP
33. DATA ALTER(1,1)/1170/,ALTER(1,2)/296/,ALTER(2,1)/2985/,ALTER(2,2) TGAP
34. 1/2111/,ALTER(3,1)/1171/,ALTER(3,2)/296/,ALTER(4,1)/1173/, TGAP
35. 2ALTER(4,2)/296/,HAL/4/ TGAP
36. DATA TARRAY/298.0,300.0,400.0,500.0,600.0,700.0,800.0,900.0, TGAP
37. 11000.0,1200.0,1600.0,1800.0,2000.0/ TGAP
38. DATA ENDCS1/1H=/,ENDCS2/1H=/,ENDCS3/1H=/,ENDRUN/3HEND/,BLANK/1H /, TGAP
39. ISUM/100=0/ TGAP
40. C1.0 INITIALIZE VARIABLE. TGAP
41. CASE=0 TGAP
42. C2.0 READ IN DATA. TGAP
43. C READ IN PRINTOUT OPTIONS (IPRINT) AS WELL AS THE TGAP
44. C OPTIONAL VARIABLES COMPRISING THE EXTERNAL SYMMETRY NUMBER TGAP
45. C (NOSN), THE NUMBER OF ENANTIOMERS (NENAN), AND THE NUMBER OF TGAP
46. C MESO STRUCTURES (MESO). A MOLECULE IDENTIFICATION LABEL TGAP
47. C (LABEL) MAY BE INPUT IF DESIRED. TGAP
48. 1 READ(5,2)IEND,IPRINT,NOSN,NENAN,MESO,LABEL TGAP
49. 2 FORMAT(A3,4I3,15X,50A1) TGAP
50. C IF END CARD PRESENT, STOP. TGAP
51. IF(IEND.EQ.ENDRUN)STOP TGAP
52. NO=0 TGAP
53. C READ IN GRAPHIC STRUCTURE OF MOLECULE. TGAP
54. 3 NO=NO+1 TGAP
55. READ(5,4)(GRID(NO,L),L=1,80) TGAP
56. 4 FORMAT(80A1) TGAP
57. IF(GRID(NO,1).NE.ENDCS1.OR.GRID(NO,2).NE.ENDCS2.OR.GRID(NO,3).NE. TGAP
58. IENDCS3)GO TO 3 TGAP
59. C END OF CASE DATA INPUT CARD REACHED. DELETE LAST CARD TGAP
60. C FROM NO COUNTER AND INCREMENT THE VARIABLE CASE. TGAP
61. NO=NO-1 TGAP
62. IF(NO.LE.0)GO TO 1 TGAP
63. CASE=CASE+1 TGAP
64. C3.0 PRINT OUT GROUP ADDITIVITY DATA TABLES ON FIRST PASS PROVIDING TGAP
65. C JPRINT IS NON-ZERO. TGAP
66. JPRINT=IPRINT/10 TGAP
67. JPRINT=IPRINT-10=JPRINT TGAP
68. IF(CASE.NE.1)GO TO 498 TGAP
69. KPRINT=IPRINT/100 TGAP
70. KPRINT=(IPRINT-100=KPRINT)/10 TGAP
71. 498 IF(CASE.EQ.1.AND.JPRINT.NE.0)CALL GADATA TGAP
72. C4.0 HEADIN: PRINTOUT OPTIONS. TGAP
73. WRITE(6,9) TGAP
74. 9 FORMAT(1M) TGAP

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17 APR 73 0.02-36

75.		IF(KPRINT.NE.0.AND.KPRINT.NE.2)GO TO 502	TGAP	502
76.	C	PRINT OUT TITLE.	TGAP	
77.		WRITE(6,500)	TGAP	
78.		500 FORMAT(1H,37X,54HGROUP ADDITIVITY THERMOCHEMICAL PROPERTIES P	TGAP	
79.		INORAM //)	TGAP	
80.		502 IF(KPRINT.NE.0.AND.KPRINT.NE.3)GO TO 506	TGAP	506
81.	C	PRINT OUT CASE NUMBER.	TGAP	
82.		WRITE(6,504)CASE	TGAP	
83.		504 FORMAT(1H,55X,12HCASE NUMBER,16//)	TGAP	
84.		506 WRITE(6,508)	TGAP	
85.		508 FORMAT(1H,54X,20HMOLECULAR STRUCTURE //)	TGAP	
86.	CS.0	CENTER STRUCTURAL DATA FOR PRINTOUT PURPOSES.	TGAP	
87.	C	FIND LEFT(MBL) AND RIGHT(MBR) BOUNDARIES OF ARRAY LABEL.	TGAP	
88.		MBL=50	TGAP	
89.		MBR=1	TGAP	
90.		DO402 L=1,50	TGAP	
91.		IF(LABEL(L).EQ.BLANK)GO TO 602	TGAP	602
92.		IF(L.GE.MBL)GO TO 600	TGAP	600
93.		MBL=L	TGAP	
94.		600 IF(L.LE.MBR)GO TO 602	TGAP	602
95.		MBR=L	TGAP	
96.		602 CONTINUE	TGAP	
97.	C	FIND INITIAL LOCATION IN KGRID INTO WHICH COLUMN OF DATA	TGAP	
98.	C	FROM ARRAY LABEL IS TO BE TRANSFERRED.	TGAP	
99.	C	BLANK OUT KGRID ARRAY AND DETERMINE IF IDENTIFICATION NAME	TGAP	
100.	C	WAS INPUT.	TGAP	
101.		DO606 L=1,103	TGAP	
102.		KGRID(L)=BLANK	TGAP	
103.		IF(MBL.EQ.50.AND.MBR.EQ.1)GO TO 616	TGAP	616
104.		LL=64-(MBR-MBL+1)/2	TGAP	
105.	C	TRANSFER DATA FROM LABEL INTO DESIGNATED LOCATIONS OF KGRID	TGAP	
106.	C	AND PRINT OUT.	TGAP	
107.		DO610 L=MBL,MBR	TGAP	
108.		KGRID(LL)=LABEL(L)	TGAP	
109.		LL=LL+1	TGAP	
110.		WRITE(6,612)(KGRID(L),L=1,88)	TGAP	
111.		612 FORMAT(1H,88A1//)	TGAP	
112.	C	FIND LEFT(MDL) AND RIGHT(MBR) GRID BOUNDARIES.	TGAP	
113.		616 MBL=80	TGAP	
114.		MBR=1	TGAP	
115.		DO8 K=1,NO	TGAP	
116.		DO8 L=1,80	TGAP	
117.		IF(KGRID(K,L).EQ.BLANK)GO TO 8	TGAP	8
118.		IF(L.GE.MBL)GO TO 7	TGAP	7
119.		MBL=L	TGAP	
120.		7 IF(L.LE.MBR)GO TO 8	TGAP	8
121.		MBR=L	TGAP	
122.		8 CONTINUE	TGAP	
123.	C	FIND INITIAL LOCATION IN KGRID INTO WHICH COLUMN OF DATA FROM	TGAP	
124.	C	ARRAY GRID IS TO BE TRANSFERRED AND BLANK OUT KGRID ARRAY.	TGAP	
125.		LS=64-(MBR-MBL+1)/2	TGAP	
126.		DO9 L=1,103	TGAP	
127.		KGRID(L)=BLANK	TGAP	
128.	C	TRANSFER COLUMN OF DATA FROM GRID INTO DESIGNATED LOCATIONS	TGAP	
129.	C	OF KGRID AND PRINT OUT.	TGAP	
130.		DO12 K=1,NO	TGAP	
131.		LL=LS	TGAP	
132.		DO10 L=MBL,MBR	TGAP	
133.		KGRID(LL)=KGRID(K,L)	TGAP	
134.		LL=LL+1	TGAP	
135.		WRITE(6,11)(KGRID(L),L=1,103)	TGAP	
136.		11 FORMAT(1H,103A1)	TGAP	
137.		12 CONTINUE	TGAP	
138.	CS.0	TRANSFERS CONTROL TO SECTION ONE OF THE PROGRAM WHICH	TGAP	
139.	C	IDENTIFIES THE GROUPS AND THEIR STRUCTURAL AND WEIGHT DATA.	TGAP	
140.		IERR=0	TGAP	
141.		CALL STAND(IERR)	TGAP	
142.		IF(IERR.13,14,15	TGAP	
143.	C	ERROR EXISTS. TRANSFER TO PRINTOUT ROUTINE AND EXIT FROM	TGAP	14 13
144.	C	CASE CALCULATION.	TGAP	
145.		13 CALL PRINT	TGAP	

146.		GO TO 1	TGAP	
147.	C7.0	TRANSFERS CONTROL TO SECTION TWO OF THE PROGRAM WHICH FINDS THE	TGAP	
148.	C	CHAIN SEGMENTS AND UNIQUE RINGS (IF ANY).	TGAP	
149.		14 CALL CHAINMLK, IERR)	TGAP	
150.	C	IF ERROR EXISTS TRANSFER TO PRINTOUT ROUTINE AND EXIT FROM	TGAP	
151.	C	CASE CALCULATION.	TGAP	
152.		IF(IERR)13, 15, 13	TGAP	15 13
153.	C8.0	TRANSFER CONTROL TO SECTION THREE OF THE PROGRAM WHICH FINDS	TGAP	
154.	C	ALL SECOND-ORDER AND RING CORRECTIONS AS WELL AS CONTRIBUTIONS	TGAP	
155.	C	DUE TO INTERNAL AND EXTERNAL ROTATIONAL SYMMETRY AND OPTICAL	TGAP	
156.	C	ISOMERISM.	TGAP	
157.		15 CALL CORCIG(NOSM, MENAN, MESO, LX, HSYM, SSYM, CPSYM)	TGAP	
158.	C9.0	COMPUTE AND PRINT OUT THERMOCHEMICAL PROPERTIES OF MOLECULE.	TGAP	
159.	C	TRANSFER THERMOCHEMICAL CONTRIBUTIONS DERIVED FROM SECTION	TGAP	
160.	C	THREE TO CORRESPONDING VARIABLES DELH, S, AND CP.	TGAP	
161.		DELH=MSYM	TGAP	
162.		S=SSYM	TGAP	
163.		DO21 J=1, 9	TGAP	
164.		CP(J)=CPSYM(J)	TGAP	
165.	C	FIND ORDER MAX ELEMENTS OF ARRAY SUM WOULD HAVE IF ARRANGED	TGAP	
166.	C	IN NUMERICAL ORDER AND STORE SAID ORDER (RELATIVE TO INITIAL	TGAP	
167.	C	ORDER) IN ORDSUM.	TGAP	
168.		MAX=163	TGAP	
169.		CALL ORDER(MAX, ORDSUM, SUM)	TGAP	
170.	C	FIND LOCATION IN GROUP ADDITIVITY DATA ARRAYS CONTAINING THE	TGAP	
171.	C	DATA CORRESPONDING TO THE COMPUTED WEIGHT MOLWT(K) OF GROUP K	TGAP	
172.		LFLAGG=0	TGAP	
173.		DO69 K=1, KCC	TGAP	
174.		ISER=SEARCH(SUM, ORDSUM, 163, MOLWT(K), IT)	TGAP	
175.	C	WAS WEIGHT MATCH ACHIEVED	TGAP	
176.		IF(I SER.NE.0)GO TO 25	TGAP	25 67
177.		IF(IT.GT.0.AND.IT.LE.163)GO TO 67	TGAP	
178.	C	NO. DOES AN ALTERNATE DATA GROUP HEIGHTY EXIST FOR GROUP K	TGAP	
179.		25 DO33 L=1, NAL	TGAP	
180.		IF(MOLWT(K).NE.ALTER(L, 1))GO TO 33	TGAP	33 67
181.	C	YES IT DOES. FIND ITS LOCATION IN DATA ARRAYS. OTHERWISE	TGAP	
182.	C	PRINT OUT MESSAGE INDICATING DATA ARE MISSING.	TGAP	
183.		ISER=SEARCH(SUM, ORDSUM, 163, ALTER(L, 2), IT)	TGAP	63 67
184.		IF(I SER)63, 67, 63	TGAP	
185.		33 CONTINUE	TGAP	
186.		63 WRITE(6, 65)K, MOLWT(K)	TGAP	
187.		65 FORMAT(1H0, 26X, 14HDATA FOR GROUP, 14, 18H WITH A WEIGHT OF, 16,	TGAP	
188.		135H ARE NOT IN PROGRAM DATA LIBRARY.)	TGAP	
189.		LFLAGG=1	TGAP	
190.	C	MOST LIKELY, A MATCH WAS ACHIEVED. NOW ADD THE THERMO-	TGAP	
191.	C	CHEMICAL DATA FOR GROUP K TO DELH, S, AND CP.	TGAP	
192.		67 DELH=DELH+HF298(IT)	TGAP	
193.		S=S+S298(IT)	TGAP	
194.		DO68 J=1, 9	TGAP	
195.		68 CP(J)=CP(J)+CPK(IT, J)	TGAP	
196.		69 CONTINUE	TGAP	
197.	C	DETERMINE IF THERMOCHEMICAL DATA OUTPUT IS COMPLETE. IF NOT,	TGAP	
198.	C	PRINT OUT WARNING MESSAGE.	TGAP	
199.		IF(LFLAGG.EQ.0)GO TO 75	TGAP	75
200.		WRITE(6, 73)	TGAP	
201.		73 FORMAT(// 1H0, 1X, 126HWARNING --- ALL OF THE THERMOCHEMICAL VALUE	TGAP	
202.		IS FOR ONE OR MORE GROUPS ARE MISSING. THE THERMOCHEMICAL DATA BELO	TGAP	
203.		W ARE INCOMPLETE.)	TGAP	
204.		75 IF(LFLAGG.EQ.0)GO TO 83	TGAP	83
205.		WRITE(6, 77)	TGAP	
206.		77 FORMAT(// 1H0, 21X, 87HWARNING --- ENTROPY AND FREE ENERGY DATA BELO	TGAP	
207.		W MAY BE OFF A FEW PERCENT DUE TO POSSIBLE 1/1N, 2/1N, 2/1N CONTRIBUTIO	TGAP	
208.		2/1N) FROM EXTERNAL ROTATIONAL SYMMETRY OR AND OPTICAL ISOMERISM.)	TGAP	
209.	C	PRINT OUT NET HEAT CAPACITY COEFFICIENTS OF MOLECULE. ALSO	TGAP	
210.	C	COMPUTE AND PRINT OUT THE HEAT CAPACITY, ENTROPY, ENTHALPY,	TGAP	
211.	C	RIGID FREE ENERGY, H-H298), AND TOTAL ENTHALPY FOR	TGAP	
212.	C	TEMPERATURES SPECIFIED IN ARRAY TARRAY.	TGAP	
213.		83 HCOHS=(1/4*(CP(4)+298.0/4.0+CP(3)/3.0)+298.0+CP(2)/2.0)+298.0+	TGAP	
214.		1/CP(1))+298.0)/1000.0	TGAP	
215.		SCONS=S-CP(1)+ALOG(298.0)-((CP(4)+298.0/3.0+CP(3)/2.0)+298.0+	TGAP	
216.		1/CP(2))+298.0	TGAP	

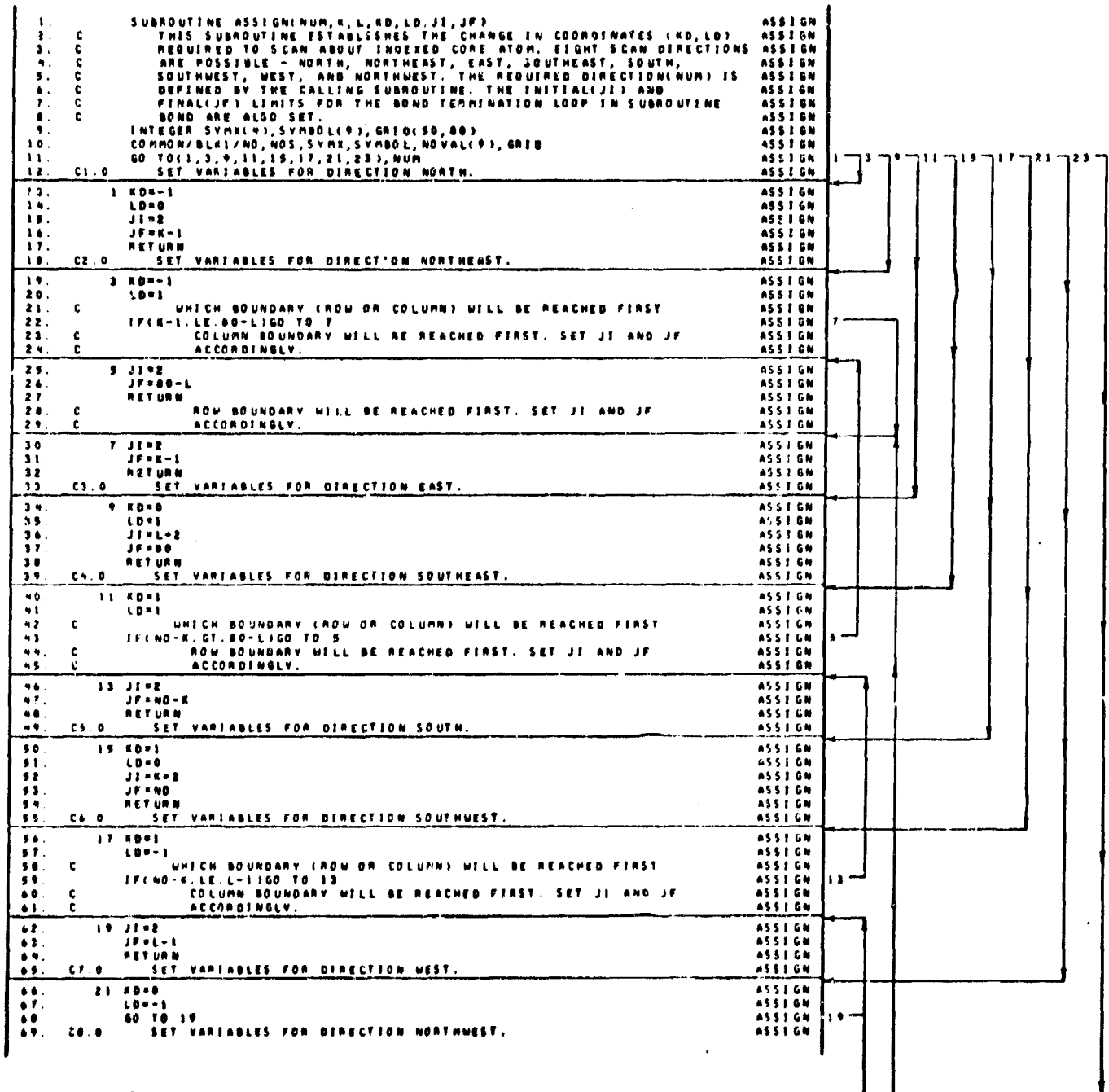
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217.      0085      J=1,14          T&AP
218.      CPT(J)=CP(1)+(CP(4)-TARRAV(J)+CP(3))*TARRAV(J)+CP(2)*TARRAV(J) T&AP
219.      ST(J)=CP(1)+ALOG(TARRAV(J))+((CP(4)-TARRAV(J))/3.0+CP(3)/2.0) T&AP
220.      1*TARRAV(J)+CP(2))*TARRAV(J)+SCONS T&AP
221.      MST(J)=(((CP(4)-TARRAV(J))/4.0+CP(3))/3.0)*TARRAV(J)+CP(2)/2.0+ T&AP
222.      1TARRAV(J)+CP(1))*TARRAV(J)/1000.0 T&AP
223.      HSDT(J)=MST(J)-HCONS T&AP
224.      FT(J)=-(HSDT(J)+1000.0-TARRAV(J)+ST(J))/TARRAV(J) T&AP
225.      HTT(J)=HSDT(J)+DELM T&AP
226.      65 CONTINUE T&AP
227.      WRITE(6,87)(CP(J),J=1,4) T&AP
228.      87 FORMAT(//1H,4X,40THERMOCHEMICAL PROPERTIES OF MOLECULE // T&AP
229.      11H,51X,24HEAT CAPACITY COEFFICIENTS /1H,20X,12NCAL/DEG-MOLE T&AP
230.      25X,15NCAL/DEG**2-MOLE,5X,15NCAL/DEG**3-MOLE,5X,15NCAL/DEG**4-MOLE/ T&AP
231.      31H,22X,2E19.0,2E20.8) T&AP
232.      WRITE(6,88) T&AP
233.      88 FORMAT(//1H,15X,1MT,11X,4MC(P),14X,1MS,11X,9MH(T)-M(O),3X, T&AP
234.      116H-(G(T)-H(298))/T,5X,11MH(T)-H(298),3X,22HDELHF(298)+H(T)-H(298) T&AP
235.      2/1H,11X,5HDEG K,5X,12NCAL/DEG-MOLE,5X,12NCAL/DEG-MOLE,5X, T&AP
236.      39HKCAL/MOLE,5X,12NCAL/DEG-MOLE,6X,9HKCAL/MOLE,11X,9HKCAL/MOLE) T&AP
237.      WRITE(6,89)(TARRAV(J),CPT(J),ST(J),MST(J),FT(J),HSDT(J),HTT(J), T&AP
238.      1J=1,14) T&AP
239.      89 FORMAT(1H,8X,F8.1,SF16.6,F20.6) T&AP
240.      GO TO 1 T&AP
241.      END T&AP

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ASSIGN



70. 22 00-1
71. 00-1
72. 17010-01-01-1107, 7, 19
73. 000

ASSIGN
ASSIGN
ASSIGN
ASSIGN

10 000 70 0-00-10

ASYMC

```
1.      SUBROUTINE ASYMC(NASYMC)                                ASYMC
2.      C      THIS SUBROUTINE DETERMINES THE NUMBER OF ASYMMETRIC CARBON ASYMC
3.      C      ATOMS PRESENT IN THE MOLECULE.                   ASYMC
4.      C      INTEGER SYMX(4),SYMBOL(9),GRID(50,80)           ASYMC
5.      C      INTEGER WEIGHT(9)                                 ASYMC
6.      C      DIMENSION IOPATR(100),JBR(100),KCSAME(6,100)     ASYMC
7.      C      COMMON/BLK1/NO,NOS,SYMX,SYMBOL,NVAL(9),GRID     ASYMC
8.      C      COMMON/BLK2/WEIGHT,MMGT(9),MOLWT(100),IX(100,9,6),NC(100),KCC ASYMC
9.      C      COMMON/BLK3/IRING(40,30),IMATX(50,80),NW(100),IBC(100),KON(100), ASYMC
10.     C      IDBR(100),IB(100,8),IRG,NOBR                    ASYMC
11.     C      EQUIVALENCE (IOPATR(1),IMATX(2,49)),(JBR(1),IMATX(2,43)), ASYMC
12.     C      I(KCSAME(1,1),GRID(4,48))                       ASYMC
13.     C1.0 INITIALIZE COUNTER NASYMC.                         ASYMC
14.     C      NASYMC=0                                         ASYMC
15.     C2.0 EXECUTE SEARCH FOR ASYMMETRIC ATOMS.               ASYMC
16.     C      DO9 K=1,KCC                                       ASYMC
17.     C      IF(KCSAME(1,K).NE.0.OR.IX(K,1).NE.2.OR.IBC(K).NE.0.OR. ASYMC
18.     C      IJBR(K).NE.4)GO TO 9                               ASYMC
19.     C      CORE ATOM K IS A NON-RING CARBON ATOM WITH FOUR LIGANDS ALL ASYMC
20.     C      OF WHICH ARE DISSIMILAR.                         ASYMC
21.     C      NASYMC=NASYMC+1                                   ASYMC
22.     C      IOPATR(NASYMC)=K                                  ASYMC
23.     S CONTINUE                                             ASYMC
24.     RETURN                                                  ASYMC
25.     END                                                      ASYMC
```

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BOND

```
1. SUBROUTINE BOND(KX, LX, KD, LD, JJ, JF, I, IERR) BOND
2. C THIS SUBROUTINE DETERMINES THE TYPE OF BOND AT A SPECIFIED BOND
3. C DIRECTION OF THE INDEXED CORE ATOM. IT ALSO SCANS SYMBOL INPUT BOND
4. C ARRAY ALONG THIS DIRECTION UNTIL A SYMBOL UNEQUAL TO THE BOND
5. C DESIGNATED BOND IS DETECTED. BOND
6. C INTEGER SYM(4), SYMBOL(9), GRID(50, 60) BOND
7. C COMMON/BLKI/NO, NOS, SYM, SYMBOL, NOVAL(9), GRID BOND
8. C1.0 DETERMINE IF INPUT SYMBOL IS A BOND SYMBOL. BOND
9. C DO1 I=1,3 BOND
10. C IF(GRID(KX, LX).EQ.SYM(I))GO TO 11 BOND
11. C CONTINUE BOND
12. C NO, IT IS NOT. PRINT ERROR MESSAGE, SET ERROR FLAG, AND EXIT. BOND
13. C WRITE(6, 5)KX, LX BOND
14. C 5 FORMAT(// 1H0, 20X, 22MERROR - BOND SYMBOL AT, 14, 1H, , 14, 4H MISSING BOND
15. C 1 OR INCORRECT. CASE TERMINATED.) BOND
16. C7 IERR=1 BOND
17. C RETURN BOND
18. C YES, IT IS. BOND
19. C2.0 FIND LOCATION OF NON-BOND SYMBOL AND EXIT. BOND
20. C11 DO 13 JJ=J1, JF BOND
21. C KX=KX+KD BOND
22. C LX=LX+LD BOND
23. C IF(GRID(KX, LX).NE.SYM(I))RETURN BOND
24. C13 CONTINUE BOND
25. C THERE IS NO NON-BOND SYMBOL. PRINT ERROR MESSAGE, SET ERROR BOND
26. C FLAG, AND EXIT. BOND
27. C WRITE(6, 15)KX, LX BOND
28. C 15 FORMAT(1H0, 15X, 22MFREE RADICAL AT GRID COORDINATES, 15, 1H, , 15) BOND
29. C GO TO 7 BOND
30. C END BOND
```

CHAINM

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1. SUBROUTINE CHAINM(LX, IERR)
2. C THIS SUBROUTINE IS THE CONTROL ELEMENT FOR SECTION TWO OF THE
3. C PROGRAM. THIS SECTION IDENTIFIES THE CHAIN FORMATIONS PRESENT
4. C IN THE MOLECULE AS WELL AS THE NUMBER OF UNIQUE RINGS AND THE
5. C RING COMPONENTS.
6. C INTEGER WEIGHT(9)
7. C DIMENSION AA(4), JUNCT(5, 100), NOBRD(100)
8. C COMMON/BLK2/WEIGHT, MWGT(9), MOLWT(100), IX(100, 5, 6), NC(100), KCC
9. C COMMON/BLK3/IRING(40, 30), IMATX(50, 80), NM(100), IBC(100), KON(100),
10. C IDBR(100), IR(100, 8), IRG, NOBR
11. C COMMON/BLK4/NBC(60, 50), NBS(60, 2), NBR(60, 20), IAC, NOMFUS, IACTOT
12. C EQUIVALENCE (JUNCT(1, 1), IMATX(3, 1)), (NOBRD(1), IMATX(3, 11))
13. C DATA AA/4M, IR, 4RING(1, 1), 4MNBC(1, 1)
14. C1.0 INITIALIZE VARIABLES.
15. C LM=1
16. C LZ=1
17. C NBP=0
18. C MDIF=0
19. C DD1 = LM, KCF
20. C 1 IBCCL=0
21. C2.0 SEARCH FOR TERMINAL GROUP.
22. C DD3 = LM, KCC
23. C IF(NC(L).EQ.1)GO TO 5
24. C 3 CONTINUE
25. C NO TERMINAL GROUP IS PRESENT.
26. C KCM=1
27. C MDIF=KC
28. C GO TO 7
29. C TERMINAL GROUP IS PRESENT.
30. C 5 KCM=1
31. C3.0 IF BRANCH ATOMS ARE PRESENT, SET BRANCH COMPUTATION VARIABLES
32. C NOBRD AND JUNCT.
33. C 7 IF(NOBR.EQ.0)GO TO 12
34. C DD1 = LM, NOBR
35. C KK=IDBR(L)
36. C NOBRD(KK)=1
37. C JF=NC(KK)
38. C DD10 = JF, JF
39. C JUNCT(J, KK)=IX(KK, J+1, 6)
40. C 10 CONTINUE
41. C4.0 STORE FIRST ATOM OF FIRST CHAIN IN NBC. IS IT A BRANCH ATOM
42. C 12 NBCCL(L, LM)=IX(KC, 1, 6)
43. C IF(NC(L).LE.2)GO TO 13
44. C KC IS A BRANCH ATOM. FIND NEW KC.
45. C NBP=NBP+1
46. C NBC(L, NBP)=LM
47. C NOBRD(KC)=0
48. C IFLAG1=1
49. C CALL NEWKC(KCPV, KC, IFLAG1, IFLAG2)
50. C GO TO 13
51. C KC IS NOT A BRANCH ATOM. FIND NEW KC.
52. C 13 KCPV=KC
53. C KC=IX(KC, 2, 6)
54. C5.0 START OF CHAIN EVALUATION CYCLE.
55. C 15 LMLM=1
56. C SET LM. IF NUMBER OF CHAINS EXCEEDS DIMENSION (50) OF ARRAY
57. C NBC, PRINT OUT MESSAGE AND EXIT.
58. C IF(LM.GE.50)GO TO 21
59. C NBC(LM, LM)=IX(KC, 1, 6)
60. C IS RING STRUCTURE PRESENT IN MOLECULE
61. C IF(ING.EQ.0)GO TO 18
62. C YES, DETERMINE IF RING STRUCTURE IS CONTAINED IN CHAIN.
63. C LMLM=1
64. C DD1 = KM=1, LM
65. C IF(NBC(L, KM).NE.NBC(L, LM))GO TO 17
66. C RING STRUCTURE CONTAINED IN CHAIN. STORE RING
67. C COMPONENTS.
68. C CALL RING(LM, LM, IERR)
69. C IF(IERR.EQ.0)GO TO 18
70. C NUMBER OF RING COMPONENTS EXCEEDS DIMENSION OF ARRAY
71. C IRING. PRINT OUT MESSAGE AND EXIT.
72. C NALY=LM-KM
73. C WRITE(6, 30)AA(1), AA(2), IAC, NALY

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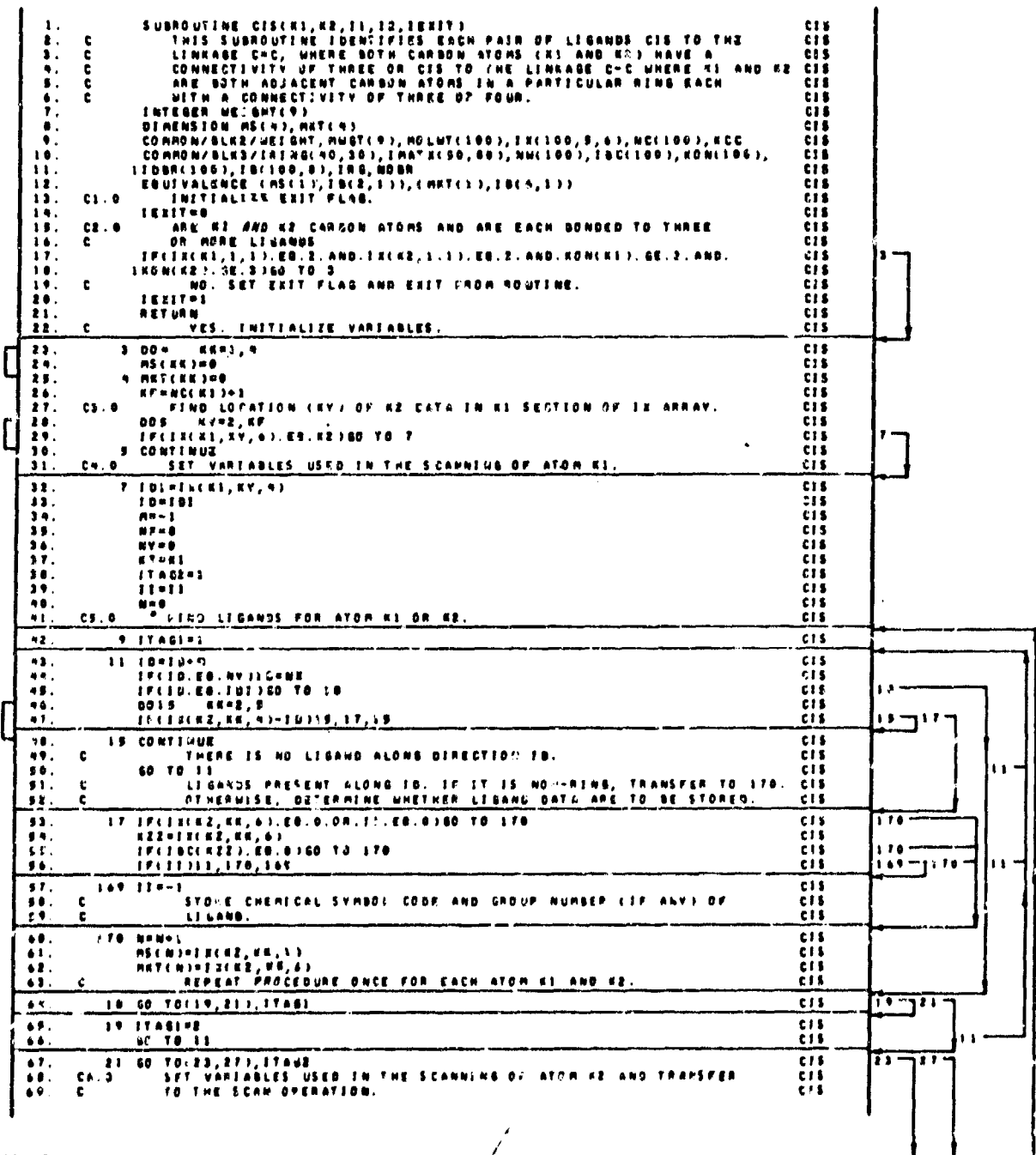
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74.	RETURN	CHAINR	
75.	16 LM=LM-1	CHAINR	
76.	C IF KK=1, CHAIN IS A DUPLICATE. DISCARD CHAIN LX.	CHAINR	
77.	IF(KK.NE.-1)GO TO 19	CHAINR	17
78.	LXL=LX-1	CHAINR	
79.	GO TO 20	CHAINR	20
80.	17 CONTINUE	CHAINR	
81.	18 IF(NC(KC)-2)19,25,27	CHAINR	19-25-27
82.	C KC IS TERMINAL ATOM.	CHAINR	
83.	19 LXL=LX	CHAINR	
84.	C SET NBS ARRAY.	CHAINR	
85.	20 NBS(LX,1)=LM	CHAINR	
86.	NBS(LX,2)=NBP	CHAINR	
87.	C IF UNUSED BRANCH ATOMS REMAIN, SET UP NEW CHAIN. OTHERWISE,	CHAINR	
88.	GO TO 23.	CHAINR	23
89.	IF(NBP.LE.0)GO TO 23	CHAINR	
90.	CALL NEWCOL(LX,LXL,NBP,LX,KC,KCPV,LA,IERR)	CHAINR	23
91.	IF(IERR.EQ.0)GO TO 22	CHAINR	22
92.	21 WRITE(6,30)AA(3),AA(4),LX,LM	CHAINR	
93.	30 FORMAT(// 1H0,34X,26HARRAY DIMENSION EXCEEDED -,2A4,12,1H,,12,	CHAINR	
94.	120H). CASE TERMINATED.)	CHAINR	
95.	RETURN	CHAINR	
96.	22 IF(NBP.GT.0)GO TO 15	CHAINR	15
97.	C IF MORE THAN ONE RING IS PRESENT, DELETE NON-UNIQUE	CHAINR	
98.	RINGS FROM SET.	CHAINR	
99.	23 IF(INC.GT.1)CALL LESSEN(INC)	CHAINR	
100.	C IF RINGS ARE PRESENT, POSSIBLY REDEFINE CHAIN SET.	CHAINR	
101.	IF(INC.GT.0)CALL RESETR(MDIF,LX)	CHAINR	
102.	C CHECK ALL CHAINS FOR POSSIBLE FINAL REDEFINITION.	CHAINR	
103.	CALL CHANGE(LX)	CHAINR	
104.	RETURN	CHAINR	
105.	C KC IS A CHAIN ATOM. STORE KC DATA IN VARIABLES, FIND NEW KC,	CHAINR	
106.	AND CONTINUE SEARCH.	CHAINR	
107.	25 IF(KCPV.EQ.IX(KC,2,4))GO TO 26	CHAINR	26
108.	KCPV=KC	CHAINR	
109.	KC=IX(KC,2,4)	CHAINR	
110.	GO TO 15	CHAINR	15
111.	26 KCPV=KC	CHAINR	
112.	KC=IX(KC,3,4)	CHAINR	
113.	GO TO 15	CHAINR	15
114.	C KC IS A BRANCH ATOM. STORE KC DATA IN VARIABLES, FIND NEW KC,	CHAINR	
115.	AND CONTINUE SEARCH.	CHAINR	
116.	27 NBP=NBP+1	CHAINR	
117.	NBS(LX,NBP)=LM	CHAINR	
118.	CALL NEWKC(KCPV,KC,0,IFLAG2)	CHAINR	
119.	GO TO 15	CHAINR	15
120.	END	CHAINR	

CHANGE

1.		SUBROUTINE CHANGE(LI)	CHANGE
2.	C	THIS SUBROUTINE REDEFINES ALL EXISTING CHAINS IN ARRAY NBC IF	CHANGE
3.	C	A CHAIN EXISTS THAT (1) HAS ONE BRANCH ATOM ONLY (2) AND ITS	CHANGE
4.	C	UPPER RESIDUAL (I2) IS GREATER THAN ITS LOWER RESIDUAL (I1).	CHANGE
5.	C	IF MORE THAN ONE SUCH CHAIN EXISTS, THE ONE WITH THE MAXIMUM	CHANGE
6.	C	I2-I1 IS CHOSEN AS THE REFERENCE.	CHANGE
7.		COMMON/BLK4/NBC(60,5),NR(40,2),NBR(60,20),IRC,NONFUS,IRCTOT	CHANGE
8.	C1.0	INITIALIZE VARIABLE.	CHANGE
9.		MAXD=0	CHANGE
10.	C2.0	INITIALIZE CYCLE THAT SEARCHES FOR CHAIN WITH ONE BRANCH ATOM	CHANGE
11.	C	AND MAXIMUM I2-I1.	CHANGE
12.		DO4 L=1,LI	CHANGE
13.		IF(NBC(L,2).NE.1)GO TO 4	CHANGE
14.	C	CHAIN L HAS ONLY ONE BRANCH ATOM.	CHANGE
15.		I1=NBR(L,1)-1	CHANGE
16.		I2=NBS(L,1)-NBR(L,1)	CHANGE
17.		MDIF=I2-I1	CHANGE
18.		IF(MDIF.LE.MAXD)GO TO 4	CHANGE
19.	C	MDIF MAXIMUM VALUE THUS FAR. STORE CHAIN PROPERTIES.	CHANGE
20.		MAXD=MDIF	CHANGE
21.		MAXL=L	CHANGE
22.	4	CONTINUE	CHANGE
23.		IF(MAXD.EQ.0)RETURN	CHANGE
24.	C3.0	POSITIVE DIFFERENTIAL OBTAINED. REDEFINE ALL CHAINS EXCEPT MAXL	CHANGE
25.		MAXIZ=NBR(MAXL,1)	CHANGE
26.		DO10 L=1,LI	CHANGE
27.		IF(L.EQ.MAXL)GO TO 10	CHANGE
28.	C	CHAIN L IS NOT CHAIN MAXL (REFERENCE). REDEFINE ITS VARIABLES	CHANGE
29.		JF=NBS(L,1)	CHANGE
30.		MX=JF-1	CHANGE
31.		DO10 J=MAXIZ,JF	CHANGE
32.		MX=MX-1	CHANGE
33.		MY=NBC(L,1)	CHANGE
34.	10	NBC(L,MY)=NBC(L,MX)	CHANGE
35.		MX=NBS(MAXL,1)-1	CHANGE
36.		JF=NBS(MAXL,1)-MAXIZ	CHANGE
37.		DO10 J=1,JF	CHANGE
38.		MX=MX-1	CHANGE
39.	12	NBC(L,J)=NBC(MAXL,MX)	CHANGE
40.		NBS(L,1)=NBS(L,1)+MAXD	CHANGE
41.		JF=NBS(L,2)	CHANGE
42.		DO16 J=1,JF	CHANGE
43.	16	NBR(L,J)=NBR(L,J)+MAXD	CHANGE
44.	10	CONTINUE	CHANGE
45.		JF=NBS(MAXL,1)/2	CHANGE
46.		MX=NBS(MAXL,1)-1	CHANGE
47.	C4.0	REDEFINE VARIABLES OF CHAIN MAXL.	CHANGE
48.		DO24 J=1,JF	CHANGE
49.		MX=MX-1	CHANGE
50.		MY=NBC(MAXL,J)	CHANGE
51.		NBC(MAXL,J)=NBC(MAXL,MX)	CHANGE
52.	24	NBC(MAXL,MY)=MY	CHANGE
53.		NBR(MAXL,1)=NBR(MAXL,1)+MAXD	CHANGE
54.		RETURN	CHANGE
55.		END	CHANGE

C18



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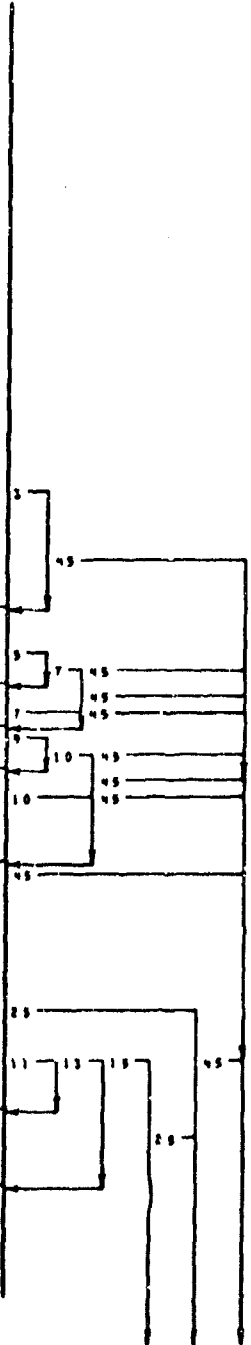
70.	23	101=121(1, RV, 4)49	CIS
71.		17(111(1, RV, 4), 07, 4)101=101-0	CIS
72.		10=101	CIS
73.		R=1	CIS
74.		R1=1	CIS
75.		RV=9	CIS
76.		RZ=K2	CIS
77.		1YAG2=2	CIS
78.		11=12	CIS
79.		60 YR 9	CIS
80.	27	RETURN	CIS
81.		END	CIS

CISCOR

```

1. SUBROUTINE CISCOR(K1,K2,I1,I2,IGS,IGSCIS,ICIS,CISH,CISS) CISCOR
2. C THIS SUBROUTINE DETERMINES WHETHER THE LIGANDS OF ATOMS K1 AND CISCOR
3. C K2 EXHIBIT A CIS INTERACTION. IF SO, IT ESTABLISHES THE NUMBER, CISCOR
4. C TYPE, AND MAGNITUDE OF THIS CORRECTION. CISCOR
5. C INTEGER WEIGHT(9) CISCOR
6. C DIMENSION HCAUS(3,150),KFGAUS(150),KTGAUS(150),DATCIS(2,150), CISCOR
7. C IAS(4),MRT(4) CISCOR
8. C COMMON/BLR2/WEIGHT,AMST(9),MOLWT(100),IX(100,9,6),NC(100),KCC CISCOR
9. C COMMON/BLR3/IRING(40,30),IMATR(50,80),NM(100),IBC(100),KON(100), CISCOR
10. C IIDBR(100),IS(100,8),IRB,NOBR CISCOR
11. C EQUIVALENCE (HCAUS(1,1),IMATR(1,72)),(KFGAUS(1),IMATR(1,63)), CISCOR
12. C IKTGAUS(1),IMATR(1,60)),(DATCIS(1,1),IMATR(1,66)),(MS(1), CISCOR
13. C ZIB(2,1)),(MRT(1),IBC(1)) CISCOR
14. C1.0 IDENTIFY THE CIS COMPONENTS OF ATOMS K1 AND K2. CISCOR
15. C CALL CIS(K1,K2,I1,I2,TEXT) CISCOR
16. C IF K1 AND K2 ARE BOTH CARBON ATOMS WITH A CONNECTIVITY OF CISCOR
17. C THREE OR MORE CONTINUE. OTHERWISE EXIT FROM ROUTINE. CISCOR
18. C IF ITEXT.NE.0 RETURN CISCOR
19. C2.0 INITIALIZE VARIABLES. CISCOR
20. C KLM=0 CISCOR
21. C KTCRA=0 CISCOR
22. C KBU=0 CISCOR
23. C KTL=0 CISCOR
24. C KTR=0 CISCOR
25. C KCIS=0 CISCOR
26. C KNEW=0 CISCOR
27. C3.0 EXECUTE LOOP THAT TESTS CIS COMPONENTS. CISCOR
28. C DO45 L=1,2 CISCOR
29. C IF IAS(L).NE.1.OR.MS(L*2).NE.1 GO TO 5 CISCOR
30. C BOTH CIS ATOMS ARE HYDROGEN ATOMS. THERE IS NO CIS CORRECTION CISCOR
31. C IN THIS CASE. INCREMENT HYDROGEN COUNTER AND TRANSFER. CISCOR
32. C KLM=KLM+1 CISCOR
33. C GO TO 45 CISCOR
34. C ARE BOTH CIS ATOMS CARBON ATOMS EACH WITH A CONNECTIVITY CISCOR
35. C GREATER THAN TWO. CISCOR
36. C 3 L1=MRT(L) CISCOR
37. C L2=MRT(L+2) CISCOR
38. C IF IAS(L).NE.2 GO TO 5 CISCOR
39. C IF ICON(L1)-2149,45,7 CISCOR
40. C 5 IF IAS(L).NE.6 GO TO 45 CISCOR
41. C IF ICON(L1)-1149,45,7 CISCOR
42. C 7 IF IAS(L+2).NE.2 GO TO 9 CISCOR
43. C IF ICON(L2)-2149,45,10 CISCOR
44. C 9 IF IAS(L+2).NE.6 GO TO 45 CISCOR
45. C IF ICON(L2)-1149,45,10 CISCOR
46. C YES THEY ARE. ARE BOTH CIS ATOMS RING ATOMS AND PART OF THE CISCOR
47. C SAME RING SYSTEM IF SO, THERE IS NO CIS INTERACTION CISCOR
48. C BETWEEN THIS PAIR. TRANSFER TO 45. CISCOR
49. C 10 IF IBC(L1)=IBC(L2).NE.0.AND.IBC(L1).EQ.IBC(L2) GO TO 45 CISCOR
50. C CIS INTERACTION EXISTS. SET VARIABLES AND INCREMENT CIS CISCOR
51. C COUNTER KCIS. CISCOR
52. C KTL=0 CISCOR
53. C KCL=0 CISCOR
54. C KCP=0 CISCOR
55. C KCS=0 CISCOR
56. C KCIS=KCIS+1 CISCOR
57. C IF ICON(L1).NE.4 GO TO 25 CISCOR
58. C LIGAND ON ATOM K1 HAS A CONNECTIVITY OF FOUR. CISCOR
59. C K5=KCON(L1)+1 CISCOR
60. C GO TO I(49,11,12,13,14),K5 CISCOR
61. C LIGAND HAS NO CORE LIGANDS EXCEPT K1. INCREASE COUNTER CISCOR
62. C AND TRANSFER. CISCOR
63. C 11 KBU=KBU+1 CISCOR
64. C GO TO 25 CISCOR
65. C LIGAND HAS THREE CORE LIGANDS IN ADDITION TO K1. PROCESS CISCOR
66. C VARIABLES. CISCOR
67. C 13 KTL=KTL+1 CISCOR
68. C KTL=0 CISCOR
69. C LIGAND HAS ONE OR TWO CORE LIGANDS IN ADDITION TO K1. IF CISCOR
70. C AT LEAST ONE IS A CARBON ATOM, INCREMENT KCL COUNTER. IF CISCOR
71. C LATTER LIGAND HAS ONLY ONE CORE ATOM AND PARENT LIGAND HAS CISCOR
72. C ONLY TWO, INCREMENT KCS COUNTER. CISCOR

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73.	19 0023	N=2, 45	CIS COR	
74.		IF (ISCLL, 0, 0) .EQ. 01. OR. (ISCLL, 0, 1) .NE. 2160 TO 21	CIS COR	21
75.		PCLNCL=1	CIS COR	
76.		NCNCLL, 0, 0	CIS COR	21
77.		IF (NCLCCH, 0) .ST. 1. OR. (NCLL, 1) .NE. 2160 TO 21	CIS COR	
78.		NC3=NC3-1	CIS COR	
79.		GO TO 29	CIS COR	29
80.	21	CONTINUE	CIS COR	
81.	20	IF (NCLL, 0) .NE. 4160 TO 45	CIS COR	45
82.	C	LEGAND ON ATOM 42 HAS A CONNECTIVITY OF FOUR.	CIS COR	
83.		45=NCLL-1	CIS COR	45
84.		GO TO 46, 31, 35, 39, 33, 45	CIS COR	33
85.	C	LEGAND HAS NO CORE LEGAND EXCEPT 42. INCREMENT COUNTER	CIS COR	45
86.	C	AND TRANSFER.	CIS COR	
87.	31	EDU=EDU+1	CIS COR	
88.		GO TO 45	CIS COR	45
89.	C	LEGAND HAS THREE CORE LEGANDS IN ADDITION TO 42. PROCESS	CIS COR	
90.	C	VARIABLES.	CIS COR	
91.	33	ATOM=ATOM+1	CIS COR	
92.		IF (ATALL, 0) .1. INTETRA=ATCTRA+1	CIS COR	
93.		LEGAND HAS ONE OF TWO CORE LEGANDS IN ADDITION TO 42. IF	CIS COR	
94.	C	AT LEAST ONE IS A CARBON ATOM. INCREMENT RCA COUNTER. IF	CIS COR	
95.	C	LATTER LEGAND HAS ONLY ONE CORE ATOM AND PARENT LEGAND HAS	CIS COR	
96.	C	ONLY TWO. INCREMENT RCS COUNTER.	CIS COR	
97.	35	0037	CIS COR	37
98.		IF (ISCLL, 0, 0) .EQ. 02. OR. (ISCLL, 0, 1) .NE. 2160 TO 37	CIS COR	
99.		NCNCL=1	CIS COR	
100.		NCNCLL, 0, 0	CIS COR	
101.		IF (NCLCCH, 0) .ST. 1. OR. (NCLL, 1) .NE. 2160 TO 37	CIS COR	37
102.		NC3=NC3-1	CIS COR	
103.		GO TO 43	CIS COR	43
104.	37	CONTINUE	CIS COR	
105.	C	IF NCL, RCA, AND RCS WERE ALL ACTIVATED, SET COUNTER NENE.	CIS COR	
106.	41	IF (NCL, 0) .AND. (RCA, 0) .AND. (RCS, 0) .INENE=NENE+1	CIS COR	
107.	45	CONTINUE	CIS COR	
108.		IF (NCL, 0) .OR. (RCA, 0) .OR. (RCS, 0)	CIS COR	
109.	C	CIS INTERACTION(S) PRESENT. FIND AND APPLY APPROPRIATE	CIS COR	
110.	C	CORRECTIONS.	CIS COR	
111.	C	PROCESS VARIABLES.	CIS COR	
112.		165CIS=165CIS-1	CIS COR	
113.		1CIS=1CIS+RCS	CIS COR	
114.		165=165-1	CIS COR	
115.		RTGAUS=165/4	CIS COR	
116.		RTGAUS=165/4	CIS COR	
117.		RTGAUS=165/4	CIS COR	
118.		RTGAUS=165/4	CIS COR	
119.		RTGAUS=165/4	CIS COR	
120.		RTGAUS=165/4	CIS COR	
121.		GO TO 47, 49, 53, 57, 43, 45 OR	CIS COR	
122.	C	ONE TERTIARY CARBON GROUP PRESENT. SET CORRECTION FOR THE	CIS COR	47
123.	C	HEAT OF FORMATION.	CIS COR	49
124.	49	DATCIS1, 165/4, 0	CIS COR	53
125.	53	IF (NCL, 0) .NE. 2160 TO 73	CIS COR	73
126.	C	TWO CIS INTERACTIONS PRESENT. ADD THIS CORRECTION	CIS COR	73
127.		DATCIS1, 165/4+DATCIS1, 165/4, 0	CIS COR	73
128.		GO TO 73	CIS COR	73
129.	C	TWO TERTIARY CARBON GROUPS PRESENT. ARE THEY BOTH CIS	CIS COR	
130.	57	IF (NCL, 0) .NE. 2160 TO 37	CIS COR	37
131.	C	YES. SET CORRECTION FOR THE HEAT OF FORMATION	CIS COR	
132.		DATCIS1, 165/4+165/4, 0	CIS COR	57
133.		GO TO 73	CIS COR	
134.	C	NO. SET CORRECTION FOR THE HEAT OF FORMATION	CIS COR	
135.	57	DATCIS1, 165/4, 0	CIS COR	
136.		GO TO 73	CIS COR	73
137.	C	THREE TERTIARY CARBON GROUPS PRESENT. SET CORRECTION FOR	CIS COR	
138.	C	THE HEAT OF FORMATION	CIS COR	
139.	59	DATCIS1, 165/4+165/4, 0	CIS COR	
140.		GO TO 73	CIS COR	73

141. C	FOUR TERTIARY CARBON GROUPS PRESENT. SET CORRECTION FOR	CIS COR	
142. C	THE HEAT OF FORMATION.	CIS COR	
143.	43 DAYCIS1, 165 120.0	CIS COR	
144.	GO TO 73	CIS COR	
145. C	NO TERTIARY CARBON GROUPS PRESENT. ARE THERE ONE OR TWO CIS	CIS COR	
146. C	INTERACTIONS	CIS COR	
147.	45 IFICIS1, 60.2160 TO 60	CIS COR	69
148. C	ONE. SET CORRECTION FOR THE HEAT OF FORMATION.	CIS COR	
149.	DAYCIS1, 165 121.0	CIS COR	
150.	GO TO 73	CIS COR	73
151. C	TWO. SET CORRECTION FOR THE HEAT OF FORMATION.	CIS COR	
152.	47 DAYCIS1, 165 123.0	CIS COR	
153.	73 IFICIS1, 60.0 OR 60U, 61.0160 TO 73	CIS COR	73
154. C	3-ENE STRUCTURE PRESENT. SET CORRECTION FOR THE ENTROPY.	CIS COR	
155.	DAYCIS2, 165 124.0=PLAOTINE3	CIS COR	
156.	GO TO 77	CIS COR	77
157. C	OUT-2-ENE STRUCTURE PRESENT. SET CORRECTION FOR THE ENTROPY.	CIS COR	
158.	75 IFICIS1, 60.1 OR 60U, 61.0160 TO 77	CIS COR	77
159.	DAYCIS2, 165 125.0	CIS COR	
160. C	FIND SUM TOTAL OF CIS CORRECTIONS FOR THE HEAT OF FORMATION	CIS COR	
161. C	AND ENTROPY.	CIS COR	
162.	77 CIS=CIS+DAYCIS1, 165 3	CIS COR	
163.	CIS=CIS+DAYCIS2, 165 3	CIS COR	
164.	RETURN	CIS COR	
165.	END	CIS COR	

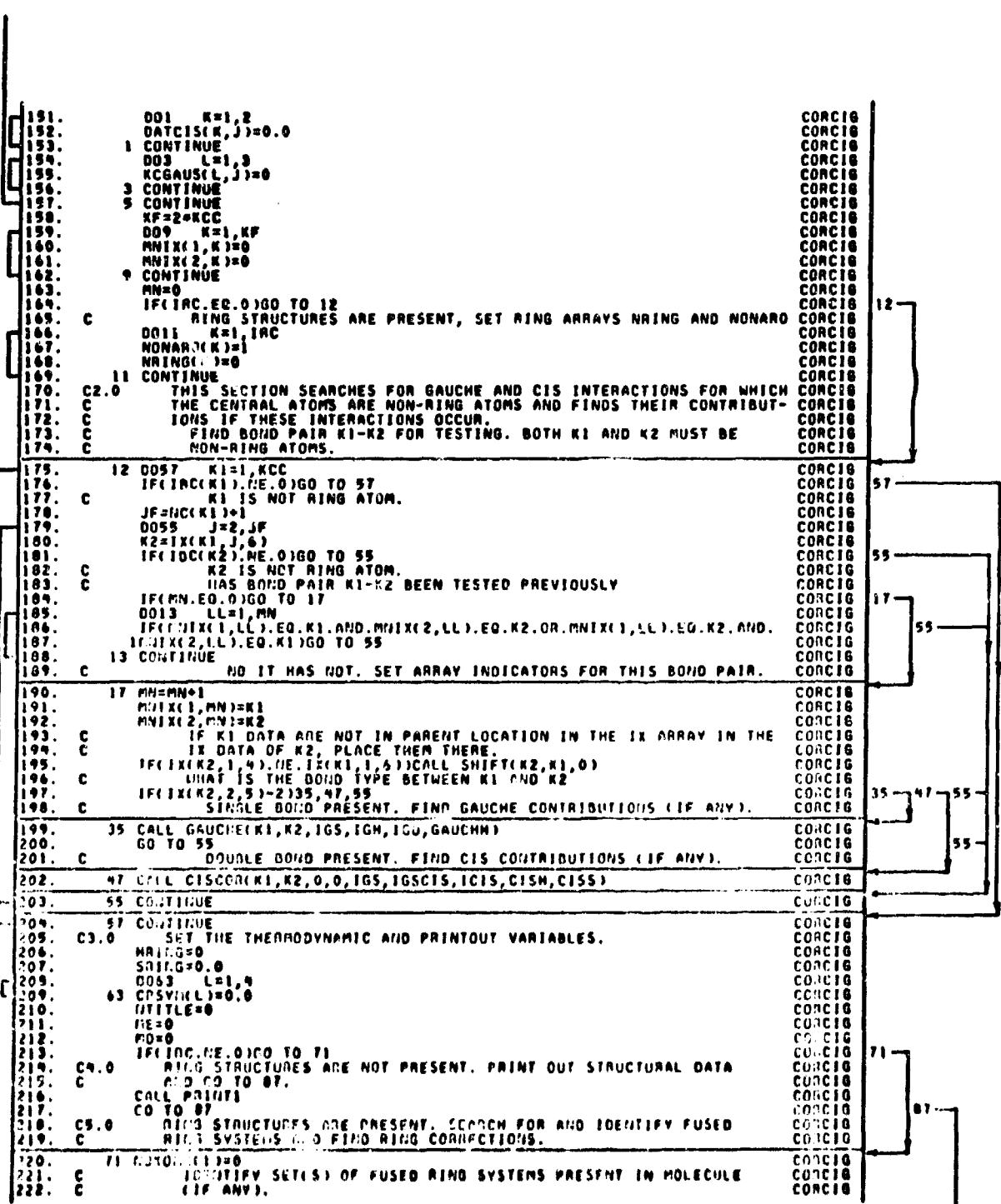
CORCIG

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1. SUBROUTINE CORCIG(NOSM,NENAN,MESO,LX,MSYM,SSYM,CPSYM) CORCIG
2. THIS SUBROUTINE IS THE CONTROL ELEMENT FOR SECTION THREE OF THE CORCIG
3. PROGRAM. THIS SECTION SEARCHES FOR AND ACCOUNTS FOR ALL SECOND- CORCIG
4. ORDER INTERACTIONS AND RING CORRECTIONS AS WELL AS CONTRIBU- CORCIG
5. TIONS DUE TO INTERNAL AND EXTERNAL ROTATIONAL SYMMETRY AND CORCIG
6. OPTICAL ISOMERISM. CORCIG
7. INTEGER SYM(4),SYMBOL(9),GRID(50,80) CORCIG
8. INTEGER WEIGHT(9) CORCIG
9. INTEGER RINGL(40) CORCIG
10. DIMENSION CPSYM(4),NOKOMB(11),KCGAUS(3,150),KFGAUS(150), CORCIG
11. 1KTGAUS(150),DATCIS(2,150),MDEL(40),IM(150),CPALT(4),NRING(40), CORCIG
12. 2KRCOR(100),KRCNWT(100),NONARO(40),MNIX(2,200),MARD(100) CORCIG
13. DIMENSION TYPE(4,8),CPCIS(4),DORTHO(6),RINGD(6,50) CORCIG
14. DIMENSION A1(6),A2(6),A3(6),A4(6),A5(6),A6(6),A7(6),A8(6),A9(6), CORCIG
15. 1A10(6),A11(6),A12(6),A13(6),A14(6),A15(6),A16(6),A17(6),A18(6), CORCIG
16. 2A19(6),A20(6),A21(6),A22(6),A23(6),A24(6),A25(6),A26(6),A27(6), CORCIG
17. 3A28(6),A29(6),A30(6) CORCIG
18. DIMENSION A31(6),A32(6),A33(6),A34(6),A35(6),A36(6),A37(6),A38(6), CORCIG
19. 1A39(6),A40(6),A41(6),A42(6),A43(6),A44(6) CORCIG
20. DIMENSION A45(6),A46(6),A47(6),A48(6),A49(6),A50(6) CORCIG
21. COMMON/DLK1/NO,NOS,SYM,SYMBOL,NOVAL(9),GRID CORCIG
22. COMMON/DLK2/WEIGHT,MWGT(9),MOLWT(100),IX(100,5,6),NC(100),KCC CORCIG
23. COMMON/DLK3/RING(40,30),IMATX(50,80),NWC(100),IAC(100),KON(100), CORCIG
24. 1IGR(100),IB(100,8),IRG,NOBR CORCIG
25. COMMON/DLK4/KDC(60,50),NBS(60,2),NBX(60,20),IRC,NONFUS,IRCTOT CORCIG
26. COMMON/DLK5/NOATM,KUMATM(5),MDC(50),MBS(2),JW,JY,LFLAG5,LFLAG6 CORCIG
27. EQUIVALENCE (RINGD(1,1),A1),(RINGD(1,2),A2),(RINGD(1,3),A3), CORCIG
28. 1(RINGD(1,4),A4),(RINGD(1,5),A5),(RINGD(1,6),A6),(RINGD(1,7),A7), CORCIG
29. 2(RINGD(1,8),A8),(RINGD(1,9),A9),(RINGD(1,10),A10),(RINGD(1,11), CORCIG
30. 3A11),(RINGD(1,12),A12),(RINGD(1,13),A13),(RINGD(1,14),A14), CORCIG
31. 4(RINGD(1,15),A15),(RINGD(1,16),A16),(RINGD(1,17),A17), CORCIG
32. 5(RINGD(1,18),A18),(RINGD(1,19),A19),(RINGD(1,20),A20), CORCIG
33. 6(RINGD(1,21),A21),(RINGD(1,22),A22),(RINGD(1,23),A23), CORCIG
34. 7(RINGD(1,24),A24),(RINGD(1,25),A25),(RINGD(1,26),A26), CORCIG
35. 8(RINGD(1,27),A27),(RINGD(1,28),A28),(RINGD(1,29),A29), CORCIG
36. 9(RINGD(1,30),A30) CORCIG
37. EQUIVALENCE (RINGD(1,31),A31),(RINGD(1,32),A32),(RINGD(1,33),A33), CORCIG
38. 1(RINGD(1,34),A34),(RINGD(1,35),A35),(RINGD(1,36),A36), CORCIG
39. 2(RINGD(1,37),A37),(RINGD(1,38),A38),(RINGD(1,39),A39), CORCIG
40. 3(RINGD(1,40),A40),(RINGD(1,41),A41),(RINGD(1,42),A42), CORCIG
41. 4(RINGD(1,43),A43),(RINGD(1,44),A44),(RINGD(1,45),A45), CORCIG
42. 5(RINGD(1,46),A46),(RINGD(1,47),A47),(RINGD(1,48),A48), CORCIG
43. 6(RINGD(1,49),A49),(RINGD(1,50),A50) CORCIG
44. EQUIVALENCE (NRENZ,IO(10,1)),(NOSIX,IB(11,1)),(MD,IB(12,1)), CORCIG
45. 1(MDEL(1),IB(13,1)),(RINGL(1),IO(95,1)),(NOKOMB(1),IB(80,8)), CORCIG
46. 2(KCGAUS(1,1),IMATX(1,72)),(KFGAUS(1),IMATX(1,63)),(KTGAUS(1), CORCIG
47. 3IMATX(1,60)),(DATCIS(1,1),IMATX(1,66)),(IM(1),IMATX(1,57)), CORCIG
48. 4(CPALT(1),IO(91,8)),(NRING(1),GRID(1,75)),(KRCOR(1),GRID(1,76)), CORCIG
49. 5(KRCNWT(1),GRID(1,78)),(NENAN,GRID(1,80)),(NONARO(1), CORCIG
50. 6IMATX(2,49)),(MNIX(1,1),GRID(4,1)),(NIGENZ,IO(96,8)),(MARD(1), CORCIG
51. 7GRID(1,25)) CORCIG
52. DATA TYPE(1,1)/4H RING,TYPE(2,1)/4H CO2,TYPE(3,1)/4H H2O, CORCIG
53. 1TYPE(4,1)/4H H2O,TYPE(1,2)/4H H2O,TYPE(2,2)/4H CO2,TYPE(3,2) CORCIG
54. 2/4H H2O,TYPE(4,2)/4H H2O,TYPE(1,3)/4H PAR,TYPE(2,3)/4H CO2, CORCIG
55. 3TYPE(3,3)/4H H2O,TYPE(4,3)/4H H2O,TYPE(1,4)/4H H2O,TYPE(2,4) CORCIG
56. 4/4H CO2,TYPE(3,4)/4H H2O,TYPE(4,4)/4H H2O,TYPE(1,5)/4H GAZ, CORCIG
57. 5TYPE(2,5)/4H H2O,TYPE(3,5)/4H ALK,TYPE(4,5)/4H H2O,TYPE(1,6) CORCIG
58. 6/4H CO2,TYPE(2,6)/4H H2O,TYPE(3,6)/4H ALK,TYPE(4,6)/4H H2O, CORCIG
59. 7TYPE(1,7)/4H GAZ,TYPE(2,7)/4H H2O,TYPE(3,7)/4H ETH,TYPE(4,7) CORCIG
60. 8/4H H2O,TYPE(1,8)/4H H2O,TYPE(2,8)/4H H2O,TYPE(3,8)/4H H2O, CORCIG
61. 9TYPE(4,8)/4H H2O CORCIG
62. DATA CPCIS(1)-2.71900850E+0,5.85308034E-3,-4.78484651E-6,1.39424152 CORCIG
63. 1E-9 CORCIG
64. DATA DORTHO /0.57,-1.61,3.67654979E-1,4.40466325E-3, CORCIG
65. 1-6.2451047E-6,2.89796366E-9,DORPAR/-1.50/ CORCIG
66. COMMON/CONSTANTS FOR HYDROCARBON, OXYGEN-CONTAINING, AND CORCIG
67. NITROGEN-CONTAINING RINGS. CORCIG
68. DATA A1/27.4,32.1,-5.59519091E+0,1.15774509E-2, CORCIG
69. 1-1.11935029E-5,3.49006739E-9/ CORCIG
70. DATA A2/43.733,6.400,0/ CORCIG
71. DATA A3/26.2,29.0,-7.96086542E+0,1.38122922E-2, CORCIG
72. 1-9.77151219E-6,2.53582451E-9/ CORCIG
73. DATA A4/29.8,29.0,-4.15702016E+0,7.04990289E-3, CORCIG
74. 1-9.93025400E-6,1.69080107E-9/ CORCIG
75. DATA A5/6.3,27.3,-1.20102313E+1,1.73221158E-2, CORCIG
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76. I -0.04512613E-6, 1.64564380E-9/ CORC18
77. DATA A6/ 5.9, 25.8, -7.96443944E+0, 6.47567798E-3, CORC18
78. I 4.7177450E-7, -1.15478934E-9/ CORC18
79. DATA A7/6.0,5=0.0/ CORC18
80. DATA A8/ 0.00000001, 19.8, -1.31204886E+1, 2.55471733E-2, CORC18
81. I -1.13372646E-5, 1.03305952E-9/ CORC18
82. DATA A9/ 1.4, 21.5, -9.86261273E+0, 2.40236698E-2, CORC18
83. I -1.96337388E-5, 5.57399852E-9/ CORC18
84. DATA A10/4.8,5=0.0/ CORC18
85. DATA A11/0.5,5=0.0/ CORC18
86. DATA A12/6.4,15.9,4=0.0/ CORC18
87. DATA A13/5.4,5=0.0/ CORC18
88. DATA A14/6.0,5=0.0/ CORC18
89. DATA A15/4.7,23.7,4=0.0/ CORC18
90. DATA A16/5.9,16.5,4=0.0/ CORC18
91. DATA A17/6.0,5=0.0/ CORC18
92. DATA A18/15.5,5=0.0/ CORC18
93. DATA A19/0.9,5=0.0/ CORC18
94. DATA A20/17.1,5=0.0/ CORC18
95. DATA A21/12.8,5=0.0/ CORC18
96. DATA A22/9.9,5=0.0/ CORC18
97. DATA A23/12.8,5=0.0/ CORC18
98. DATA A24/63.5,67.6,4=0.0/ CORC18
99. DATA A25/68.4,69.2,4=0.0/ CORC18
100. DATA A26/55.3,5=0.0/ CORC18
101. DATA A27/32.7,5=0.0/ CORC18
102. DATA A28/28.9,5=0.0/ CORC18
103. DATA A29/29.6,5=0.0/ CORC18
104. DATA A30/31.1,5=0.0/ CORC18
105. DATA A31/27.6, 31.4, 4.53771953E+0, -3.66170519E-2, CORC18
106. I 5.70918434E-5, -2.73125817E-8/ CORC18
107. DATA A32/26.4, 27.7, -5.31540263E+0, 2.40262420E-3, CORC18
108. I -4.32548458E-6, 7.38512391E-9/ CORC18
109. DATA A33/6.7,5=0.0/ CORC18
110. DATA A34/2.2,5=0.0/ CORC18
111. DATA A35/3.5,5=0.0/ CORC18
112. DATA A36/5.4,5=0.0/ CORC18
113. DATA A37/3.4,5=0.0/ CORC18
114. DATA A38/-6.2,5=0.0/ CORC18
115. DATA A39/2.5,5=0.0/ CORC18
116. DATA A40/6.0,5=0.0/ CORC18
117. DATA A41/3.4,5=0.0/ CORC18
118. DATA A42/1.1,5=0.0/ CORC18
119. DATA A43/1.4,5=0.0/ CORC18
120. DATA A44/4.6,5=0.0/ CORC18
121. DATA A45/27.7,31.6,4=0.0/ CORC18
122. DATA A46/26.2,29.3,4=0.0/ CORC18
123. DATA A47/6.8, 26.7, -7.49239560E+0, 1.47421187E-3, CORC18
124. I 1.18614544E-5, -8.02285243E-9/ CORC18
125. DATA A48/1.0,5=0.0/ CORC18
126. DATA A49/3.4,5=0.0/ CORC18
127. DATA A50/8.5,5=0.0/ CORC18
128. C1.0 INITIALIZE VARIABLES FOR THIS ROUTINE AND SUBSEQUENT CORC18
129. C ROUTINES IN SECTION THREE OF THE PROGRAM. CORC18
130. IGS=0 CORC18
131. IRNG2=0 CORC18
132. IRNG3=0 CORC18
133. ICRTHO=0 CORC18
134. IORPAR=0 CORC18
135. IGO=0 CORC18
136. GAUCHN=0.0 CORC18
137. ICIS=0 CORC18
138. IJSCIS=0 CORC18
139. CISM=0.0 CORC18
140. CISS=0.0 CORC18
141. IBN=0 CORC18
142. IDTE=0 CORC18
143. DTEH=0.0 CORC18
144. NTBENZ=0 CORC18
145. DOS J=1,KCC CORC18
146. MAROT J=0 CORC18
147. KFGAUSI J=0 CORC18
148. KTBGAI J=0 CORC18
149. KRCMORI J=0 CORC18
150. KRCNAT J=0 CORC18

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223.	CALL FUSION	CORCIG
224.	NNBENZ=0	CORCIG
225.	NNBENZ=9	CORCIG
226.	NOSIX=0	CORCIG
227.	C FIND SUBSCRIPT CORRESPONDING TO LOCATION OF THERMOCHEMICAL	CORCIG
228.	C CORRECTIONS FOR RING K.	CORCIG
229.	0075 K=1, IRC	CORCIG
230.	CALL CYCORR(K, L1)	CORCIG
231.	IF(L1.GT.0)GO TO 73	CORCIG
232.	ME=ME+1	CORCIG
233.	73 RINGL(K)=L1	CORCIG
234.	75 CONTINUE	CORCIG
235.	IF(NBENZ.GT.0.OR.NNBENZ.GT.0)GO TO 77	CORCIG
236.	C BENZENE OR PYRIDINE-LIKE RINGS ARE NOT PRESENT. PRINT OUT	CORCIG
237.	C STRUCTURAL DATA AND GO TO 79.	CORCIG
238.	CALL PRINT1	CORCIG
239.	GO TO 79	CORCIG
240.	C FIND WEIGHT CORRECTIONS AND ORTHO (PARA) CORRECTIONS FOR	CORCIG
241.	C BENZENE AND PYRIDINE-LIKE RINGS.	CORCIG
242.	77 CALL HEXGON(IGS, IORTHO, IORPAR, DORTHO, DORPAR, HRING, SRING, CPSYM)	CORCIG
243.	79 IF(NOKOMB(1).EQ.0)GO TO 83	CORCIG
244.	C FUSED RINGS ARE PRESENT. FIND RING CORRECTIONS FOR CERTAIN	CORCIG
245.	C HYDROCARBON FUSED RING SYSTEMS.	CORCIG
246.	C CALL CRING(IGS, IRNG2, RINGD(1, 24), HRING, SRING, CPSYM)	CORCIG
247.	C FIND CORRECTIONS FOR A NITROGEN-CONTAINING FUSED RING SYSTEM.	CORCIG
248.	C CALL NRING(IGS, IRNG3, RINGD(1, 49), HRING, SRING, CPSYM)	CORCIG
249.	C DELETE RING CORRECTION FLAGS FROM RING SETS WHICH FORM PART	CORCIG
250.	C OF FUSED RING SETS AND HENCE HAVE THEIR RING CORRECTIONS	CORCIG
251.	C ALREADY INCLUDED THEREIN.	CORCIG
252.	83 J=0	CORCIG
253.	85 J=J+1	CORCIG
254.	IF(J.GT.MD)GO TO 86	CORCIG
255.	K=MOEL(J)	CORCIG
256.	RINGL(K)=0	CORCIG
257.	GO TO 85	CORCIG
258.	C SEARCH FOR ADDITIONAL RING CORRECTIONS AS WELL AS FOR	CORCIG
259.	C GAUCHE AND CIS INTERACTIONS IN WHICH ONE OR BOTH OF THE	CORCIG
260.	C CENTRAL ATOMS ARE NON-AROMATIC RING ATOMS AND FIND THEIR	CORCIG
261.	C CONTRIBUTIONS IF THESE OCCUR.	CORCIG
262.	86 CALL SORNG(IGS, IGH, IGO, IGSCIS, ICIS, GAUCHM, CISM, CISS)	CORCIG
263.	87 IF(IGS.EQ.0)GO TO 95	CORCIG
264.	C6.0 RING AND/OR SECOND-ORDER INTERACTIONS PRESENT. ESTABLISH THE	CORCIG
265.	C NUMERICAL ORDER OF THESE DATA.	CORCIG
266.	CALL ORDER(IGS, IM, RTGAUS)	CORCIG
267.	IF(IGO.EQ.0)GO TO 95	CORCIG
268.	C7.0 GAUCHE ETHER STRUCTURES PRESENT. SEARCH FOR THE PRESENCE OF	CORCIG
269.	C DITERTIARY ETHER STRUCTURES.	CORCIG
270.	CALL DITERE(IGS, IGO, IDTE, DTEN)	CORCIG
271.	C8.0 FIND THE LIGAND ATOMIC COMPOSITION OF EACH CORE ATOM AND THE	CORCIG
272.	C SYMMETRY ELEMENTS OF EACH NON-RING CORE ATOM IN THE MOLECULE.	CORCIG
273.	95 JW=9	CORCIG
274.	JY=9	CORCIG
275.	CALL SYMTRY(LX)	CORCIG
276.	C9.0 FIND NUMBER OF ASYMMETRIC ATOMS PRESENT.	CORCIG
277.	CALL ASYMC(NASYMC)	CORCIG
278.	C10.0 FIND LONGEST CHAIN IN MOLECULE.	CORCIG
279.	CALL MAXCH(LX, NASYMC)	CORCIG
280.	C11.0 FIND EXTERNAL ROTATIONAL SYMMETRY OF MOLECULE.	CORCIG
281.	CALL EXTROT(NDSEC, NASYMC, NPSUDA, KCSUDA, NOME50)	CORCIG
282.	C12.0 COMPUTE INTERNAL ROTATIONAL ENTROPY CONTRIBUTIONS (IF ANY).	CORCIG
283.	CALL INTROT(IGS, INA, ROTINS)	CORCIG
284.	IRCMD=IRC-MD-ME	CORCIG
285.	KSUM=IGS+IRCMD	CORCIG
286.	IF(KSUM.EQ.0)GO TO 291	CORCIG
287.	C13.0 PRINT OUT DATA FOR RING CORRECTIONS AND SECOND-ORDER RING	CORCIG
288.	C INTERACTIONS.	CORCIG
289.	C PRINT OUT TITLE.	CORCIG
290.	CALL PRINT2(TITLE)	CORCIG
291.	IF(IRCMD.EQ.0)GO TO 171	CORCIG
292.	C PRINT OUT DATA FOR RING CORRECTIONS.	CORCIG
293.	00169 K=1, IRC	CORCIG

294.	L1=RINGL(K)	CORCIG	
295.	IF(L1.EQ.0)GO TO 169	CORCIG	169
296.	NRING=NRING+RINGD(1,L1)	CORCIG	
297.	SRING=SRING+RINGD(2,L1)	CORCIG	
298.	DO161 KK=1,4	CORCIG	
299.	161 CPSYM(KK)=CPSYM(KK)+RINGD(KK+2,L1)	CORCIG	
300.	WRITE(6,169)(TYPE(L,1),L=1,4),K,(RINGD(KK,L1),KK=1,6)	CORCIG	
301.	165 FORMAT(1H,4A4,9X,14,12X,1H1,F13.3,4X,F13.3,3X,4E13.4)	CORCIG	
302.	169 CONTINUE	CORCIG	
303.	171 IF(IGS.EQ.0)GO TO 251	CORCIG	251
304.	C THERE ARE ADDITIONAL RING CORRECTIONS AND/OR SECOND-ORDER	CORCIG	
305.	C INTERACTIONS PRESENT IN THE MOLECULE. PRINT PERTINENT DATA.	CORCIG	
306.	IF(IRNG2.EQ.0)GO TO 177	CORCIG	177
307.	DO175 K=1,IRNG2	CORCIG	
308.	C THERE ARE FUSED CARBON RING CORRECTIONS. PRINT OUT DATA.	CORCIG	
309.	IBX=IM(K)	CORCIG	
310.	I=KFGAUS(IBX)	CORCIG	
311.	WRITE(6,173)(TYPE(L,1),L=1,4),KCGAUS(1,IBX),KCGAUS(2,IBX),	CORCIG	
312.	1(RINGD(L,1),L=1,6)	CORCIG	
313.	173 FORMAT(1H,4A4,7X,214,10X,1H1,F13.3,4X,F13.3,3X,4E13.4)	CORCIG	
314.	175 CONTINUE	CORCIG	
315.	177 IF(IRNG3.EQ.0)GO TO 183	CORCIG	183
316.	C THERE ARE FUSED NITROGEN RING CORRECTIONS. PRINT OUT DATA.	CORCIG	
317.	KI=IRNG2+1	CORCIG	
318.	KF=IRNG2+IRNG3	CORCIG	
319.	DO181 K=KI,KF	CORCIG	
320.	IBX=IM(K)	CORCIG	
321.	WRITE(6,179)(TYPE(L,1),L=1,4),(KCGAUS(L,IBX),L=1,3),RINGD(1,4)	CORCIG	
322.	179 FORMAT(1H,4A4,5X,314,8X,1H1,F13.3,4X,F13.3,3X,4E13.4)	CORCIG	
323.	181 CONTINUE	CORCIG	
324.	183 IF(ORTHO.EQ.0)GO TO 189	CORCIG	189
325.	C THERE ARE ORTHO BENZENE CORRECTIONS. PRINT OUT DATA.	CORCIG	
326.	KI=IRNG2+IRNG3+1	CORCIG	
327.	KF=IRNG2+IRNG3+ORTHO	CORCIG	
328.	DO107 K=KI,KF	CORCIG	
329.	IGX=IM(K)	CORCIG	
330.	WRITE(6,185)(TYPE(L,2),L=1,4),KCGAUS(1,IBX),KCGAUS(2,IBX),	CORCIG	
331.	1(ORTHO(KK),KK=1,6)	CORCIG	
332.	185 FORMAT(1H,4A4,7X,214,10X,1H1,F13.3,4X,F13.3,3X,4E13.4)	CORCIG	
333.	187 CONTINUE	CORCIG	
334.	189 IF(IORPAR.EQ.0)GO TO 195	CORCIG	195
335.	C THERE ARE ORTHO AND/OR PARA PYRIDINE CORRECTIONS. PRINT	CORCIG	
336.	C OUT DATA.	CORCIG	
337.	KI=IRNG2+IRNG3+ORTHO+1	CORCIG	
338.	KF=KI-1+IORPAR	CORCIG	
339.	DO193 K=KI,KF	CORCIG	
340.	IBX=IM(K)	CORCIG	
341.	J=KFGAUS(IBX)	CORCIG	
342.	WRITE(6,191)(TYPE(L,J),L=1,4),KCGAUS(1,IBX),KCGAUS(2,IBX),DORPAR	CORCIG	
343.	191 FORMAT(1H,4A4,7X,214,10X,1H1,F13.3)	CORCIG	
344.	193 CONTINUE	CORCIG	
345.	195 IF(IGSCIS.EQ.0)GO TO 211	CORCIG	211
346.	C THERE ARE CIS CORRECTIONS. PRINT OUT DATA.	CORCIG	
347.	TCIS=ICIS	CORCIG	
348.	DO199 L=1,4	CORCIG	
349.	199 CPSYM(L)=CPSYM(L)+TCIS+CPCIS(L)	CORCIG	
350.	KI=IRNG2+IRNG3+ORTHO+IORPAR+1	CORCIG	
351.	KF=KI-1+IGSCIS	CORCIG	
352.	DO207 K=KI,KF	CORCIG	
353.	IBX=IM(K)	CORCIG	
354.	DO101 L=1,4	CORCIG	
355.	201 CPALT(L)=PLDALT(KFGAUS(IBX))+CPCIS(L)	CORCIG	
356.	WRITE(6,205)(TYPE(L,4),L=1,4),KCGAUS(1,IBX),KCGAUS(2,IBX),	CORCIG	
357.	1(KFGAUS(IBX),DTCIS(1,IBX),DTCIS(2,IBX),CPALT(L),L=1,4)	CORCIG	
358.	205 FORMAT(1H,4A4,7X,214,111,F13.3,4X,F13.3,3X,4E13.4)	CORCIG	
359.	207 CONTINUE	CORCIG	
360.	211 IF(IGH.EQ.0)GO TO 239	CORCIG	239
361.	C THERE ARE GAUCHE CORRECTIONS. PRINT OUT DATA.	CORCIG	
362.	KI=IRNG2+IRNG3+ORTHO+IORPAR+IGSCIS+1	CORCIG	
363.	KF=KI-1+IGH	CORCIG	
364.	DO221 K=KI,KF	CORCIG	
365.	IBX=IM(K)	CORCIG	

346.	J=KYGauss(10X)		CORC18
347.	WRITE(6,219)(TYPE(L,J),L=1,4),KCGAUS(1,10X),KCGAUS(2,10X),		CORC18
348.	KFGAUS(10X),DATCIS(1,10X)		CORC18
349.	219 FORMAT(1M,4A4,7X,214,111,F13.3)		CORC18
350.	221 CONTINUE		CORC18
351.	IF(IOTE.EQ.0)GO TO 239		CORC18
352.	C THERE ARE DITERIARY ETHER STRUCTURES. PRINT OUT DATA.		CORC18
353.	KI=IRNG2+IRNG3+IORTMO+IORPAR+ISCSIS+IGM+1		CORC18
354.	KF=KI-1+IDTE		CORC18
355.	DO235 K=KI,KF		CORC18
356.	WRITE(6,231)(TYPE(L,8),L=1,4),(KCGAUS(L,K),L=1,3),KFGAUS(K),		CORC18
357.	1DATCIS(1,K)		CORC18
358.	231 FORMAT(1M,4A4,5X,314,19,F13.3)		CORC18
359.	235 CONTINUE		CORC18
360.	239 IF(INR.EQ.0)GO TO 251		CORC18
361.	C THERE ARE INTERNAL ROTATION CONTRIBUTIONS. PRINT OUT DATA.		CORC18
362.	KI=IGS-INR+1		CORC18
363.	DO243 K=KI,IGS		CORC18
364.	WRITE(6,241)KCGAUS(1,K),DATCIS(2,K)		CORC18
365.	241 FORMAT(10N INTERNAL ROTATION,67,16,12X,1H1,17X,F13.3)		CORC18
366.	243 CONTINUE		CORC18
367.	C14.0 FIND CONTRIBUTIONS TO THE ENTROPY ARISING FROM INTERNAL AND		CORC18
368.	C EXTERNAL ROTATIONAL SYMMETRY AND OPTICAL ISOMERISM.		CORC18
369.	251 CALL ENTSYM,NOSN,NENAN,MESO,MASYMC,NOSNC,NPSUDA,KCSUDA,NOMESO,		CORC18
370.	1SSN,SOPTS)		CORC18
371.	C15.0 FIND SUMS OF ALL AFSREMENTIONED CONTRIBUTIONS TO THE HEAT OF		CORC18
372.	C FORMATION AND ENTRUPY.		CORC18
373.	MSYM=CISH+GAUCH4+DTEM+MNINA		CORC18
374.	SSYM=CISS+ROTINS+SRING+SSN+SOPTS		CORC18
375.	RETURN		CORC18
376.	END		CORC18

239

251

CRINGS

1.		SUBROUTINE CRINGS(IGS,IRNG2,RDATA,HRING,SRING,CPSYM)	CRINGS
2.	C	THIS SUBROUTINE SEARCHES FOR CERTAIN FUSED CARBON RING SYSTEMS.	CRINGS
3.	C	IF PRESENT, IT APPLIES APPROPRIATE RING CORRECTIONS TO THE	CRINGS
4.	C	THERMODYNAMIC PROPERTIES.	CRINGS
5.		INTEGER WEIGHT(9)	CRINGS
6.		DIMENSION MDL(40),KOMB(40,10),NOKOMB(11),CPSYM(4),RDATA(6,7),	CRINGS
7.		IKRPROP(6,40),NOK(10,10),KJ(2),KTGAUS(150),KFGAUS(150),	CRINGS
8.		ZKCGAUS(3,150)	CRINGS
9.		COMMON/BLK2/WEIGHT,MWGT(9),MOLWT(100),IX(100,5,6),NC(100),KCC	CRINGS
10.		COMMON/BLK3/IRING(40,30),IMATX(50,80),NWC(100),IBC(100),KONI(100),	CRINGS
11.		IIDRR(100),IBC(100,8),IRG,NDBR	CRINGS
12.		COMMON/BLK4/NDC(60,50),NBS(60,2),MAX(60,20),IRC,NONFUS,IRCTDT	CRINGS
13.		EQUIVALENCE (MD,IB(12,1)),(MDEL(1),IB(13,1)),(KOMB(1,1),IB(62,4)),	CRINGS
14.		IC(BKOMB(1),IB(80,8)),(NOK(1,1),IMATX(1,55)),(KRPROP(1,1),	CRINGS
15.		2NDX(2,1)),(KTGAUS(1),IMATX(1,60)),(KFGAUS(1),IMATX(1,63)),	CRINGS
16.		3KCGAUS(1,1),IMATX(1,72)),(KJ(1),NWX(20,20))	CRINGS
17.	C1.0	INITIALIZE CYCLE THAT TESTS EACH FUSED RING SET.	CRINGS
18.		IC=NOKOMB(1)	CRINGS
19.		DO11 I=1,IC	CRINGS
20.		IF(NOKOMB(I)=1).NE.2)GO TO 11	CRINGS
21.	C2.0	THERE ARE TWO RINGS IN FUSED RING SET I.	CRINGS
22.		K1=KOMB(1,I)	CRINGS
23.		K2=KOMB(2,I)	CRINGS
24.	C3.0	FIND THE FIRST 3-CENTERED RING (IF ANY) IN SET I.	CRINGS
25.		IF(IRING(K1,1).NE.3)GO TO 1	CRINGS
26.	C	RING 1 IS 3-CENTERED.	CRINGS
27.		KJ(1)=K1	CRINGS
28.		KJ(2)=K2	CRINGS
29.		GO TO 3	CRINGS
30.	1	IF(IRING(K2,1).NE.3)GO TO 11	CRINGS
31.	C	RING 2 IS 3-CENTERED.	CRINGS
32.		KJ(1)=K2	CRINGS
33.		KJ(2)=K1	CRINGS
34.	C4.0	AT LEAST ONE OF THE TWO RINGS IS 3-CENTERED. NOW DETERMINE	CRINGS
35.	C	OTHER RING PROPERTIES.	CRINGS
36.	3	KSUM=KRPROP(1,K1)+KRPROP(3,K1)+KRPROP(5,K1)+KRPROP(1,K2)+	CRINGS
37.		IKRPROP(3,K2)+KRPROP(5,K2)	CRINGS
38.		IF(KSUM.NE.0)GO TO 11	CRINGS
39.	C5.0	BOTH RINGS ARE SATURATED CARBON BASED RINGS.	CRINGS
40.		N1=KJ(2)	CRINGS
41.		N2=IRING(N1,1)	CRINGS
42.	C6.0	NOW HOW MANY COMMON ATOMS DO RINGS POSSESS	CRINGS
43.		IF(NOK(2,1)-2)5,7,11	CRINGS
44.	C	RINGS HAVE 1 ATOM IN COMMON.	CRINGS
45.	5	IF(N2.NE.3)GO TO 11	CRINGS
46.	C	SECOND RING IS ALSO 3-CENTERED. SET RING CORRECTION FLAG	CRINGS
47.	C	FOR SPIROPENTANE.	CRINGS
48.		N3=1	CRINGS
49.		GO TO 9	CRINGS
50.	C	RINGS HAVE 2 ATOMS IN COMMON.	CRINGS
51.	7	IF(N2.GT.8)GO TO 11	CRINGS
52.	C	SECOND RING IS 3,4,5,6,7, OR 8-CENTERED. SET RING	CRINGS
53.	C	CORRECTION FLAG FOR BICYCLO-(1,1,0)-OCTANE,	CRINGS
54.	C	-(2,1,0)-PENTANE, -(3,1,0)-HEXANE, -(4,1,0)-HEPTANE,	CRINGS
55.	C	-(5,1,0)-OCTANE, OR -(6,1,0)-NONANE.	CRINGS
56.		N3=N2-1	CRINGS
57.	C7.0	STORE TWO RING NUMBERS IN MDL.	CRINGS
58.	9	MD=MD+1	CRINGS
59.		MDL(MD)=KJ(1)	CRINGS
60.		MD=MD+1	CRINGS
61.		MDL(MD)=KJ(2)	CRINGS
62.	C8.0	SET I IS ONE OF THE AFOREMENTIONED FUSED CARBON RING SYSTEMS.	CRINGS
63.	C	AND CORRECTIONS TO THERMODYNAMIC PROPERTIES, STORE PERTINENT	CRINGS
64.	C	PRINTOUT DATA, AND CONTINUE THE TEST OF OTHER FUSED RING SETS.	CRINGS
65.		HRING=IRING+RDATA(1,N3)	CRINGS
66.		SRING=SRING+RDATA(2,N3)	CRINGS
67.		DO10 KK=1,4	CRINGS
68.		CPSY(KK)=CPSY(KK)+RDATA(KK+2,N3)	CRINGS
69.	10	CONTINUE	CRINGS
70.		IRNG2=IRNG2+1	CRINGS
71.		IGS=IGS+1	CRINGS
72.		KTGAUS(IGS)=1	CRINGS
73.		KFGAUS(IGS)=N3+23	CRINGS

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74.      KCGAUS(1,185)=KJ(1)
75.      KCGAUS(2,185)=KJ(2)
76.      11 CONTINUE
77.      RETURN
78.      END
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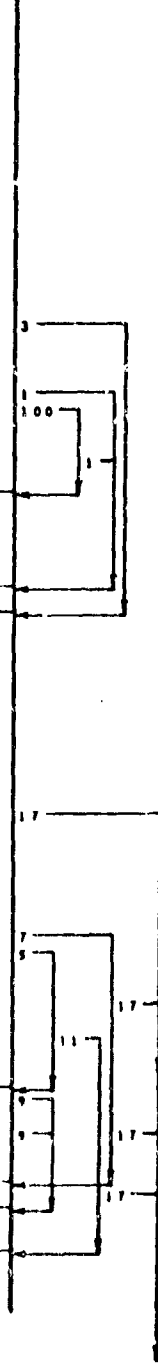
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CTWO

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1.      SUBROUTINE CTWO(IGS,IMR)
2.      C      THIS SUBROUTINE CHECKS FOR THE PRESENCE OF NO2 GROUPS AND
3.      C      MONOCYCLIC AROMATIC RINGS WHICH EXHIBIT TWOFOLD INTERNAL
4.      C      ROTATIONAL SYMMETRY ABOUT AN AXIS WITH A NONLINEAR
5.      C      CONFIGURATION. IF PRESENT, IT STORES THE PERTINENT I.D.
6.      C      NUMBERS AND CONTRIBUTIONS TO THE ENTROPY.
7.      C      INTEGER SYM(4),SYMBOL(9),GRID(90,80)
8.      C      INTEGER NHEIGHT(9)
9.      C      DIMENSION KCXDD(3),KCGAUS(3,190),DATCIS(2,190),KTGAUS(190),
10.     C      KTBNZ(40)
11.     C      COMMON/BLK1/NO,NOS,SYMZ,SYMBOL,NOVAL(9),GRID
12.     C      COMMON/BLK2/WEIGHT,HWGT(9),MOLWT(100),IK(100,5,6),NC(100),KCC
13.     C      COMMON/BLK3/IRING(40,30),IMATX(50,80),NMI(100),IBC(100),KON(100),
14.     C      IDBR(100),IB(100,8),IRG,NOBR
15.     C      EQUIVALENCE (KCGAUS(1,1),IMATX(1,72)),(DATCIS(1,1),IMATX(1,66)),
16.     C      (KTBNZ,IB(96,8)),(KTBNZ(1),GRID(41,27)),(KTGAUS(1),IMATX(1,60))
17.     C1.0   CHECK FOR NO2 GROUPS WHICH ARE NOT BONDED TO LINEAR LIGANDS.
18.     C      DO3   I=1,KCC
19.     C      IF(NC(I).EQ.KON(I))GO TO 3
20.     C      J=NC(I)+2
21.     C      JF=KON(J)+1
22.     C      DO1   J=J,JF
23.     C      IF(IX(I,J,1).NE.9)GO TO 1
24.     C      IF(IBC(I).NE.0)GO TO 100
25.     C      NO2 GROUP PRESENT.
26.     C      CALL LINEAR(100,1,LINE,KSVM)
27.     C      IF(LINE.EQ.1)GO TO 1
28.     C      NO2 LIGAND NONLINEAR.
29.     C      100 IMR=IMR+1
30.     C      IGS=IGS+1
31.     C      KCGAUS(1,IGS)=1
32.     C      KTGAUS(IGS)=9
33.     C      DATCIS(2,IGS)=-1.37746
34.     C      1 CONTINUE
35.     C      3 CONTINUE
36.     C2.0   IF MONOCYCLIC AROMATIC RINGS ARE NOT PRESENT, RETURN. OTHERWISE
37.     C      CONTINUE.
38.     C      IF(KTBNZ.EQ.0)RETURN
39.     C3.0   INITIALIZE MAIN CYCLE THAT SEARCHES FOR THE PRESENCE OF
40.     C      INTERNAL TWOFOLD SYMMETRY.
41.     C      DO17  N=1,KTBNZ
42.     C      K=KTBNZ(N)
43.     C      TEST ALL COMPONENTS OF RING K.
44.     C      DO17  J=2,7
45.     C      K1=IRING(K,J)
46.     C      IF(KON(K1).LE.2)GO TO 17
47.     C      CONNECTIVITY OF ATOM K1 IS GREATER THAN 2.
48.     C      IO=1
49.     C      JF=KON(K1)+1
50.     C      FIND THE RING AND NON-RING LIGANDS OF RING ATOM K1.
51.     C      DO11  I=2,JF
52.     C      KC=IF(K1,I,6)
53.     C      IF(KC.EQ.0)GO TO 7
54.     C      IF(IBC(KC).NE.IBC(K1))GO TO 5
55.     C      LIGAND IS A RING ATOM. STORE ITS GROUP NUMBER.
56.     C      IO=IO+1
57.     C      IF(IO.GT.3)GO TO 17
58.     C      KCXDD(10)=KC
59.     C      GO TO 11
60.     C      LIGAND IS A NON-RING (CORE ATOM. IF NONLINEAR, TRANSFER TO
61.     C      9. OTHERWISE, TRANSFER TO 17.
62.     C      5 IF(IBC(KC).NE.0)GO TO 9
63.     C      CALL LINEAR(R1,KC,LINE,KSVM)
64.     C      IF(LINE=1)9,17,9
65.     C      LIGAND IS A NON-RING NON-CORE ATOM. IF NONLINEAR, (I.E.,
66.     C      NO OR NO2) CONTINUE. OTHERWISE, TRANSFER TO 17.
67.     C      7 IF(IX(K1,9,1).LT.0)GO TO 11
68.     C      9 KCXDD(11)=K1
69.     C      KCXDD(2)=KXDD(11)
70.     C      11 CONTINUE
71.     C      IFUNCT=1
72.     C      DETERMINE IF RING IS SYMMETRICAL.

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73.	CALL EQUAL(KCRO1,KCRO2,1,1,0,1,1,0,1,IFUNCT)	CTMO	
74.	IF(IFUNCT.NE.2)GO TO 17	CTMO	17
75.	C RING HAS TWOFOLD SYMMETRY. STORE PERTINENT VARIABLES.	CTMO	
76.	I NR=2 NR+1	CTMO	
77.	I SS=I SS+1	CTMO	
78.	RCBAUS(1,I SS)=R1	CTMO	
79.	RTGAUS(I SS)=0	CTMO	
80.	DATCIS(2,I SS)=-1.37796	CTMO	
81.	17 CONTINUE	CTMO	
82.	RETURN	CTMO	
83.	END	CTMO	

1.		SUBROUTINE CYCORR(M, LI)	CYCORR
2.	C	THIS SUBROUTINE DETERMINES THE TYPE OF RING CORRECTION THAT	CYCORR
3.	C	IS TO BE APPLIED TO A NON-FUSED RING. IT ALSO SETS VARIOUS	CYCORR
4.	C	RING ARRAYS AND OTHER INDICATORS, IF BENZENE OR PYRIDINE	CYCORR
5.	C	TYPE RINGS ARE PRESENT.	CYCORR
6.		INTEGER SYMR(4), SYMBOL(9), GRID(50,80)	CYCORR
7.		INTEGER MEISHT(9)	CYCORR
8.		DIMENSION MS(4), RMT(4), KTEMP(8), IBONDS(30), IBONDD(30),	CYCORR
9.		IKBENZ(40), KSI(40), LOCO(30), LOCN(30), LOCCD(30), KRPROP(6,40),	CYCORR
10.		ZMVM(2), NRING(50), KRCONR(100), KRCONM(100), KNBENZ(40)	CYCORR
11.		COMMON/BLK1/MO, NOS, SYMR, SYMBOL, NOVAL(9), GRID	CYCORR
12.		COMMON/BLK2/MGHT, MWGT(9), MOLWT(100), IN(100, 9, 6), NCI(100), KCC	CYCORR
13.		COMMON/BLK3/TRING(40, 30), IMATK(50, 80), NM(100), IBC(100), KON(100),	CYCORR
14.		IIDBR(100), IB(100, 8), IRB, NOBR	CYCORR
15.		COMMON/BLK4/NBC(60, 50), NBS(60, 2), NBI(60, 20), IAC, NONFUS, IACTOT	CYCORR
16.		EQUIVALENCE (MS(1), IB(2, 3)), (RMT(1), IB(6, 1)), (KTEMP(1), IB(9, 1)),	CYCORR
17.		(IBONDS(1), IB(2, 3)), (IBONDD(1), IB(5, 3)), (NUMC, IB(76, 2)), (NUMD,	CYCORR
18.		ZI(17, 2)), (LOCCD(1), IMATK(1, 47)), (NUMN, IB(76, 2)), (LOCN(1),	CYCORR
19.		SI(17, 2)), (NUMCO, IB(79, 2)), (LOCCO(1), IMATK(41, 45)), (NBENZ,	CYCORR
20.		4)B(10, 1)), (NOSIX, IB(11, 1)), (KBENZ(1), IB(53, 1)), (KSI(1), IB(61, 2)),	CYCORR
21.		5)KRPROP(1, 1), NBI(2, 1)), (MVM(1), GRID(41, 75)), (NRING(1), GRID(1, 75)),	CYCORR
22.		6)KRCONR(1), GRID(1, 76)), (KRCONM(1), GRID(1, 78)), (KNBENZ, GRID(1, 80)),	CYCORR
23.		7)KNBENZ(1), GRID(2, 80))	CYCORR
24.	C1.0	INITIALIZE VARIABLES.	CYCORR
25.		LI=0	CYCORR
26.		DO1 M=1,6	CYCORR
27.		KRPROP(M,R)=0	CYCORR
28.		CONTINUE	CYCORR
29.		NUM=IRING(M, 1)	CYCORR
30.		IF (NUM.GT.9)RETURN	CYCORR
31.		MF=NUM+1	CYCORR
32.		IDIF=0	CYCORR
33.		ISB=0	CYCORR
34.		IDB=0	CYCORR
35.		NUMC=0	CYCORR
36.		NUMD=0	CYCORR
37.		NUMN=0	CYCORR
38.		NUMCO=0	CYCORR
39.	C2.0	FIND NUMBER OF CARBON, OXYGEN, NITROGEN, -C(40)-, SINGLE BONDS,	CYCORR
40.	C	AND DOUBLE BONDS PRESENT IN RING BACKBONE AND THE LOCATION OF	CYCORR
41.	C	EACH ONE, EXCEPT FOR THE CARBON ATOMS.	CYCORR
42.		DO2 I=1, MF	CYCORR
43.		KI=IRING(I, R)	CYCORR
44.		IF (I>KI, 1, 1).NE.2)GO TO 3	CYCORR
45.		NUMC=NUMC+1	CYCORR
46.		GO TO 9	CYCORR
47.		3 IF (I>KI, 1, 1).NE.3)GO TO 5	CYCORR
48.		NUMD=NUMD+1	CYCORR
49.		LOCCD(NUMD)=M	CYCORR
50.		GO TO 9	CYCORR
51.		5 IF (I>KI, 1, 1).NE.4)GO TO 7	CYCORR
52.		NUMN=NUMN+1	CYCORR
53.		LOCN(NUMN)=M	CYCORR
54.		GO TO 9	CYCORR
55.		7 IF (I>KI, 1, 1).NE.6)RETURN	CYCORR
56.		NUMCO=NUMCO+1	CYCORR
57.		LOCCO(NUMCO)=M	CYCORR
58.		9 IF (M.LT. MF)GO TO 11	CYCORR
59.		K2=IRING(M, 2)	CYCORR
60.		GO TO 13	CYCORR
61.		11 K2=IRING(M, 1)	CYCORR
62.		13 KONMAX=NCI(K1)+1	CYCORR
63.		DO15 N=2, KONMAX	CYCORR
64.		IF (I>KI, N, 6).EQ.K2)GO TO 17	CYCORR
65.		CONTINUE	CYCORR
66.		17 IF (I>KI, N, 5).NE.1)GO TO 19	CYCORR
67.		ISB=ISB+1	CYCORR
68.		IBONDS(ISB)=M	CYCORR
69.		GO TO 21	CYCORR
70.		19 IF (I>KI, N, 5).NE.2)GO TO 21	CYCORR
71.		IDB=IDB+1	CYCORR

72.	100000100100	CYCORR							
73.	21 CONTINUE	CYCORR							
74.	CD 0 IF MORE THAN ONE DOUBLE BOND IS PRESENT, FIND SEPARATION	CYCORR							
75.	C BETWEEN THE FIRST AND SECOND	CYCORR							
76.	IF 100, CT, 110117(100001001-10000100-1)	CYCORR							
77.	CD 0 STORE VARIABLES ASSOCIATED WITH RING 0 IN UNPRDT.	CYCORR							
78.	APRPT(1,0)=NUM	CYCORR							
79.	APRPT(2,0)=LCC(1)	CYCORR							
80.	APRPT(3,0)=NUM	CYCORR							
81.	APRPT(4,0)=LCC(1)	CYCORR							
82.	APRPT(5,0)=100	CYCORR							
83.	APRPT(6,0)=1000011	CYCORR							
84.	NUM=0	CYCORR							
85.	IF NUM=NUMC-NUM101, 00, 001	CYCORR	25	101					001
86.	CD 0 RING IS HOMOCYCLOPENTANE - ALL ATOMS IN RING BACKBONE ARE CARBON.	CYCORR							
87.	20 IF NUMC=100, 07, 001	CYCORR	27	00					001
88.	C 0- OR 4-MEMBERED RING PRESENT CONTAINING ONE -C(=O)- GROUP.	CYCORR							
89.	27 IF NUM.NE.0 AND NUM.NE.010RETURN	CYCORR							
90.	29 GO TO 31, 27, 43, 55, 75, 100, 1001, 00	CYCORR	31	07					
91.	C 3-MEMBERED RING IS PRESENT.	CYCORR							
92.	31 IF 100=100, 00, 001	CYCORR	33	00					001
93.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C	CYCORR							
94.	33 L1=0	CYCORR							
95.	RETURN	CYCORR							
96.	C THE COMPONENTS OF THE RING BACKBONE ARE C=C-C	CYCORR							
97.	35 L1=0	CYCORR							
98.	RETURN	CYCORR							
99.	C 4-MEMBERED RING IS PRESENT.	CYCORR							
100.	37 IF 100=100, 01, 001	CYCORR	39	01					001
101.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C-C	CYCORR							
102.	39 L1=0	CYCORR							
103.	RETURN	CYCORR							
104.	C THE COMPONENTS OF THE RING BACKBONE ARE C=C-C-C	CYCORR							
105.	41 L1=0	CYCORR							
106.	RETURN	CYCORR							
107.	C 5-MEMBERED RING IS PRESENT.	CYCORR							
108.	43 IF 100=100, 00, 01	CYCORR	45	00	01				
109.	45 IF NUMC=00, 100 TO 07	CYCORR	47						
110.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C-C-C	CYCORR							
111.	L1=0	CYCORR							
112.	RETURN	CYCORR							
113.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C-C-C(=O)	CYCORR							
114.	47 L1=0	CYCORR							
115.	RETURN	CYCORR							
116.	C THE COMPONENTS OF THE RING BACKBONE ARE C=C-C-C-C	CYCORR							
117.	49 L1=0	CYCORR							
118.	RETURN	CYCORR							
119.	C THE COMPONENTS OF THE RING BACKBONE ARE C=C-C=C-C	CYCORR							
120.	51 L1=0	CYCORR							
121.	RETURN	CYCORR							
122.	C 6-MEMBERED RING IS PRESENT.	CYCORR							
123.	53 IF 100=100, 00, 01	CYCORR	55	00	01				
124.	55 IF NUMC=00, 100 TO 07	CYCORR	57						
125.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C-C-C-C	CYCORR							
126.	L1=0	CYCORR							
127.	RETURN	CYCORR							
128.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C-C-C-C(=O)	CYCORR							
129.	57 L1=0	CYCORR							
130.	RETURN	CYCORR							
131.	C THE COMPONENTS OF THE RING BACKBONE ARE C=C-C-C-C-C	CYCORR							
132.	59 L1=0	CYCORR							
133.	RETURN	CYCORR							
134.	61 IF 100=100, 00, 001	CYCORR	63	00					001
135.	63 IF NUMC=00, 100 TO 04	CYCORR	65						
136.	S RING HAS TWO DOUBLE BONDS AND NO -C(=O)- GROUPS. STORE	CYCORR							

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127.	C	RING NUMBER IN 0010.	CYCORD	
128.		NOSE1=NOSE2=1	CYCORD	
129.		NOSE1=NOSE2=1	CYCORD	
130.		NOSE1=NOSE2=1	CYCORD	
131.	C	IF I(1) EQ 0, 1 TO 00	CYCORD	03
132.	C	THE COMPONENTS OF THE RING BACKBONE ARE C=C-C=C-C=C	CYCORD	
133.		LIST	CYCORD	
134.	C	RETURN	CYCORD	
135.	C	THE COMPONENTS OF THE RING BACKBONE ARE C=C-C=C-C=C	CYCORD	
136.		LIST	CYCORD	
137.		RETURN	CYCORD	
138.	C	DETERMINE IF RING IS OF BENZENE OR PYRIDINE TYPE. IF SO,	CYCORD	
139.		STORE RING NUMBER IN APPROPRIATE ARRAYS.	CYCORD	
140.			CYCORD	
141.	C	IF (NURC.NE.4 OR 150.NE.5) RETURN	CYCORD	
142.		NO	CYCORD	
143.			CYCORD	
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162.	C	BENZENE RING PRESENT.	CYCORD	
163.			CYCORD	
164.	C	RETURN	CYCORD	
165.	C	PYRIDINE-TYPE RING PRESENT.	CYCORD	
166.			CYCORD	
167.			CYCORD	
168.			CYCORD	
169.	C	7-MEMBERED RING IS PRESENT.	CYCORD	
170.			CYCORD	
171.	C	IF I(1) EQ 0, 1 TO 00	CYCORD	01 02 07
172.	C	THE COMPONENTS OF THE RING BACKBONE ARE C=C-C=C-C=C-C=C	CYCORD	
173.		LIST	CYCORD	
174.	C	RETURN	CYCORD	
175.	C	THE COMPONENTS OF THE RING BACKBONE ARE C=C-C=C-C=C-C=C	CYCORD	
176.		LIST	CYCORD	
177.	C	RETURN	CYCORD	
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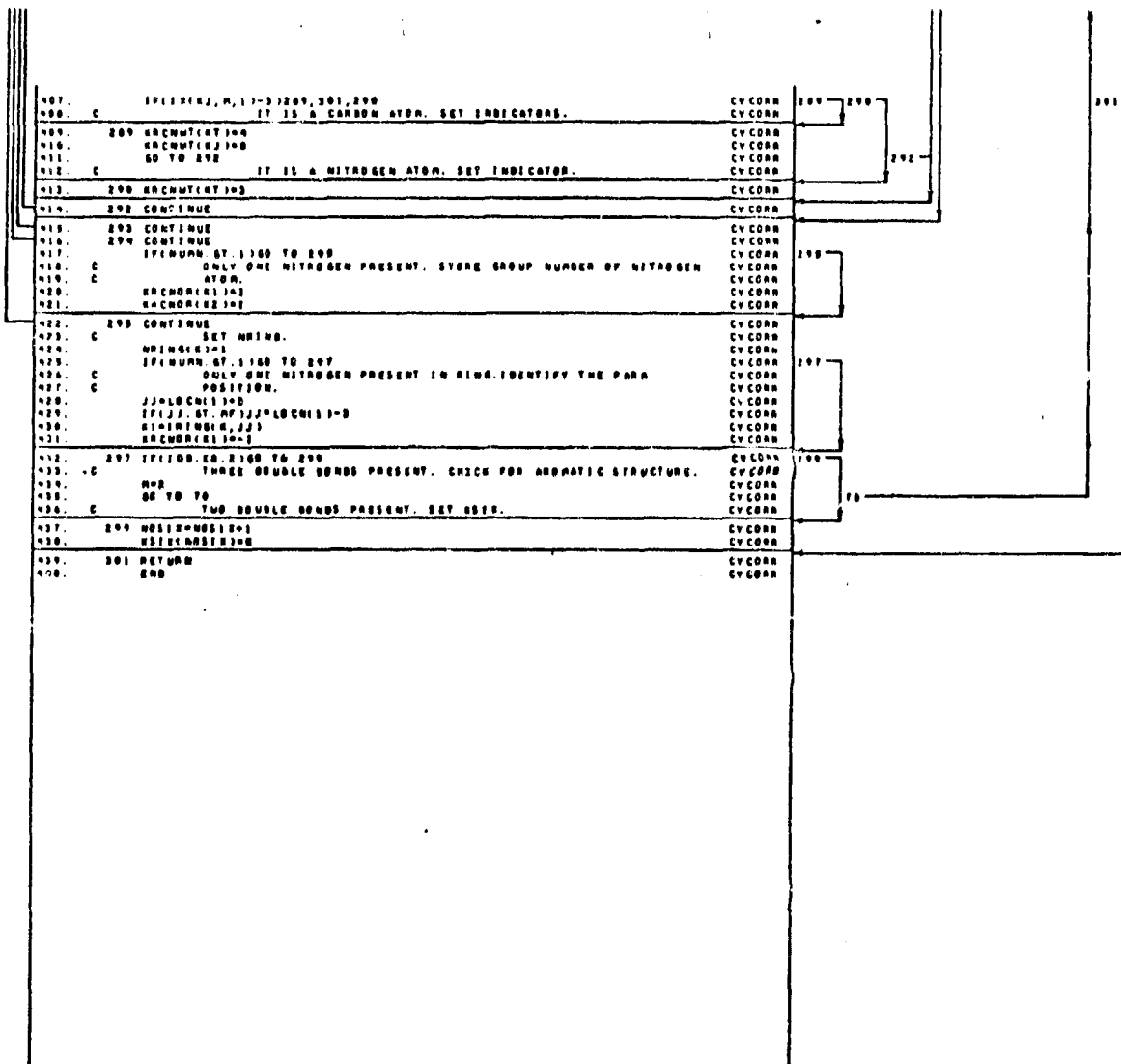
204.	SEARCHED	CYCORR	120
205.	INDEXED, NO. 0100 TO 100	CYCORR	120
206.	STEREISOM	CYCORR	120
207.	00 TO 157	CYCORR	120
208.	120 STERISOM	CYCORR	120
209.	120 CONTINUE	CYCORR	120
210.	IF(STERISOM=STERISOM)-3-3120,120,120	CYCORR	120
211.	120 IF(UMR, NO. 0100 TO 101	CYCORR	120
212.	C RING IS 0-MEMBERED.	CYCORR	120
213.	C THE COMPONENTS OF THE RING BACKBONE ARE C16 C-C-C-C-C-C-C	CYCORR	120
214.	C L1=17	CYCORR	120
215.	C RETURN	CYCORR	120
216.	C RING IS 0-MEMBERED.	CYCORR	120
217.	C THE COMPONENTS OF THE RING BACKBONE ARE C16	CYCORR	120
218.	C C-C-C-C-C-C-C	CYCORR	120
219.	C	CYCORR	120
220.	141 L1=22	CYCORR	120
221.	C RETURN	CYCORR	120
222.	143 IF(UMR, NO. 0100 TO 107	CYCORR	120
223.	C RING IS 0-MEMBERED.	CYCORR	120
224.	C THE COMPONENTS OF THE RING BACKBONE ARE TRANS	CYCORR	120
225.	C C-C-C-C-C-C-C	CYCORR	120
226.	C L1=10	CYCORR	120
227.	C RETURN	CYCORR	120
228.	C RING IS 0-MEMBERED.	CYCORR	120
229.	C THE COMPONENTS OF THE RING BACKBONE ARE TRANS	CYCORR	120
230.	C C-C-C-C-C-C-C	CYCORR	120
231.	C	CYCORR	120
232.	147 L1=13	CYCORR	120
233.	C RETURN	CYCORR	120
234.	149 IF(UMR, NO. 0100 TO 101	CYCORR	120
235.	C (0101)10000100-11-10000100-21	CYCORR	120
236.	C (0101)1000	CYCORR	120
237.	C IF(UMR, NO. 0, AND, 10, NO. 0) RETURN	CYCORR	120
238.	C THE COMPONENTS OF THE RING BACKBONE ARE C16-C16-C16-C16	CYCORR	120
239.	C L1=10	CYCORR	120
240.	C RETURN	CYCORR	120
241.	C 151 IF(UMR, NO. 0) RETURN	CYCORR	120
242.	C THE COMPONENTS OF THE RING BACKBONE ARE C16-C16-C16-C16	CYCORR	120
243.	C L1=10	CYCORR	120
244.	C RETURN	CYCORR	120
245.	C 0-MEMBERED RING IS PRESENT.	CYCORR	120
246.	157 IF(UMR-1-101,107,101	CYCORR	120
247.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C-C-C-C-C	CYCORR	120
248.	C	CYCORR	120
249.	160 L1=21	CYCORR	120
250.	C RETURN	CYCORR	120
251.	C 0, 0 RING IS HETEROGENEOUS, IS IT COMPOSED OF CARBON AND OXYGEN	CYCORR	120
252.	C ATOMS	CYCORR	120
253.	161 IF(UMR-CUMR-CUMR, NO. 00100 TO 001	CYCORR	120
254.	C YES IT IS, CHECK IF C16(1) GROUP(S) IS(ARE) ADJACENT TO THE	CYCORR	120
255.	C OXYGEN ATOM.	CYCORR	120
256.	C CALL OXYTRIC(L,C(1),1,TESTE)	CYCORR	120
257.	C IF(UMR, NO. 1 TO 0) TO 011	CYCORR	120
258.	C ONLY ONE OXYGEN PRESENT.	CYCORR	120
259.	C IF(100-1103,100,007	CYCORR	120
260.	C	CYCORR	120
261.	163 IF(1TEST2-11103,101,100	CYCORR	120
262.	C RING IS UNSATURATED, 0-MEMBERED AND HAS NO -C=C- GROUPS.	CYCORR	120
263.	C	CYCORR	120
264.	165 IF(UMR, NO. 010000	CYCORR	120
265.	C 00 TO 107,109,191,193,2013,NO	CYCORR	120
266.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C	CYCORR	120
267.	C	CYCORR	120
268.	167 L1=31	CYCORR	120
269.	C RETURN	CYCORR	120
270.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C-C	CYCORR	120
271.	C	CYCORR	120
272.	169 L1=30	CYCORR	120
273.	C RETURN	CYCORR	120
274.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C-C	CYCORR	120
275.	C	CYCORR	120
276.	171 L1=30	CYCORR	120
277.	C RETURN	CYCORR	120
278.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-C-C-C	CYCORR	120
279.	C	CYCORR	120

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271.	193 L1=04	CYCORR	
272.	RETURN	CYCORR	
273.	198 IPIUM.NE.0160 TO 197	CYCORR	197
274.	C THE COMPONENTS OF THE RING BACKBONE ARE C(=O)-P-C(=O)-C-C	CYCORR	
275.	L1=05	CYCORR	
276.	RETURN	CYCORR	
277.	197 IPIUM.NE.0160RETURN	CYCORR	
278.	C THE COMPONENTS OF THE RING BACKBONE ARE C(=O)-O-C(=O)-C-C-C	CYCORR	
279.	L1=03	CYCORR	
280.	RETURN	CYCORR	
281.	199 IPII*EST2-11205,301,303	CYCORR	281-289
282.	201 IPIUM.NE.01RETURN	CYCORR	
283.	201*LOC011-LOC0111	CYCORR	
284.	202*NUM-203	CYCORR	
285.	IPIJ01.NE.0. AND 202.NE.01RETURN	CYCORR	
286.	C THE COMPONENTS OF THE RING BACKBONE ARE C(=O)-O-C(=O)-C-C	CYCORR	
287.	L1=00	CYCORR	
288.	RETURN	CYCORR	
289.	203 IPIUM.NE.01RETURN	CYCORR	
290.	C THE COMPONENTS OF THE RING BACKBONE ARE C-O-C-C-C-C	CYCORR	
291.	L1=00	CYCORR	
292.	RETURN	CYCORR	
293.	207 IPIUM.NE.0. OF. ITEST2.NE.01RETURN	CYCORR	
294.	C THE COMPONENTS OF THE RING BACKBONE ARE C-C-O-C-C	CYCORR	
295.	L1=30	CYCORR	
296.	RETURN	CYCORR	
297.	211 IPIUM.NE.0. OR. 100.NE.0. OR. NUMC.NE.01RETURN	CYCORR	
298.	1012-LOC012-LOC013	CYCORR	
299.	IPIJND-31210,317,301	CYCORR	214-217
300.	214 IPII012.CO.0160 TO 213	CYCORR	214
301.	C THE COMPONENTS OF THE RING BACKBONE ARE C-O-C-O-C-C	CYCORR	
302.	L1=00	CYCORR	
303.	RETURN	CYCORR	
304.	C THE COMPONENTS OF THE RING BACKBONE ARE C-O-C-C-N-C	CYCORR	
305.	219 L1=0A	CYCORR	
306.	RETURN	CYCORR	
307.	217 IPIUM.NE.01RETURN	CYCORR	
308.	104*LOC011-LOC011-1050	CYCORR	
309.	IPII04.NE.01RETURN	CYCORR	
310.	C THE COMPONENTS OF THE RING BACKBONE ARE C-O-C-O-C-O	CYCORR	
311.	L1=07	CYCORR	
312.	RETURN	CYCORR	
313.	IF.0 RING IS HETEROGENEOUS. IS IT COMPOSED OF CARBON AND NITROGEN	CYCORR	
314.	C ATOMS	CYCORR	
315.	241 IPIUMC*NUMC*NUMH.NE.01RETURN	CYCORR	
316.	C YES IS IS. CHECK IF C(=O) GROUP(S) IS(ARE) ADJACENT TO THE	CYCORR	
317.	C NITROGEN ATOM.	CYCORR	
318.	CALL DICTAID,LOC011, ITEST2	CYCORR	
319.	IPII00-11202,301,273	CYCORR	
320.	C NO DOUBLE BONDS PRESENT IN RING.	CYCORR	242-271
321.	242 IPIUMC*01RETURN	CYCORR	
322.	C ONLY ONE NITROGEN ATOM PRESENT IN RING.	CYCORR	243-267
323.	IPIIEST2-11203,301,307	CYCORR	
324.	243 IPIUMC*01RETURN	CYCORR	
325.	GO TO 1253,250,241,249,301,NE	CYCORR	153-250-301-309
326.	C THE COMPONENTS OF THE RING BACKBONE ARE C-N-C	CYCORR	
327.	251 L1=0B	CYCORR	
328.	RETURN	CYCORR	
329.	C THE COMPONENTS OF THE RING BACKBONE ARE C-N-C-C	CYCORR	
330.	259 L1=06	CYCORR	
331.	RETURN	CYCORR	
332.	C THE COMPONENTS OF THE RING BACKBONE ARE C-N-C-C-C	CYCORR	
333.	261 L1=0F	CYCORR	
334.	RETURN	CYCORR	
335.	C THE COMPONENTS OF THE RING BACKBONE ARE C-N-C-C-C-C	CYCORR	
336.	263 L1=0E	CYCORR	
337.	RETURN	CYCORR	

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227.	RETURN	CYCORD	
228.	227 IFENUR, NE, SIGNURE	CYCORD	
229.	C THE COMPONENTS OF THE RING BACKBONE ARE C100, N-C101, C-C	CYCORD	
230.	LOOP	CYCORD	
231.	RETURN	CYCORD	
232.	271 IFENUR, NE, O, OR, NUNCO, OT, O, OR, IOD, OT, SIGNURE	CYCORD	
233.	C RING IS O-MEMBERED, HAS OO -C100, AND HAS TWO OR MORE	CYCORD	
234.	DOUBLE BONDS, PYRIDINE OR PYRIDINE-LIKE STRUCTURE PRESENT.	CYCORD	
235.	C SET IDENTIFICATION INDICATORS FOR RING COMPONENTS, INFO USED	CYCORD	
236.	C IN SUBROUTINE HEREON TO ESTABLISH WEIGHT OF EACH GROUP.	CYCORD	
237.	DO200 J=1, NUNO	CYCORD	
238.	IFILDCN(J)	CYCORD	
239.	IFIRING(J, I)	CYCORD	
240.	AVN(I)=LOCN(J)	CYCORD	
241.	AVN(I)=LOCN(J)-1	CYCORD	
242.	IFILDCN(J).EQ.2 AVN(I)=LOCN(J)	CYCORD	
243.	C DETERMINE GROUP NUMBER OF ATOM WHICH IS SINGLE (S1) AND	CYCORD	
244.	DOUBLE (S2) BONDED TO THE NITROGEN ATOM J.	CYCORD	
245.	DO275 K=1, 2	CYCORD	
246.	DO275 L=1, 100	CYCORD	
247.	IF (AVN(LK).EQ.1) DO275 L100 TO 270	CYCORD	270
248.	270 CONTINUE	CYCORD	
249.	RETURN	CYCORD	
250.	270 GO TO 201, 203, 205	CYCORD	201 203
251.	201 S1=AVN(I)	CYCORD	
252.	S2=AVN(I)+1	CYCORD	
253.	IF (S2 .GT. NP) S2=0	CYCORD	
254.	GO TO 203	CYCORD	203
255.	203 S1=AVN(I)+1	CYCORD	
256.	IF (S1 .GT. NP) S1=0	CYCORD	
257.	S2=AVN(I)	CYCORD	
258.	205 S1=INDNCH, S2	CYCORD	
259.	S3=INDNCH, S3	CYCORD	
260.	IF (S1, S2, S3 .EQ. 2, OR, IOD, S, I, I, NE, 2) RETURN	CYCORD	
261.	C BOTH S1 AND S2 ARE CARBON ATOMS.	CYCORD	
262.	AVN(I)=0	CYCORD	
263.	AVN(I)=0	CYCORD	
264.	AVN(I)=0	CYCORD	
265.	C SET INDICATORS.	CYCORD	
266.	DO270 L=1, 2	CYCORD	
267.	AT=AVN(L)	CYCORD	
268.	S1=0	CYCORD	
269.	S2=AVN(L)+1	CYCORD	
270.	DO275 M=1, 100	CYCORD	
271.	IF (S1, S2, S3 .EQ. 2, OR, IOD, S, I, I, NE, 2) RETURN	CYCORD	
272.	C SET INDICATOR FOR NON-RING CORE ATOM BONDED TO S1.	CYCORD	
273.	AVN(I)=0	CYCORD	
274.	GO TO 203	CYCORD	203
275.	203 IF (S1, S2, S3 .EQ. 2, OR, IOD, S, I, I, NE, 2) RETURN	CYCORD	203
276.	C SET INDICATOR FOR NON-RING CORE ATOM BONDED TO S2.	CYCORD	
277.	AVN(I)=0	CYCORD	
278.	GO TO 203	CYCORD	203
279.	C CORE ATOM BONDED TO S1 OR S2 IS PART OF RING BACKBONE.	CYCORD	
280.	200 IF (S1, S2, S3 .EQ. 2, OR, IOD, S, I, I, NE, 2) RETURN	CYCORD	200 201
281.	201 IF (S1, S2, S3 .EQ. 2, OR, IOD, S, I, I, NE, 2) RETURN	CYCORD	
282.	C IT IS A NITROGEN ATOM. SET INDICATOR.	CYCORD	
283.	AVN(I)=0	CYCORD	
284.	GO TO 203	CYCORD	203
285.	C IT IS A CARBON ATOM.	CYCORD	
286.	207 GO TO 2000, 2001, L	CYCORD	2000 200
287.	C IT IS BONDED TO S1. SET INDICATORS.	CYCORD	
288.	2000 IDENTIFICATION	CYCORD	
289.	IDENTIFICATION	CYCORD	
290.	GO TO 203	CYCORD	203
291.	C IT IS BONDED TO S2. EXAMINE CORE ATOMS ON RING WHICH	CYCORD	
292.	ARE ONE REMOVED FROM S2.	CYCORD	
293.	2001 IDENTIFICATION	CYCORD	
294.	DO295 K=1, NP	CYCORD	
295.	IF (S1, S2, S3 .EQ. 2, OR, IOD, S, I, I, NE, 2) RETURN	CYCORD	200



DATA1

```
1. BLOCK DATA DATA1 DATA1
2. C THIS BLOCK DATA CONTAINS THE DATA FROM BENSONS GROUP ADDITIVITY DATA1
3. C TABLES. THE TABULAR INPUT PER GROUP COMPRISES THE (1)CHEMICAL DATA1
4. C GROUP SYMBOL (GROUP1, GROUP2, GROUP3), (2)ASSIGNED GROUP DATA1
5. C WEIGHT(SUM), (3)HEAT OF FORMATION(HF298) AND (4)ENTROPY(S298) DATA1
6. C AT 298 DEG. K., AND THE COEFFICIENTS FOR THE HEAT CAPACITY DATA1
7. C EQUATION  $CP = CP1 + CP2(T) + CP3(T)^2 + CP4(T)^3$ . DATA1
8. C INTEGER GROUP1(100), GROUP2(100), GROUP3(100) DATA1
9. C INTEGER SUM(100) DATA1
10. C DIMENSION CP1(100), CP2(100), CP3(100), CP4(100) DATA1
11. C COMMON/BLK4/NBC(60,50), NBS(60,2), NBX(60,20), IRC, NDNFUS, IRCTOT DATA1
12. C COMMON/BLK7/SUM, HF298(100), S298(100), CPX(100,4) DATA1
13. C EQUIVALENCE (GROUP1(1), NBC(2,1)), (GROUP2(1), NBC(2,12)), DATA1
14. C (GROUP3(1), NBC(2,25)) DATA1
15. C EQUIVALENCE (CPX(1,1), CP1(1)), (CPX(1,2), CP2(1)), (CPX(1,3), CP3(1)), DATA1
16. C (CPX(1,4), CP4(1)) DATA1
17. C1.0 DATA FOR HYDROCARBONS. DATA1
18. DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L), DATA1
19. ACP1(L), CP2(L), CP3(L), CP4(L), L=1, 9) DATA1
20. B4HCMM, 4MC, 4M, 296, -10.08, 30.41, DATA1
21. C-1.67923034E-1, 2.44328426E-2, -1.16714356E-5, 2.18035135E-9, DATA1
22. D4HCNC, 4MC, 4M, 399, -4.95, 9.42, DATA1
23. E-2.55391108E-1, 2.28786843E-2, -1.32552624E-5, 2.96652455E-9, DATA1
24. F4HCNC, 4MC, 4M, 502, -1.90, -12.07, DATA1
25. G-1.72331790E+0, 2.65408863E-2, -2.04191614E-5, 5.63747170E-9, DATA1
26. H4HCCC, 4MC, 4M, 605, 0.50, -35.10, DATA1
27. I-4.07843204E+0, 3.81256429E-2, -3.60167656E-5, 1.06820609E-8, DATA1
28. J4HDM, 4M, 4M, 1031, 6.26, 27.61, DATA1
29. K-1.35786856E-1, 1.94481085E-2, -1.06666187E-5, 2.32949382E-9, DATA1
30. L4HDM, 4M, 4M, 1134, 8.59, 7.97, DATA1
31. M-8.45867337E-1, 1.28226160E-2, -6.32082053E-6, 1.11437915E-9, DATA1
32. N4HDC, 4M, 4M, 1237, 10.34, -12.70, DATA1
33. O-2.21784832E+0, 7.71249371E-3, -4.94590091E-6, 1.09689094E-9, DATA1
34. P4HDM, 4M, 4M, 2008, 6.78, 6.30, DATA1
35. Q-1.03607557E+0, 2.38648291E-2, -1.96511772E-5, 5.76029184E-9, DATA1
36. R4HDC, 4M, 4M, 2111, 8.86, -14.60, DATA1
37. S-3.33905417E-1, 1.87546888E-2, -1.82762574E-5, 5.74280363E-9, DATA1
38. DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L), DATA1
39. ACP1(L), CP2(L), CP3(L), CP4(L), L=10, 18) DATA1
40. B4HDZ, 4M, 4M, 2011, 6.78, 6.30, DATA1
41. C-1.03807557E+0, 2.38648291E-2, -1.96511772E-5, 5.76029184E-9, DATA1
42. D4HDZ, 4M, 4M, 2114, 8.64, -14.60, DATA1
43. E-3.33905417E-1, 1.87546888E-2, -1.82762574E-5, 5.74280363E-9, DATA1
44. F4HDM, 4M, 4M, 2009, 6.76, 6.30, DATA1
45. G-1.03807557E+0, 2.38648291E-2, -1.96511772E-5, 5.76029184E-9, DATA1
46. H4HDC, 4M, 4M, 1273, -4.76, 9.80, DATA1
47. I-1.97016033E+0, 2.92031432E-2, -1.99328415E-5, 5.14872893E-9, DATA1
48. J4HDM, 4M, 4M, 2147, -4.29, 10.20, DATA1
49. K-3.73854403E+0, 3.57678715E-2, -2.69846033E-5, 7.46954866E-9, DATA1
50. L4HDM, 4M, 4M, 2150, -4.29, 10.20, DATA1
51. M-3.73854403E+0, 3.57678715E-2, -2.69846033E-5, 7.46954866E-9, DATA1
52. N4HCT, 4M, 4M, 1274, -4.73, 10.30, DATA1
53. O-1.37099386E+0, 2.94749983E-2, -1.56770613E-5, 3.74328008E-9, DATA1
54. P4HDC, 4M, 4M, 1276, -4.86, 9.34, DATA1
55. Q-1.28315922E+0, 3.00487640E-2, -2.21458365E-5, 5.87065982E-9, DATA1
56. R4HDC, 4M, 4M, 1376, -1.48, -11.60, DATA1
57. S-3.60401932E-1, 3.37235704E-2, -2.82179473E-5, 8.23527062E-9, DATA1
58. DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L), DATA1
59. ACP1(L), CP2(L), CP3(L), CP4(L), L=19, 27) DATA1
60. B4HCT, 4M, 4M, 1377, -1.72, -11.19, DATA1
61. C-2.83092066E+0, 2.91372022E-2, -2.28409405E-5, 6.4142777E-9, DATA1
62. D4HCT, 4M, 4M, 1379, -0.98, -12.15, DATA1
63. E-2.85108084E+0, 3.41308621E-2, -2.90251609E-5, 8.72526375E-9, DATA1
64. F4HDC, 4M, 4M, 1479, 1.60, -34.72, DATA1
65. G-5.66578889E+0, 4.37931905E-2, -4.17270981E-5, 1.24739551E-8, DATA1
66. H4HDC, 4M, 4M, 1482, 2.81, -39.18, DATA1
67. I-6.37314891E+0, 4.99863297E-2, -5.01919550E-5, 1.53979446E-8, DATA1
68. J4M, 4M, 4M, 1024, 26.93, 24.70, DATA1
69. K-2.56220694E+0, 1.15236646E-2, -8.70323055E-6, 2.54450214E-9, DATA1
70. L4M, 4M, 4M, 1127, 27.59, 6.39, DATA1
71. M-1.46686730E+0, 6.94339008E-3, -5.46269683E-6, 2.00146454E-9, DATA1
72. N4M, 4M, 4M, 2001, 29.20, 6.43, DATA1
73. O-1.11432395E+0, 1.54355057E-2, -1.17471535E-5, 3.01714266E-9, DATA1
74. P4M, 4M, 4M, 2004, 29.30, 6.43, DATA1
75. R-1.11432395E+0, 1.54355057E-2, -1.17471535E-5, 3.01714266E-9, DATA1
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76.	R4HZM	,4M	,4M	1016,	3.30,	11.53,	DATA1
77.	S	-1.6891748E+0,	2.01929000E-2,	-1.35394127E-5,	3.43535328E-9/		DATA1
78.	DATA	(GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L),					DATA1
79.	ACP1(L), CP2(L), CP3(L), CP4(L), L=28, 33)/						DATA1
80.	B4HZC	,4M	,4M	1119,	5.51,	-7.69,	DATA1
81.	C	7.14972161E-1,	7.07999179E-3,	-2.19924970E-6,	-1.21381310E-10,		DATA1
82.	D4HZD	,4M	,4M	1993,	5.68,	-7.80,	DATA1
83.	E	2.03920577E+0,	5.75753208E-3,	-7.13712848E-6,	-3.50617941E-11,		DATA1
84.	F4HZT	,4M	,4M	1994,	5.68,	-7.80,	DATA1
85.	G	-2.03920577E+0,	5.75753208E-3,	-2.13712848E-6,	-3.50617941E-11,		DATA1
86.	H4HZZ	,4M	,4M	1996,	4.96,	-4.64,	DATA1
87.	I	-7.11108376E-1,	1.79264165E-2,	-1.59957077E-5,	4.70062916E-9,		DATA1
88.	J4HA	,4M	,4M	997,	34.20,	6.00,	DATA1
89.	K	1.88644431E+0,	8.73926593E-3,	-7.16630431E-6,	2.02379753E-9,		DATA1
90.	L4HZ1	,4M	,4M	999,	4.84,	-4.6329,	DATA1
91.	M	-4.45622480E-2,	1.28983697E-2,	-1.02396205E-5,	2.93610786E-9/		DATA1
92.	C2.0	DATA FOR OXYGEN-CONTAINING GROUPS.					DATA1
93.	DATA	(GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L),					DATA1
94.	ACP1(L), CP2(L), CP3(L), CP4(L), L=51, 57)/						DATA1
95.	B4H(CO), 4H(CO), 4HC	,4M	,4M	1502,	-29.2,	0.0,	DATA1
96.	C	4*0.0,					DATA1
97.	D4H(CO), 4HOD	,4M	,4M	1855,	-33.5,	0.0,	DATA1
98.	E	4*0.0,					DATA1
99.	F4H(CO), 4HOZ	,4M	,4M	1858,	-46.0,	0.0,	DATA1
100.	G	4*0.0,					DATA1
101.	H4H(CO), 4HOC	,4M	,4M	981,	-33.4,	14.78,	DATA1
102.	I	3.19242434E+00,	1.02961486E-02,	-3.35001576E-06,	-7.82103825E-10,		DATA1
103.	J4H(CO), 4HOM	,4M	,4M	878,	-29.5,	34.93,	DATA1
104.	K	4.63300963E+00,	6.58441850E-03,	6.03395343E-06,	-5.05496292E-09,		DATA1
105.	L4H(CO), 4HDM	,4M	,4M	1717,	-31.7,	0.0,	DATA1
106.	M	4*0.0,					DATA1
107.	N4H(CO), 4HZZ	,4M	,4M	2700,	-39.1,	0.0,	DATA1
108.	O	4*0.0/					DATA1
109.	DATA	(GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L),					DATA1
110.	ACP1(L), CP2(L), CP3(L), CP4(L), L=58, 64)/						DATA1
111.	B4H(CO), 4HZC	,4M	,4M	1823,	-37.6,	0.0,	DATA1
112.	C	4*0.0,					DATA1
113.	D4H(CO), 4HZM	,4M	,4M	1720,	-31.7,	0.0,	DATA1
114.	E	4*0.0,					DATA1
115.	F4H(CO), 4HCC	,4M	,4M	946,	-31.5,	15.01,	DATA1
116.	G	3.30891440E+00,	7.16369917E-03,	2.33322491E-06,	-3.19746180E-09,		DATA1
117.	H4H(CO), 4HCM	,4M	,4M	843,	-29.6,	34.93,	DATA1
118.	I	4.63300963E+00,	6.58441850E-03,	6.03395343E-06,	-5.05496292E-09,		DATA1
119.	J4H(CO), 4HMM	,4M	,4M	740,	-27.7,	53.67,	DATA1
120.	K	6.26038702E+00,	4.58150196E-03,	1.12433979E-05,	-7.28097943E-09,		DATA1
121.	L4H(CO), 4H(CO), 4M)	,4M	,4M	1324,	-50.9,	0.0,	DATA1
122.	M	4*0.0,					DATA1
123.	N4H(CO), 4H(D	,4M	,4M	1003,	-19.0,	0.0,	DATA1
124.	O	4*0.0/					DATA1
125.	DATA	(GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L),					DATA1
126.	ACP1(L), CP2(L), CP3(L), CP4(L), L=65, 71)/						DATA1
127.	B4H(CO), 4H(D	,4M	,4M	1842,	-41.5,	0.0,	DATA1
128.	C	4*0.0,					DATA1
129.	D4H(CO), 4H(C	,4M	,4M	968,	-41.3,	8.39,	DATA1
130.	E	4*0.0,					DATA1
131.	F4H(CO), 4H(M	,4M	,4M	865,	-60.3,	24.52,	DATA1
132.	G	-1.86524457E+00,	2.61105691E-02,	-2.66193574E-05,	1.01501091E-08,		DATA1
133.	H4HODC	,4M	,4M	447,	-4.5,	9.4,	DATA1
134.	I	3.99375985E+00,	-1.96318580E-03,	3.45093879E-06,	-1.19120711E-09,		DATA1
135.	J4HODD	,4M	,4M	482,	19.0,	9.4,	DATA1
136.	K	3.99375985E+00,	-1.96318580E-03,	3.45093879E-06,	-1.19120711E-09,		DATA1
137.	L4HODH	,4M	,4M	344,	-18.27,	27.85,	DATA1
138.	M	2.49720532E+00,	1.4323353E-02,	-9.11292325E-06,	2.67551005E-09,		DATA1
139.	N4HODD	,4M	,4M	2160,	-32.8,	8.1,	DATA1
140.	O	4*0.0/					DATA1
141.	DATA	(GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L),					DATA1
142.	ACP1(L), CP2(L), CP3(L), CP4(L), L=72, 78)/						DATA1
143.	B4HODC	,4M	,4M	1286,	-31.3,	0.0,	DATA1
144.	C	4*0.0,					DATA1
145.	D4HODZ	,4M	,4M	2166,	-19.3,	0.0,	DATA1
146.	E	4*0.0,					DATA1
147.	F4HODC	,4M	,4M	1289,	-22.6,	0.0,	DATA1
148.	G	4*0.0,					DATA1
149.	H4HODZM	,4M	,4M	1186,	-37.9,	29.1,	DATA1
150.	I	4.00163263E+00,	-5.24726811E-03,	1.40015611E-05,	-6.95695002E-09,		DATA1

191.	J4H0CC, 4M, 4M, 412, -23.7, 0.40, DATA1
192.	K 3.73567870E-00, -2.79311733E-03, 7.37218681E-06, -3.49635604E-09, DATA1
193.	L4H0CM, 4M, 4M, 309, -37.80, 29.67, DATA1
194.	M 5.95817829E+00, -6.71425028E-03, 1.68870991E-05, -8.32589317E-09, DATA1
195.	N4H0'CO, 4M)D, 4M, 1828, 6.3, 0.0, DATA1
196.	O 400.0, DATA1
197.	DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L), DATA1
198.	ACPI(L), CP2(L), CP3(L), CP4(L), L=79, 93) DATA1
199.	B4H0(CO, 4M)C, 4M, 1793, 9.4, 0.0, DATA1
200.	C 400.0, DATA1
201.	D4H0(CO, 4M)M, 4M, 1690, 7.60, 0.0, DATA1
202.	E 400.0, DATA1
203.	F4H0D0, 4M, 4M, 2146, 8.9, 0.0, DATA1
204.	G 400.0, DATA1
205.	H4H0DC, 4M, 4M, 1272, 10.3, 0.0, DATA1
206.	I 400.0, DATA1
207.	J4H0DM, 4M, 4M, 1169, 0.6, 8.0, DATA1
208.	K 8.45867337E-01, 1.28224360E-02, -6.32082053E-06, 1.11437915E-09, DATA1
209.	L4H2(CO, 4M), 4M, 1675, 9.7, 0.0, DATA1
210.	M 400.0, DATA1
211.	N4H2O, 4M, 4M, 1154, -1.0, -10.2, DATA1
212.	O-4.44977239E+00, 4.04574195E-02, -4.83862365E-05, 1.90830840E-09, DATA1
213.	DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L), DATA1
214.	ACPI(L), CP2(L), CP3(L), CP4(L), L=86, 92) DATA1
215.	B4H0(CO, 4M)CO, 4M)MM, 1511, -7.2, 0.0, DATA1
216.	C 400.0, DATA1
217.	D4H0(CO, 4M)CCH, 4M, 1050, -1.8, -12.0, DATA1
218.	E 400.0, DATA1
219.	F4H0(CO, 4M)CMH, 4M, 955, -3.0, 9.4, DATA1
220.	G 3.39420138E-01, 2.51711439E-02, -2.04641082E-05, 7.34887474E-09, DATA1
221.	H4H0(CO, 4M)CCC, 4M, 1161, 1.6, 0.0, DATA1
222.	I 400.0, DATA1
223.	J4H0(CO, 4M)MMM, 4M, 852, -10.00, 30.41, DATA1
224.	K-1.67923834E-01, 2.44328426E-02, -1.16714356E-05, 2.18035135E-09, DATA1
225.	L4H0CO, 4M, 4M, 475, -16.8, 0.0, DATA1
226.	M 400.0, DATA1
227.	N4H0CO, 4M, 4M, 572, -17.2, 0.0, DATA1
228.	O 400.0, DATA1
229.	DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L), DATA1
230.	ACPI(L), CP2(L), CP3(L), CP4(L), L=93, 99) DATA1
231.	B4H0COH, 4M, 4M, 409, -17.7, 0.0, DATA1
232.	C 400.0, DATA1
233.	D4H0COZK, 4M, 4M, 1311, -6.6, 9.7, DATA1
234.	E 400.0, DATA1
235.	F4H0COH, 4M, 4M, 1300, -3.9, 0.0, DATA1
236.	G 400.0, DATA1
237.	H4H0CO, 4M, 4M, 646, -6.30, -33.56, DATA1
238.	I-6.21467381E+00, 5.16292395E-02, -6.19187997E-05, 2.47600205E-09, DATA1
239.	J4H0CO, 4M, 4M, 537, -7.00, -11.00, DATA1
240.	K-5.35977826E+00, 4.78986890E-02, -5.25420190E-05, 2.04415825E-09, DATA1
241.	L4H0COH, 4M, 4M, 43, -8.5, 10.03, DATA1
242.	M-3.46110576E+00, 3.69163436E-02, -3.24811370E-05, 1.13583539E-09, DATA1
243.	N4H0COH, 4M, 4M, 331, -10.00, 30.41, DATA1
244.	O-1.75871384E-01, 2.44607515E-02, -1.16902894E-05, 2.18283350E-09, DATA1
245.	CS.0 DATA FOR NITROGEN-CONTAINING GROUPS. DATA1
246.	DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L), DATA1
247.	ACPI(L), CP2(L), CP3(L), CP4(L), L=110, 124) DATA1
248.	B4H0CMH, 4M, 4M, 712, -10.00, 30.41, DATA1
249.	C-1.67923834E-01, 2.44328426E-02, -1.16714356E-05, 2.18035135E-09, DATA1
250.	D4H0CM, 4M, 4M, 819, -6.6, 9.8, DATA1
251.	E-1.84194751E+00, 3.01279382E-02, -2.33046702E-05, 7.40890103E-09, DATA1
252.	F4H0C, 4M, 4M, 918, -5.2, -11.7, DATA1
253.	G-3.73791206E+00, 3.82564997E-02, -3.82709110E-05, 1.34873957E-09, DATA1
254.	H4H0C, 4M, 4M, 1021, -3.2, -24.1, DATA1
255.	I-5.61176857E+00, 4.75192184E-02, -5.35080656E-05, 2.01088418E-09, DATA1
256.	J4H0CMH, 4M, 4M, 699, 4.0, 20.71, DATA1
257.	K 2.87594738E+00, 1.00598791E-02, -2.32720336E-06, -1.39650146E-10, DATA1
258.	L4H0CCH, 4M, 4M, 802, 15.4, 0.94, DATA1
259.	M 9.59545130E-03, 1.70299403E-02, -1.09771783E-05, 2.57028800E-09, DATA1
260.	N4H0C, 4M, 4M, 935, 24.4, -13.46, DATA1
261.	O-1.81182942E+00, 7.33777734E-02, -2.09418857E-05, 6.03373847E-09, DATA1
262.	DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L), DATA1
263.	ACPI(L), CP2(L), CP3(L), CP4(L), L=125, 131) DATA1
264.	B4H0MMH, 4M, 4M, 1119, 11.4, 29.13, DATA1
265.	C 9.75906852E-01, 2.11752446E-02, -1.46899632E-05, 3.94852974E-09, DATA1

226.	D4HNNCH, 4M	, 4M	1218,	20.9	9.61,		DATA1
227.	E 9.56846121E-01,	1.64883897E-02,	-1.24831746E-05,	3.51125561E-09,			DATA1
228.	F4HNNCC, 4M	, 4M	1321,	29.2	-13.80,		DATA1
229.	G 4*0.0,						DATA1
230.	H4HNNZM, 4M	, 4M	2099,	22.1	0.0		DATA1
231.	I 4*0.0,						DATA1
232.	J4HNNM, 4M	, 4M	479,	0.0	0.0		DATA1
233.	K 4*0.0,						DATA1
234.	L4HNNIC, 4M	, 4M	583,	21.3	0.7		DATA1
235.	M 4*0.0,						DATA1
236.	N4HNNIZ, 4M	, 4M	1459,	16.7	0.0		DATA1
237.	O 4*0.0,						DATA1
238.	DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L),						DATA1
239.	ACPI(L), CP2(L), CP3(L), CP4(L), L=132, 138) /						DATA1
240.	B4HNNZM, 4M	, 4M	527,	25.1	26.0		DATA1
241.	C 2.41191140E+00,	7.15235247E-03,	-2.21801632E-06,	8.55800248E-11,			DATA1
242.	D4HNNCC, 4M	, 4M	630,	32.5	8.0		DATA1
243.	E 4*0.0,						DATA1
244.	F4HNNZM, 4M	, 4M	1576,	4.8	29.71,		DATA1
245.	G 2.8*594738E+00,	1.00598791E-02,	-2.32720336E-06,	-1.39650146E-10,			DATA1
246.	H4HNNZM, 4M	, 4M	1679,	14.9	0.0		DATA1
247.	I 4*0.0,						DATA1
248.	J4HNNZCC, 4M	, 4M	1782,	26.2	0.0		DATA1
249.	K 4*0.0,						DATA1
250.	L4HNNZM, 4M	, 4M	2556,	18.3	0.0		DATA1
251.	M 4*0.0,						DATA1
252.	N4HNNZM, 4M	, 4M	1539,	-0.5	-9.69,		DATA1
253.	C-3.57157539E+00,	3.69462129E-02,	-4.48672434E-05,	1.80561699E-08,			DATA1
254.	DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L),						DATA1
255.	ACPI(L), CP2(L), CP3(L), CP4(L), L=139, 145) /						DATA1
256.	B4HNNZM, 4M	, 4M	1046,	23.0	0.0		DATA1
257.	C 4*0.0,						DATA1
258.	D4H(CO), 4MNM	, 4M	1259,	-29.6	34.93,		DATA1
259.	E 4.63300543E+00,	6.58441850E-03,	6.03395343E-06,	-9.05496292E-09,			DATA1
260.	F4H(CO), 4MNC	, 4M	1362,	-32.8	16.2		DATA1
261.	G 3.64767855E+00,	3.89405707E-03,	7.00136594E-06,	-3.37854793E-09,			DATA1
262.	H4HNC(CO), 4MNM	, 4M	1255,	-14.9	24.69,		DATA1
263.	I-3.25292052E+00,	3.09737873E-02,	-2.42737069E-05,	7.77065898E-09,			DATA1
264.	J4HNC(CO), 4MNC	, 4M	1350,	-4.4	3.9		DATA1
265.	K 4*0.0,						DATA1
266.	L4HNC(CO), 4MCC	, 4M	1461,	0.0	0.0		DATA1
267.	M 4*0.0,						DATA1
268.	N4HNC(CO), 4MNM	, 4M	2239,	0.4	0.0		DATA1
269.	O 4*0.0,						DATA1
270.	DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L),						DATA1
271.	ACPI(L), CP2(L), CP3(L), CP4(L), L=146, 152) /						DATA1
272.	B4HNC(CO), 4MNC	, 4M	1914,	-18.5	0.0		DATA1
273.	C 4*0.0,						DATA1
274.	D4HNC(CO), 4M(CO), 4MCC	, 4M	2017,	-5.9	0.0		DATA1
275.	E 4*0.0,						DATA1
276.	F4HNC(CO), 4M(CO), 4MCC	, 4M	2894,	-0.5	0.0		DATA1
277.	G 4*0.0,						DATA1
278.	H4HNC(CO), 4MNC	, 4M	679,	22.5	40.20,		DATA1
279.	I 1.59367113E+00,	3.80737392E-02,	-2.26626252E-05,	4.49026495E-09,			DATA1
280.	J4HNC(CO), 4MNC	, 4M	792,	25.8	19.80,		DATA1
281.	K 4.45475478E+00,	2.59532780E-02,	-1.4581110E-05,	2.77018921E-09,			DATA1
282.	L4HNC(CO), 4MCC	, 4M	885,	0.0	-2.80,		DATA1
283.	M 4*0.0,						DATA1
284.	N4HNC(CO), 4MNC	, 4MCC	1165,	0.0	28.40,		DATA1
285.	O 4*0.0,						DATA1
286.	DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L), S298(L),						DATA1
287.	ACPI(L), CP2(L), CP3(L), CP4(L), L=153, 159) /						DATA1
288.	B4HNC(CO), 4MNM	, 4M	1414,	37.4	36.58,		DATA1
289.	C 1.62789124E+00,	3.41575604E-02,	-2.50052036E-05,	6.52183340E-09,			DATA1
290.	D4HNC(CO), 4M(CO), 4M		1797,	84.1	0.0		DATA1
291.	E 4*0.0,						DATA1
292.	F4HNC(CO), 4MNM	, 4M	1247,	0.0	44.4		DATA1
293.	G 3.05906524E-01,	9.04788384E-02,	-3.7813518E-05,	1.01928047E-08,			DATA1
294.	H4HNC(CO), 4M	, 4M	137,	35.0	20.50,		DATA1
295.	I 3.13115650E+00,	2.94963575E-02,	-2.70020814E-05,	9.27540003E-09,			DATA1
296.	J4HNC(CO), 4M	, 4M	1397,	63.0	35.40,		DATA1
297.	K 6.32800189E+00	1.66234963E-02,	-1.18436933E-05,	3.18238362E-09,			DATA1
298.	L4HNC(CO), 4MNC	, 4M	912,	-15.1	40.4		DATA1
299.	M 4*0.0,						DATA1
300.	N4HNC(CO), 4MCC	, 4M	619,	-15.0	76.9		DATA1


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301.      0 400.0/                               DATA
302.      DATA (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), KP290(L), Z290(L),   DATA
303.      ACPI(L), CP2(L), CP3(L), CP4(L), L=140, 163)/                            DATA
304.      B4MCION, 4ND ICC, 4MC      ,       710,       0.0 ,       3.9 ,        DATA
305.      C 400.0,                               DATA
306.      D4MCION, 4ND IIC, 4ND ICH,       720,       -14.0 ,       0.0 ,        DATA
307.      E 400.0,                               DATA
308.      F4NDINO, 4ND IC , 4N      ,       500,       -5.0 ,       41.9 ,        DATA
309.      G 4.39094421E+00, 1.91590634E-02, -1.22787841E-05, 2.66823631E-09,   DATA
310.      H4NDION, 4ND IC , 4N      ,       525,       -15.4 ,       40.50,        DATA
311.      I 400.0/                               DATA
312.      END

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DELETE

1.		SUBROUTINE DELETE(KIRD,ISBE,KTY)	DELETE
2.	C	THIS SUBROUTINE DISENGAGES FROM USE ALL THE PAIRS OF CHAIN	DELETE
3.	C	RING ATOMS AND THEIR NON-RING LIGANDS WHICH HAVE BEEN FOUND	DELETE
4.	C	TO BE DISSIMILAR BY THE COMPARISON TESTS OF SUBROUTINE EQUALR.	DELETE
5.		INTEGER SVXK(4),SYMBOL(9),GRID(50,80)	DELETE
6.		DIMENSION JDONE(100),KCCR(2,30),IDX(8,99)	DELETE
7.		COMMON/BLK1/ND,NOS,SVXK,SYMBOL,NOVAL(9),GRID	DELETE
8.		COMMON/BLK3/IRING(40,30),IMATX(50,80),NW(100),IBC(100),KON(100),	DELETE
9.		JDRK(100),IB(100,8),IRG,NORR	DELETE
10.		EQUIVALENCE (JDONE(1),IMATX(2,47)),(KCCR(1,1),GRID(1,23)),	DELETE
11.		1(IDX(1,1),GRID(3,1))	DELETE
12.	C1.0	THIS SECTION DISENGAGES FROM USE ALL THOSE PAIRS OF CHAIN	DELETE
13.	C	ATOMS FROM THE TWO RINGS, A AND B, UNDER COMPARISON WHICH ARE	DELETE
14.	C	EACH BONDED TO TWO OTHER RING ATOMS AND WHICH FOLLOW THE	DELETE
15.	C	PREVIOUS BRANCH RING ATOM. THE LATTER IS AN ATOM BONDED TO	DELETE
16.	C	THREE OTHER RING ATOMS, NAMELY, ATOMS THAT FORM PART OF THE	DELETE
17.	C	RING BACKBONE.	DELETE
18.		KK=KTY	DELETE
19.		DO3 K=1,KTY	DELETE
20.		IF(KCCR(1,KK)EQ.KIRD)GO TO 9	DELETE
21.		K1=KCCR(1,KK)	DELETE
22.		JDONE(K1)=9	DELETE
23.		K2=KCCR(2,KK)	DELETE
24.		JDONE(K2)=9	DELETE
25.		KK=KK-1	DELETE
26.		3 CONTINUE	DELETE
27.	C2.0	IF NONE OF THE AFOREMENTIONED CHAIN RING ATOMS ARE PRESENT,	DELETE
28.	C	EXIT FROM ROUTINE.	DELETE
29.		5 KD=KTY-KK	DELETE
30.		IF(KD.EQ.0)RETURN	DELETE
31.	C3.0	THIS SECTION ALSO DISENGAGES FROM USE ANY PAIRS OF NON-RING	DELETE
32.	C	ATOMS BONDED TO THE AFOREMENTIONED CHAIN RING ATOMS.	DELETE
33.		K1=KTY	DELETE
34.		KTY=KK	DELETE
35.		K2=ISBE	DELETE
36.		OO11 K=1,KD	DELETE
37.		IF(KCCR(1,K1)NE.IDX(1,K2))GO TO 9	DELETE
38.		K2=K2-1	DELETE
39.		9 K1=K1-1	DELETE
40.		11 CONTINUE	DELETE
41.		ISBE=K2	DELETE
42.		RETURN	DELETE
43.		END	DELETE

DELTA1

1.		SUBROUTINE DELTA1(KT)	DELTA1
2.	C	THIS SUBROUTINE DETERMINES THAT PART OF THE WEIGHT OF GROUP KT	DELTA1
3.	C	THAT IS COMPOSED OF THE SUM OF THE ASSIGNED WEIGHTS OF THE	DELTA1
4.	C	GROUP CORE ATOM AND OF THE ATOMIC CONSTITUENTS BONDED TO THE	DELTA1
5.	C	CORE ATOM.	DELTA1
6.		INTEGER WEIGHT(9)	DELTA1
7.		COMMON/BLK2/WEIGHT, MWGT(9), MOLWT(100), IX(100,5,6), NC(100), KCC	DELTA1
8.	C1.	SET KSUM.	DELTA1
9.		KSUM=0	DELTA1
10.		I=IX(KT,1,1)	DELTA1
11.	C2.	ADD WEIGHT OF CORE ATOM KT TO MOLWT(KT).	DELTA1
12.		MOLWT(KT)=MOLWT(KT)+WEIGHT(I)	DELTA1
13.	C3.	ADD WEIGHTS OF LIGAND ATOMS BONDED TO KT.	DELTA1
14.		DO 11 KM=2,9	DELTA1
15.		I=IX(KT,KM,1)	DELTA1
16.		IF(I.EQ.0)GO TO 17	DELTA1
17.	C	ADD WEIGHT OF LIGAND KM.	DELTA1
18.		MOLWT(KT)=MOLWT(KT)+WEIGHT(I)	DELTA1
19.	C	DETERMINE WHETHER WEIGHT OF ATOM KM HAS TO BE MODIFIED.	DELTA1
20.	C	IS BOND BETWEEN KT AND KM MULTIPLE	DELTA1
21.		IF(IX(KT,KM,5).EQ.1)GO TO 11	DELTA1
22.	C	YES, IT IS.	DELTA1
23.		IF(IX(KT,1,1).NE.2)GO TO 3	DELTA1
24.	C	ATOM KT IS CARBON ATOM.	DELTA1
25.		IF(IX(KT,KM,1).NE.2)GO TO 9	DELTA1
26.	C	ATOM KM IS ALSO CARBON ATOM.	DELTA1
27.	C	IS BOND BETWEEN KT AND KM TRIPLE	DELTA1
28.		IF(IX(KT,KM,5).EQ.3)GO TO 1	DELTA1
29.	C	NO, IT IS DOUBLE. APPLY CORRECTION FOR C=C.	DELTA1
30.	C	INCREMENT KSUM.	DELTA1
31.		MOLWT(KT)=MOLWT(KT)+750	DELTA1
32.		KSUM=KSUM+1	DELTA1
33.		GO TO 11	DELTA1
34.	C	YES, IT IS. APPLY CORRECTION FOR C C	DELTA1
35.		1 MOLWT(KT)=MOLWT(KT)+764	DELTA1
36.		GO TO 11	DELTA1
37.		3 IF(IX(KT,1,1).NE.4.OR.IX(KT,KM,5).NE.2)GO TO 11	DELTA1
38.	C	KT IS OF TYPE N. NOW DETERMINE KM.	DELTA1
39.		IF(IX(KT,KM,1)-3)9,11,7	DELTA1
40.	C	APPLY CORRECTION FOR N=C OR C=N	DELTA1
41.		5 MOLWT(KT)=MOLWT(KT)-202	DELTA1
42.		GO TO 11	DELTA1
43.	C	APPLY CORRECTION FOR N=N	DELTA1
44.		7 MOLWT(KT)=MOLWT(KT)-570	DELTA1
45.		GO TO 11	DELTA1
46.	C	IF KM IS OF TYPE N, APPLY CORRECTION FOR C=N (GO TO 5).	DELTA1
47.		9 IF(IX(KT,KM,1).EQ.4.AND.IX(KT,KM,5).EQ.2)GO TO 5	DELTA1
48.		11 CONTINUE	DELTA1
49.	C4.	TWO CORRECTIONS HAVE BEEN APPLIED FOR C=C. BOND IS ACTUALLY	DELTA1
50.	C	C=C=C. APPLY WEIGHT CORRECTION FOR ALLENE.	DELTA1
51.		13 IF(KSUM.NE.2)RETURN	DELTA1
52.		MOLWT(KT)=MOLWT(KT)-672	DELTA1
53.		RETURN	DELTA1
54.		END	DELTA1

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DELTA2

1.		SUBROUTINE DELTA2(KT, JT)	DELTA2
2.	C	THIS SUBROUTINE ADDS ALL OF THE SECOND-ORDER MULTIPLE-BOND	DELTA2
3.	C	CONTRIBUTIONS TO THE GROUP (KT) WEIGHT VALUE. THE CONTRIBUTIONS	DELTA2
4.	C	CONSIDERED HERE ARE THOSE ARISING FROM ANY MULTIPLE BONDS WHICH	DELTA2
5.	C	LIGANDS BONDED TO THE CORE ATOM (JT) MAY HAVE. THE BOND	DELTA2
6.	C	BETWEEN KT AND JT IS, OF COURSE, NOT INCLUDED.	DELTA2
7.		INTEGER WEIGHT(4)	DELTA2
8.		COMMON/BLK2/WEIGHT, MWGT(4), MOLWT(100), IX(100,5,6), NC(100), KCC	DELTA2
9.	C1.	IS ATOM JT A CARBON ATOM	DELTA2
10.		IF(IX(JT,1,1).NE.2)RETURN	DELTA2
11.	C	YES, IT IS.	DELTA2
12.	C2.0	FIND LOCATION OF DATA IN GROUP JT ASSOCIATED WITH LIGAND KT.	DELTA2
13.		DO3 KM=2,5	DELTA2
14.		IF(IX(KT,1,2).EQ.IX(JT,KM,2).AND.IX(KT,1,3).EQ.IX(JT,KM,3))GO TO 7	DELTA2
15.		5 CONTINUE	DELTA2
16.	7	KV=KM	DELTA2
17.	C3.0	INITIATE CYCLE THAT ASSIGNS THE SECOND-ORDER CORRECTIONS.	DELTA2
18.		DO13 KM=2,5	DELTA2
19.		IF(KM.EQ.KV)GO TO 13	DELTA2
20.	C	BOND BETWEEN KT AND JT IS EXCLUDED.	DELTA2
21.		IF(IX(JT,KM,1).NE.2.OR.IX(JT,KM,5).EQ.1)GO TO 13	DELTA2
22.	C	ATOM KM IS ALSO A CARBON ATOM AND BOND BETWEEN JT AND KM	DELTA2
23.	C	IS MULTIPLE.	DELTA2
24.	C	IS BOND BETWEEN JT AND KM TRIPLE	DELTA2
25.		IF(IX(JT,KM,5).EQ.3)GO TO 3	DELTA2
26.	C	NO, IT IS DOUBLE. IS IT AN ALLENE TYPE BOND	DELTA2
27.		IF(IX(KT,1,1).EQ.2.AND.IX(JT,KV,5).EQ.2)GO TO 1	DELTA2
28.	C	NO, APPLY CORRECTION FOR C=C	DELTA2
29.		MOLWT(KT)=MOLWT(KT)+ 874	DELTA2
30.		RETURN	DELTA2
31.	C	YES, APPLY CORRECTION FOR C=C=C	DELTA2
32.	1	MOLWT(KT)=MOLWT(KT)+0	DELTA2
33.		RETURN	DELTA2
34.	C	YES, IT IS TRIPLE. APPLY CORRECTION FOR C C	DELTA2
35.	3	MOLWT(KT)=MOLWT(KT)+ 875	DELTA2
36.		RETURN	DELTA2
37.	13	CONTINUE	DELTA2
38.		RETURN	DELTA2
39.		END	DELTA2

DITERE

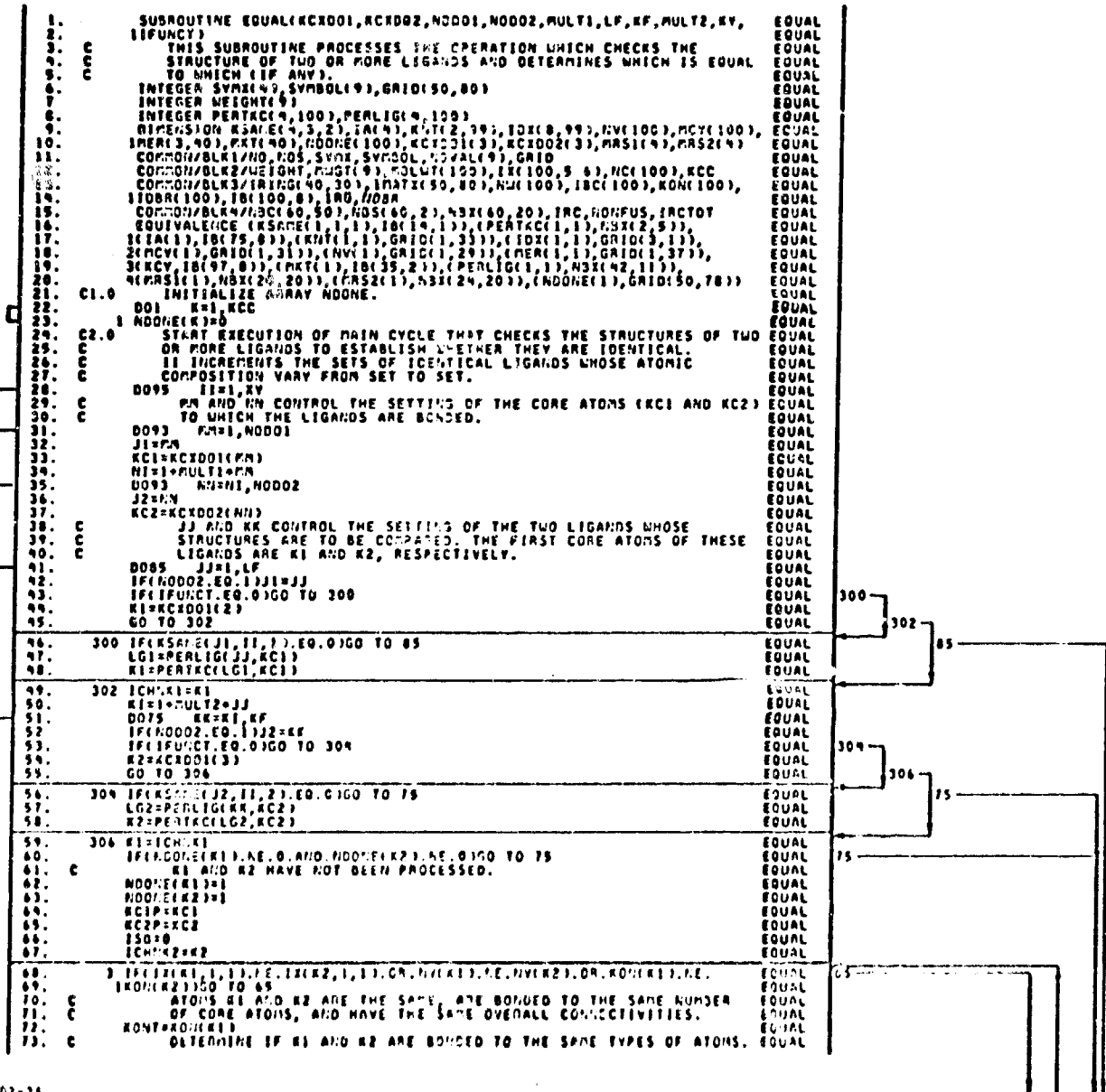
1.		SUBROUTINE DITERE(IGS, IGO, IDTE, OTEM)	DITERE
2.	C	THIS SUBROUTINE DETERMINES WHETHER THERE ARE ONE OR MORE	DITERE
3.	C	DITERTIARY ETHER GROUPS PRESENT. IF SO, IT STORES THE	DITERE
4.	C	MAGNITUDE OF EACH CORRECTION AND SETS THE OTHER PERTINENT	DITERE
5.	C	VARIABLES.	DITERE
6.		INTEGER SUM1, SUM2	DITERE
7.		INTEGER WEIGHT(9)	DITERE
8.		DIMENSION KCGAUS(3, 150), KFCAUS(150), KTGAUS(150), DATCIS(2, 150),	DITERE
9.		IPM(150)	DITERE
10.		COMMON/BLK2/WEIGHT, RWGT(9), MOLWT(100), IX(100, 5, 6), NC(100), KCC	DITERE
11.		COMMON/BLK3/IRING(40, 30), IMATX(50, 80), MW(100), IBC(100), KON(100),	DITERE
12.		IGBR(100), IB(100, 8), IRO, NOBR	DITERE
13.		EQUIVALENCE (KCGAUS(1, 1), IMATX(1, 72)), (KFCAUS(1), IMATX(1, 63)),	DITERE
14.		(KTGAUS(1), IMATX(1, 60)), (DATCIS(1, 1), IMATX(1, 66)), (IPM(1),	DITERE
15.		ZIMATX(1, 97))	DITERE
16.	C1.0	IF NUMBER OF GAUCHE ETHER CORRECTIONS ARE EVEN, CONTINUE.	DITERE
17.	C	OTHERWISE PRINT ERROR MESSAGE AND EXIT.	DITERE
18.		JJ=100/2	DITERE
19.		IF(100.EQ.2+JJ)GO TO 63	DITERE
20.		WRITE(6, 61)	DITERE
21.		61 FORMAT(///1H9, 4HERROR IN GAUCHE ETHER CALCULATION. CONTINUE.///)	DITERE
22.		RETURN	DITERE
<hr/>			
23.	63	LI=IGS-100+1	DITERE
24.		LF=105	DITERE
25.	C2.0	TEST EACH PAIR OF GAUCHE ETHERS FOR DITERTIARY ETHER STRUCTURE.	DITERE
26.		DO45 L=LI, LF, 2	DITERE
27.	C	FIND GROUP NUMBERS OF NON-OXYGEN CORE ATOMS.	DITERE
28.		IBX=IPM(L)	DITERE
29.		KC1=KCGAUS(1, IBX)	DITERE
30.		KC2=KCGAUS(1, IBX+1)	DITERE
31.		SUM1=IX(KC1, 1, 1)+IX(KC2, 1, 1)	DITERE
32.		SUM2=MW(KC1)+MW(KC2)	DITERE
33.		IF(SUM1.NE.4.OR.SUM2.NE.8)GO TO 65	DITERE
34.	C	BOUNDARY LIGANDS ARE CARBON ATOMS AND EACH HAS A	DITERE
35.	C	CONNECTIVITY OF FOUR. DITERTIARY GROUP IS PRESENT. SET	DITERE
36.	C	VARIABLES AND CONTINUE.	DITERE
37.		IGS=IGS+1	DITERE
38.		KCGAUS(1, IGS)=KC1	DITERE
39.		KCGAUS(2, IGS)=KCGAUS(2, IBX)	DITERE
40.		KCGAUS(3, IGS)=KC2	DITERE
41.		KTGAUS(IGS)=8	DITERE
42.		KFCAUS(IGS)=1	DITERE
43.		DATCIS(1, IGS)=0.4	DITERE
44.		OTEM=OTEM+DATCIS(1, IGS)	DITERE
45.		IDTE=IDTE+1	DITERE
46.	65	CONTINUE	DITERE
47.		RETURN	DITERE
48.		END	DITERE

ENTSYM

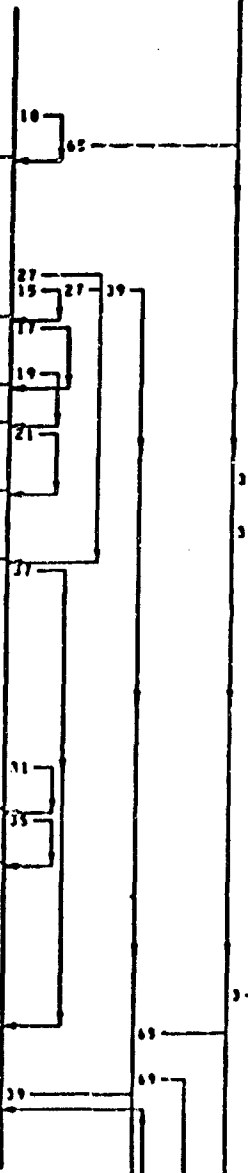
1.	SUBROUTINE ENTSYM(NOSN, NENAN, MESO, NASYMC, NOSNC, NPSUDA, RCSUDA,	ENTSYM
2.	INORSO, SSN, SOPTS)	ENTSYM
3.	C THIS SUBROUTINE COMPUTES THE CONTRIBUTIONS TO THE ENTROPY DUE	ENTSYM
4.	C TO INTERNAL AND EXTERNAL ROTATIONAL SYMMETRY AND OPTICAL	ENTSYM
5.	C ISOMERISM USING COMPUTED DATA AS WELL AS INPUT DATA (IF ANY).	ENTSYM
6.	DIMENSION TOUT(12), IOPATN(100)	ENTSYM
7.	COMMON/BLKS/IRING(40,30), IMATR(50,80), NM(100), IRC(100), KDN(100),	ENTSYM
8.	1IDBR(100), ID(100,8), IRG, NOBR	ENTSYM
9.	COMMON/BLKS/NDATA, NUMATR(5), MDC(50), MDS(2), JM, JY, LFLAGS, LFLAGG	ENTSYM
10.	EQUIVALENCE (IOPATN(1), IMATR(2,45))	ENTSYM
11.	DATA TOUT/1M, 4M, 1M, 4MUT, 1M, 1M, 4MCOMP, 4MUTED, 1M, 4M NOT,	ENTSYM
12.	14M CAL, 4MCULA, 4MBLE /	ENTSYM
13.	C1.0 INITIALIZE VARIABLE.	ENTSYM
14.	LFLAGG=0	ENTSYM
15.	C2.0 WAS THE NUMBER OF ENANTIOMERS INPUT	ENTSYM
16.	C YES. FIND TOTAL NUMBER, NOPTS, AND ENTROPY OF MIXING.	ENTSYM
17.	IF(NENAN.EQ.0)GO TO 1	ENTSYM
18.	NOPTS=NENAN+MESO	ENTSYM
19.	OPTS=NOPTS	ENTSYM
20.	SOPTS=-1.98726+ALOG(OPTS)	ENTSYM
21.	SOPTS=SOPTS	ENTSYM
22.	GO TO 3	ENTSYM
23.	C NO. SET NOPTS=0.	ENTSYM
24.	1 NOPTS=0	ENTSYM
25.	3 MESOC=0	ENTSYM
26.	AFREQ=1.000	ENTSYM
27.	C3.0 WERE ANY ASYMMETRIC ATOMS FOUND BY PROGRAM	ENTSYM
28.	IF(NASYMC.GT.0)GO TO 9	ENTSYM
29.	C NO. SET RELEVANT VARIABLES.	ENTSYM
30.	NENANC=0	ENTSYM
31.	NOPTSC=0	ENTSYM
32.	SOPTSC=0.0	ENTSYM
33.	GO TO 19	ENTSYM
34.	C YES. COMPUTE ENTROPY OF MIXING USING THE NUMBER OF ASYMMETRIC	ENTSYM
35.	C ATOMS CALCULATED.	ENTSYM
36.	9 IF(NOMESO.EQ.0)GO TO 13	ENTSYM
37.	N=NASYMC+NPSUDA	ENTSYM
38.	NENANC=2+((N-1)	ENTSYM
39.	IF(N/2.EQ.2+N)GO TO 11	ENTSYM
40.	MESOC=2+((N-1)/2)	ENTSYM
41.	NENANC=NENANC+MESOC	ENTSYM
42.	GO TO 15	ENTSYM
43.	11 MESOC=2+((N-2)/2)	ENTSYM
44.	GO TO 15	ENTSYM
45.	13 NENANC=2+NASYMC	ENTSYM
46.	15 NOPTSC=NENANC+MESOC	ENTSYM
47.	IF(NOMESO.EQ.2)AFREQ=FLOAT(MESOC*2/NOPTSC)	ENTSYM
48.	OPTS=NOPTSC	ENTSYM
49.	SOPTSC=-1.98726+ALOG(OPTS)	ENTSYM
50.	C4.0 WAS AN EXTERNAL SYMMETRY NUMBER INPUT	ENTSYM
51.	19 IF(NOSN.EQ.0)GO TO 23	ENTSYM
52.	C YES. COMPUTE EXTERNAL ROTATIONAL ENTROPY CONTRIBUTION FROM	ENTSYM
53.	C INPUT DATA.	ENTSYM
54.	SN=NOSN	ENTSYM
55.	IF(MESO.LE.0)GO TO 21	ENTSYM
56.	AFREQ=FLOAT(MESO*2/NOPTS)	ENTSYM
57.	GO TO 22	ENTSYM
58.	21 IF(MESOC.LE.0)GO TO 22	ENTSYM
59.	AFREQ=FLOAT(MESOC*2/NOPTSC)	ENTSYM
60.	22 SSNI=-1.98726+ALOG(SN)	ENTSYM
61.	SSN=SSNI	ENTSYM
62.	C NOW COMPUTE SAME PROPERTY FROM COMPUTED DATA.	ENTSYM
63.	23 SN=NOSNC	ENTSYM
64.	SSNC=-1.98726+AFREQ+ALOG(SN)	ENTSYM
65.	C5.0 IF SYMMETRY AND/OR OPTICAL DATA WERE INPUT, THE ENTROPY	ENTSYM
66.	C CONTRIBUTIONS USED IN THE THERMO CALCULATIONS ARE THOSE DERIVED	ENTSYM
67.	C FROM THE INPUT DATA.	ENTSYM
68.	IF(NOSN.EQ.0)SSN=SSNC	ENTSYM
69.	IF(NOPTS.EQ.0)SOPTS=SOPTSC	ENTSYM
70.	C6.0 SET FLAG IF DATUM WAS NOT INPUT AND PROPERTY IS NOT COMPUTABLE.	ENTSYM

71.	IF(JM.EQ.9.AND.NOSM.EQ.0.OR.JY.EQ.9.AND.NOPTS.EQ.0) LFLAG=1	ENTSYM
72.	C7.0 PRINT OUT EXTERNAL ROTATIONAL SYMMETRY CONTRIBUTION.	ENTSYM
73.	WRITE(6,25)	ENTSYM
74.	25 FORMAT(//1H0,42X,45HEXTERNAL ROTATIONAL SYMMETRY CONTRIBUTION	ENTSYM
75.	1//1H,45X,6NSOURCE,9X,15NSYMMETRY NUMBER,7X,7ENTROPY)	ENTSYM
76.	IF(NOSM.EQ.0) GO TO 31	ENTSYM
77.	C SYMMETRY DATA WAS INPUT. PRINT OUT CONTRIBUTION COMPUTED	ENTSYM
78.	C THEREWITH.	ENTSYM
79.	WRITE(6,29)(TOUT(K),K=1,4),NOSM,SSNI	ENTSYM
80.	29 FORMAT(1H,30X,44X,7X,15,7X,7F14.5)	ENTSYM
81.	C PRINT OUT CONTRIBUTION FROM COMPUTED DATA.	ENTSYM
82.	31 WRITE(6,29)TOUT(JM),TOUT(JM+1),TOUT(JM+2),TOUT(JM+3),NOSMC,SSMC	ENTSYM
83.	C0.0 PRINT OUT OPTICAL ISOMERS CONTRIBUTION.	ENTSYM
84.	WRITE(6,35)	ENTSYM
85.	35 FORMAT(//1H0,49X,30OPTICAL ISOMER CONTR/UTION //1X,11X,	ENTSYM
86.	16NSOURCE,9X,10NASYMMETRIC,4X,16PSEUDOASYMMETRIC,4X,11MENANTIONER	ENTSYM
87.	25,4X,4HRESO,4X,21TOTAL OPTICAL ISOMERS,7X,7ENTROPY)	ENTSYM
88.	IF(NOPTS.EQ.0) GO TO 41	ENTSYM
89.	C OPTICAL DATA WERE INPUT. PRINT OUT CONTRIBUTION COMPUTED	ENTSYM
90.	C THEREWITH.	ENTSYM
91.	WRITE(6,39)(TOUT(K),K=1,4),NENAN,RESO,NOPTS,SOPTS1	ENTSYM
92.	39 FORMAT(1H,6X,44X,39X,15,7X,15,11X,15,10X,7F14.5)	ENTSYM
93.	C PRINT OUT CONTRIBUTION FROM COMPUTED DATA.	ENTSYM
94.	41 WRITE(6,45)TOUT(JY),TOUT(JY+1),TOUT(JY+2),TOUT(JY+3),NASYMC,	ENTSYM
95.	1NPSUDA,NENANC,RESOC,NOPTSC,SOPTSC	ENTSYM
96.	45 FORMAT(1H,6X,44X,5X,15,12X,15,12X,15,7X,15,11X,15,10X,7F14.5)	ENTSYM
97.	IF(NASYMC.EQ.0) RETURN	ENTSYM
98.	C9.0 IF ASYMMETRIC ATOMS WERE FOUND BY PROGRAM, PRINT OUT THEIR	ENTSYM
99.	C GROUP NUMBERS.	ENTSYM
100.	WRITE(6,49)(IOPAT(K),K=1,NASYMC)	ENTSYM
101.	49 FORMAT(//1H0,14X,44NGROUP NUMBER OF ASYMMETRIC CARBON ATOM: *	ENTSYM
102.	1,10(15,1H,1)(1H,32X,10(15,1H,1))	ENTSYM
103.	IF(NPSUDA.EQ.0) RETURN	ENTSYM
104.	C IF PSEUDOASYMMETRIC ATOM IS PRESENT, PRINT OUT ITS GROUP	ENTSYM
105.	C NUMBER.	ENTSYM
106.	WRITE(6,51)PCSUDA	ENTSYM
107.	51 FORMAT(//1H0,10X,49NGROUP NUMBER OF PSEUDOASYMMETRIC CARBON ATOM	ENTSYM
108.	1H,15)	ENTSYM
109.	RETURN	ENTSYM
110.	END	ENTSYM

EQUAL



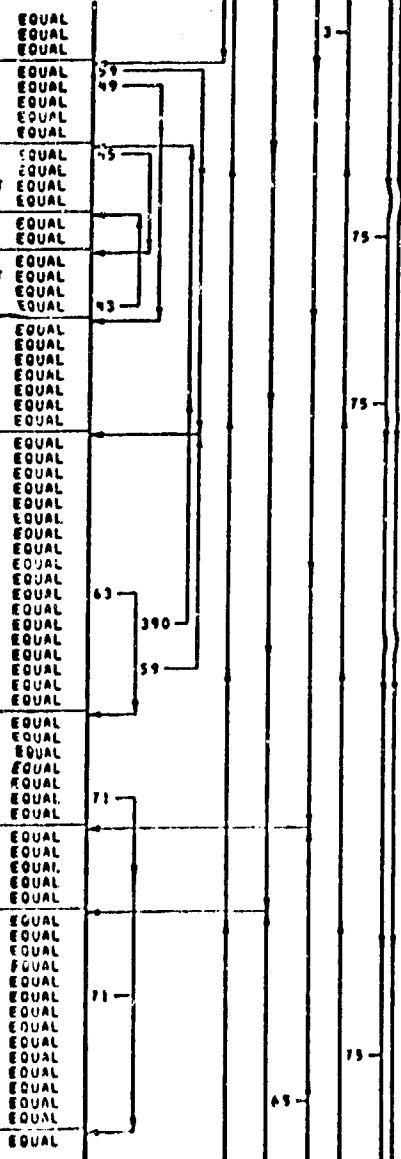
74.	C	IF NOT, GO TO 65. OTHERWISE, CONTINUE.	EQUAL
75.		DO3 K=1, KONT	EQUAL
76.		IAK)=I(K2, K+1, 1)	EQUAL
77.		CONTINUE	EQUAL
78.		DO1 J=1, KCM	EQUAL
79.		DO3 K=1, KONT	EQUAL
80.		IF(I(K1, J)+1, 1).EQ. IAK) GO TO 10	EQUAL
81.		CONTINUE	EQUAL
82.		GO TO 65	EQUAL
83.		10 IAK)=0	EQUAL
84.		31 CONTINUE	EQUAL
85.	C	K1 AND K2 ARE THE SAME. IF A SINGLE RING IS BEING ANALYZED,	EQUAL
86.		TRANSFER TO 27. OTHERWISE, FIND THE NEW VALUES OF K1 AND K2	EQUAL
87.		NAMELY, THOSE UNPROCESSED CORE ATOMS WHICH ARE BONDED TO	EQUAL
88.		OLD K1 AND K2 PAIR, EACH OF WHICH IS LOCATED IN ONE OR THE	EQUAL
89.		OTHER OF THE TWO TEST LIGANDS.	EQUAL
90.		IF(IFUNCT).E.0) GO TO 27	EQUAL
91.		IF(NV(K1)-2) 19, 19, 27	EQUAL
92.	C	K1 AND K2 ARE CHAIN ATOMS. FIND THE NEW K1 AND K2.	EQUAL
93.		15 IF(I(K1, 2, 6)).NE. KCIP) GO TO 17	EQUAL
94.		KCIP=K1	EQUAL
95.		K1=I(K1, 3, 6)	EQUAL
96.		GO TO 19	EQUAL
97.		17 KCIP=K1	EQUAL
98.		K1=I(K1, 2, 6)	EQUAL
99.		19 IF(I(K2, 2, 6)).NE. KC2P) GO TO 21	EQUAL
100.		KC2P=K2	EQUAL
101.		K2=I(K2, 3, 6)	EQUAL
102.		GO TO 3	EQUAL
103.		21 KC2P=K2	EQUAL
104.		K2=I(K2, 2, 6)	EQUAL
105.		GO TO 3	EQUAL
106.	C	K1 AND K2 ARE BRANCH ATOMS. FIND THE NEW K1 AND K2.	EQUAL
107.		27 IF(I(K1) + I(K2)).NE.0) GO TO 37	EQUAL
108.	C	NEITHER K1 NOR K2 ARE RING ATOMS.	EQUAL
109.		ISB=ISB+1	EQUAL
110.	C	STORE K1 AND K2 IN IDX. ISB IS THE COUNTER THAT	EQUAL
111.	C	SPECIFIES THE NUMBER OF BRANCHES ENCOUNTERED.	EQUAL
112.		IDX(1, ISB)=K1	EQUAL
113.		IDX(2, ISB)=K2	EQUAL
114.		N1=1	EQUAL
115.		N2=5	EQUAL
116.		N1=NV(K1)+1	EQUAL
117.	C	ALSO STORE THEREIN THE GROUP NUMBERS OF THE CORE ATOMS	EQUAL
118.	C	OF K1 AND K2 WHICH HAVE TO BE CHECKED FOR EQUALITY.	EQUAL
119.		DO3 L=2, N1	EQUAL
120.		IF(I(K1, L, 6)).EQ. KCIP) GO TO 31	EQUAL
121.		N1=N1+1	EQUAL
122.		IDX(N1, ISB)=I(K1, L, 6)	EQUAL
123.		31 IF(I(K2, M, 6)).EQ. KC2P) GO TO 35	EQUAL
124.		N2=N2+1	EQUAL
125.		IDX(N2, ISB)=I(K2, M, 6)	EQUAL
126.		35 CONTINUE	EQUAL
127.		NDX(1, ISB)=2	EQUAL
128.		NDX(2, ISB)=2	EQUAL
129.		KCIP=K1	EQUAL
130.	C	FIND NEW K1 AND K2 AND RECYCLE.	EQUAL
131.		K1=IDX(2, ISB)	EQUAL
132.		KC2P=K2	EQUAL
133.		K2=IDX(1, ISB)	EQUAL
134.		GO TO 3	EQUAL
135.	C	K1 AND/OR K2 ARE/IS RING ATOM(S).	EQUAL
136.		37 IF(I(K1) + I(K2)).EQ.0) GO TO 65	EQUAL
137.	C	BOTH K1 AND K2 ARE RING ATOMS. CHECK THEIR EQUALITY.	EQUAL
138.		CALL EQUAL(K1, KCIP, KC2P, K1, K2, ISB, N1, N2, IFUNCT)	EQUAL
139.		IFERR=1. EQ.0) GO TO 69	EQUAL
140.		IF(ISB. EQ. 1) 39, KC2P) GO TO 39	EQUAL
141.		39 KCIP=IDX(1, ISB)	EQUAL
142.		KC2P=IDX(2, ISB)	EQUAL
143.		K1=IDX(2, ISB)	EQUAL



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144.      K2=IDX(6,ISB)
145.      GO TO 3
146. C
147.      39 IF(15B.GT.0)GO TO 59
148.      2F(1)FUNCT.NE.0)GO TO 49
149.      ALL ATOMS OF THE TWO TEST LIGANDS HAVE BEEN PROCESSED.
150.      LATTER ARE EQUAL. PRINT MESSAGE. STORE SYMMETRY DATA AND
151.      FIND NEW LIGAND PAIR COMBINATION TO TEST.
152.      390 IF(KC1.NE.KC2)GO TO 45
153.      WRITE(6,97)ICHNK1,ICHNK2,KC1
154.      40 FORMAT(// 1M0,30X,15HCOMPLEX LIGANDS,14,5M AND,14,14M OF CORE AT
155.      10M,14,12M ARE EQUAL.)
156.      43 CALL SAME(KCXDOO(1),ICHNK1,ICHNK2,MRS1(J1),MRS2(J2))
157.      GO TO 75
158.      45 WRITE(6,97)ICHNK1,ICHNK2,KC1,KC2
159.      47 FORMAT(// 1M0,30X,15HCOMPLEX LIGANDS,14,5M AND,14,15M OF CORE AT
160.      10M,14,5M AND,14,12M ARE EQUAL.)
161.      GO TO 43
162.      49 IFUNCT#2
163.      K1=KCDOO(1)
164.      WRITE(6,91)IDC(K1),K1
165.      51 FORMAT(// 1M0,44X,4HRING,14,20M IS SYMMETRICAL ABOUT ATOM,14,
166.      11M.)
167.      GO TO 75
168. C
169.      59 MX1=KNT(1,ISB)
170.      MX2=KNT(2,ISB)+4
171.      MAKE NEGATIVE TO INDICATE CHAINS MX1 AND MX2 OF BRANCH
172.      ISB HAVE BEEN FOUND EQUAL.
173.      IDX(MX1,ISB)=-145)IDX(MX1,ISB)
174.      IDY(MX2,ISB)=-145)IDX(MX2,ISB)
175.      KNT(1,ISB)=KNT(1,ISB)+1
176.      KX=IDX(1,ISB)
177.      HAVE ALL CHAINS OF BRANCH ISB IN LIGAND ONE BEEN CHECKED
178.      IF IDY, GO TO 63.
179.      IF(KNT(1,ISB).LE.(V(KX))GO TO 63
180.      YES. ARE THERE BRANCHES REMAINING TO BE TESTED
181.      IF(15B.LE.1)GO TO 390
182.      YES. FIND NEW BRANCH AND RECYCLE BRANCH TEST.
183.      ISB=ISB-1
184.      GO TO 59
185. C
186.      NO. FIND K1 OF NEW CHAIN SEGMENT AND RESET KNT FOR
      LIGAND TWO.
187.      63 KCIP=IDX(1,ISB)
188.      KC2P=IDX(5,ISB)
189.      MX1=KNT(1,ISB)
190.      K1=IDX(MX1,ISB)
191.      KNT(2,ISB)=2
192.      GO TO 71
193. C
194.      65 KCIP=IDX(1,ISB)
195.      KC2P=IDX(5,ISB)
196.      MX1=KNT(1,ISB)
197.      K1=IDX(MX1,ISB)
198. C
199.      69 KNT(2,ISB)=KNT(2,ISB)+1
200.      KX=IDX(5,ISB)
201.      HAVE ALL CHAINS OF BRANCH ISB IN LIGAND TWO BEEN
202.      CHECKED AGAINST THE SPECIFIED CHAIN OF LIGAND ONE IF
203.      NOT, GO TO 71.
204.      IF(KNT(2,ISB).LE.(V(KX))GO TO 71
205.      YES. ARE THERE BRANCHES REMAINING TO BE TESTED IF
206.      NOT GO TO 75 TO FIND NEW LIGAND PAIR COMBINATION TO
207.      TEST.
208.      IF(15B.LE.1)GO TO 75
209.      YES. FIND NEW BRANCH AND RECYCLE BRANCH TEST.
210.      ISB=ISB-1
211.      GO TO 69
212. C
213.      71 MX2=KNT(2,ISB)+4

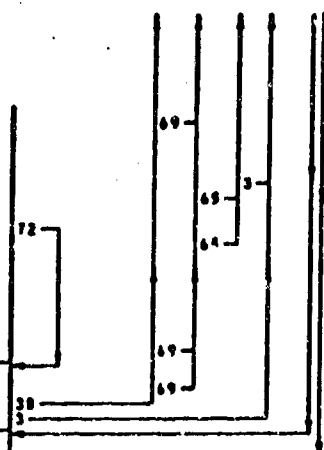
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214.      IF(IOR(MX2,ISB).LT.0)GO TO 69      EQUAL
215.      K2=IDN(MX2,ISB)                    EQUAL
216.      C      IF NEITHER K1 NOR K2 ARE RING ATOMS, GO TO 3 (RECYCLE) EQUAL
217.      C      TEST)                       EQUAL
218.      IF(IBC(K1)=IBC(K2)).EQ.0)GO TO 3    EQUAL
219.      IF(IBC(K1)=IBC(K2)).EQ.0)GO TO 69    EQUAL
220.      C      BOTH K1 AND K2 ARE RING ATOMS. CHECK THEIR EQUALITY. EQUAL
221.      IF(MCV(K1)=MCV(K2)).EQ.0)GO TO 72    EQUAL
222.      IF(MCV(K1).NE.MCV(K2))GO TO 69      EQUAL
223.      KCV=MCV(K1)                          EQUAL
224.      ISB=MER(3,KCV)                       EQUAL
225.      KCIP=IDN(1,ISB)                     EQUAL
226.      KCZP=IDN(2,ISB)                     EQUAL
227.      K1=MER(1,KCV)                       EQUAL
228.      K2=MER(2,KCV)                       EQUAL
229.      IF(KX(KCV)).EQ.1)GO TO 69           EQUAL
230.      72 CALL EQUALR(KC1,KCIP,KCZP,K1,K2,ISB,KRING1,IFUNCT) EQUAL
231.      IFRING1.EQ.0)GO TO 69               EQUAL
232.      IF(150.EQ.MER(3,KCV))GO TO 30      EQUAL
233.      GO TO 3                             EQUAL
234.      75 CONTINUE                        EQUAL
235.      85 CONTINUE                        EQUAL
236.      93 CONTINUE                        EQUAL
237.      95 CONTINUE                        EQUAL
238.      RETURN                              EQUAL
239.      END                                 EQUAL

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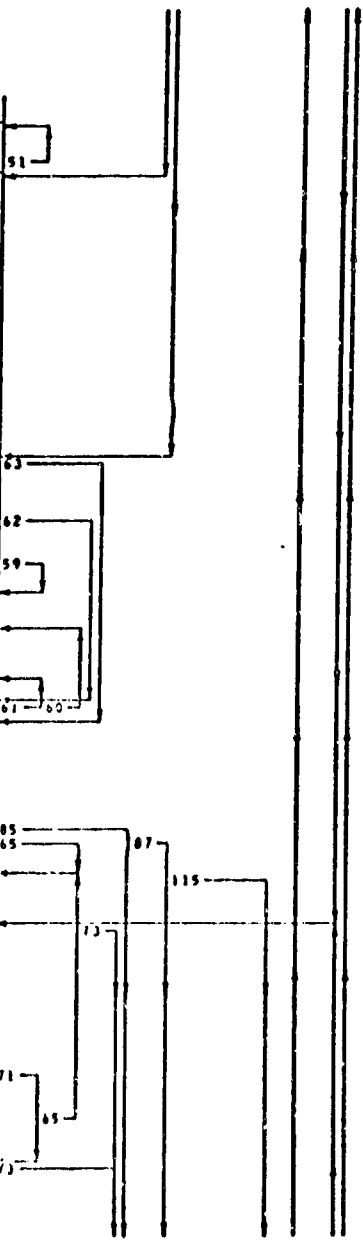
EQUALR

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1. SUBROUTINE EQUALR(KC,KC1P,KC2P,K1,K2,ISB,KRING1,IFUNCT) EQUALR
2. THIS SUBROUTINE DETERMINES WHETHER THE BACKBONE STRUCTURES EQUALR
3. OF TWO RINGS, A AND B, ARE THE SAME. NON-RING LIGANDS BOND TO EQUALR
4. THESE RINGS ARE ALSO CLASSIFIED AND STORED, BUT THEIR EQUALR
5. SYMMETRIES ARE NOT TESTED HERE. THEY ARE CHECKED IN SUBROUTINE EQUALR
6. EQUAL. IF IFUNCT IS NONZERO, THE SYMMETRY OF ONE RING, NOT TWO, EQUALR
7. IS TO BE DETERMINED. EQUALR
8. INTEGER SYM(4),SYNDUL(9),GRID(50,50) EQUALR
9. DIMENSION MCV(100),JDONE(100),IDNR(8,30),IDYR(3),NVC(100),PAT(40), EQUALR
10. IKNT(2,99),IDXB(99),NVR(100),KNTA(2,30),KRC(3,40),KCCA(2,30), EQUALR
11. ZIAC(4),IADDC(3) EQUALR
12. COMMON/DLK1/NO,NOS,SYM,SYMBOL,NOVAL(9),GRID EQUALR
13. COMMON/DLK2/WEIGHT,PLOT(9),MOLWT(100),IIX(100,5,6),NCI(100),KCC EQUALR
14. COMMON/DLK3/IRING(40,30),IPATX(50,80),NVC(100),IBC(100),KCC(100), EQUALR
15. IIDR(100),IB(100,8),IRG,NORR EQUALR
16. COMMON/DLK4/IBCI(60,50),IISF(60,2),NDX(60,20),IRC,NORFUS,IACTOT EQUALR
17. EQUIVALENCE (MCV(1),GRID(1,31)),(JDONE(1),IPATX(2,97)),(IDYR(1), EQUALR
18. IGRID(40,16)),(IDNR(1,1),GRID(1,17)),(NVC(1),GRID(1,29)), EQUALR
19. ZIACX(1),IB(35,2)),(KNTA(1,1),GRID(1,33)),(IDXB(1),GRID(3,1)), EQUALR
20. SINVR(1),NVR(22,18)),(KNTA(1,1),GRID(4,21)),(KRC(1,1),GRID(1,37)), EQUALR
21. KCV,IB(97,8)),(KCCA(1,3),GRID(1,23)),(IAC(1),IB(75,8)), EQUALR
22. SICRDC(1),GRID(1,42)) EQUALR
23. C1.0 INITIALIZE SYMMETRY INDICATOR. EQUALR
24. KRING1=0 EQUALR
25. IF(IFUNCT.NE.0)GO TO 0 EQUALR
26. C2.0 HAVE RING ATOMS K1 AND K2 BEEN TESTED PREVIOUSLY EQUALR
27. IF(MCV(K1).NE.MCV(K2)).EQ.0)GO TO 3 EQUALR
28. C YES. FIND KCV AND TRANSFER TO 7. EQUALR
29. KCV=MCV(K1) EQUALR
30. GO TO 7 EQUALR
31. C NO. INCREMENT KCV AND TRANSFER TO FIRSTA FOR PRELIMINARY EQUALR
32. SYMMETRY TESTS OF THE TWO RINGS. EQUALR
33. C
34. 3 KCV=KCV+1 EQUALR
35. CALL FIRSTA(KC,K1,K2,KRING2) EQUALR
36. IF(KRING2.EQ.0)RETURN EQUALR
37. C3.0 IS RING B BEING TESTED FOR THE FIRST OR SECOND TIME EQUALR
38. 7 IF(KNT(KCV).EQ.0)GO TO 9 EQUALR
39. C FIRST TIME. EQUALR
40. 0 KZSET=2 EQUALR
41. GO TO 11 EQUALR
42. C SECOND TIME.
43. 9 KZSET=3 EQUALR
44. C4.0 INITIALIZE VARIABLES. EQUALR
45. 11 DD(1)=J=1,KCC EQUALR
46. JDONE(J)=0 EQUALR
47. 13 CONTINUE EQUALR
48. KC1PR=KC1P EQUALR
49. K1R=K1 EQUALR
50. K2R=K2 EQUALR
51. ISL=0 EQUALR
52. KTT=0 EQUALR
53. ISBE=ISB EQUALR
54. IDX=1 EQUALR
55. 15 N1R=0 EQUALR
56. N2R=0 EQUALR
57. N1E=0 EQUALR
58. N2E=0 EQUALR
59. ISCR=ISOR+1 EQUALR
60. ISPE=ISOE+1 EQUALR
61. KONF=KON(K1R)+1 EQUALR
62. C5.0 THIS SECTION FINDS THE DIRECTION OF A POTENTIAL BOND ONE EQUALR
63. RECEIVED FROM BOND K1R-KC1PR AND THE NUMBER OF RING AND NON-RING EQUALR
64. LIGANDS BOND TO ATOMS K1R AND K2R OF RING STRUCTURES A AND EQUALR
65. B, RESPECTIVELY. EQUALR
66. C
67. 0027 R=0,KONF EQUALR
68. IF(IIX(K1R,K,6)).NE.KC1PR)GO TO 19 EQUALR
69. I1D=IIX(K1R,K,4)+1 EQUALR
70. IF(I1D.GT.0)I1D=I1D-1 EQUALR
71. GO TO 23 EQUALR
72. 19 K5=IIX(K1R,K,6) EQUALR
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73.	IF(IACKS).EQ.0)GO TO 21	EQUAL	21
74.	N1R=N1R+1	EQUAL	
75.	IDXR(N1R+1,ISDR)=IX(K1R,K,6)	EQUAL	
76.	IDXR(N1R)=IX(K1R,K,6)	EQUAL	
77.	GO TO 23	EQUAL	23
78.	21 N1E=N1E+1	EQUAL	
79.	IDX(N1E+1,ISDE)=IX(K1E,K,6)	EQUAL	
80.	23 IF(I(AZR,K,6).EQ.AC7)/GO TO 27	EQUAL	27
81.	K5=IX(K2R,K,6)	EQUAL	
82.	IF(IACKS).EQ.0)GO TO 25	EQUAL	25
83.	N2R=N2R+1	EQUAL	
84.	IDXR(N2R+1,ISDR)=IX(K2R,K,6)	EQUAL	
85.	GO TO 27	EQUAL	27
86.	25 N2E=N2E+1	EQUAL	
87.	IDX(N2E+1,ISDE)=IX(K2R,K,6)	EQUAL	
88.	27 CONTINUE	EQUAL	
89.	C 0 ARE THE NUMBER OF RING AND NON-RING LIGANDS THE SAME FOR ATOMS	EQUAL	
90.	K1R AND K2R	EQUAL	
91.	IF(N1R.EQ.N2R.AND.N1E.EQ.N2E)GO TO 31	EQUAL	
92.	C NO. IF SINGLE RING IS BEING TESTED, RETURN. OTHERWISE,	EQUAL	
93.	C REDUCE SUBSCRIPTS AND TRANSFER.	EQUAL	
94.	IF(IFUNCT.NE.0)RETURN	EQUAL	
95.	ISDR=ISDR-1	EQUAL	
96.	ISDE=ISDE-1	EQUAL	
97.	GO TO 67	EQUAL	
98.	C YES. ARE K1R AND K2R BONDED TO NON-RING LIGANDS	EQUAL	
99.	31 IF(N1E.GT.0)GO TO 33	EQUAL	31
100.	C NO. IF SINGLE RING IS BEING TESTED AND NO IS PRESENT,	EQUAL	
101.	C RETURN. OTHERWISE, REDUCE SUBSCRIPT AND TRANSFER.	EQUAL	
102.	IF(IFUNCT.NE.0.AND.NC(K1R).EQ.2.AND.IX(K1R,3,1).EQ.0)RETURN	EQUAL	
103.	ISDE=ISDE-1	EQUAL	
104.	GO TO 35	EQUAL	35
105.	C YES. IF SINGLE RING IS BEING TESTED, DETERMINE IF BOND HAS	EQUAL	
106.	C TWOFOLD SYMMETRY.	EQUAL	
107.	33 IF(IFUNCT.EQ.0)GO TO 34	EQUAL	33
108.	CALL LINEAR(K1,IDX2,ISDF),LINE,KSYN)	EQUAL	
109.	IF(LINE.NE.1.AND.KSYN.NE.2)RETURN	EQUAL	
110.	C FINISH SETTING IDENTIFIERS ASSOCIATED WITH THE NON-RING	EQUAL	
111.	C LIGANDS.	EQUAL	34
112.	34 IDX1,ISDE)=K1R	EQUAL	
113.	IDX5,ISDE)=K2R	EQUAL	
114.	KNY1,ISBC)=2	EQUAL	
115.	KNY2,ISBC)=2	EQUAL	
116.	NV(K1R)=N1E+1	EQUAL	
117.	NV(K2R)=N1E(K1R)	EQUAL	
118.	C TO HOW MANY OTHER RING ATOMS ARE RING ATOMS K1R AND K2R	EQUAL	
119.	C BONDED	EQUAL	
120.	35 IF(N1R.GT.1)GO TO 39	EQUAL	35
121.	C ONE IN ADDITION TO PARENT RING ATOM, K1R AND K2R ARE CHAIN	EQUAL	
122.	C RING ATOMS. FIND NEW K1R AND K2R.	EQUAL	
123.	KC1P=K1R	EQUAL	
124.	K1R=IDX(2,ISDR)	EQUAL	
125.	KC2P=K2R	EQUAL	
126.	K2R=IDX(6,ISDR)	EQUAL	
127.	ISDR=ISDR-1	EQUAL	
128.	GO TO 37	EQUAL	37
129.	C TWO OR MORE IN ADDITION TO PARENT RING ATOM, K1R AND K2R	EQUAL	
130.	C ARE BRANCH RING ATOMS. FIND NEW K1R AND K2R.	EQUAL	
131.	39 CALL ORDER(N1R,1ROD,1DRD)	EQUAL	
132.	K1=1-ROD(1)	EQUAL	
133.	K2=1-ROD(N1R)	EQUAL	
134.	C FIND LIGAND OF ATOM K1R THAT IS AT OR NEAR BOND	EQUAL	
135.	C DIRECTIO: MID.	EQUAL	
136.	IF(1DRD(K1)-MID(1),45,49	EQUAL	45 49 91
137.	41 N1=K1	EQUAL	
138.	CO TO 53	EQUAL	53
139.	49 N1=K2	EQUAL	
140.	GO TO 53	EQUAL	53
141.	49 IF(1DRD(K1).GE.MID(1)GO TO 41	EQUAL	

142.	K5=1	EQUALR
143.	51 K5=K5+1	EQUALR
144.	MX=(H00(K5))	EQUALR
145.	IF(IIDR(MX).LT.NID)GO TO 51	EQUALR
146.	53 K=IDR(2,ISDR)	EQUALR
147.	IDR(2,ISDR)=IDR(MX+1,ISDR)	EQUALR
148.	IDR(MX+1,ISDR)=K	EQUALR
149.	C SET IDENTIFIERS ASSOCIATED WITH RING LIGANDS AND FIND	EQUALR
150.	C NEW K1R AND K2R.	EQUALR
151.	K1=0	EQUALR
152.	IF(K1R.EQ.K1)K1=1	EQUALR
153.	NVR(K1R)=NVR+1-N1	EQUALR
154.	NVR(K2R)=NVR(K1R)	EQUALR
155.	KNTR(1,ISDR)=2	EQUALR
156.	KNTR(2,ISDR)=2	EQUALR
157.	IF(ISDR.EQ.1)KNTR(2,ISDR)=K2SET	EQUALR
158.	IDR(1,ISDR)=K1R	EQUALR
159.	IDR(5,ISDR)=K2R	EQUALR
160.	KC1PR=K1R	EQUALR
161.	K1R=IDR(2,ISDR)	EQUALR
162.	KC2PR=K2R	EQUALR
163.	K2R=IDR(MX,ISDR)+4	EQUALR
164.	K2R=IDR(MX,ISDR)	EQUALR
165.	57 IF(IFUNCT.EQ.0.OR.K1R.NE.K2R)GO TO 65	EQUALR
166.	C SINGLE RING IS BEING TESTED AND K1R EQUALS K2R.	EQUALR
167.	C DETERMINE IF FINAL LIGAND TO BE TESTED WHICH IS BONDED	EQUALR
168.	C TO THE RING HAS TWOFOLD SYMMETRY.	EQUALR
169.	IF(NCK(K1R).EQ.2)GO TO 62	EQUALR
170.	DO50 K=2,4	EQUALR
171.	K5=IX(K1R,K,6)	EQUALR
172.	IF(IDCK(K5).EQ.0)GO TO 59	EQUALR
173.	58 CONTINUE	EQUALR
174.	59 CALL LIFERR(K1R,K5,LINE,KSYM)	EQUALR
175.	IF(LINE.NE.1.AND.KSYM.NE.2)RETURN	EQUALR
176.	60 K1R=K1	EQUALR
177.	KCY=1	EQUALR
178.	KCY=1+ISB	EQUALR
179.	61 RETURN	EQUALR
180.	52 IF(IX(K1R,1)-8)GO,61,60	EQUALR
181.	63 J00=(KC1PR+1)	EQUALR
182.	J00=(KC2PR+1)	EQUALR
183.	KTT=KTT+1	EQUALR
184.	KCCR(1,KTT)=KC1PR	EQUALR
185.	KCCR(2,KTT)=KC2PR	EQUALR
186.	C4.0 ARE THE NEW K1R AND K2R ATOMS EQUAL TO THE STARTING VALUES	EQUALR
187.	C K1 AND K2, RESPECTIVELY IF SO, GO TO 85 AND CHANGE ISB.	EQUALR
188.	IF(K1R.EQ.K1.AND.K2R.EQ.K2)GO TO 85	EQUALR
189.	GO TO 65,87,188	EQUALR
190.	C7.0 TRANSFER POINT WHEN ISB=1.	EQUALR
191.	65 IF(J00.EK2R).EQ.0)GO TO 115	EQUALR
192.	C K2R HAS BEEN TESTED PREVIOUSLY. ARE THERE ANY BRANCH RING	EQUALR
193.	C ATOMS LEFT TO TEST IF NOT, GO TO 73.	EQUALR
194.	67 IF(ISDR.LE.0)GO TO 73	EQUALR
195.	C DISENGAGE INTERVENING CHAIN ATOMS(IF ANY). FIND NEW K2R (AND	EQUALR
196.	C K1R IF ALTERED).	EQUALR
197.	IF(KTT.GT.0)CALL DELETE(IDR(1,ISDR),ISBE,KTT)	EQUALR
198.	KC1PR=IDR(1,ISDR)	EQUALR
199.	KC2PR=IDR(5,ISDR)	EQUALR
200.	K1R=IDR(1,ISDR)	EQUALR
201.	K1R=IDR(MX,ISDR)	EQUALR
202.	KNTR(2,ISDR)=KNTR(2,ISDR)+1	EQUALR
203.	KX=IDR(K5,ISDR)	EQUALR
204.	IF(KNTR(2,ISDR).GT.NVR(MX))GO TO 71	EQUALR
205.	KX=KNTR(2,ISDR)+4	EQUALR
206.	K2R=IDR(KX,ISDR)	EQUALR
207.	GO TO 65	EQUALR
208.	C ALL LIGANDS OF BRANCH ISDR IN RING B HAVE BEEN TESTED. ARE	EQUALR
209.	C THERE ANY LEFT BRANCHES TO TEST	EQUALR
210.	71 IF(ISCALF.LT.0)GO TO 73	EQUALR
211.	C YES. FIND NEW BRANCH SUBSCRIPT AND RETURN TO 67.	EQUALR



212.	ISBR=ISBR-1	EQUALR
213.	GO TO 67	EQUALR
214.	73 IF(NT(KCY).EQ.1)GO TO 103	EQUALR
215.	C NO. REPEAT ENTIRE TEST CYCLE, SCANNING RING B IN THE	EQUALR
216.	C REVERSE DIRECTION.	EQUALR
217.	NT(KCY)=1	EQUALR
218.	GO TO 9	EQUALR
219.	C RESET IAX AND GO TO 91.	EQUALR
220.	65 IBR=2	EQUALR
221.	GO TO 91	EQUALR
222.	C0.0 TRANSFER POINT WHEN IBR=2.	EQUALR
223.	C0.0 HAVE ATOMS K1R OR/AND K2R BEEN TESTED PREVIOUSLY IF NOT,	EQUALR
224.	C GO TO 115.	EQUALR
225.	67 IF(JOON(K1R).EQ.1)GO TO 91	EQUALR
226.	IF(JOON(K2R).EQ.0)GO TO 115	EQUALR
227.	C YES. FIND NEW K1R.	EQUALR
228.	91 NTR(1,ISBR)=NTR(1,ISBR)+1	EQUALR
229.	NR=IDIR(1,ISBR)	EQUALR
230.	C HAVE ALL LIGANDS OF BRANCH ISBR IN RING A BEEN TESTED	EQUALR
231.	C IF NOT, GO TO 99.	EQUALR
232.	IF(NTR(1,ISBR).LE.NV(NR))GO TO 99	EQUALR
233.	C ARE THERE ANY MORE BRANCHES TO TEST	EQUALR
234.	IF(ISBR.LE.1)GO TO 92	EQUALR
235.	C YES. FIND NEW BRANCH SUBSCRIPT AND RETURN TO 91.	EQUALR
236.	ISBR=ISBR-1	EQUALR
237.	GO TO 91	EQUALR
238.	C NO. BACKBONE STRUCTURE OF BOTH RINGS IS IDENTICAL. SET	EQUALR
239.	C PERTINENT ARRAYS AND EXIT FROM ROUTINE.	EQUALR
240.	92 KRING1=1	EQUALR
241.	KR(1,KCY)=K1	EQUALR
242.	KR(2,KCY)=K2	EQUALR
243.	KR(3,KCY)=ISB	EQUALR
244.	IF(15DE.EQ.155)RETURN	EQUALR
245.	K1=ISD+1	EQUALR
246.	DO93 K=K1,10BE	EQUALR
247.	MX=10X(1,K)	EQUALR
248.	KCY(MX)=KCY	EQUALR
249.	K2=10X(5,K)	EQUALR
250.	KCY(K2)=KCY	EQUALR
251.	93 CONTINUE	EQUALR
252.	RETURN	EQUALR
253.	C SET K1R AND FIND NEW K2R TO TEST (IF ANY).	EQUALR
254.	99 KC1PR=IDIR(1,ISBR)	EQUALR
255.	KC2PR=IDIR(5,ISBR)	EQUALR
256.	NR=NTR(1,ISBR)	EQUALR
257.	K1R=IDIR(NR,ISBR)	EQUALR
258.	NTR(2,ISBR)=2	EQUALR
259.	101 NR=NTR(2,ISBR)+1	EQUALR
260.	K2R=IDIR(NR,ISBR)	EQUALR
261.	IF(JOON(K2R).EQ.0)GO TO 115	EQUALR
262.	NTR(2,ISBR)=NTR(2,ISBR)+1	EQUALR
263.	NR=IDIR(NR,ISBR)	EQUALR
264.	IF(NTR(2,ISBR).LE.NV(NR))GO TO 101	EQUALR
265.	C NO MORE NEW K2R ATOMS AVAILABLE.	EQUALR
266.	103 NT(KCY)=0	EQUALR
267.	KCY=KCY-1	EQUALR
268.	IF(KCY.EQ.0)RETURN	EQUALR
269.	C RESET ALL VALUES ASSOCIATED WITH KCY TO THEIR INITIAL	EQUALR
270.	C VALUES AND RETURN.	EQUALR
271.	DO107 K=1,KCC	EQUALR
272.	IF(KCY(K).LE.KCY)GO TO 107	EQUALR
273.	KR(KCY(K))	EQUALR
274.	KR(K2R)	EQUALR
275.	KCY(K)=0	EQUALR
276.	107 CONTINUE	EQUALR
277.	RETURN	EQUALR
278.	C10.0 CHECK SIMILARITY OF RING ATOMS K1R AND K2R.	EQUALR
279.	115 IF(ABS(K1R-1).LE.ABS(K2R-1).OR.ABS(K1R).LE.ABS(K2R).OR.ABS(K1R).	EQUALR
280.	ABS(K2R))GO TO 67	EQUALR
281.	C ATOMS K1R AND K2R ARE THE SAME, ARE BONDED TO THE SAME NUMBER	EQUALR

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282. C      OF CORE ATOMS, AND HAVE THE SAME OVERALL CONNECTIVITIES.
283.      CONTXON(K1N)
284. C      DETERMINE IF K1R AND K2R ARE BONDED TO THE SAME TYPES OF
285. C      ATOMS. IF NOT, GO TO 67. OTHERWISE, GO TO 15.
286.      GO119 K=1,CONT
287.      JAK1=1;IKK2A,K=1,1)
288.      119 CONTINUE
289.      GO125 J=1,CONT
290.      GO125 K=1,CONT
291.      IF(IISER1A,J=1,1).EQ.IAK1)GO TO 123
292.      121 CONTINUE
293.      GO TO 67
294.      123 IAK1=0
295.      125 CONTINUE
296.      GO TO 15
297.      END

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EQUALR
EQUALR
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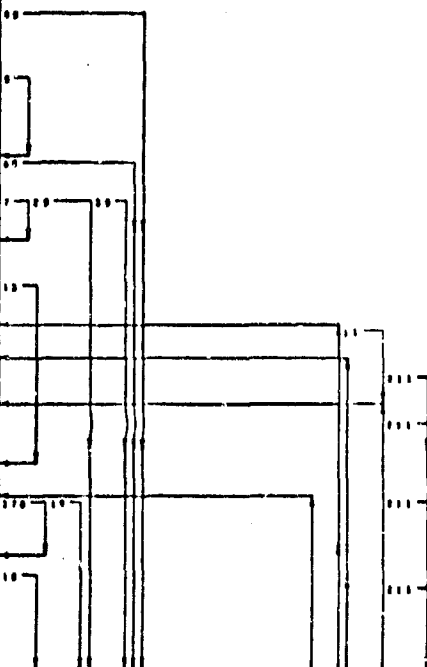
123

67

15

ESTROT

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1. SUBROUTINE (ZROT) NSNC, NSVNC, NSVND, NSVND, NSVND, NSVND
2. C THIS SUBROUTINE COMPUTES THE INTERNAL ROTATION SYMMETRY NUMBER
3. C OF THE MOLECULE
4. INTEGER SYMNC, SYMND, SYMNC, SYMND, SYMNC, SYMND
5. INTEGER M(NT)
6. DIMENSION (NT, 100), LINE(3), ASYND(3), ASYND(3), 100, NSVND(10, 100),
7. INTAL(3), INTAL(3), INTAL(3), INTAL(3), INTAL(3), INTAL(3), INTAL(3), INTAL(3),
8. INTAL(3), INTAL(3), INTAL(3), INTAL(3), INTAL(3), INTAL(3), INTAL(3), INTAL(3),
9. COMMON/BLZ/NSVNC, NSVND, SYMNC, SYMND, SYMNC, SYMND, SYMNC, SYMND
10. COMMON/BLZ/INTAL(10, 100), INTAL(10, 100), INTAL(10, 100), INTAL(10, 100),
11. INTAL(10, 100), INTAL(10, 100), INTAL(10, 100), INTAL(10, 100), INTAL(10, 100),
12. COMMON/BLZ/NSVND, NSVND, SYMNC, SYMND, SYMNC, SYMND, SYMNC, SYMND
13. EQUIVALENCE (INTAL, SYMNC, 10), (INTAL, SYMND, 10), (INTAL, SYMNC, 10),
14. (INTAL, SYMND, 10), (INTAL, SYMNC, 10), (INTAL, SYMND, 10), (INTAL, SYMNC, 10),
15. (INTAL, SYMND, 10), (INTAL, SYMNC, 10), (INTAL, SYMND, 10), (INTAL, SYMNC, 10),
16. (INTAL, SYMND, 10), (INTAL, SYMNC, 10), (INTAL, SYMND, 10), (INTAL, SYMNC, 10),
17. (INTAL, SYMND, 10), (INTAL, SYMNC, 10), (INTAL, SYMND, 10), (INTAL, SYMNC, 10),
18. (INTAL, SYMND, 10), (INTAL, SYMNC, 10), (INTAL, SYMND, 10), (INTAL, SYMNC, 10),
19. (INTAL, SYMND, 10), (INTAL, SYMNC, 10), (INTAL, SYMND, 10), (INTAL, SYMNC, 10),
20. (INTAL, SYMND, 10), (INTAL, SYMNC, 10), (INTAL, SYMND, 10), (INTAL, SYMNC, 10),
21. C1.0 INITIALIZE VARIABLES.
22. NSVNC=0
23. NSVND=0
24. NSVND=0
25. NSVND=0
26. NSVND=0
27. NSVND=0
28. NSVND=0
29. NSVND=0
30. NSVND=0
31. NSVND=0
32. NSVND=0
33. NSVND=0
34. NSVND=0
35. NSVND=0
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41. NSVND=0
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43. NSVND=0
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47. NSVND=0
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53. NSVND=0
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59. NSVND=0
60. NSVND=0
61. NSVND=0
62. NSVND=0
63. NSVND=0
64. NSVND=0
65. NSVND=0
66. NSVND=0
67. NSVND=0
68. NSVND=0
69. NSVND=0
70. NSVND=0
71. NSVND=0
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73	GO TO 211	ESTROT	
74	10 INTMIN=INTMIN+1	ESTROT	
75	4101 INTMIN=INTMIN+1	ESTROT	
76	GO TO 211	ESTROT	
77	C	NEITHER 1 NOR 2 ARE LINEAR. ARE THEY OF SAME SYMMETRY	
78	10 IF (ASVRI1) NE. ASVRI2 OR. ASVRI3. LT. 2 RETURN	ESTROT	
79	C	YES.	
80	NO ASVRI1	ESTROT	
81	GO TO 211	ESTROT	
82	C	NO ASVRI1	
83	C	NO ASVRI1	
84	C	NO ASVRI1	
85	C	NO ASVRI1	
86	C	NO ASVRI1	
87	C	NO ASVRI1	
88	C	NO ASVRI1	
89	C	NO ASVRI1	
90	C	NO ASVRI1	
91	C	NO ASVRI1	
92	20 CONTINUE	ESTROT	
93	JUMP	ESTROT	
94	RETURN	ESTROT	
95	C	NO ASVRI1	
96	C	NO ASVRI1	
97	30 IF (TOTAL1, AC1) EQ. 2. AND. TOTAL2, AC2) EQ. 2. GO TO 11	ESTROT	
98	IF (TOTAL1, AC1) EQ. 2. AND. TOTAL2, AC2) EQ. 2. GO TO 11	ESTROT	
99	27 IF (ASVRI1, AC1) EQ. 2. OR. NOSAME1, AC1) NE. 2. GO TO 211	ESTROT	
100	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
101	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
102	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
103	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
104	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
105	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
106	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
107	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
108	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
109	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
110	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
111	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
112	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
113	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
114	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
115	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
116	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
117	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
118	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
119	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
120	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
121	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
122	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
123	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
124	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
125	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
126	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
127	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
128	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
129	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
130	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
131	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
132	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
133	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
134	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
135	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
136	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
137	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
138	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
139	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	
140	C	LEGANDS MP1, 2 NOT EQUAL TO 2, AND 2 OR MORE ASYMMETRIC	

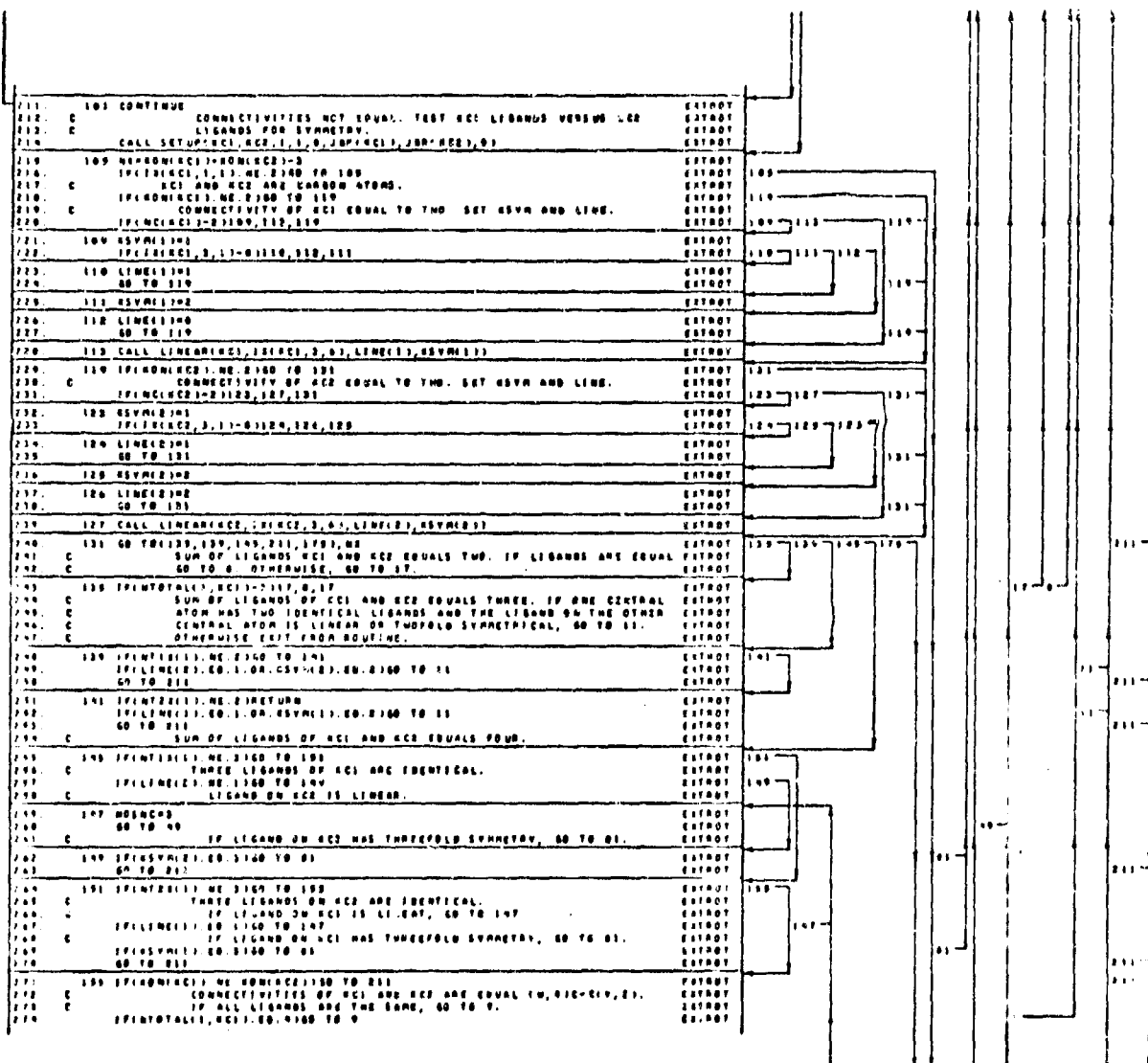
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141. C M IS NOT LINEAR NOR HAS THREEFOLD SYMMETRY. ESTROT
142. C NOORCS ESTROT
143. C RETURN ESTROT
144. C M VS LINEAR. ESTROT
145. C NOORCS ESTROT
146. C GO TO 40 ESTROT
147. C 00 IPIRICE(1,1).NE.0100 TO 70 ESTROT
148. C C1 IS A CD ATOM. ESTROT
149. C IPIRICE(1,1).NE.0100 TO 011 ESTROT
150. C CONNECTIVITY OF ONE, GO TO 11. ESTROT
151. C C1 HAS A CONNECTIVITY OF ONE - CO(1). IF N IS 0 WITH A ESTROT
152. C 71 NOIRICE(1,0) ESTROT
153. C IPIRICE(1,1).AND.IRICE(1,1).GO.0100 TO 11 ESTROT
154. C FIND SYMMETRY OF A. ESTROT
155. C CALL LINEAR(1,0,LINE(1),NOIRICE) ESTROT
156. C NOORCS ESTROT
157. C RETURN ESTROT
158. C C1 HAS A CONNECTIVITY OF TWO. IF THE TWO LIGANDS ARE ESTROT
159. C EQUAL, GO TO 11. ESTROT
160. C 72 IPIRICE(1,1).NE.0101,11,011 ESTROT
161. C IF C1 IS AN OXYGEN ATOM, GO TO 70. ESTROT
162. C 70 IPIRICE(1,1).GO.0100 TO 70 ESTROT
163. C C1 IS A DIFFERENT ATOM. IF THE THREE LIGANDS ARE THE SAME, ESTROT
164. C SET INDICATOR OF WHETHER EITHER. ESTROT
165. C IPIRICE(1,1).NE.0101 ESTROT
166. C 01 NOORCS ESTROT
167. C GO TO 011 ESTROT
168. C 00.0 THE MOLECULE HAS AN EVEN NUMBER OF ATOMS IN ITS LOWEST CHAIN. ESTROT
169. C FIND THE CENTRAL ATOMS, C1 AND C2, IN THE LOWEST CHAIN. ESTROT
170. C 00 NOIRICE(1,0) ESTROT
171. C NOORCS ESTROT
172. C IPIRICE(1,1).NE.0100 TO 00 ESTROT
173. C IPIRICE(1,1).NE.0100 TO 00.0100 ESTROT
174. C TWO CENTRAL ATOMS, C1 AND C2, ARE RING ATOMS. TRANSFER TO ESTROT
175. C RING SYMMETRY TEST ROUTINE. ESTROT
176. C CALL SYMM(1,NOIRICE) ESTROT
177. C RETURN ESTROT
178. C C1 AND C2 ARE NOT RING ATOMS. ARE THESE TWO ATOMS IDENTICAL ESTROT
179. C 00 IPIRICE(1,1).NE.IRICE(1,1).RETURN ESTROT
180. C YES. SELECT LOCATIONS OF PARENT ATOMS IN IS ARRAY, IF ESTROT
181. C NECESSARY. ESTROT
182. C IPIRICE(1,1).NE.NOIRICE(1,0) ESTROT
183. C IPIRICE(1,1).NE.NOIRICE(1,0) ESTROT
184. C ARE CONNECTIVITIES OF C1 AND C2 THE SAME ESTROT
185. C IPIRICE(1,1).NE.NOIRICE(1,0) ESTROT
186. C YES. SET EPL00 AND COPY DATA FOR C1 AND C2 CONTAINED ESTROT
187. C IN ARRAYS NTOTAL, NCSARE, AND NCSARE INTO THE TEMPORARY ESTROT
188. C ARRAYS. ESTROT
189. C EPL00 ESTROT
190. C 0001 J=1,0 ESTROT
191. C NTOTAL(1)=NTOTAL(1,0) ESTROT
192. C NCSARE(1)=NCSARE(1,0) ESTROT
193. C NCSARE(1)=NCSARE(1,0) ESTROT
194. C 71 NTOTAL(1)=NTOTAL(1,0) ESTROT
195. C 0000 J=1,0 ESTROT
196. C NCSARE(1)=NCSARE(1,0) ESTROT
197. C NCSARE(1)=NCSARE(1,0) ESTROT
198. C 0000 J=1,0 ESTROT
199. C NCSARE(1)=NCSARE(1,0) ESTROT
200. C 70 NTOTAL(1)=NTOTAL(1,0) ESTROT
201. C COPY VALUES OF NTOTAL FOR C1 AND C2 IN N10 AND N100, ESTROT
202. C RESPECTIVELY, EXCLUDING THE CENTRAL LIGANDS C1 AND ESTROT
203. C C2, IF PRESENT. ESTROT
204. C 0010 J=1,0 ESTROT
205. C IPIRICE(1,1).NE.0100 TO 00 ESTROT
206. C NCSARE(1)=0 ESTROT
207. C NCSARE(1)=0 ESTROT
208. C 70 IPIRICE(1,1).NE.0100 TO 101 ESTROT
209. C NCSARE(1)=0 ESTROT
210. C NCSARE(1)=0 ESTROT

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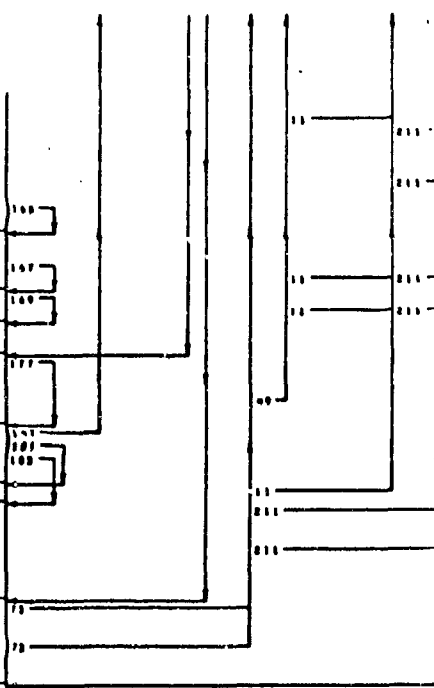


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276. C      IF W=2 AND Y=2, GO TO 11.          EXTRDY
277.      IFNT(11).EQ.2 AND NT(11).EQ.2100 TO 11  EXTRDY
278.      IFNC(AME1),NC1).EQ.2 OR NC(AME1),NC1).EQ.0100 TO 111  EXTRDY
279.      C      HCl HAS TWO EQUAL LEAGMS AND CCl DOES ALSO. DETERMINE  EXTRDY
280.      C      WHETHER OR NOT 102. IF 10, GO TO 11.  EXTRDY
281.      CALL CIRCLE,CC1,0,0,1000)          EXTRDY
282.      IFLEW17.EQ.1700 TO 111             EXTRDY
283.      00100 J=1,4                         EXTRDY
284.      IF(NT(17).EQ.0100 TO 100           EXTRDY
285.      NT(17)-NT(17)                         EXTRDY
286.      100 CONTINUE                          EXTRDY
287.      00100 J=1,2                         EXTRDY
288.      IF(NC(AME1),NC1).EQ. NT(17)100 TO 107  EXTRDY
289.      IF(NC(AME1),NC1)-NT(17)-01011,11,111  EXTRDY
290.      107 IF(NC(AME1),NC1).EQ. NT(17)100 TO 109  EXTRDY
291.      IF(NC(AME1),NC1)-NT(17)-01011,11,111  EXTRDY
292.      109 CONTINUE                          EXTRDY
293.      C      SUM OF LEAGMS OF HCl AND CCl SHOULD BE 10, 0, 100-010, 0, 11.  EXTRDY
294.      170 IF(NT(17).EQ.17) NT(17).EQ.2100 TO 177  EXTRDY
295.      C      ALL SIX LEAGMS ARE EQUAL.          EXTRDY
296.      000000=0                             EXTRDY
297.      000 TO 00                             EXTRDY
298.      C      IF W=1000 AND Y=1000, GO TO 107  EXTRDY
299.      107 IF(NT(17).EQ.2 AND NT(17).EQ.2100 TO 107  EXTRDY
300.      IF(NT(17).EQ.2 AND NT(17).EQ.2100 TO 101  EXTRDY
301.      IF(NT(17).EQ.2 OR NT(17).EQ.2100 TO 100  EXTRDY
302.      C      IF W=1000 AND Y=1000, GO TO 11.  EXTRDY
303.      101 IF(NT(17).EQ.2 AND NT(17).EQ.2100 TO 11  EXTRDY
304.      100 IF(NT(17).EQ.2 OR NT(17).EQ.2100 TO 111  EXTRDY
305.      C      IF W=2 AND Y=2, MOLECULE HAS ACSD STRUCTURE.  EXTRDY
306.      C      SET INDICATOR.                    EXTRDY
307.      IF(NT(17),NC1)-NT(17),NC1)-NT(17),NC1).EQ.0100 TO 111  EXTRDY
308.      000000=2                             EXTRDY
309.      RETURN                                 EXTRDY
310.      C      IF HCl AND CCl ARE BOTH REVISED ATOMS OR BOTH CO, GO TO 70.  EXTRDY
311.      100 IF(17)CC1,1,1).EQ.3 OR 17)NC1,1,1).EQ.0100 TO 70  EXTRDY
312.      C      HCl AND CCl ARE REVISIED ATOMS  EXTRDY
313.      C      IF SUM OF LEAGMS OF HCl AND CCl EQUALS FOUR, GO TO 70.  EXTRDY
314.      IF(NT).EQ.1700 TO 70                 EXTRDY
315.      C=0  RESET NT(17) FOR HCl AND CCl TO THEIR ORIGINAL VALUES, IF  EXTRDY
316.      C      APPLIED IN THIS SUBROUTINE.        EXTRDY
317.      011 IF(NT(17).EQ.3)RETURN             EXTRDY
318.      00010 J=1,6                         EXTRDY
319.      NT(17),NC1)-NT(17),NC1)              EXTRDY
320.      011 17),NC1)-NT(17),NC1)            EXTRDY
321.      00000                                EXTRDY
322.      00000                                EXTRDY

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FIND

1.		SUBROUTINE FIND(KC,X,L,M,NUR,MR,IERR)	FIND
2.	C	THIS SUBROUTINE DETERMINES WHETHER THE FIRST ATOM TO BE	FIND
3.	C	INDEXED IS A CORE ATOM OR AN UNIVALENT ATOM. IF THE LATTER, IT	FIND
4.	C	DETERMINES THE LOCATION OF ONE OF THE CORE ATOMS BONDED TO	FIND
5.	C	THIS NON-CORE AND FIRST INDEXED ATOM. THE DATA FOR THIS NON-	FIND
6.	C	CORE ATOM ARE STORED IN ARRAY IX.	FIND
7.		INTEGER SYMX(4),SYMBOL(9),GRID(50,00)	FIND
8.		INTEGER WEIGHT(6)	FIND
9.		COMMON/BLK1/NO,NOS,SYMX,SYMBOL,NOVAL(9),GRID	FIND
10.		COMMON/BLK2/WEIGHT,MMGT(9),MOLWT(100),IX(100,5,6),NCC(100),KCC	FIND
11.	C1.0	FIND NUMBER OF LIGANDS(MP) BONDED TO INDEXED ATOM. HOW MANY	FIND
12.	C	ARE THERE	FIND
13.		CALL NUMBER(NUR,NX,K,L,MP,KX,LI,KD,LD,JI,JF)	FIND
14.		IF(MP-1)3,7,9	FIND
15.	C	ZERO LIGANDS - PRINT ERROR MESSAGE, SET ERROR FLAG, AND EXIT.	FIND
16.		3 WRITE(6,5)K,L	FIND
17.		5 FORMAT(// 1N0, 39X,24HERROR - ISOLATED ATOM AT,14,14,,14,19H. CAS	FIND
18.		1E TERMINATED.)	FIND
19.		IERR=1	FIND
20.		RETURN	FIND
21.	C	ONE LIGAND - INDEXED ATOM IS NOT CORE ATOM. FIND CORE ATOM.	FIND
22.	C	STORE DATA OF INDEXED ATOM IN IX ARRAY IN LOCATION	FIND
23.	C	ASSIGNED TO A LIGAND.	FIND
24.		7 IX(KC,2,1)=M	FIND
25.		IX(KC,2,2)=K	FIND
26.		IX(KC,2,3)=L	FIND
27.	C	FIND BOND TYPE AND LOCATION OF SYMBOL OF CORE LIGAND	FIND
28.	C	BONDED TO INDEXED ATOM.	FIND
29.		CALL BOND(KX,LI,KD,LD,JI,JF,IX(KC,2,5),IERR)	FIND
30.		IF(IERR.EQ.1)RETURN	FIND
31.	C	IDENTIFY SYMBOL.	FIND
32.		CALL IDENT(NX,KX,LI,M,IERR)	FIND
33.		IF(IERR.EQ.1)RETURN	FIND
34.	C	COMPUTE BOND DIRECTION FROM CORE ATOM TO INDEXED ATOM AND	FIND
35.	C	STORE.	FIND
36.		NZ=MR+4	FIND
37.		IF(NZ.GT.8)NZ=NZ-8	FIND
38.		IX(KC,2,4)=NZ	FIND
39.	C	SET COORDINATES OF CORE ATOM, MR, AND NUR.	FIND
40.		K=KX	FIND
41.		L=LI	FIND
42.		MR=3	FIND
43.		GO TO 11	FIND
44.	C	TWO LIGANDS - INDEXED ATOM IS CORE ATOM. SET MR AND NUR.	FIND
45.		9 MR=2	FIND
46.		11 NUR=NUR	FIND
47.		RETURN	FIND
48.		END	FIND

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FIRSTA

1.	SUBROUTINE FIRSTA(KC,K1,K2,KRING2)	FIRSTA
2.	C THIS SUBROUTINE DETERMINES IF ATOMS K1 AND K2 FORM PART OF TWO	FIRSTA
3.	C DIFFERENT FUSED RING SYSTEMS. IF SO, IT COMPARES SEVERAL OF THE	FIRSTA
4.	C COMPOSITION AND STRUCTURAL PROPERTIES OF THE TWO FUSED RING	FIRSTA
5.	C SYSTEMS TO DETERMINE WHETHER OR NOT THEY ARE SIMILAR. IF THE	FIRSTA
6.	C TWO RINGS ARE NOT FUSED, IT COMPARES THEIR RING SIZE.	FIRSTA
7.	INTEGER SYMX(4),SYMBOL(9),GRID(6,6)	FIRSTA
8.	DIMENSION NOKOMB(11),KORB(40,10),NOK(10,10),KAPROP(6,40),IA(40),	FIRSTA
9.	IE(40),IC(40),SD(40)	FIRSTA
10.	COMMON/BLK1/NO,NOS,CYMX,SYMBOL,NOVAL(9),GRID	FIRSTA
11.	COMMON/BLK3/IRING(40,30),IMATX(50,60),NM(100),IAC(100),KON(100),	FIRSTA
12.	IIDBR(100),IB(100,6),IRG,NOBR	FIRSTA
13.	COMMON/BLK4/NBC(60,30),NBS(60,2),NBX(60,20),IRC,NONFUS,IRCTOT	FIRSTA
14.	COMMON/BLK5/NDATA,NUMATRS),MBC(50),MBS(2),JM,JV,LFLAG,FLAGG	FIRSTA
15.	EQUIVALENCE (NOKOMB(1),IB(60,6)),(KOMB(1,1),ID(42,4)),(NDR(1,1),	FIRSTA
16.	IMATX(1,50)),(KAPROP(1,1),NBX(2,1)),(IA(1),GRID(1,27)),IE(1),	FIRSTA
17.	ZI(22,3)),(IC(1),IMATX(2,50)),(ID(1),IMATX(42,50))	FIRSTA
18.	C1.0 INITIALIZE VARIABLE KRING2.	FIRSTA
19.	KRING2=0	FIRSTA
20.	C2.0 ARE ATOMS K1 AND K2 IN SAME RING SYSTEM	FIRSTA
21.	IF(IBC(K1).NE.IBC(K2))GO TO 5	FIRSTA
22.	C YES. SET FLAGS AND EXIT FROM ROUTINE.	FIRSTA
23.	WRITE(6,3)K1,K2,KC	FIRSTA
24.	3 FORMAT(// 1H0,23I,9HATOMS,14,6H AND,14,40H ARE IN SAME RING SY	FIRSTA
25.	STEM. ASYMMETRY OF,14,20H NOT DETERMINABLE.)	FIRSTA
26.	JM=0	FIRSTA
27.	JV=0	FIRSTA
28.	RETURN	FIRSTA
29.	C NO. CONTINUE WITH TEST.	FIRSTA
30.	5 IF((IBC(K1)+IBC(K2))/100-1)7,47,9	FIRSTA
31.	C3.0 K1 AND K2 ARE NON-FUSED RINGS. IF THEIR RING SIZE IS EQUAL,	FIRSTA
32.	C GO TO 45. OTHERWISE, RETURN.	FIRSTA
33.	7 IC1=IBC(K1)	FIRSTA
34.	IC2=IBC(K2)	FIRSTA
35.	IF(IRING(IC1,1).EQ.IRING(IC2,1))GO TO 45	FIRSTA
36.	RETURN	FIRSTA
37.	C4.0 K1 AND K2 BELONG TO SEPARATE FUSED RING SYSTEMS.	FIRSTA
38.	9 IC1=IBC(K1)-100	FIRSTA
39.	IC2=IBC(K2)-100	FIRSTA
40.	IF(NOKOMB(IC1+1).NE.NOKOMB(IC2+1))RETURN	FIRSTA
41.	C5.0 SAME NUMBER OF FUSED RINGS IN BOTH SYSTEMS.	FIRSTA
42.	IF(NOK(1,IC1).NE.NOK(1,IC2).OR.NOK(2,IC1).NE.NOK(2,IC2).OR.	FIRSTA
43.	NOK(3,IC1).NE.NOK(3,IC2))RETURN	FIRSTA
44.	C6.0 BOTH SYSTEMS HAVE THE SAME NUMBER OF RING PAIRS, SAME NUMBER OF	FIRSTA
45.	C ATOMS COMMON TO ANY FUSED RING PAIR, AND SAME NUMBER OF ATOMS	FIRSTA
46.	C COMMON TO ALL RING PAIRS.	FIRSTA
47.	KV=NOKOMB(IC1+1)	FIRSTA
48.	C7.0 TEST THE EQUALITY OF THE TWO FUSED RING SYSTEMS FURTHER.	FIRSTA
49.	DO 11 K=1,KV	FIRSTA
50.	JX=NOMB(K,IC2)	FIRSTA
51.	IA(K)=IRING(JX,1)	FIRSTA
52.	IE(K)=KAPROP(1,JX)	FIRSTA
53.	IC(K)=KAPROP(3,JX)	FIRSTA
54.	ID(K)=KAPROP(5,JX)	FIRSTA
55.	11 CONTINUE	FIRSTA
56.	DO 11 J=1,KV	FIRSTA
57.	JY=NOMB(J,IC1)	FIRSTA
58.	C DETERMINE IF RINGS EXIST, ONE ON EACH SYSTEM, WHICH HAVE THE	FIRSTA
59.	C SAME NUMBER OF COMPONENTS. IF NOT, RETURN.	FIRSTA
60.	DO 19 K=1,KV	FIRSTA
61.	IF(IRING(JX,1).EQ.IA(K))GO TO 17	FIRSTA
62.	19 CONTINUE	FIRSTA
63.	RETURN	FIRSTA
64.	17 IA(K)=1	FIRSTA
65.	C DETERMINE IF DUPLICATE RINGS EXIST, ONE IN EACH SYSTEM, WHICH	FIRSTA
66.	C HAVE THE SAME NUMBER OF OTHER ATOMS IN THEIR BACKBONE. IF	FIRSTA
67.	C NOT, RETURN.	FIRSTA
68.	DO 19 K=1,KV	FIRSTA
69.	IF(KAPROP(1,JX).EQ.IE(K))GO TO 21	FIRSTA
70.	19 CONTINUE	FIRSTA
71.	RETURN	FIRSTA
72.	21 IE(K)=1	FIRSTA
73.	C DETERMINE IF DUPLICATE RINGS EXIST, ONE IN EACH SYSTEM, WHICH	FIRSTA

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74.	C	HAVE THE SAME NUMBER OF NITROGEN ATOMS IN THEIR BACKBONE. IF	FIRSTA	
75.	C	NOT, RETURN.	FIRSTA	
76.		DO23 K=1, KY	FIRSTA	
77.		IF(KRPROP(3, JX).EQ. IC(K)) GO TO 25	FIRSTA	25
78.		23 CONTINUE	FIRSTA	
79.		RETURN	FIRSTA	
80.		25 IC(K)=-1	FIRSTA	
81.	C	DETERMINE IF DUPLICATE RINGS EXIST, ONE IN EACH SYSTEM, WHICH	FIRSTA	
82.	C	HAVE THE SAME NUMBER OF DOUBLE BONDS. IF NOT, RETURN.	FIRSTA	
83.		DO27 K=1, KY	FIRSTA	
84.		IF(KRPROP(5, JX).EQ. ID(K)) GO TO 29	FIRSTA	29
85.		27 CONTINUE	FIRSTA	
86.		RETURN	FIRSTA	
87.		29 ID(K)=-1	FIRSTA	
88.		31 CONTINUE	FIRSTA	
89.	C4.0	ABOVE COMPARISONS SUCCESSFUL. DO RING SYSTEMS POSSESS ONE OR	FIRSTA	
90.	C	MORE ATOMS COMMON TO ALL RING PAIRS	FIRSTA	
91.		IF(NOR(3, IC1).EQ.0) GO TO 45	FIRSTA	45
92.	C	YES THEY DO. NOW DETERMINE IF THE SAME TYPES OF ATOMS ARE	FIRSTA	
93.	C	SHARED IN BOTH SYSTEMS. IF NOT, RETURN.	FIRSTA	
94.		KF=NOR(3, IC1)	FIRSTA	
95.		DO35 K=1, KP	FIRSTA	
96.		IA(K)=NOR(K+3, IC2)	FIRSTA	
97.		35 CONTINUE	FIRSTA	
98.		DO41 J=1, KP	FIRSTA	
99.		DO37 K=1, KP	FIRSTA	
100.		IF(NOR(J+3, IC1).EQ. IA(K)) GO TO 39	FIRSTA	39
101.		37 CONTINUE	FIRSTA	
102.		RETURN	FIRSTA	
103.		39 IA(K)=-1	FIRSTA	
104.		41 CONTINUE	FIRSTA	
105.	C7.0	ALL COMPARISONS SUCCESSFUL. SET FLAG = 1.	FIRSTA	
106.		45 KRING2=1	FIRSTA	
107.		47 RETURN	FIRSTA	
108.		END	FIRSTA	

FUSION

1.		SUBROUTINE FUSION	FUSION
2.	C	THIS SUBROUTINE IDENTIFIES THE SET(S) OF FUSED RING SYSTEM(S)	FUSION
3.	C	THAT MAY BE PRESENT IN THE MOLECULE.	FUSION
4.		INTEGER SYM(4), SYMBOL(9), GRID(50,60)	FUSION
5.		DIMENSION JSCAN(40), KOMB(40,10), NOKOMB(11), NOK(10,10),	FUSION
6.		KCOMMON(40,9,10)	FUSION
7.		COMMON/BLK1/NO, NOS, SYM1, SYM0L, NOVAL(9), GRID	FUSION
8.		COMMON/BLK3/IRING(40,30), IMATX(50,60), NW(100), IBC(100), KOW(100)	FUSION
9.		IIDBR(100), IB(100,8), IRB, NOBR	FUSION
10.		COMMON/BLK4/NBCC(60,50), NBS(60,2), NOK(60,20), IPC, NONFUS, IACTOT	FUSION
11.		EQUVALENCE (JSCAN(1), IMATX(11,40)), (KOMB(1,1), IB(62,4)),	FUSION
12.		(NCKOMB(1), IR(60,8)), (NOK(1,1), IMATX(1,58)), KCOMMON(1,1,1),	FUSION
13.		ZGRID(2,1)	FUSION
14.	C1.	INITIALIZE VARIABLES.	FUSION
15.		IC=0	FUSION
16.		NDIF=0	FUSION
17.		DD1 L=1,IRC	FUSION
18.		JSCAN(L)=0	FUSION
19.		DD100 K=1,10	FUSION
20.		DD100 J=1,9	FUSION
21.		KCOMMON(L,J,K)=0	FUSION
22.	100	CONTINUE	FUSION
23.	1	CONTINUE	FUSION
24.		DD2 K=1,10	FUSION
25.		DD2 J=1,10	FUSION
26.		NOK(J,K)=0	FUSION
27.	7	CONTINUE	FUSION
28.	C2.	INCREMENT COUNTER THAT DEFINES THE NUMBER OF RING SETS.	FUSION
29.	3	IC=IC+1	FUSION
30.	C3.	INITIALIZE COUNTER THAT DEFINES THE NUMBER OF RINGS IN SET IC.	FUSION
31.	5	KV=0	FUSION
32.	C4.	THIS CYCLE SELECTS THE RING SET(S).	FUSION
33.		DD7 L=1,IRC	FUSION
34.		IF(JSCAN(L).EQ.0)GO TO 8	FUSION
35.	7	CONTINUE	FUSION
36.	C	NO MORE RING SETS ARE PRESENT. FINALIZE VARIABLES. TERMINATE	FUSION
37.	C	MAJOR CYCLE AND EXIT.	FUSION
38.		IC=IC-1	FUSION
39.		NOKOMB(1)=IC	FUSION
40.		NONFUS=IRC-NDIF	FUSION
41.		IACTOT=NONFUS+NOKOMB(1)	FUSION
42.		RETURN	FUSION
43.	C	MORE RING COMPONENTS ARE PRESENT. RING L IS SELECTED AS TEST	FUSION
44.	C	COMPONENT. THIS IS ALSO INDICATED BY SETTING SCAN INDICATOR	FUSION
45.	C	VARIABLE.	FUSION
46.	8	KV=KV+1	FUSION
47.		NOMB(KV,IC)=L	FUSION
48.		JSCAN(L)=1	FUSION
49.		RSUBN1	FUSION
50.	C5.	THIS CYCLE FINDS THOSE RING COMPONENTS (IF ANY) PRESENT IN	FUSION
51.	C	SET IC.	FUSION
52.	11	KB=KV	FUSION
53.		DD2B J=1,IRC	FUSION
54.	C	WAS RING J SCANNED PREVIOUSLY	FUSION
55.	C	IF(JSCAN(J).NE.0)GO TO 25	FUSION
56.	C	IGNORE J.	FUSION
57.		IF(JSCAN(J).NE.0)GO TO 25	FUSION
58.	C	RING J NOT SCANNED PREVIOUSLY.	FUSION
59.		KTEST=0	FUSION
60.		JF=IRING(J,1)+1	FUSION
61.	C	DETERMINE WHETHER RING J IS FUSED TO OTHER RINGS K IN SET IC.	FUSION
62.		DD10 K=1,KV	FUSION
63.		NUM=0	FUSION
64.		IRK=KOMB(K,IC)	FUSION
65.		KF=IRING(IRK,1)+1	FUSION
66.	C	DO RINGS J AND IRK HAVE ATOMS IN COMMON	FUSION
67.		DD13 JJ=2,JF	FUSION
68.		DD13 KK=2,KF	FUSION
69.	C	IF NOT, GO TO 13.	FUSION
70.		IF(IRING(IRK,JK).NE.IRING(J,JJ))GO TO 13	FUSION
71.	C	YES - RINGS J AND IRK ARE FUSED. INCREMENT COUNTER AND	FUSION
72.	C	STORE FUSED ATOMS IN KCOMMON.	FUSION
73.		NUM=NUM+1	FUSION

74.		KOMMON(KSUB, NUM+3, IC)=IRING(IRR, KK)	FUSION	
75.	13	CONTINUE	FUSION	
76.	C	HOW MANY ATOMS DO THEY HAVE IN COMMON	FUSION	
77.	C	ZERO, IF NUM EQUALS ZERO.	FUSION	
78.		IF(NUM.EQ.0)GO TO 19	FUSION	19
79.	C	RINGS J AND IRR HAVE TWO OR MORE ATOMS IN COMMON. STORE	FUSION	
80.	C	THIS NUMBER AND THE TWO I. D. RING NUMBERS IN KOMMON.	FUSION	
81.	C	INCREMENT COUNTER KSUB AND KTEST.	FUSION	
82.		KOMMON(KSUB, 1, IC)=IK	FUSION	
83.		KOMMON(KSUB, 2, IC)=J	FUSION	
84.		KOMMON(KSUB, 3, IC)=NUM	FUSION	
85.		KSUB=KSUB+1	FUSION	
86.		KTEST=KTEST+1	FUSION	
87.	19	CONTINUE	FUSION	
88.	C	DID AT LEAST ONE OF THE RINGS IN CURRENT SET HAVE ATOM(S) IN	FUSION	
89.	C	COMMON WITH TEST RING J	FUSION	
90.		IF(KTEST.EQ.0)GO TO 25	FUSION	25
91.	C	YES, RING J SHOULD BE ADDED TO IC SET. STORE I. D. NUMBER OF	FUSION	
92.	C	RING IN KOMB AND SET JSCAN(J).	FUSION	
93.		KV=KV+1	FUSION	
94.		KOMB(KV, IC)=J	FUSION	
95.		JSCAN(J)=1	FUSION	
96.	25	CONTINUE	FUSION	
97.	C6.	WERE NEW RINGS ADDED TO IC SET	FUSION	
98.	C	IF YES, GO TO 13.	FUSION	
99.		IF(KV.GT. KB)GO TO 11	FUSION	11
100.	C	NO, NEW RINGS WERE NOT ADDED.	FUSION	
101.	C7.	HOW MANY TOTAL RINGS IN SET IC	FUSION	
102.	C	IF LESS THAN TWO, FUSEG SET IC NOT PRESENT. IGNORE IC AND GO	FUSION	
103.	C	TO 5.	FUSION	
104.		IF(KV-1)5, 9, 33	FUSION	33
105.	C	IC SET EXISTS. STORE NUMBER OF RING COMPONENTS IN NOKOMB.	FUSION	
106.	C	ALSO ADD NUMBER OF FUSED RING COMPONENTS TO VARIABLE NOIF.	FUSION	
107.	33	NOKOMB(IC+1)=KV	FUSION	
108.		NDIF=NDIF+KV	FUSION	
109.		KSUB=KSUB-1	FUSION	
110.	C8.	STORE NUMBER OF RING PAIRS IN SET IC IN NOK(1, IC).	FUSION	
111.		NOK(1, IC)=KSUB	FUSION	
112.		KCT=KOMMON(1, 3, IC)	FUSION	
113.		IF(KSUB.GT.1)GO TO 36	FUSION	36
114.	C	ONLY ONE PAIR OF FUSED RINGS PRESENT IN IC. STORE COMMON	FUSION	
115.	C	ATOMS IN NOK(4, IC), NOK(5, IC), ...	FUSION	
116.		D035 J=1, KCT	FUSION	
117.		NOK(J+3, IC)=KOMMON(1, J+3, IC)	FUSION	
118.	35	CONTINUE	FUSION	
119.		NOK(3, IC)=KCT	FUSION	
120.		GO TO 45	FUSION	45
121.	C	MORE THAN ONE PAIR OF FUSED RINGS ARE PRESENT IN SET IC.	FUSION	
122.	C	DETERMINE IF ALL RING PAIRS IN IC HAVE SAME NUMBER OF ATOMS	FUSION	
123.	C	IN COMMON.	FUSION	
124.	36	D037 K=2, KSUB	FUSION	
125.		IF(KCT.AE.KOMMON(J, 3, IC))GO TO 51	FUSION	51
126.		37 CONTINUE	FUSION	
127.	C	YES THEY DO. NOW DETERMINE HOW MANY OF THE RING ATOMS ARE	FUSION	
128.	C	COMMON TO ALL FUSED RING PAIRS IN SET IC. STORE THESE IN	FUSION	
129.	C	NOK(4, IC), NOK(5, IC), ...	FUSION	
130.		JJ=0	FUSION	
131.		D043 L=1, KCT	FUSION	
132.		D041 K=2, KSUB	FUSION	
133.		D039 J=1, KCT	FUSION	
134.		IF(KOMMON(1, L+3, IC).EQ.KOMMON(K, J+3, IC))GO TO 41	FUSION	41
135.	39	CONTINUE	FUSION	
136.		GO TO 43	FUSION	43
137.	C	ATOM KOMMON(1, L+3, IC) IS COMMON TO ALL FUSED RING PAIRS	FUSION	
138.	C	IN SET IC.	FUSION	
139.	41	CONTINUE	FUSION	
140.		JJ=JJ+1	FUSION	
141.		NOK(JJ+3, IC)=KOMMON(1, L+3, IC)	FUSION	
142.	43	CONTINUE	FUSION	
143.	C	STORE TOTAL OF ABOVE ATOMS IN NOK(3, IC) AND STORE TOTAL	FUSION	
144.	C	NUMBER OF ATOMS COMMON TO ANY FUSED RING PAIR SET IC IN	FUSION	
145.	C	NOK(2, IC).	FUSION	

146.	NOR(3,IC)=JJ	FUSION
147.	45 NOR(2,IC)=KCT	FUSION
148.	C9 SET THE LOCATIONS OF THE IC ARRAY CORRESPONDING TO THE GROUP	FUSION
149.	C NUMBERS OF THE COMPONENTS OF THE RINGS OF SET IC EQUAL TO THE	FUSION
150.	C SET NUMBER (IC) + 100.	FUSION
151.	S1 DOSS L=1, KY	FUSION
152.	J=KOMB(L,IC)	FUSION
153.	KP=IRING(J,1)+1	FUSION
154.	DOSS KK=2, KP	FUSION
155.	JJ=IRING(J, KK)	FUSION
156.	IBC(JJ)=IC+100	FUSION
157.	S3 CONTINUE	FUSION
158.	GO TO 3	FUSION
159.	END	FUSION

GADATA

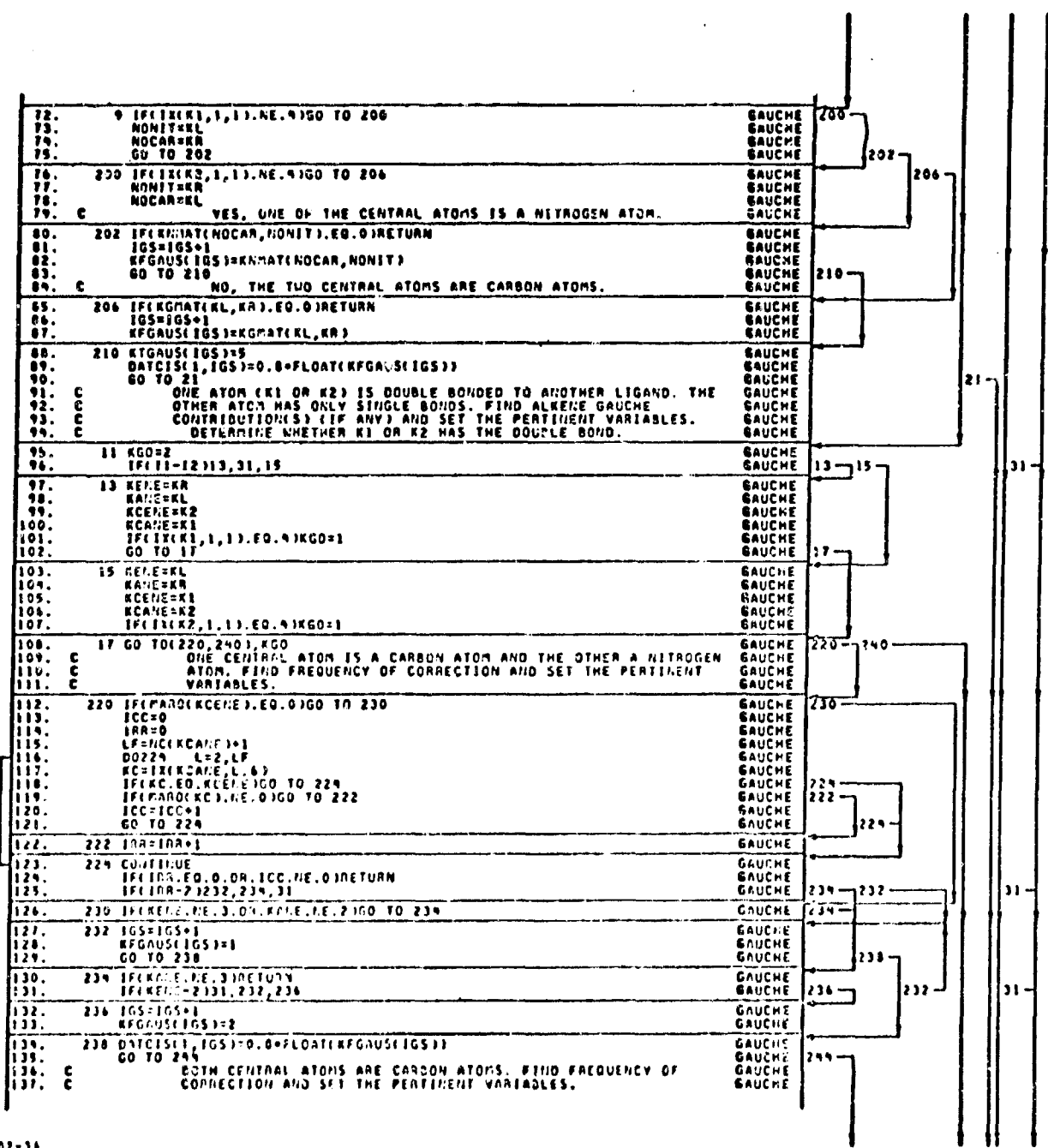
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1.      SUBROUTINE GADATA                                GADATA
2.      C      THIS SUBROUTINE PRINTS OUT THE GROUP ADDITIVITY LIBRARY DATA  GADATA
3.      C      IF CALLED FOR BY THE INPUT DATA.                                GADATA
4.      INTEGER GROUP1(100), GROUP2(100), GROUP3(100)  GADATA
5.      INTEGER SUM(100)                                GADATA
6.      DIMENSION CP1(100), CP2(100), CP3(100), CP4(100)  GADATA
7.      COMMON/BLK4/NBC(40,50), NBS(40,2), NBS(40,20), IAC, NONFUS, IACTOT  GADATA
8.      COMMON/BLK7/SUM, HF298(100), S298(100), CPX(100,4)  GADATA
9.      EQUIVALENCE (CPX(1,1), CP1(1)), (CPX(1,2), CP2(1)), (CPX(1,3), CP3(1)),  GADATA
10.     (CPX(1,4), CP4(1))  GADATA
11.     EQUIVALENCE (GROUP1(1), NBC(2,1)), (GROUP2(1), NBC(2,12)),  GADATA
12.     (GROUP3(1), NBC(2,28))  GADATA
13.     C1.0 PRINT OUT HEADING AND UNITS OF OUTPUT.  GADATA
14.     WRITE(6,998)  GADATA
15.     998 FORMAT(1H1,35X,40HTABLES OF THERMOCHEMICAL GROUP CONTRIBUTIONS  GADATA
16.     1//)  GADATA
17.     WRITE(6,996)  GADATA
18.     996 FORMAT(1H0, 4X,5HGROUP, 7X,6HWEIGHT, 2X,17HHEAT OF FORMATION, 2X,  GADATA
19.     17HENTROPY, 20X,24HHEAT CAPACITY COEFFICIENTS/ 1M ,20X,9HMCAL/MOLE,  GADATA
20.     3 4X,12HMCAL/DEG-MOLE, 3X,12HMCAL/DEG-MOLE, 2X,15HMCAL/DEG+2-MOLE,  GADATA
21.     3 2X,15HMCAL/DEG+3-MOLE, 2X,15HMCAL/DEG+4-MOLE/1M ,30X,5H298 K,  GADATA
22.     49X,5H298 K)  GADATA
23.     C2.0 PRINT OUT TABLE OF HYDROCARBONS.  GADATA
24.     WRITE(6,994)  GADATA
25.     994 FORMAT(1H0, 49X,21HDATA FOR HYDROCARBONS//)  GADATA
26.     WRITE(6,3) (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L),  GADATA
27.     15298(L), CP1(L), CP2(L), CP3(L), CP4(L), L=1,33)  GADATA
28.     3 FORMAT(1M ,2A4,AS,10,6X,F10.4,4X,F10.4,F17.10,F16.10,2F17.10)  GADATA
29.     C3.0 PRINT OUT TABLE OF OXYGEN-CONTAINING GROUPS.  GADATA
30.     WRITE(6,992)  GADATA
31.     992 FORMAT(1H0, 43X,33HDATA FOR OXYGEN-CONTAINING GROUPS//)  GADATA
32.     WRITE(6,5) (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L),  GADATA
33.     15298(L), CP1(L), CP2(L), CP3(L), CP4(L), L=1,99)  GADATA
34.     5 FORMAT(1M ,2A4,AS,10,6X,F10.4,4X,F10.4,F17.10,F16.10,2F17.10)  GADATA
35.     C4.0 PRINT OUT TABLE OF NITROGEN-CONTAINING GROUPS.  GADATA
36.     WRITE(6,990)  GADATA
37.     990 FORMAT(1H0, 42X, 35HDATA FOR NITROGEN-CONTAINING GROUPS//)  GADATA
38.     WRITE(6,7) (GROUP1(L), GROUP2(L), GROUP3(L), SUM(L), HF298(L),  GADATA
39.     15298(L), CP1(L), CP2(L), CP3(L), CP4(L), L=110,163)  GADATA
40.     7 FORMAT(1M ,2A4,AS,10,6X,F10.4,4X,F10.4,F17.10,F16.10,2F17.10)  GADATA
41.     RETURN  GADATA
42.     END  GADATA

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GAUCHE

1.		SUBROUTINE GAUCHE(K1, P2, IGS, IGM, IGO, GAUCMH)	GAUCHE
2.	C	THIS SUBROUTINE DETERMINES WHETHER THE LIGANDS OF ATOMS K1 AND	GAUCHE
3.	C	K2 ARE GAUCHE TO EACH OTHER. IF SO, IT DETERMINES THE NUMBER,	GAUCHE
4.	C	TYPE, AND MAGNITUDE OF THE GAUCHE CORRECTION.	GAUCHE
5.		INTEGER SYM(4), SYZOL(4), GRID(50, 60)	GAUCHE
6.		INTEGER WEIGHT(4)	GAUCHE
7.		DIMENSION KCGAUS(3, 150), KFGAUS(150), KTGGAUS(150), DATCIS(2, 150),	GAUCHE
8.		IKGMAT(4, 4), KGMAT(4, 3), PARO(100)	GAUCHE
9.		COMMON/BLK1/NO, NOS, SYM1, SYM2OL, NOVAL(4), GRID	GAUCHE
10.		COMMON/BLK2/WEIGHT, FWT(4), POLUT(100), IZI(100, 5, 6), NC(100), KCC	GAUCHE
11.		COMMON/BLK3/IRING(40, 30), IMATX(50, 60), NWE(100), IBC(100), KONE(100),	GAUCHE
12.		IIGCR(100), IBI(100, 8), IAG, NOBR	GAUCHE
13.		EQUIVALENCE (KCGAUS(1, 1), IMATX(1, 72)), (KFGAUS(1), IMATX(1, 63)),	GAUCHE
14.		IKETGAUS(1), IMATX(1, 60), DATCIS(1, 1), IMATX(1, 66), PARO(1),	GAUCHE
15.		ZGRID(1, 25)	GAUCHE
16.	C	KGMAT DEFINES THE NUMBER OF ALKANE GAUCHE CORRECTIONS WHEN K1	GAUCHE
17.	C	AND K2 ARE BOTH CARBON ATOMS.	GAUCHE
18.		DATA KGMAT(1, 1)/0/, KGMAT(1, 2)/0/, KGMAT(1, 3)/0/, KGMAT(1, 4)/0/,	GAUCHE
19.		IKGMAT(2, 1)/0/, KGMAT(2, 2)/0/, KGMAT(2, 3)/1/, KGMAT(2, 4)/2/,	GAUCHE
20.		IKGMAT(3, 1)/0/, KGMAT(3, 2)/1/, KGMAT(3, 3)/2/, KGMAT(3, 4)/1/,	GAUCHE
21.		IKGMAT(4, 1)/0/, KGMAT(4, 2)/2/, KGMAT(4, 3)/2/, KGMAT(4, 4)/0/	GAUCHE
22.	C	KGMAT DEFINES THE NUMBER OF ALKANE GAUCHE CORRECTIONS WHEN K1	GAUCHE
23.	C	OR K2 IS A NITROGEN ATOM.	GAUCHE
24.		DATA KGMAT(1, 1)/0/, KGMAT(1, 2)/0/, KGMAT(1, 3)/0/, KGMAT(1, 4)/0/,	GAUCHE
25.		IKGMAT(2, 2)/0/, KGMAT(2, 3)/1/, KGMAT(2, 4)/0/, KGMAT(3, 2)/0/, KGMAT(3, 3)/0/,	GAUCHE
26.		IKGMAT(4, 1)/0/, KGMAT(4, 2)/2/, KGMAT(4, 3)/2/	GAUCHE
27.	C1.0	IF BOTH K1 AND K2 ARE NITROGEN ATOMS, EXIT FROM ROUTINE.	GAUCHE
28.		IF(IKX(K1, 1), 1).EQ.4.AND.IKX(K2, 1), 1).EQ.4)RETURN	GAUCHE
29.	C	IF K1 OR K2 IS AN OXYGEN ATOM, GO TO 23	GAUCHE
30.		IF(IKX(K1, 1), 1).EQ.3.OR.IKX(K2, 1), 1).EQ.3)GO TO 23	GAUCHE
31.		IF(KON(K1).LT.3.AND.IKX(K1, 1), 1).NE.6)RETURN	GAUCHE
32.		IF(KON(K2).LT.3.AND.IKX(K2, 1), 1).NE.6)RETURN	GAUCHE
33.	C2.0	CORE ATOMS K1 AND K2 ARE EITHER CARBON OR NITROGEN ATOMS.	GAUCHE
34.		FIND NUMBER OF LIGANDS BONDED TO K1 AND K2 WHICH ARE HEAVY	GAUCHE
35.	C	(NON-HYDROGEN) ATOMS.	GAUCHE
36.		KL=0	GAUCHE
37.		KR=0	GAUCHE
38.		LF=KON(K1)+1	GAUCHE
39.		DO150 L=2, LF	GAUCHE
40.		IF(IKX(K1, L), 6).EQ.K2.OR.IKX(K1, L), 1).EQ.1)GO TO 150	GAUCHE
41.		KL=KL+1	GAUCHE
42.		150 CONTINUE	GAUCHE
43.		LF=KON(K2)+1	GAUCHE
44.		DO180 L=2, LF	GAUCHE
45.		IF(IKX(K2, L), 6).EQ.K1.OR.IKX(K2, L), 1).EQ.1)GO TO 180	GAUCHE
46.		KR=KR+1	GAUCHE
47.		180 CONTINUE	GAUCHE
48.		KL=KL+1	GAUCHE
49.		KR=KR+1	GAUCHE
50.	C	DETERMINE IF GAUCHE ALKANE OR GAUCHE ALKENE INTERACTIONS	GAUCHE
51.	C	ARE PRESENT.	GAUCHE
52.		I1=0	GAUCHE
53.		I2=0	GAUCHE
54.	C	DETERMINE IF K1 OR K2 ARE JOINED BY A DOUBLE BOND TO OTHER	GAUCHE
55.	C	LIGANDS. IF SO, SET THE CORRESPONDING FLAG(S) EQUAL TO 1.	GAUCHE
56.		DO12 L=2, 5	GAUCHE
57.		IF(IKX(K1, L), 5)-2)0, 6, 3)	GAUCHE
58.		6 I1=1	GAUCHE
59.		8 IF(IKX(K2, L), 5)-2)12, 10, 3)	GAUCHE
60.		10 I2=1	GAUCHE
61.		12 CONTINUE	GAUCHE
62.		IF(IKX(K1, 1), 1).NE.6)GO TO 190	GAUCHE
63.		KL=KL+1	GAUCHE
64.		I1=1	GAUCHE
65.		190 IF(IKX(K2, 1), 1).NE.6)GO TO 192	GAUCHE
66.		KR=KR+1	GAUCHE
67.		I2=1	GAUCHE
68.		192 IF(I1+I2-1)9, 11, 3)	GAUCHE
69.	C	ALL BONDS OF ATOMS K1 AND K2 ARE SINGLE. FIND ALKANE GAUCHE	GAUCHE
70.	C	CONTRIBUTIONS: IF ANY AND SET THE PERTINENT VARIABLES.	GAUCHE
71.	C	IS K1 OR K2 A NITROGEN ATOM	GAUCHE



138.	240	IF (KENE.NE.3.OR.KANE.NE.3.AND.KANE.NE.4)RETURN	GAUCHE	
139.		IGS=ISS+1	GAUCHE	
140.		RFGAUS(IGS)=2	GAUCHE	
141.		DATCIS(IGS)=0.5	GAUCHE	
142.	249	RFGAUS(IGS)=6	GAUCHE	
143.	21	RCGAUS(1,IGS)=K1	GAUCHE	
144.		RCGAUS(2,IGS)=K2	GAUCHE	
145.		GO TO 28	GAUCHE	28
146.	23	IF (IKK(1,1,1).EQ.3.AND.IKK(2,1,1).EQ.3)RETURN	GAUCHE	
147.	C3.0	CORE ATOMS K1 AND K2 ARE NOT BOTH OXYGEN ATOMS. SEARCH FOR	GAUCHE	
148.	C	ETHER OXYGEN GAUCHE CONTRIBUTION(S).	GAUCHE	
149.		IF (NJK(1).LT.3.OR.IKK(2,1,1).NE.3)GO TO 24	GAUCHE	24
150.		KHEAVY=K1	GAUCHE	
151.		KOXY=K2	GAUCHE	
152.		GO TO 25	GAUCHE	25
153.	24	IF (IKK(1,1,1).NE.3.OR.NJK(2).LV.3)RETURN	GAUCHE	
154.		KHEAVY=K2	GAUCHE	
155.		KOXY=K1	GAUCHE	
156.	C	ONE ATOM (K1 OR K2) IS AN OXYGEN ATOM THE OTHER ATOM IS A	GAUCHE	
157.		HEAVY ATOM WHICH HAS THE CORRECT NUMBER OF NON-HYDROGEN	GAUCHE	
158.		ATOMS.	GAUCHE	
159.	25	IF (IKKHEAVY(1,1).NE.2.AND.IKKHEAVY(1,1).NE.6.OR.NMK(KOXY).NE.2)	GAUCHE	
160.		RETURN	GAUCHE	
161.	C	THE OXYGEN ATOM HAS TWO CORE LIGANDS. DETERMINE IF THE OTHER	GAUCHE	
162.		ATOM BONDED TO THE OXYGEN ATOM IS ALSO A CARBON ATOM, BUT	GAUCHE	
163.		NOT -CN.	GAUCHE	
164.		DO250 L=2,3	GAUCHE	
165.		IF (IK(KOXY,L,6).EQ.KHEAVY)GO TO 250	GAUCHE	250
166.		IF (IK(KOXY,L,1).NE.2)GO TO 248	GAUCHE	248
167.		LL=IK(KOXY,L,1)	GAUCHE	
168.		IF (K(LL).GE.3)GO TO 240	GAUCHE	240
169.	248	IF (IK(KOXY,L,1).EQ.6)GO TO 250	GAUCHE	240
170.	250	CONTINUE	GAUCHE	
171.		RETURN	GAUCHE	
172.	C	YES IT IS. FIND NUMBER OF LIGANDS BONDED TO KHEAVY WHICH	GAUCHE	
173.	C	ARE HEAVY (NON-HYDROGEN) ATOMS.	GAUCHE	
174.	260	NL=0	GAUCHE	
175.		LF=KON(KHEAVY)+1	GAUCHE	
176.		DO290 L=2,LF	GAUCHE	
177.		IF (IK(KHEAVY,L,6).EQ.KOXY.OR.IK(KHEAVY,L,1).EQ.1)GO TO 290	GAUCHE	290
178.		NL=NL+1	GAUCHE	
179.	390	CONTINUE	GAUCHE	
180.	C	DETERMINE IF INTERACTION EXISTS. IF SO, FIND FREQUENCY	GAUCHE	
181.	C	OF CORRECTION AND SET THE PERTINENT VARIABLES.	GAUCHE	
182.		IF (KL.LT.3)RETURN	GAUCHE	
183.		IGS=IGS+1	GAUCHE	
184.		IF (N:(KHEAVY).NE.3)GO TO 26	GAUCHE	26
185.		RFGAUS(IGS)=1	GAUCHE	
186.		GO TO 27	GAUCHE	27
187.	26	RFGAUS(IGS)=2	GAUCHE	
188.	27	RFGAUS(IGS)=7	GAUCHE	
189.		RCGAUS(1,IGS)=KHEAVY	GAUCHE	
190.		RCGAUS(2,IGS)=KOXY	GAUCHE	
191.		DATCIS(1,IGS)=0.3*FLOAT(RFGAUS(IGS))	GAUCHE	
192.		IGO=IGO+1	GAUCHE	
193.	C4.0	FIND SUM TOTAL OF GAUCHE CORRECTIONS FOR THE HEAT OF FORMATION	GAUCHE	
194.	C	AND INCREMENT GAUCHE COUNTER IGM.	GAUCHE	
195.	28	GAUCHH=GAUCHH+DATCIS(1,IGS)	GAUCHE	
196.		IGH=IGH+1	GAUCHE	
197.	31	RETURN	GAUCHE	
198.		END	GAUCHE	

HEXGON

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1. SUBROUTINE HEXGON(IGS, IORTHO, IORPAR, DORTHO, DONPAR, HRING, SRING, HEXGON
2. ICPSYR) HEXGON
3. THIS SUBROUTINE ASSIGNS THE NECESSARY WEIGHT CORRECTIONS TO HEXGON
4. GROUPS OF FUSED RING SYSTEMS CONTAINING BENZENE CARBONS AND/OR HEXGON
5. PYRIDINE-LIKE STRUCTURES WHICH FORM CONJUGATED SIX-MEMBERED HEXGON
6. RINGS AND/OR TO NON-FUSED RINGS OF THE AFOREMENTIONED HEXGON
7. STRUCTURES AND TO ALL GROUPS BONDED TO THESE RING ATOMS. IT HEXGON
8. ALSO PRINTS OUT THE ASSIGNED WEIGHTS, THE COMPOSITION OF THE HEXGON
9. MOLECULE, AND THE IX ARRAY. HEXGON
10. INTEGER SYM(4), SYMBOL(9), GRID(50,80) HEXGON
11. INTEGER WEIGHT(9) HEXGON
12. DIMENSION KBENZ(40), KSIX(40), MDEL(40), IC2A(10), JDONE(40), HEXGON
13. IKOMB(40,10), NOKOMB(11), MFIX(100), CPSYM(4), DORTHO(6), JBOND(100), HEXGON
14. ZNOR(10,10), HRING(40), KACNOR(100), KRCNWT(100), KNBENZ(40), KTBENZ(40) HEXGON
15. J, NONARD(40), KTGAUS(150), KCGAUS(3,150), MARO(100) HEXGON
16. COMMON/BLK1/NO, NOS, SYM, SYMBOL, NOVAL(9), GRID HEXGON
17. COMMON/BLK2/WEIGHT, MWBT(9), MOLWT(100), IX(100,5,6), NC(100), KCC HEXGON
18. COMMON/BLK3/IRING(40,30), IMATX(50,80), NWC(100), IBC(100), KNC(100), HEXGON
19. IIOBR(100), IB(100,8), IRG, NOER HEXGON
20. COMMON/BLK4/NBC(60,50), NBS(60,2), NBX(60,20), IAC, NONFUS, IACTOT HEXGON
21. EQUIVALENCE (NBENZ, IB(10,1)), (MOSIX, IB(11,1)), (MO, IB(12,1)), HEXGON
22. I(MDEL(1), IB(13,1)), (KBENZ(1), IB(93,1)), (KSIX(1), IB(81,2)), HEXGON
23. Z(JDONE(1), IB(81,3)), (IC2, IB(21,4)), (IC2A(1), IB(22,4)), (KOMB(1,1), HEXGON
24. IB(62,4)), (NOKOMB(1), IB(60,8)), (MFIX(1), IMATX(1,55)), (JBOND(1), HEXGON
25. IMATX(1,51)), (NOK(1,1), IMATX(1,55)), (NRING(1), GRID(1,75)) HEXGON
26. 5(KRCNOR(1), GRID(1,76)), (KRCNWT(1), GRID(1,78)), (KNBENZ, GRID(1,80)), HEXGON
27. 6(KNBENZ(1), GRID(2,80)), (NTBENZ, IB(96,8)), (KTBENZ(1), GRID(41,27)), HEXGON
28. 7(NONARD(1), IMATX(2,49)), (KTGAUS(1), IMATX(1,60)), (KCGAUS(1,1), HEXGON
29. IMATX(1,72)), (MARO(1), GRID(1,25)) HEXGON
30. C1. INITIALIZE VARIABLES. HEXGON
31. IC2=0 HEXGON
32. DO1 L=1, IAC HEXGON
33. JDONE(L)=0 HEXGON
34. 1 CONTINUE HEXGON
35. DO3 KC=1, KCC HEXGON
36. MFIX/KC)=0 HEXGON
37. JBOND(KC)=0 HEXGON
38. 3 CONTINUE HEXGON
39. IF(NBENZ.EQ.0)GO TO 9 HEXGON
40. DO7 L=1, NBENZ HEXGON
41. 7 KTBENZ(L)=KBENZ(L) HEXGON
42. 9 IF(NNBENZ.EQ.0)GO TO 15 HEXGON
43. I=NBENZ+1 HEXGON
44. DO11 L=1, NNBNZ HEXGON
45. KTBENZ(I)=KNBENZ(I.) HEXGON
46. 11 I=I+1 HEXGON
47. 15 NTBENZ=NBENZ+NNBNZ HEXGON
48. C2. IF FUSED RING SYSTEMS ARE NOT PRESENT, GO TO 43. OTHERWISE, HEXGON
49. CONTINUE. HEXGON
50. IF(NOKOMB(1).EQ.0)GO TO 43 HEXGON
51. IC=NOKOMB(1) HEXGON
52. C3. DETERMINE WHETHER ANY OF FUSED RING SETS ARE COMPOSED OF PURE HEXGON
53. CARBON OR CARBON-NITROGEN BACKBONE, 6-CENTERED RINGS OF THE HEXGON
54. TYPE DESIGNATED IN ARRAY KSIX, AT LEAST ONE OF WHICH MUST HAVE HEXGON
55. A BENZENE OR PYRIDINE-LIKE STRUCTURE WITH 3 DOUBLE BONDS PER HEXGON
56. RING. HEXGON
57. DO37 J=1, IC HEXGON
58. C DOES EACH ADJOINING RING PAIR IN FUSED RING SET J HAVE TWO HEXGON
59. ATOMS IN COMMON AND A CARBON OR PYRIDINE-TYPE UNSATURATED HEXGON
60. STRUCTURE HEXGON
61. C IF(NOK(2,J).NE.2)GO TO 37 HEXGON
62. NN=0 HEXGON
63. C EACH RING IN SET J HAS 2 ATOMS IN COMMON WITH EACH RING TO HEXGON
64. WHICH IT IS FUSED. NOW TEST WHETHER RINGS IN SET J ARE HEXGON
65. UNSATURATED, 6-CENTERED CARBON OR PYRIDINE-LIKE RINGS OF HEXGON
66. TYPE DESIGNATED BY ARRAY KSIX. HEXGON
67. MPOS=0 HEXGON
68. MTEMP=MB HEXGON
69. KY=NOKOMB(J+1) HEXGON
70. DO27 K=1, KY HEXGON
71. DO29 I=1, NOSIX HEXGON
72. IF(NOMB(K,J).EQ.KSIX(I))GO TO 27 HEXGON
73. 25 CONTINUE HEXGON
74. GO TO 37 HEXGON
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76.	C	27 CONTINUE	HEXGON	
77.	C	RINGS IN SET J ARE OF TYPE DESIGNATED BY K&K ARRAY. DOES AT	HEXGON	
78.	C	LEAST ONE OF THE RINGS IN FUSED RING SET J HAVE 3 DOUBLE	HEXGON	
79.	C	BONDS WITHIN THE RING	HEXGON	
80.	C	DO33 K=1,RY	HEXGON	
81.	C	DO32 I=1,RYBENZ	HEXGON	
82.	C	IF(NONAR(J),J).EQ.(RYBENZ(I))GO TO 33	HEXGON	33
83.	C	32 CONTINUE	HEXGON	
84.	C	RING K DOES NOT HAVE 3 DOUBLE BONDS. SET VARIABLE	HEXGON	
85.	C	IDENTIFYING THIS RING IF IT IS A RING WITH A PURE CARBON	HEXGON	
86.	C	BACKBONE.	HEXGON	
87.	C	JK=KOMB(K,J)	HEXGON	
88.	C	IF(NRING(J).EQ.0)GO TO 320	HEXGON	320
89.	C	NN=0	HEXGON	
90.	C	GO TO 33	HEXGON	33
91.	C	320 NN=NN+1	HEXGON	
92.	C	NDLE(N)=KOMB(K,J)	HEXGON	
93.	C	GO TO 33	HEXGON	33
94.	C	RING K HAS 3 DOUBLE BONDS. INDICATE THIS BY SETTING NPAS	HEXGON	
95.	C	AND JDO=0.	HEXGON	
96.	C	32 NPAS=1	HEXGON	
97.	C	JJ=RYBENZ(I)	HEXGON	
98.	C	JDO=JDO+1	HEXGON	
99.	C	IF(I.EQ.0).AND.(NN=0)	HEXGON	
100.	C	33 CONTINUE	HEXGON	
101.	C	DOES SET J CONTAIN AT LEAST ONE RING WITH 3 DOUBLE BONDS	HEXGON	
102.	C	IF(NPAS.EQ.1)GO TO 34	HEXGON	34
103.	C	NO. RESET NN TO ITS INITIAL VALUE AT START OF CYCLE. TEST	HEXGON	
104.	C	REMAINING FUSED RING SETS.	HEXGON	
105.	C	NN=NTMP	HEXGON	
106.	C	GO TO 37	HEXGON	37
107.	C	YES. FUSED SET IS OF DESIRED TYPE. SET VARIABLE IDENTIFYING	HEXGON	
108.	C	THIS FUSED RING SET AND ZERO OUT THE LOCATIONS IN THE	HEXGON	
109.	C	NONAR0 ARRAY CORRESPONDING TO THE 10 NUMBERS OF THE RINGS	HEXGON	
110.	C	IN THE SET. CONTINUE TEST OF FUSED RING SETS.	HEXGON	
111.	C	34 IC2=IC2+1	HEXGON	
112.	C	IC2A(IC2)=J	HEXGON	
113.	C	IF(NN.EQ.0)NN=1	HEXGON	
114.	C	DO360 K=1,RY	HEXGON	
115.	C	JJ=KOMB(K,J)	HEXGON	
116.	C	NONAR0(J)=0	HEXGON	
117.	C	DO350 I=2,7	HEXGON	
118.	C	KC=IRING(I,J)	HEXGON	
119.	C	350 NAR0(K)=NN	HEXGON	
120.	C	360 CONTINUE	HEXGON	
121.	C	37 CONTINUE	HEXGON	
122.	C	CORRECT WEIGHT OF RING ATOMS IN BENZENE OR PYRIDINE-LIKE	HEXGON	
123.	C	STRUCTURES WHICH DO NOT FORM PART OF FUSED RING SET.	HEXGON	
124.	C	43 JA=999	HEXGON	
125.	C	DO55 L=1,NTRENT	HEXGON	
126.	C	JJ=RYBENZ(L)	HEXGON	
127.	C	IF(JDO=0)GO TO 55	HEXGON	55
128.	C	BENZENE OR PYRIDINE-LIKE RING JJ IS NOT PART OF FUSED RING	HEXGON	
129.	C	SET. REDUCE WEIGHT OF ALL ATOMS COMPRISING BACKBONE OF RING	HEXGON	
130.	C	JJ. SET IDENTIFIER OF ATOMS EQUAL TO JA (EQUAL TO OR LESS	HEXGON	
131.	C	THAN -500).	HEXGON	
132.	C	NN=1	HEXGON	
133.	C	IF(L.EQ.0)NN=2	HEXGON	
134.	C	JK=JL	HEXGON	
135.	C	NT=0	HEXGON	
136.	C	IF(IRING(JJ,K))	HEXGON	
137.	C	NAR0(K)=NN	HEXGON	
138.	C	(PLAS=RCRCHW(K))	HEXGON	
139.	C	GO TO 45, 46, 460, 47, 470, 48, 485, 49, 495	HEXGON	
140.	C	CARBON ATOM(I) IS OF TYPE C=C-C(I)=0	HEXGON	45 46 460 47 470 48 485 49
141.	C	45 POLWTK(I)=POLWTK(I)-530	HEXGON	
142.	C	GO TO 51	HEXGON	51
143.	C	46 POLWTK(I)=POLWTK(I)+81	HEXGON	
144.	C	GO TO 51	HEXGON	51
145.	C	CARBON ATOM(I) IS OF TYPE C=C-C(I)=0	HEXGON	

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146.	460	MOLWT(KC)=MOLWT(KC)-460	HEIGON	
147.		GO TO 51	HEIGON	51
148.	C	CARBON ATOM IS OF TYPE C=C(=)-C=N	HEIGON	
149.	460	MOLWT(KC)=MOLWT(KC)-110	HEIGON	
150.		GO TO 51	HEIGON	51
151.	C	CARBON ATOM IS OF TYPE N=C=N	HEIGON	
152.	47	MOLWT(KC)=MOLWT(KC)-9	HEIGON	
153.		GO TO 51	HEIGON	51
154.	C	NITROGEN ATOM IS OF TYPE C=C-N=C	HEIGON	
155.	470	MOLWT(KC)=MOLWT(KC)-3	HEIGON	
156.		GO TO 51	HEIGON	51
157.	C	NITROGEN ATOM(=) IS OF TYPE N=C-N(=)C	HEIGON	
158.	48	MOLWT(KC)=MOLWT(KC)-877	HEIGON	
159.		GO TO 51	HEIGON	51
160.	C	CARBON ATOM IS OF TYPE C=C-C	HEIGON	52
161.	49	MOLWT(KC)=MOLWT(KC)-998	HEIGON	
162.	C	SET IDENTIFIER	HEIGON	
163.	91	MPIX(KC)=JK	HEIGON	
164.		53 CONTINUE	HEIGON	
165.	C	ZERO OUT LOCATION IN NONARD ARRAY CORRESPONDING TO RING JJ.	HEIGON	
166.		NONARD(JJ)=0	HEIGON	
167.	59	CONTINUE	HEIGON	
168.	CS.	GO TO 69 IF AFOREMENTIONED FUSED RING SYSTEMS ARE NOT PRESENT.	HEIGON	
169.		IF(ICZ.EQ.0)GO TO 69	HEIGON	69
170.		JK=0	HEIGON	
171.	CS.	CORRECT WEIGHT OF RING ATOMS IN BENZENE OR PYRIDINE-LIKE	HEIGON	
172.	C	STRUCTURES WHICH FORM PART OF A FUSED RING SET.	HEIGON	
173.	C	FIND ATOMS INVOLVED IN Z AND Z1 GROUP BOND TYPES AND CORRECT	HEIGON	
174.	C	THE GROUP WEIGHTS OF THESE ATOMS ACCORDINGLY.	HEIGON	
175.		DO68 I=1,ICZ	HEIGON	
176.		JK=JK+1	HEIGON	
177.		I=ICZM(I)	HEIGON	
178.		IF=HOKOP(I*1)	HEIGON	
179.	C	COMPUTE FREQUENCY OF OCCURRENCE OF EACH RING COMPONENT IN	HEIGON	
180.	C	EACH RING FOR ALL RINGS IN FUSED RING SYSTEM II (OR I).	HEIGON	
181.		DO57 J=1,JF	HEIGON	
182.		JJ=KOMB(J,I)	HEIGON	
183.		DO57 K=2,7	HEIGON	
184.		KC=IANG(JJ,K)	HEIGON	
185.		MPIX(KC)=MPIX(KC)+1	HEIGON	
186.		57 CONTINUE	HEIGON	
187.	C	IS RING COMPONENT OF Z, Z1, OR NIZ12 TYPE	HEIGON	
188.		DO67 KC=1,KCC	HEIGON	
189.		IF(MPIX(KC)-1)67,60,59	HEIGON	59 60 67
190.	C	RING COMPONENT IS OF Z1 TYPE. RESET WEIGHT OF ATOM AND	HEIGON	
191.	C	SET ITS IDENTIFIER EQUAL TO -1000.	HEIGON	
192.	59	MOLWT(KC)=999	HEIGON	
193.		MPIX(KC)=-1000	HEIGON	
194.		GO TO 67	HEIGON	67
195.	C	RING COMPONENT IS OF Z OR NIZ12 TYPE. REDUCE WEIGHT OF ATOM	HEIGON	
196.	C	AND SET ITS IDENTIFIER EQUAL TO JK.	HEIGON	
197.	60	RFLAG=KOMB(KC)	HEIGON	
198.		GO TO(61,61,62,620,63,630,64,625)RFLAG	HEIGON	61 62 620 625 63 630 64 65
199.	C	CARBON ATOM(=) IS OF TYPE C=C(=)-N	HEIGON	
200.	61	MOLWT(KC)=MOLWT(KC)-934	HEIGON	
201.		GO TO 66	HEIGON	66
202.	C	CARBON ATOM(=) IS OF TYPE N=C-C(=)N	HEIGON	
203.	62	MOLWT(KC)=MOLWT(KC)-921	HEIGON	
204.		GO TO 66	HEIGON	66
205.	C	CARBON ATOM(=) IS OF TYPE C=C-C(=)N	HEIGON	
206.	620	MOLWT(KC)=MOLWT(KC)-460	HEIGON	
207.		GO TO 66	HEIGON	66
208.	C	CARBON ATOM IS OF TYPE C=C(=)-C=N	HEIGON	
209.	625	MOLWT(KC)=MOLWT(KC)-110	HEIGON	
210.		GO TO 66	HEIGON	66
211.	C	CARBON ATOM IS OF TYPE N=C=N	HEIGON	
212.	63	MOLWT(KC)=MOLWT(KC)-9	HEIGON	
213.		GO TO 66	HEIGON	66

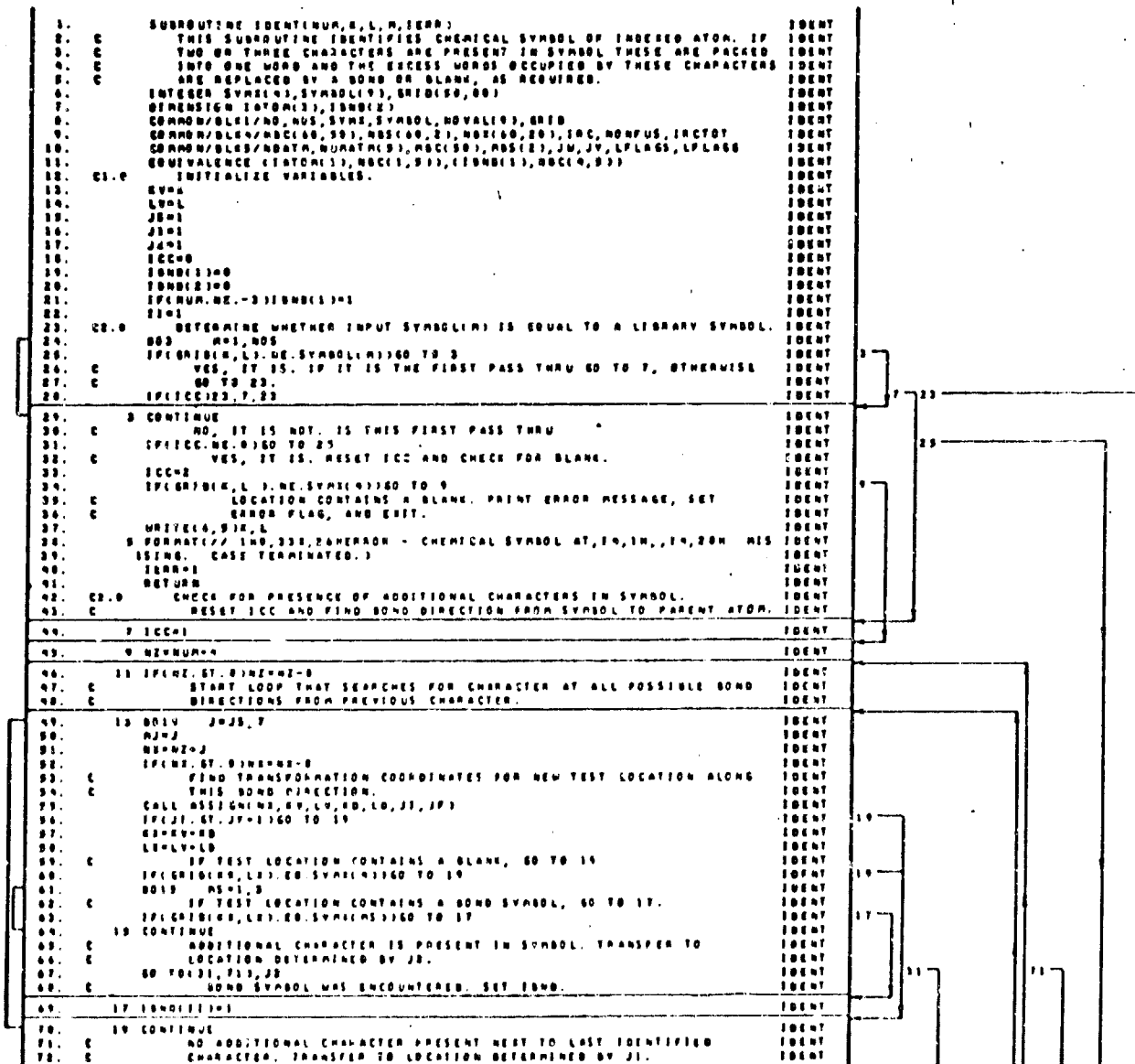
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214.	C	NITROGEN ATOM IS OF TYPE C=C-N=C	HEXGON	
215.		630 MOLWT(C)=MOLWT(C)*3	HEXGON	
216.		80 TO 80	HEXGON	
217.	C	NITROGEN ATOM=1 IS OF TYPE N=C-N=C+1=C	HEXGON	86
218.		64 MOLWT(C)=MOLWT(C)*877	HEXGON	
219.		80 TO 80	HEXGON	
220.	C	CARBON ATOM IS OF TYPE C=C-C	HEXGON	86
221.		68 MOLWT(C)=MOLWT(C)*992	HEXGON	
222.	C	SET IDENTIFIER.	HEXGON	
223.		66 MFI(XC)=J	HEXGON	
224.		87 CONTINUE	HEXGON	
225.		88 CONTINUE	HEXGON	
226.	C	APPLY WEIGHT CORRECTION TO NON-RING CORE ATOMS BONDED TO RING	HEXGON	
227.	C	AND RECORD NON-RING HEAVY ATOMS BONDED TO RING.	HEXGON	
228.		59 JOR=0	HEXGON	
229.		8000 KC=1,KCC	HEXGON	
230.	C	SEARCH FOR RING ATOMS.	HEXGON	
231.		IF(MF(XC).EQ.0)GO TO 89	HEXGON	89
232.	C	KC IS RING ATOM.	HEXGON	
233.		IF(MF(XC).LE.-1000)GO TO 89	HEXGON	89
234.	C	KC IS A 2 TYPE ATOM IN A FUSED OR NONFUSED RING SYSTEM.	HEXGON	89
235.		IF(XC(4,1).LE.-1000)GO TO 89	HEXGON	89
236.	C	NON-RING LIGAND BONDED TO GROUP KC IS A HEAVY ATOM. NOW	HEXGON	
237.	C	DETERMINE WHETHER IT IS A CORE ATOM AND PERFORM	HEXGON	
238.	C	APPROPRIATE OPERATIONS.	HEXGON	
239.		JR=MFI(XC)	HEXGON	
240.		8075 J=0	HEXGON	
241.	C	IF HEAVY LIGAND IS NOT CORE ATOM GO TO 71. OTHERWISE	HEXGON	
242.	C	CONTINUE.	HEXGON	
243.		IF(XC(J,4).EQ.0)GO TO 71	HEXGON	71
244.		IF(XC(J,6)	HEXGON	
245.		IF(MF(XC).EQ.JR.OR.MF(XC).EQ.-1000)GO TO 73	HEXGON	73
246.	C	APPLY WEIGHT CORRECTION TO LIGAND AT BONDED TO RING ATOM KC	HEXGON	
247.		IF(MF(XC).EQ.0)GO TO 71	HEXGON	71
248.		MULTEXT=MOLWT(C)*3	HEXGON	
249.		GO TO 71	HEXGON	71
250.		70 MOLWT(C)=MOLWT(C)*877	HEXGON	
251.	C	STORE CORE ATOM TO WHICH HEAVY LIGAND IS BONDED IN JBOND.	HEXGON	
252.		71 JOR=JOR+1	HEXGON	
253.		JBOND=JORB	HEXGON	
254.		73 CONTINUE	HEXGON	
255.		89 CONTINUE	HEXGON	
256.	C	PRINT OUT COMPOSITION OF MOLECULE, ASSIGNED WEIGHTS OF GROUPS,	HEXGON	
257.	C	AND IS READY. (IF THIS SUBROUTINE IS NOT ACTIVATED, THIS PRINT-	HEXGON	
258.	C	OUT OCCURS IN SUBROUTINE CORCIS).	HEXGON	
259.		CALL PRINT1	HEXGON	
260.	C	SEARCH AND CORRECT FOR ORTHO AND PARA GROUPS.	HEXGON	
261.		IF(JOR.LE.1)RETURN	HEXGON	
262.		80128 J=1,JOR	HEXGON	
263.		IF(J=1)	HEXGON	
264.	C	IF NO MORE ATOMS ARE AVAILABLE TO TEST, EXIT FROM SUBROUTINE.	HEXGON	
265.		IF(XC(J,1).EQ.0)GO TO 129	HEXGON	129
266.	C	K1 IS A CORE ATOM BONDED TO HEAVY NON-RING ATOM.	HEXGON	
267.		K1=JBOND(J)	HEXGON	
268.	C	TEST K1 AGAINST REMAINING CORE ATOMS, STARTING WITH K1.	HEXGON	
269.		80120 K=1,JOR	HEXGON	
270.	C	ATOM K2 IS ANOTHER RING CORE ATOM BONDED TO HEAVY NON-RING	HEXGON	
271.	C	ATOM.	HEXGON	
272.		K2=JBOND(K)	HEXGON	
273.		IF(MF(XC).NE.MF(XC))GO TO 120	HEXGON	120
274.	C	K1 AND K2 ARE IN THE SAME RING SYSTEM. NOW DETERMINE IF	HEXGON	
275.	C	THEY ARE ORTHO TO EACH OTHER.	HEXGON	
276.		80120 L=2,0	HEXGON	
277.		IF(XC(L,4).EQ.K2)GO TO 102	HEXGON	102
278.	C	100 CONTINUE	HEXGON	
279.	C	K1 AND K2 ARE NOT ORTHO.	HEXGON	
280.		80 TO 120	HEXGON	120
281.	C	K1 AND K2 ARE ORTHO. ADD CORRECTIONS TO THERMODYNAMIC	HEXGON	
282.	C	PROPERTIES AND STORE PERTINENT OUTPUT DATA.	HEXGON	
283.		102 NRING=NRING+80RTM(L)	HEXGON	

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284.		SRING=SRING+DORTH0(Z)	HEXGON
285.		DO109 KK=1,4	HEXGON
286.		CPSYM(KK)=CPSYM(KK)+DORTH0(KK+2)	HEXGON
287.	104	CONTINUE	HEXGON
288.		IORTH0=IORTH0+1	HEXGON
289.		IGS=IGS+1	HEXGON
290.		KTGAUS(IGS)=R	HEXGON
291.		KCGAUS(1,IGS)=R1	HEXGON
292.		KCGAUS(2,IGS)=R2	HEXGON
293.	120	CONTINUE	HEXGON
294.	122	CONTINUE	HEXGON
295.	C10	SEARCH AND CORRECT FOR HEAVY GROUPS BONDED TO RING AND WHICH	HEXGON
296.	C	ARE ORTHO OR PARA TO NITROGEN ATOM IN PYRIDINE-LIKE STRUCTURES.	HEXGON
297.	C	THIS CORRECTION APPLIES ONLY TO RINGS CONTAINING ONLY ONE	HEXGON
298.	C	NITROGEN ATOM.	HEXGON
299.	125	DO139 KC=1,KCC	HEXGON
300.		IF(KRCNOR(KC).EQ.0)GO TO 139	HEXGON
301.	C	GROUP ATOM KC CONTAINED IN PYRIDINE-LIKE STRUCTURE. NOW	HEXGON
302.	C	DETERMINE WHETHER KC IS BONDED TO HEAVY NON-RING ATOM.	HEXGON
303.		DO137 J=1,JOR	HEXGON
304.		IF(KC.NE.JBOND(J))GO TO 137	HEXGON
305.	C	YES, KC IS BONDED TO HEAVY NON-RING ATOM. ADD CORRECTION	HEXGON
306.	C	FOR THE HEAT OF FORMATION AND SCORE PERTINENT OUTPUT DATA.	HEXGON
307.		HRING=HRING+DORPAR	HEXGON
308.		IORPAR=IORPAR+1	HEXGON
309.		IGS=IGS+1	HEXGON
310.		IF(KRCNOR(KC).LT.0)GO TO 131	HEXGON
311.	C	HEAVY ATOM IS ORTHO TO NITROGEN ATOM.	HEXGON
312.		KTGAUS(IGS)=2	HEXGON
313.		KCGAUS(1,IGS)=KRCNOR(KC)	HEXGON
314.		KCGAUS(2,IGS)=JBOND(J)	HEXGON
315.		GO TO 137	HEXGON
316.	C	HEAVY ATOM IS PARA TO NITROGEN ATOM.	HEXGON
317.	131	KTGAUS(IGS)=3	HEXGON
318.		KCGAUS(1,IGS)=IABS(KRCNOR(KC))	HEXGON
319.		KCGAUS(2,IGS)=JBOND(J)	HEXGON
320.	137	CONTINUE	HEXGON
321.	139	CONTINUE	HEXGON
322.		RETURN	HEXGON
323.		END	HEXGON

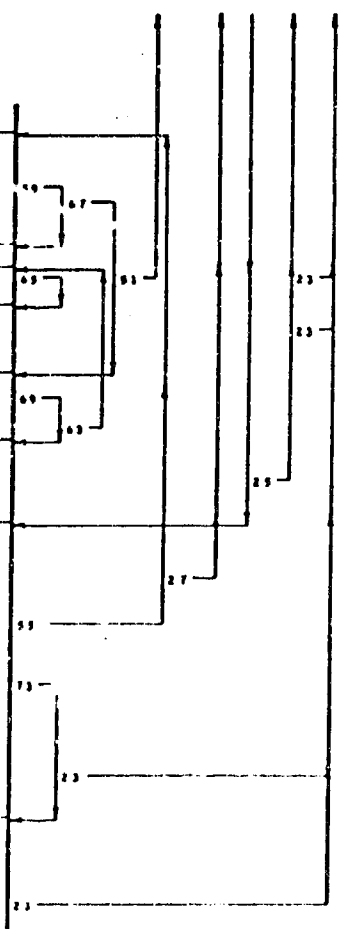
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73.	GO TO(21,35,37),J1	IDENT	21	35	37	
74.	C IF FIRST SYMBOL WAS NOT A LIBRARY SYMBOL(LCCV2), GO TO 25.	IDENT				25
75.	21 IFLICC.EQ.2162 TO 29	IDENT				
76.	C3.0 SYMBOL HAS BEEN IDENTIFIED. SUM ATOMS IN SYMBOL N INTO NUMATN	IDENT				
77.	C AND EXIT.	IDENT				
78.	23 KPP=1	IDENT				
79.	CALL SUMATRN,CP,DURAT-1)	IDENT				
80.	RETURN	IDENT				
81.	C SET ERROR FLAG.	IDENT				
82.	25 IARR=1	IDENT				
83.	C PRINT SPACE MESSAGE AND EXIT.	IDENT				
84.	27 WRITE(6,29)	IDENT				
85.	29 FORMAT(1MO,1SD,5NHERRON - INCORRECT SPECIES DESIGNATION. CASE YER	IDENT				
86.	INITATED.7	IDENT				
87.	RETURN	IDENT				
88.	C4.0 SYMBOL CONTAINS AT LEAST TWO AND POSSIBLY THREE CHARACTERS.	IDENT				
89.	C SEARCH FOR THIRD CHARACTER Z IN SYMBOL ZAY WHERE X, LOCATED	IDENT				
90.	C AT H,L, IS FIRST CHARACTER OF SYMBOL IDENTIFIED.	IDENT				
91.	C STORE FIRST CHARACTER IN IATON(1) AND SECOND CHARACTER	IDENT				
92.	C IN IATOP(2).	IDENT				
93.	31 IATON(1)=GRICIG, L1	IDENT				
94.	IATON(2)=GRICIG, L2)	IDENT				
95.	C STORE AND SET PERTINENT VARIABLES AND RETURN TO SEARCH FOR	IDENT				
96.	C THIRD CHARACTER.	IDENT				
97.	KZ=KZ	IDENT				
98.	LK2=L2	IDENT				
99.	KOZ=K2	IDENT				
100.	LOZ=L2	IDENT				
101.	NS=KZ	IDENT				
102.	JZ=Z	IDENT				
103.	JZ=KZ-1	IDENT				
104.	IF(JZ.EQ.7)GO TO 35	IDENT	35			
105.	JZ=Z	IDENT				
106.	ICT=1	IDENT				
107.	GO TO 11	IDENT				
108.	C5.0 SYMBOL IS NOT ZAY. NOW SEARCH FOR THIRD CHARACTER Z IN SYMBOL	IDENT				
109.	C ZWZ WHERE Z IS LOCATED AT H,L.	IDENT				
110.	C STORE AND SET PERTINENT VARIABLES AND RETURN TO SEARCH FOR	IDENT				
111.	C THIRD CHARACTER.	IDENT				
112.	35 JS=1	IDENT				
113.	KV=KZ	IDENT				
114.	LV=LZ	IDENT				
115.	LV=LZ	IDENT				
116.	JS=2	IDENT				
117.	KV=KZ-1	IDENT				
118.	ZV=Z	IDENT				
119.	GO TO 11	IDENT				
120.	C6.0 SYMBOL COMPOSED OF TWO CHARACTERS. IDENTIFY SYMBOL AND PACK	IDENT				
121.	C THE TWO CHARACTERS INTO ONE WORD.	IDENT				
122.	C IDENTIFY SYMBOL.	IDENT				
123.	37 CALL MULTICATOP,2,R,IARR)	IDENT				
124.	IF(LICAR.EQ.1)GO TO 27	IDENT				
125.	C IF THIS IS FIRST SYMBOL OF MOLECULE TO BE IDENTIFIED, GO TO	IDENT	27			
126.	C 39.	IDENT				
127.	IPINUM.EQ.-3)GO TO 39	IDENT				
128.	C IF BOND IS ATTACHED TO CHARACTER 1, GO TO 51.	IDENT	39			
129.	IF(IIBND(1).EQ.1)GO TO 51	IDENT				
130.	C CASE 1 - PACK TWO CHARACTERS INTO ONE WORD.	IDENT				
131.	39 C101=Z2,L22=SYMBOL(1)	IDENT				
132.	C1010=L1+SYMBOL(1)	IDENT				
133.	K=KZ	IDENT				
134.	L=LZ	IDENT				
135.	NUM=NS	IDENT				
136.	GO TO 23	IDENT				
137.	C CASE 2 - PACK TWO CHARACTERS INTO ONE WORD.	IDENT				
138.	31 ICT=0	IDENT				
139.	Z=KZ	IDENT				
140.	L=LZ	IDENT				
141.	K=KZ	IDENT				
142.	L=LZ	IDENT				
143.	C7.0 FINAL SETTINGS FOR TWO OR THREE CHARACTER CASES. STORE SYMBOL	IDENT				

146.	C	AT R, L.	IDENT
145.		58 GRID(R, L)=SYMBOL(R)	IDENT
146.		58=58+50	IDENT
147.		L2=L2+50	IDENT
148.		IF(NE, L2, 1.00, 52, 57, 50) GO TO 59	IDENT
149.		IF(LE, 52, 1.00, 52, 50) GO TO 67	IDENT
150.	C	EXTENSION COORDINATE OUTSIDE GRID BOUNDARY. STORE BLANK IN	IDENT
151.	C	GRID(R, L) AND TRANSFER TO LOCATION DETERMINED BY ICT.	IDENT
152.		59 GRID(R, L)=SYMBOL(R)	IDENT
153.		63 IPICT=1323, 59, 69	IDENT
154.	C	SYMBOL OF TYPE 59. SET LOCATION CONTAINING CHARACTER V.	IDENT
155.		65 GRID(R2, L2)=GRID(R, L)	IDENT
156.		GO TO 83	IDENT
157.	C	RESET THE LAST CHARACTER IDENTIFIED WHEN TWO OR THREE	IDENT
158.	C	CHARACTERS ARE PRESENT IN SYMBOL.	IDENT
159.		67 50=50	IDENT
160.		IF(NE, R2, L2, 1.00, 59, 59) GO TO 69	IDENT
161.		GRID(R2, L2)=GRID(R, L)	IDENT
162.		GO TO 63	IDENT
163.		69 CONTINUE	IDENT
164.	C	NO MATCH OBTAINED. ERROR EXIT.	IDENT
165.		GO TO 25	IDENT
166.	C	SYMBOL COMPOSED OF THREE CHARACTERS IDENTIFY SYMBOL AND	IDENT
167.	C	PACK THE THREE CHARACTERS INTO ONE WORD.	IDENT
168.		71 IATOR(3)=GRID(R, L)	IDENT
169.	C	IDENTIFY SYMBOL.	IDENT
170.		CALL MULTIPLY(3, R, IATOR)	IDENT
171.		IF(NE, 57, 0) GO TO 27	IDENT
172.	C	IF BOND IS ATTACHED TO CHARACTER 1, GO TO 55. OTHERWISE STORE	IDENT
173.	C	A BLANK IN R, L.	IDENT
174.		IF(1=NO) 55, 50, 1) GO TO 55	IDENT
175.		GRID(R, L)=SYMBOL(R)	IDENT
176.	C	BOND IS ATTACHED TO CHARACTER 2. REDEFINE REMAINING	IDENT
177.	C	CHARACTERS AND EXIT.	IDENT
178.		IF(1=NO) 55, 50, 2) GO TO 73	IDENT
179.		GRID(R2, L2)=SYMBOL(R)	IDENT
180.		GRID(R, L)=SYMBOL(R)	IDENT
181.		5=52	IDENT
182.		5=52	IDENT
183.		NUM=5	IDENT
184.		GO TO 23	IDENT
185.	C	BOND IS NOT ATTACHED TO CHARACTER 2. REDEFINE REMAINING	IDENT
186.	C	CHARACTERS AND EXIT.	IDENT
187.		73 GRID(R2, L2)=SYMBOL(R)	IDENT
188.		GRID(R2, L2)=SYMBOL(R)	IDENT
189.		5=52	IDENT
190.		5=52	IDENT
191.		NUM=5	IDENT
192.		GO TO 23	IDENT
193.		END	IDENT



INTROT

```

1      SUBROUTINE INTROT(IGS,INR,ROTINS)
2.    C0.0  THIS SUBROUTINE DETERMINES WHICH CARBON ATOMS (IF ANY) HAVE
3.    C      THREEFOLD INTERNAL ROTATIONAL SYMMETRY AND HAVE NOT BEEN
4.    C      INCLUDED IN THE EXTERNAL ROTATIONAL SYMMETRY CONTRIBUTIONS.
5.    C      IT ALSO DETERMINES THE PRESENCE OF STRUCTURES WITH TWOFOLD
6.    C      INTERNAL ROTATIONAL SYMMETRY SUCH AS NO2 GROUPS AND CERTAIN
7.    C      MONOCYCLIC AROMATIC RINGS. IF ANY OF THESE ARE PRESENT, THE
8.    C      TOTAL INTERNAL ROTATION CONTRIBUTION TO THE ENTROPY IS COMPUTED
9.    C      INTEGER SYM(4),SYMBOL(9),GRID(50,80)
10.   C      INTEGER WEIGHT(9)
11.   C      DIMENSION IKC(100),KINT(100),NTOTAL(3,150),KCGAUS(3,100),
12.   C      IOATCIS(2,150),KTGAUS(150)
13.   C      COMMON/BLK1/NO,NOS,SYM,SYMBOL,NOVAL(9),GRID
14.   C      COMMON/BLK2/WEIGHT,NGT(9),MOLWT(100),IX(100,5,4),NC(100),KCC
15.   C      COMMON/BLK3/RING(40,30),IMATX(50,80),NM(100),IRC(100),KOW(100),
16.   C      IDBR(100),IB(100,8),IRG,NBR
17.   C      EQUIVALENCE (IKC(1),GRID(1,79)),(INTMIN,GRID(4,76)),(KINT(1),
18.   C      IGRD(5,76)),(NTOTAL(1,1),GRID(4,70)),(KCGAUS(1,1),IMATX(1,72)),
19.   C      2(DATCIS(1,1),IMATX(1,66)),(KTGAUS(1),IMATX(1,60))
20.   C1.0  INITIALIZE VARIABLES.
21.   C      INR=0
22.   C      ROTINS=0.0
23.   C      KS=IGS
24.   C2.0  DETERMINE IF THERE ARE CARBON ATOMS WITH A CONNECTIVITY OF FOUR
25.   C      AND THREEFOLD-ROTATIONAL SYMMETRY. IF SO, STORE GROUP NUMBER
26.   C      OF ATOM.
27.   C      DO2 K=1,KCC
28.   C      IF(IX(K,1).NE.2.0R.KON(K).NE.4.0R.NTOTAL(1,K).NE.3)GO TO 2
29.   C      INR=INR+1
30.   C      IGS=IGS+1
31.   C      KCGAUS(1,IGS)=K
32.   C      IMATX(1,66)=4
33.   C      DATCIS(2,IGS)=-2.0323
34.   C2  CONTINUE
35.   C      IF(INR.EQ.0.0R.INTMIN.EQ.0)GO TO 10
36.   C3.0  AFOREMENTIONED CARBON ATOMS ARE PRESENT AND SYMMETRY OF SOME OF
37.   C      THESE ATOMS HAS BEEN INCLUDED IN THE EXTERNAL ROTATIONAL
38.   C      SYMMETRY. FIND THESE ATOMS AND DISCARD THEM.
39.   C      M=KS
40.   C      DO4 K=1,INR
41.   C      M=M+1
42.   C      4 IKC(K)=KCGAUS(1,M)
43.   C      LL=0
44.   C      M=KS
45.   C      DO8 K=1,INR
46.   C      DO4 L=1,INTMIN
47.   C      IF(IX(K).EQ.KINT(L))GO TO 8
48.   C      6 CONTINUE
49.   C      LL=LL+1
50.   C      M=M+1
51.   C      KCGAUS(1,M)=IKC(K)
52.   C      8 CONTINUE
53.   C      INR=LL
54.   C      IGS=KS+INR
55.   C4.0  DETERMINE IF THERE ARE STRUCTURES WITH TWOFOLD INTERNAL
56.   C      ROTATIONAL SYMMETRY.
57.   C10  CALL CTWO(IGS,INR)
58.   C      IF(INR.FO.0)RETURN
59.   C5.0  COMPUTE TOTAL INTERNAL ROTATIONAL CONTRIBUTION.
60.   C      M=KS
61.   C      DO24 K=1,INR
62.   C      M=M+1
63.   C      ROTINS=ROTINS+DATCIS(2,M)
64.   C26  CONTINUE
65.   C      RETURN
66.   C      END

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74.	25	IF(JRING(J,1),LT,JRING(R,1),OR,JADIF(J),NE,0)GO TO 90	LESSEN	
75.	C	SET ISET.	LESSEN	
76.	27	D031 M=2,MP	LESSEN	
77.		ISET(K)=0	LESSEN	
78.	31	CONTINUE	LESSEN	
79.		IF(JOT,EQ,0)GO TO 95	LESSEN	
80.	C	TEST RING(S) EXIST THAT ARE COMPLETELY CONTAINED IN REFERENCE	LESSEN	95
81.	C	RING K. DETERMINE IF RING R IS TO BE DELETED.	LESSEN	
82.		RR=0	LESSEN	
83.	C	FIND RING NUMBERS IN JRING THAT INVOLVE TEST RINGS AND	LESSEN	
84.	C	ARE CONTAINED IN REFERENCE RING K.	LESSEN	
85.		D037 I=1,JOT	LESSEN	
86.	32	RR=RR+1	LESSEN	
87.		IF(JRDIF(RK),NE,0)GO TO 32	LESSEN	32
88.		LP=JRING(RK,1)*1	LESSEN	
89.	C	SET ISET=-1 FOR THOSE LOCATIONS IN THE REFERENCE RING IN	LESSEN	
90.	C	WHICH THE RING ATOM IS EQUAL TO A RING ATOM IN THE TEST	LESSEN	
91.	C	RING SET.	LESSEN	
92.		D033 L=2,LP	LESSEN	
93.		LX=JRING(RK,L)	LESSEN	
94.		ISET(LX)=-1	LESSEN	
95.	33	CONTINUE	LESSEN	
96.	37	CONTINUE	LESSEN	
97.	C	ARE ALL LOCATIONS IN ISET=-1. IF NOT, GO TO 49.	LESSEN	
98.		D041 M=2,MP	LESSEN	
99.		IF(ISET(M),EQ,0)GO TO 49	LESSEN	49
100.		41 CONTINUE	LESSEN	
101.	C	YES. REFERENCE RING K IS NOT A BASIC RING. DELETE RING K.	LESSEN	
102.		43 INC=INC-1	LESSEN	
103.		RR=RR-1	LESSEN	
104.		KR=RR+K	LESSEN	
105.		GO TO 90	LESSEN	
106.	45	IF(JDL,LE,1)GO TO 90	LESSEN	90
107.	C	TEST RINGS EXIST THAT ARE CONTAINED IN PART IN REFERENCE	LESSEN	90
108.	C	RING R. DETERMINE IF RING R IS TO BE DELETED.	LESSEN	
109.		RR=0	LESSEN	
110.	C	FIND RING NUMBERS OF JRING SET THAT INVOLVE TEST RINGS AND	LESSEN	
111.	C	STORE IN JRC TOGETHER WITH INCOMPATIBILITY FACTOR.	LESSEN	
112.		48 I=1,JDL	LESSEN	
113.	46	RR=RR+1	LESSEN	46
114.		IF(JADIF(RK),EQ,0)GO TO 46	LESSEN	
115.		JAC(1,1)=JADIF(RK)	LESSEN	
116.		JAC(1,2)=RK	LESSEN	
117.		48 CONTINUE	LESSEN	
118.	C	ARRANGE THE INCOMPATIBILITY FACTORS IN INCREASING NUMERICAL	LESSEN	
119.	C	ORDER IN TERMS OF THEIR SUBSCRIPTS AND STORE THE RESULTING	LESSEN	
120.	C	ORDER OF THE SUBSCRIPTS IN ARRAY IORD.	LESSEN	
121.		CALL ORDER(JDL,IORD,JRC)	LESSEN	
122.		I1=JDL*1	LESSEN	
123.	C	DETERMINE WHICH SETS OF TEST RINGS HAVE SAME CONSTITUENTS	LESSEN	
124.	C	MISSING FROM REFERENCE RING R.	LESSEN	
125.		D074 I=2,JDL	LESSEN	
126.		I1=I1-1	LESSEN	
127.		K1=IORD(I1)	LESSEN	
128.		R2=JRC(K1,2)	LESSEN	
129.		MP=JRING(R2,1)*1	LESSEN	
130.		JR=0	LESSEN	
131.		JF=I1-1	LESSEN	
132.	C	ARE ALL THE MISSING COMPONENTS OF TEST RING J2 INCLUDED	LESSEN	
133.	C	IN THE LIST OF TEST RING R2.	LESSEN	
134.		D080 I=1,JP	LESSEN	
135.		JJ=IORD(I)	LESSEN	
136.		J1=JRC(JJ,2)	LESSEN	
137.		LP=JRING(J2,1)*1	LESSEN	
138.		D096 L=2,LP	LESSEN	
139.		IF(JRING(J2,L),GT,0)GO TO 96	LESSEN	96
140.		D054 M=2,MP	LESSEN	
141.		IF(JRING(R2,MP),GT,0)GO TO 84	LESSEN	96
142.		IF(JRING(R2,MP),EQ,JRING(J2,L))GO TO 96	LESSEN	96
143.	84	CONTINUE	LESSEN	
144.		GO TO 90	LESSEN	90

145.	56 CONTINUE	LESSEN
146.	C VAS THEY ARE. SET RSTORE.	LESSEN
147.	J=J+1	LESSEN
148.	RSTORE(J)=J2	LESSEN
149.	58 CONTINUE	LESSEN
150.	IF(JE-1)74,68,62	LESSEN
151.	60 IF(JADIF(J2),NE,JADIF(R2))GO TO 74	LESSEN
152.	C TEST RINGS TEST THAT HAVE ALL OR SOME OF THE SAME	LESSEN
153.	C CONSTITUENTS AS TEST RING KE MISSING FROM REFERENCE	LESSEN
154.	C RING R.	LESSEN
155.	62 J=J+1	LESSEN
156.	RSTORE(J)=R2	LESSEN
157.	C SET ISETR.	LESSEN
158.	DO44 M=2,MF	LESSEN
159.	ISETR(M)=ISETR(M)	LESSEN
160.	64 CONTINUE	LESSEN
161.	C SET ISETR=-1 FOR THOSE LOCATIONS IN THE REFERENCE RING	LESSEN
162.	C IN WHICH THE RING ATOM IS EQUAL TO A RING ATOM IN THE	LESSEN
163.	C (PARTIAL) TEST RING SET JUST DEFINED.	LESSEN
164.	DO60 J=1,JR	LESSEN
165.	JJ=RSTORE(J)	LESSEN
166.	LF=JRING(JJ,1)-1	LESSEN
167.	DO66 L=2,LF	LESSEN
168.	LI=JRING(JJ,L)	LESSEN
169.	IF(LI.LT.0)GO TO 66	LESSEN
170.	ISETR(LI)=-1	LESSEN
171.	66 CONTINUE	LESSEN
172.	68 CONTINUE	LESSEN
173.	C IF ALL ISETR LOCATIONS =-1, REFERENCE RING R SHALL BE	LESSEN
174.	C DELETED. OTHERWISE, CONTINUE WITH TEST.	LESSEN
175.	DO70 M=2,MF	LESSEN
176.	IF(ISETR(M).EQ.0)GO TO 74	LESSEN
177.	70 CONTINUE	LESSEN
178.	GO TO 43	LESSEN
179.	74 CONTINUE	LESSEN
180.	52 CONTINUE	LESSEN
181.	IF(ERCI.EQ.1)CIPETURN	LESSEN
182.	C4.0 THIS SECTION DELETES THE RINGS THAT ARE EQUAL OR COMPOSITES.	LESSEN
183.	RORDE(1)=1	LESSEN
184.	C DETERMINE THE ORDER THE SUBSCRIPTS OF THE RING NUMBERS IN	LESSEN
185.	C RRRK WOULD HAVE IF THE RING NUMBERS WERE ARRANGED IN	LESSEN
186.	C NUMERICAL ORDER.	LESSEN
187.	IF(ER.CT.1)CALL ORDER(RR,RORR,RREN)	LESSEN
188.	J=0	LESSEN
189.	RR=1	LESSEN
190.	RR=RORR(RR)	LESSEN
191.	C FIND RING NUMBER (J) CONTAINED IN RRR. SET JSTOP.	LESSEN
192.	DO J=1	LESSEN
193.	IF(J.NE.RREN(RR))GO TO 80	LESSEN
194.	JSTOP=J	LESSEN
195.	C INCREMENT J	LESSEN
196.	82 J=J+1	LESSEN
197.	C IF J EXCEEDS INITIAL NUMBER OF RINGS, EXIT.	LESSEN
198.	IF(J.GT.1)CINCRETURN	LESSEN
199.	85 IF(J-EREN(RR))184,82,83	LESSEN
200.	C FIND NEW VALUE OF RR.	LESSEN
201.	83 RR=RR+1	LESSEN
202.	IF(RR.GT.RR)GO TO 84	LESSEN
203.	RR=RORR(RR)	LESSEN
204.	GO TO 85	LESSEN
205.	C TRANSFER DATA FROM RING J TO RING JSTOP.	LESSEN
206.	84 LF=TRING(J,1)-1	LESSEN
207.	DO86 L=1,LF	LESSEN
208.	TRING(JSTOP,L)=TRING(J,L)	LESSEN
209.	86 CONTINUE	LESSEN
210.	NALOC(JSTOP)=NALOC(J)	LESSEN
211.	JSTOP=JSTOP+1	LESSEN
212.	GO TO 82	LESSEN
213.	END	LESSEN

LINEAR

1.		SUBROUTINE LINEAR(KC,KCNEXT,LINE,KSVM)	LINEAR
2.	C	THIS SUBROUTINE ESTABLISHES THE SYMMETRY PROPERTIES OF A	LINEAR
3.	C	PARTICULAR LIGAND (KCNEXT) BONDED TO KC. IT DETERMINES THE	LINEAR
4.	C	LINEARITY AND THE ROTATIONAL SYMMETRY OF THE LIGAND.	LINEAR
5.		INTEGER SYM(4),SYMBOL(9),GRID(9,9)	LINEAR
6.		INTEGER WEIGHT(9)	LINEAR
7.		DIMENSION KCSAME(6,100),NTOTAL(1,100)	LINEAR
8.		COMMON/BLK1/ND,NDS,SYM2,SYMBOL,NDVAL(9),GRID	LINEAR
9.		COMMON/BLK2/WEIGHT,MMGT(9),MOLWT(100),IX(100,5,6),NL(100),KCL	LINEAR
10.		COMMON/BLK3/IRTAG(40,30),IMAT(50,80),NM(100),IBCL(100),KON(100),	LINEAR
11.		LIDBR(100),IR(100,8),IRG,NDBR	LINEAR
12.		COMMON/BLK4/NDATM,NUMATM(5),MBC(50),MBS(2),JW,JY,LFLAGS,LFLAGG	LINEAR
13.		EQUIVALENCE (KCSAME(1,1),GRID(4,42)),(NTOTAL(1,1),GRID(4,70))	LINEAR
14.	C1.0	INITIALIZE VARIABLES.	LINEAR
15.		LINK=0	LINEAR
16.		KSVM=1	LINEAR
17.		K1=KC	LINEAR
18.		K2=KCNEXT	LINEAR
19.		3 IF(IBC(K2) EQ.0)GO TO 19	LINEAR
20.	C2.0	ATOM KCNEXT IS A RING ATOM. SET FLAG AND RETURN	LINEAR
21.		JW=9	LINEAR
22.		RETURN	LINEAR
23.	C3.0	ATOM KCNEXT IS NOT A RING ATOM.	LINEAR
24.		1* IF(IX(K2,1,1) NE.2 AND IX(K2,1,1) NE.4)RETURN	LINEAR
25.	C4.0	ATOM IS EITHER CARBON OR CO. HOW MANY CORE ATOMS ARE BONDED	LINEAR
26.	C	TO LIGAND ATOM	LINEAR
27.		IF(NC(K2)-2)25,35,43	LINEAR
28.	C	ONE CORE ATOM.	LINEAR
29.		25 IF(IX(K2,1,1) NE.2 OR KON(K2) NE.2 OR IX(K2,3,1) GE.8)GO TO 31	LINEAR
30.	C	LIGAND IS CARBON ATOM AND HAS A CONNECTIVITY OF TWO.	LINEAR
31.		29 LINEAR	LINEAR
32.		RETURN	LINEAR
33.	C	IF LIGAND IS CO AND HAS A CONNECTIVITY OF ONE, GO TO 29	LINEAR
34.		31 IF(IX(K2,1,1) EQ.6 AND KON(K2) EQ.1)GO TO 29	LINEAR
35.		IF(NTOTAL(1,K2) NE.KON(K2)-1)RETURN	LINEAR
36.	C	THE NUMBER OF SYMMETRICAL GROUPS BONDED TO THE LIGAND	LINEAR
37.	C	EQUALS ITS CONNECTIVITY MINUS ONE	LINEAR
38.		KSVM=NTOTAL(1,K2)	LINEAR
39.		RETURN	LINEAR
40.	C	TWO CORE ATOMS IF THE CONNECTIVITY OF THE LIGAND EXCEEDS ITS	LINEAR
41.	C	NUMBER OF CORE ATOMS, OR IF THE LIGAND IS CO, RETURN	LINEAR
42.		35 IF(KON(K2) GT.NC(K2) OR IX(K2,1,1) EQ.4)RETURN	LINEAR
43.	C	FIND THE NEXT ATOM DOWN THE CHAIN AND REPEAT TESTS	LINEAR
44.		IF(IX(K2,2,6) NE.K1)GO TO 37	LINEAR
45.		K1=K2	LINEAR
46.		K2=IX(K2,3,6)	LINEAR
47.		GO TO 3	LINEAR
48.		37 K1=K2	LINEAR
49.		K2=IX(K2,2,6)	LINEAR
50.		GO TO 3	LINEAR
51.	C	THREE OR MORE CORE ATOMS	LINEAR
52.		43 KP=NC(K2)-1	LINEAR
53.		IF(KON(K2) NE.NC(K2) OR NTOTAL(1,K2) NE.KP)RETURN	LINEAR
54.	C	LIGAND HAS A CONNECTIVITY EQUAL TO ITS NUMBER OF CORE	LINEAR
55.	C	LIGANDS (NCK(K2)), AND IT HAS NCK(K2) IDENTICAL LIGANDS	LINEAR
56.	C	ARE ANY OF THESE IDENTICAL LIGANDS EQUAL TO THE PREVIOUS	LINEAR
57.	C	ATOM IN THE CHAIN. IF SO, RETURN OTHERWISE, SET SYMMETRY	LINEAR
58.	C	VALUE.	LINEAR
59.		CONT K=1,KP	LINEAR
60.		IF(KCSAME(K,K2) EQ.K1)RETURN	LINEAR
61.		47 CONTINUE	LINEAR
62.		KSVM=NTOTAL(1,K2)	LINEAR
63.		RETURN	LINEAR
64.		END	LINEAR

MAXCHN

1.		SUBROUTINE MAXCHN(LX,NASYMC)	MAXCHN
2.	C	THIS SUBROUTINE FINDS THE LONGEST CHAIN IN THE MOLECULE AND	MAXCHN
3.	C	PRINTS OUT THE GROUP NUMBERS OF THE CORE ATOM CONSTITUENTS OF	MAXCHN
4.	C	THE CHAIN. IF ASYMMETRIC ATOMS ARE PRESENT, IT ALSO DETERMINES	MAXCHN
5.	C	IF ANOTHER CHAIN OF THE SAME (MAXIMUM) LENGTH IS PRESENT WHICH	MAXCHN
6.	C	CONTAINS MORE ASYMMETRIC ATOMS THAN THE FIRST MAXIMUM CHAIN	MAXCHN
7.	C	DETECTED. IF SO, A NEW MAXIMUM CHAIN IS DEFINED.	MAXCHN
8.		DIMENSION IOPATM(100)	MAXCHN
9.		COMMON/BLK3/IRING(40,30),IMATX(50,80),NM(100),IBC(100),KON(100),	MAXCHN
10.		IOBR(100),IB(100,8),IRG,NOBR	MAXCHN
11.		COMMON/BLK4/NBC(60,50),NBS(60,2),NBX(60,20),IRC,NONFUS,IACTOT	MAXCHN
12.		COMMON/BLK5/NDATM,NUMATM(5),MBC(50),MBS(2),JW,JV,LFLAG5,LFLAG6	MAXCHN
13.		EQUIVALENCE (IOPATM(1),IMATX(2,45))	MAXCHN
14.	C1.0	SET VARIABLES.	MAXCHN
15.		KSAME=1	MAXCHN
16.		LV=1	MAXCHN
17.		KMAX=NBS(1,1)	MAXCHN
18.	C2.0	FIND THE LONGEST CHAIN IN THE MOLECULE.	MAXCHN
19.		IF(LX.LE.1)GO TO 12	MAXCHN
20.		DO11 K=P,LX	MAXCHN
21.		IF(NBS(K,1)-KMAX)11,3,7	MAXCHN
22.		1 KSAME=KSAME+1	MAXCHN
23.		GO TO 11	MAXCHN
24.		7 KSAME=1	MAXCHN
25.		KMAX=NBS(K,1)	MAXCHN
26.		LV=K	MAXCHN
27.		11 CONTINUE	MAXCHN
28.		12 LVP=LV	MAXCHN
29.	C3.0	IF ASYMMETRIC ATOMS ARE PRESENT, DETERMINE IF ANOTHER CHAIN OF	MAXCHN
30.	C	THE SAME (MAXIMUM) LENGTH IS PRESENT WHICH CONTAINS MORE	MAXCHN
31.	C	ASYMMETRIC ATOMS. IF SO, UTILIZE THIS ONE AS THE MAXIMUM CHAIN.	MAXCHN
32.		IF(NASYMC.EQ.0.OR.KSAME.EQ.1)GO TO 35	MAXCHN
33.	C	ONE OR MORE ASYMMETRIC ATOMS ARE PRESENT.	MAXCHN
34.		KOPMAX=0	MAXCHN
35.		KI=LV+1	MAXCHN
36.		13 KOP=0	MAXCHN
37.	C	FIND HOW MANY ASYMMETRIC ATOMS (KOP) ARE PRESENT IN MAXIMUM	MAXCHN
38.	C	CHAIN LV.	MAXCHN
39.		DO17 L=1,NASYMC	MAXCHN
40.		DO15 K=1,KMAX	MAXCHN
41.		IF(IOPATM(L).NE.NBC(LV,K))GO TO 15	MAXCHN
42.		KOP=KOP+1	MAXCHN
43.		GO TO 17	MAXCHN
44.		15 CONTINUE	MAXCHN
45.		17 CONTINUE	MAXCHN
46.		IF(KOP.EQ.NASYMC)GO TO 35	MAXCHN
47.	C	KOP IS LESS THAN TOTAL NUMBER OF ASYMMETRIC ATOMS PRESENT.	MAXCHN
48.	C	CONTINUE SEARCH.	MAXCHN
49.		IF(KOP.LE.KOPMAX)GO TO 21	MAXCHN
50.	C	KOP IS GREATER THAN PREVIOUS MAXIMUM NUMBER OF ASYMMETRIC	MAXCHN
51.	C	ATOMS CONTAINED IN CHAIN. DEFINE NEW MAXIMUM CHAIN.	MAXCHN
52.		KOPMAX=KOP	MAXCHN
53.		LVP=LV	MAXCHN
54.		21 IF(KI.GT.LX)GO TO 29	MAXCHN
55.	C	NOT ALL CHAINS HAVE BEEN TESTED. FIND NEW CHAIN TO TEST THAT	MAXCHN
56.	C	CONTAINS A MAXIMUM NUMBER OF CORE ATOM CONSTITUENTS.	MAXCHN
57.		DO25 L=KI,LX	MAXCHN
58.		IF(NBS(L,1).GE.KMAX)GO TO 27	MAXCHN
59.		25 CONTINUE	MAXCHN
60.		GO TO 29	MAXCHN
61.		27 L=VL	MAXCHN
62.		KI=K+1	MAXCHN
63.		GO TO 13	MAXCHN
64.		29 JV=0	MAXCHN
65.	C4.0	STORE GROUP NUMBERS OF LONGEST CHAIN IN MBC. STORE OTHER	MAXCHN
66.	C	PERTINENT CHAIN DATA IN MBL.	MAXCHN
67.		35 DO37 K=1,KMAX	MAXCHN
68.		MBC(K)=NBC(LVP,K)	MAXCHN
69.		MBS(1)=KMAX	MAXCHN
70.		MBS(2)=LVP	MAXCHN

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71.	CS.0	PRINT OUT THE TOTAL NUMBER OF CORE ATOM CONSTITUENTS IN THE	MAXCMM
72.	C	CHAIN AND THEIR GROUP NUMBERS.	MAXCMM
73.		WRITE(6,41)KMAX	MAXCMM
74.	41	FORMAT(/// IN ,20X,42HNUMBER OF CORE ATOMS IN LONGEST CHAIN = ,	MAXCMM
75.		115)	MAXCMM
76.		WRITE(6,45)(MBC(M),M=1,KMAX)	MAXCMM
77.	45	FORMAT(1H0, 7X,55HGROUP NUMBER OF CORE CONSTITUENTS OF LONGEST CHA	MAXCMM
78.		IN = ,10(15,1N,)/(1N ,62X,10(15,1N,))	MAXCMM
79.		RETURN	MAXCMM
80.		END	MAXCMM

MULTI

1.		SUBROUTINE MULTI(IATOM,KNO,M,IERR)	MULTI
2.	C	THIS SUBROUTINE IDENTIFIES MULTI-CHARACTER, MULTI-WORD INPUT	MULTI
3.	C	SYMBOL CONTAINED IN IATOM WITH THE CORRESPONDING MULTI-	MULTI
4.	C	CHARACTER SINGLE WORD PROGRAM LIBRARY SYMBOL.	MULTI
5.		INTEGER SYMBL(3,4)	MULTI
6.		DIMENSION IPIX(4),IATOM(5)	MULTI
7.		COMMON/ALK4/NBC(60,50),NRC(60,2),NOR(60,20),IRC,NOFUS,INCYOT	MULTI
8.		EQUIVALENCE (IPIX(1),NBC(1,6))	MULTI
9.		DATA SYMBL(1,1)/IMC,SYMBL(2,1)/IND,SYMBL(3,1)/INO,	MULTI
10.		ISYMBL(1,2)/IMC,SYMBL(2,2)/IMW,SYMBL(3,2)/IND,SYMBL(1,3)/IMW,	MULTI
11.		ISYMBL(2,3)/IND,SYMBL(3,3)/INO,SYMBL(1,4)/IMW,SYMBL(2,4)/IND,	MULTI
12.		ISYMBL(3,4)/IMW	MULTI
13.	C1.0	INITIALIZE CYCLE THAT SEARCHES OVER ALL MULTI-CHARACTER, MULTI-	MULTI
14.	C	WORD PROGRAM SYMBOLS(SYMBL) WHICH ARE EQUIVALENT TO THE MULTI-	MULTI
15.	C	CHARACTER, SINGLE WORD PROGRAM LIBRARY SYMBOLS(SYMBOL).	MULTI
16.		DO 11 I=1,4	MULTI
17.	C	ZERO IPIX ARRAY.	MULTI
18.		DO 1 J=1,3	MULTI
19.		IPIX(J)=0	MULTI
20.		JC=1	MULTI
21.	C	COMPARE EACH ELEMENT OF INPUT SYMBL(I) AGAINST EACH ELEMENT	MULTI
22.	C	OF LIBRARY SYMBOL(K). IS MATCH OBTAINED	MULTI
23.		DOV L=1,KNO	MULTI
24.		KI=1	MULTI
25.	2	DO 3 K=KI,KNO	MULTI
26.		IF(IATOM(I).EQ.SYMBOL(K,1))GO TO 5	MULTI
27.	3	CONTINUE	MULTI
28.	C	NO, TRY NEW LIBRARY SYMBOL.	MULTI
29.		GO TO 11	MULTI
30.	C	YES, HAS THIS LIBRARY ELEMENT ALREADY BEEN MATCHED IN THE	MULTI
31.	C	SCAN OF THIS SYMBOL	MULTI
32.	9	DOV N=1,JC	MULTI
33.		IF(IPIX(N).NE.N)GO TO 7	MULTI
34.	C	YES, IGNORE. PROCEED TO NEXT LIBRARY ELEMENT IF	MULTI
35.	C	AVAILABLE. OTHERWISE TO NEW LIBRARY SYMBOL.	MULTI
36.		KI=KI+1	MULTI
37.		IF(KI-KNO)2,2,11	MULTI
38.	7	CONTINUE	MULTI
39.	C	NO, SET IPIX AND TEST NEXT ELEMENT OF INPUT SYMBOL.	MULTI
40.		IPIX(JC)=K	MULTI
41.		JC=JC+1	MULTI
42.	9	CONTINUE	MULTI
43.		IF(I(KNO+1).NE.JC)GO TO 11	MULTI
44.	C	IDENTIFICATION ACHIEVED. SET M TO CORRECT VALUE AND EXIT.	MULTI
45.		M=I-5	MULTI
46.		RETURN	MULTI
47.	11	CONTINUE	MULTI
48.	C	IDENTIFICATION NOT ACHIEVED. SET ERROR FLAG AND EXIT.	MULTI
49.		IERR=1	MULTI
50.		RETURN	MULTI
51.		END	MULTI

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NEWCOL

1.		SUBROUTINE NEWCOL(LX, LXL, NBP, IC, KC, KCPV, LM, IERR)	NEWCOL
2.	C	THIS SUBROUTINE DEFINES THE INITIAL CONSTITUENTS OF A NEW	NEWCOL
3.	C	CHAIN. THE GROUP NUMBERS OF THE PREVIOUS CHAIN COMMON TO THE	NEWCOL
4.	C	CHAIN ARE STORED IN A NEW ROW OF ARRAY NBC. THE RELATED BRANCH	NEWCOL
5.	C	DATA FOR THE NEW CHAIN ARE STORED IN ARRAY NBX.	NEWCOL
6.		INTEGER WEIGHT(9)	NEWCOL
7.		DIMENSION JUNCT(9, 100), NOBRD(100)	NEWCOL
8.		COMMON/BLK2/WEIGHT, HMG(9), MDLUT(100), IX(100, 9, 4), NC(100), RCC	NEWCOL
9.		COMMON/BLK3/IRING(40, 30), IMATX(50, 40), NW(100), IRC(100), ROW(100),	NEWCOL
10.		IOBR(100), IO(100, 8), IRC, NOBR	NEWCOL
11.		COMMON/BLK4/NBC(60, 50), NBS(40, 2), NBX(60, 20), IRC, NONFUS, IACTOT	NEWCOL
12.		EQUIVALENCE (JUNCT(1, 1), IMATX(3, 1)), (NOBRD(1), IMATX(3, 1))	NEWCOL
13.	C1.0	FIND CORE ATOM IN CHAIN FORMATION WHICH IS ALSO A BRANCH POINT.	NEWCOL
14.	C	DETERMINE WHETHER THIS ATOM STILL HAS LIGANDS WHICH HAVE NOT	NEWCOL
15.	C	YET BEEN INCORPORATED IN A CHAIN LINK.	NEWCOL
16.		LF=NBP	NEWCOL
17.		DO3 LL=1, LF	NEWCOL
18.		LM=NBX(LX, NBP)	NEWCOL
19.		KC=NBC(LX, LM)	NEWCOL
20.		IFLAG1=0	NEWCOL
21.		LY=LM-1	NEWCOL
22.		IF(LY, ST.0)GO TO 1	NEWCOL
23.		IFLAG1=1	NEWCOL
24.		GO TO 2	NEWCOL
25.		KCPV=NBC(LX, LY)	NEWCOL
26.	C	FIND THE TENTATIVE BRANCH ATOM KC.	NEWCOL
27.	2	CALL NEWKC(KCPV, KC, IFLAG1, IFLAG2)	NEWCOL
28.	C	HAS KC ALREADY BEEN PROCESSED IF NOT, GO TO 5 OTHERWISE,	NEWCOL
29.	C	FIND NEW BRANCH ATOM.	NEWCOL
30.		IF(IFLAG2.EQ.0)GO TO 5	NEWCOL
31.		NBP=NBP-1	NEWCOL
32.	3	CONTINUE	NEWCOL
33.		LX=LXL	NEWCOL
34.		RETURN	NEWCOL
35.	C2.0	RESET TO THEIR INITIAL VALUE OF 1 THE LOCATIONS OF NOBRD	NEWCOL
36.	C	ASSOCIATED WITH THOSE BRANCH ATOMS WHICH FOLLOW IC.	NEWCOL
37.	5	LF=NBS(LX, 2)	NEWCOL
38.		DO4 LL=1, LF	NEWCOL
39.		IF(NBX(LX, LL).LE.LM)GO TO 6	NEWCOL
40.		J=NBX(LX, LL)	NEWCOL
41.		KCX=NBC(LX, J)	NEWCOL
42.		NOBRD(KCX)=1	NEWCOL
43.	6	CONTINUE	NEWCOL
44.	C3.0	COPY GROUP NUMBERS IN NBC(LX, J) INTO NBC(LX+1, J) UP TO	NEWCOL
45.	C	DESIGNATED BRANCH POINT. ALSO COPY NBX ARRAY.	NEWCOL
46.		LY=LXL-1	NEWCOL
47.		IF(LY.LE.40)GO TO 17	NEWCOL
48.		IERR=1	NEWCOL
49.		LX=LY	NEWCOL
50.		RETURN	NEWCOL
51.	17	DO19 J=1, LM	NEWCOL
52.	19	NBC(LY, J)=NBC(LX, J)	NEWCOL
53.		DO21 J=1, NBP	NEWCOL
54.	21	NBX(LY, J)=NBX(LX, J)	NEWCOL
55.		LX=LY	NEWCOL
56.		IZ=LW	NEWCOL
57.		RETURN	NEWCOL
58.		END	NEWCOL

NEWRC

1.		SUBROUTINE NEWRC(KCPV, KC, IFLAG1, IFLAG2)	NEWRC
2.	C	THIS SUBROUTINE FINDS THE NEXT CHAIN ATOM WHEN THE LAST IDENTIFIED ATOM (KC) IN THE CHAIN IS A BRANCH ATOM. THE NEW CHAIN ATOM IS SET EQUAL TO ONE OF THE UNUSED CORE ATOM LIGANDS OF KC AND IS STORED IN KC. IF ALL OF THESE LIGANDS HAVE ALREADY BEEN INCORPORATED IN SOME CHAIN LINK, THE PROGRAM EXITS FROM THE SUBROUTINE UNLESS KCPV IS NOT STORED IN THE REQUIRED ORDER.	NEWRC
3.	C		NEWRC
4.	C		NEWRC
5.	C		NEWRC
6.	C		NEWRC
7.	C		NEWRC
8.	C		NEWRC
9.	C	INTEGER WEIGHT(9)	NEWRC
10.	C	DIMENSION JUNCT(5, 100), NOBRD(100)	NEWRC
11.	C	COMMON/BLK2/WEIGHT, MMGT(9), MOLWT(100), IS(100, 5, 6), NC(100), RCC	NEWRC
12.	C	COMMON/BLK3/IRING(10, 30), IMATR(30, 80), NW(100), IBC(100), KCM(100),	NEWRC
13.	C	IDBR(100), IB(100, 8), IFB, NOBR	NEWRC
14.	C	EQUIVALENCE (JUNCT(1, 1), IMATR(3, 1)), (NOBRD(1), IMATR(3, 1))	NEWRC
15.	C1.0	SET IFLAG2 AND INCREMENT NOBRD.	NEWRC
16.	C	IFLAG2=0	NEWRC
17.	C	NOBRD(KC)=NOBRD(KC)+1	NEWRC
18.	C2.0	IS IFLAG1 EQUAL TO ONE	NEWRC
19.	C	IF(IFLAG1.NE.1)GO TO 1	NEWRC
20.	C	YES. IF ALL LIGANDS OF ATOM KC HAVE BEEN USED, GO TO 2.	NEWRC
21.	C	OTHERWISE, GO TO 9.	NEWRC
22.	C	IF(NOBRD(KC)-NC(KC))9, 2	NEWRC
23.	C	NO, IT IS NOT.	NEWRC
24.	C3.0	ALL CORE ATOM LIGANDS OF BRANCH ATOM KC MAY HAVE BEEN USED.	NEWRC
25.	C	1 IF(NOBRD(KC).LE.NC(KC))GO TO 4	NEWRC
26.	C	ALL CORE ATOM LIGANDS OF BRANCH ATOM KC HAVE BEEN USED.	NEWRC
27.	C	IF(JUNCT(1, KC).NE.KCPV)GO TO 3	NEWRC
28.	C	KCPV IS IN CORRECT LOCATION. SET IFLAG2 AND EXIT.	NEWRC
29.	C	2 IFLAG2=1	NEWRC
30.	C	RETURN	NEWRC
31.	C	KCPV IS NOT IN REQUIRED POSITION. RESET NOBRD.	NEWRC
32.	C	3 NOBRD(KC)=2	NEWRC
33.	C	IF CONDITIONS REQUIRE IT, STORE VALUE OF KCPV IN JUNCT(1, KC)	NEWRC
34.	C	SWITCHING LOCATIONS WITH GROUP NUMBER PREVIOUSLY THERE.	NEWRC
35.	C	4 IF=NC(KC)	NEWRC
36.	C	DO5 J=1, JF	NEWRC
37.	C	IF(JUNCT(J, KC).EQ.KCPV)GO TO 7	NEWRC
38.	C	5 CONTINUE	NEWRC
39.	C	7 IF(J.LT.NOBRD(KC))GO TO 9	NEWRC
40.	C	ITEMP=JUNCT(J, KC)	NEWRC
41.	C	JUNCT(J, KC)=JUNCT(1, KC)	NEWRC
42.	C	JUNCT(1, KC)=ITEMP	NEWRC
43.	C4.0	SET KCPV EQUAL TO CURRENT KC. THEN SET KC EQUAL TO ONE OF THE STILL UNUSED CORE ATOM LIGANDS BONDED TO BRANCH ATOM KC	NEWRC
44.	C		NEWRC
45.	C	9 KCPV=KC	NEWRC
46.	C	ITEMP=NOBRD(KC)	NEWRC
47.	C	KC=JUNCT(ITEMP, KC)	NEWRC
48.	C	RETURN	NEWRC
49.	C	END	NEWRC

NRINGS

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2. SUBROUTINE NRINGS(IGS,IRNG3,RDATA,HRING,SRING,CPSYM) NRINGS
3. C THIS SUBROUTINE DETERMINES WHETHER THE EXISTING SIX-MEMBERED NRINGS
4. C NITROGEN-CONTAINING RINGS FORM PART OF THE TRICYCLIC FUSED RING NRINGS
5. C SYSTEM N(2)C(6)H(12), WHERE EACH RING IS FUSED AND HAS 4 POINTS NRINGS
6. C IN COMMON WITH EACH OF OTHER TWO RINGS. IF PRESENT IT ADDS NRINGS
7. C RING CORRECTIONS TO THERMODYNAMIC PROPERTIES. NRINGS
8. C INTEGER WEIGHT(9) NRINGS
9. C DIMENSION KOMB(40,10),NOKOMB(11),NOK(10,10),KRPROP(6,40), NRINGS
10. C IJSTORE(3),RDATA(6),CPSYM(4),KTGAUS(150),KCGAUS(3,150) NRINGS
11. C COMMON/BLK2/WEIGHT,MWGT(9),MOLWT(100),IX(100,5,6),AC(100),KCC NRINGS
12. C COMMON/BLK3/IRING(40,30),IMATX(50,60),NM(100),IBC(100),KCN(100), NRINGS
13. C IIDBR(100),IB(100,8),IRG,NBR NRINGS
14. C COMMON/BLK4/NBC(60,50),NBS(60,2),NBX(60,20),IRC,NONFUS,IRCTOT NRINGS
15. C EQUIVALENCE (KOMB(1,1),IB(62,4)),(NOKOMB(1),IB(80,8)),(IJSTORE(1), NRINGS
16. C 1IB(98,8)),(NOK(1,1),IMATX(1,55)),(KRPROP(1,1),NBX(2,1)), NRINGS
17. C 2(KTGAUS(1),IMATX(1,60)),(KCGAUS(1,1),IMATX(1,72)) NRINGS
18. C1.0 INITIALIZE CYCLE THAT TESTS EACH FUSED RING SET. NRINGS
19. C IC=NOKOMB(1) NRINGS
20. C2.0 HOW MANY RINGS ARE THERE IN FUSED RING SET J NRINGS
21. C DO7 J=1,IC NRINGS
22. C KV=NOKOMB(J+1) NRINGS
23. C IF NUMBER UNEQUAL TO 3 IGNORE SET J. NRINGS
24. C IF(KV.NE.3)GO TO 7 NRINGS
25. C SET J COMPOSED OF 3 RINGS. NRINGS
26. C IF(NOK(1,J).NE.3.OR.NOK(2,J).NE.4.OR.NOK(3,J).NE.2)GO TO 7 NRINGS
27. C EACH RING IS FUSED AT 4 POINTS TO EACH OF THE OTHER TWO NRINGS
28. C RINGS AND TWO OF THESE FOUR ATOMS ARE COMMON TO ALL THREE NRINGS
29. C RINGS NRINGS
30. C K1=NOK(4,J) NRINGS
31. C K2=NOK(5,J) NRINGS
32. C IF(IX(K1,1,1).NE.4.OR.IX(K2,1,1).NE.4)GO TO 7 NRINGS
33. C THE TWO JUNCTURE ATOMS ARE NITROGEN. NRINGS
34. C NX3=0 NRINGS
35. C3.0 DETERMINE WHETHER THE 3 RINGS IN SET J ARE EACH 6-CENTERED NRINGS
36. C CARBON-NITROGEN RINGS WITH NO DOUBLE BONDS. NRINGS
37. C DO1 K=1,KV NRINGS
38. C I=KOMB(K,J) NRINGS
39. C IF(IRING(I,1).NE.6)GO TO 7 NRINGS
40. C RING I IS 6-CENTERED. NRINGS
41. C IF(KRPROP(1,1)+KRPROP(5,1).NE.0.OR.KRPROP(3,1).NE.2)GO TO 7 NRINGS
42. C RING I COMPOSED ONLY OF 4 CARBON AND 2 NITROGEN ATOMS WITH NRINGS
43. C NO DOUBLE BONDS. STORE I.O. NUMBER OF RING INVOLVED. NRINGS
44. C NX3=NX3+1 NRINGS
45. C IJSTORE(NX3)=I NRINGS
46. C1 CONTINUE NRINGS
47. C4.0 DETERMINE SEPARATION OF TWO NITROGEN ATOMS. NRINGS
48. C K2=KRPROP(4,1)+3 NRINGS
49. C K3=IRING(1,K2) NRINGS
50. C IF(IX(K3,1,1).NE.4)GO TO 7 NRINGS
51. C THE TWO NITROGEN ATOMS ARE IN THE 1 AND 4 POSITIONS. NRINGS
52. C5.0 SET J IS THE TRICYCLIC FUSED RING SYSTEM N(2)C(6)H(12). ADD NRINGS
53. C CORRECTIONS TO THERMODYNAMIC PROPERTIES, STORE PERTINENT NRINGS
54. C PRINTOUT DATA, AND CONTINUE THE TEST OF OTHER FUSED RING SETS. NRINGS
55. C HRING=HRING+RDATA(1) NRINGS
56. C SRING=SRING+RDATA(2) NRINGS
57. C DO3 KK=1,3 NRINGS
58. C CPSYM(KK)=CPSYM(KK)+RDATA(KK+2) NRINGS
59. C3 CONTINUE NRINGS
60. C IRNG3=IRNG3+1 NRINGS
61. C IGS=IGS+1 NRINGS
62. C KTGAUS(IGS)=1 NRINGS
63. C DO5 KK=1,5 NRINGS
64. C KCGAUS(KK,IGS)=IJSTORE(KK) NRINGS
65. C7 CONTINUE NRINGS
66. C RETURN NRINGS
67. C END NRINGS

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NUMBER

1.		SUBROUTINE NUMBER(NUM, NX, K, L, MP, KXX, LXX, KDD, LCD, JII, JFF)	NUMBER
2.	C	THIS SUBROUTINE DETERMINES THE NUMBER OF LIGANDS(MP) ATTACHED	NUMBER
3.	C	TO CORE ATOM NUMBER ONE OR THE NUMBER OF LIGANDS MINUS ONE OF	NUMBER
4.	C	ANY CORE ATOM WHOSE GROUP NUMBER IS GREATER THAN ONE.	NUMBER
5.		INTEGER SYMX(4), SYMBOL(9), GRID(50, 50)	NUMBER
6.		COMMON/BLK1/NO, NOS, SYMX, SYMBOL, NOVAL(9), GRID	NUMBER
7.	C1.0	INITIALIZE MP AND FIND THE REVERSE OF DIRECTION NUR.	NUMBER
8.		MP=0	NUMBER
9.		NUM=NUM+0	NUMBER
10.		IF(NUM.GT.0)NUM=NUM-0	NUMBER
11.	C2.0	INITIALIZE CYCLE THAT FINDS THE NUMBER OF LIGANDS.	NUMBER
12.		DO1 J=1,7	NUMBER
13.	C	COMPUTE BOND DIRECTION TO BE TESTED.	NUMBER
14.		NI=NUM+J	NUMBER
15.		IF(NI.GT.0)NI=NI-0	NUMBER
16.	C	FIND NEW TRANSFORMATION COORDINATES FOR THIS BOND DIRECTION.	NUMBER
17.		CALL ASSIGN(NX, K, L, KD, LD, JI, JF)	NUMBER
18.		IF(JI.GT.JF)GO TO 1	NUMBER
19.		KI=K+KB	NUMBER
20.		LI=L+LB	NUMBER
21.	C	DOES THIS LOCATION HAVE A NON-BLANK CHARACTER	NUMBER
22.		IF(GRID(KI, LI).EQ.SYMX(4))GO TO 1	NUMBER
23.	C	YES, IT DOES. INCREMENT MP.	NUMBER
24.		MP=MP+1	NUMBER
25.	C	IS THIS THE FIRST LIGAND IDENTIFIED	NUMBER
26.		IF(MP.GT.1)GO TO 1	NUMBER
27.	C	YES, IT IS. SET ALL IDENTIFYING VARIABLES FOR THIS	NUMBER
28.	C	LIGAND. CONTINUE SEARCH.	NUMBER
29.		KXX=NX	NUMBER
30.		KII=KI	NUMBER
31.		LXX=LX	NUMBER
32.		KDD=KB	NUMBER
33.		LDD=LB	NUMBER
34.		JII=JI	NUMBER
35.		JFF=JF	NUMBER
36.		CONTINUE	NUMBER
37.		RETURN	NUMBER
38.		END	NUMBER

ORDER

1.	SUBROUTINE ORDER(LIM,IA,IB)	ORDER
2.	C THIS SUBROUTINE STORES IN ARRAY IA THE ORDER THAT THE LIM	ORDER
3.	C ELEMENTS OF ARRAY IB WOULD HAVE IF ARRANGED IN ORDER OF	ORDER
4.	C ASCENDING VALUE.	ORDER
5.	DIMENSION IA(100),IB(100)	ORDER
6.	C1.0 STORE INITIAL ORDER OF ELEMENTS IN IA.	ORDER
7.	DO1 J=1,LIM	ORDER
8.	IA(J)=J	ORDER
9.	1 CONTINUE	ORDER
10.	IF(LIM.EQ.1)RETURN	ORDER
11.	C2. MORE THAN ONE ELEMENT CONTAINED IN IB. INITIALIZE CYCLE.	ORDER
12.	JF=LIM-1	ORDER
13.	DOO J=1,JF	ORDER
14.	C CHECK ORDER OF TWO ADJACENT ELEMENTS IN IA, NAMELY, J AND	ORDER
15.	C J+1. IF IB(K1) CORRESPONDING TO ELEMENT J IS GREATER THAN	ORDER
16.	C IB(K2) CORRESPONDING TO ELEMENT J+1, THEIR ORDER IN IA IS	ORDER
17.	C SWITCHED. ALL PREVIOUS ELEMENTS IN IA ARE THEN ALSO CHECKED	ORDER
18.	C AGAINST J+1 IN LIKE MANNER AND THEIR ORDER IN IA REARRANGED	ORDER
19.	C IF NECESSARY.	ORDER
20.	K3=J	ORDER
21.	K4=J+1	ORDER
22.	3 IF(K4.LE.1)GO TO 9	ORDER
23.	K1=IA(K3)	ORDER
24.	K2=IA(K4)	ORDER
25.	IF(IA(K1).LE.IB(K2))GO TO 9	ORDER
26.	JX=IA(K3)	ORDER
27.	IA(K3)=IA(K4)	ORDER
28.	IA(K4)=JX	ORDER
29.	K3=K3-1	ORDER
30.	K4=K3+1	ORDER
31.	GO TO 3	ORDER
32.	C NOW CHECK REMAINING ELEMENTS IN SAME MANNER AND CONTINUE	ORDER
33.	C UNTIL ALL ELEMENTS HAVE BEEN CHECKED.	ORDER
34.	5 CONTINUE	ORDER
35.	RETURN	ORDER
36.	END	ORDER

OXYATM

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1.      SUBROUTINE OXYATM(R, LACK, ITEST)      OXYATM
2.      C      THIS SUBROUTINE DETERMINES WHETHER THERE ARE 0, 1, OR 2 -C(=O)-      OXYATM
3.      C      GROUPS PRESENT IN RING R WHICH ARE ADJACENT TO AN OXYGEN ATOM      OXYATM
4.      C      LOCK (OR NITROGEN ATOM) LIKEWISE PART OF THE RING BACKBONE      OXYATM
5.      C      STRUCTURE.      OXYATM
6.      C      NUMBER WEIGHT(9)      OXYATM
7.      C      DIMENSION MR(30)      OXYATM
8.      C      COMMON/BLAS/IRING(40, 30), IPRAT(50, 50), NM(100), IBC(100), ROW(100),      OXYATM
9.      C      IGBR(100), IJ(100, 3), ITR, NGBR      OXYATM
10.     C      EQUIVALENCE (M(1), IPRAT(1, 1))      OXYATM
11.     C      FIND LOCATION OF C(=O) GROUPS IN RING R.      OXYATM
12.     C1.0      NOXY=0      OXYATM
13.     C      MPR=PRR(R, I)      OXYATM
14.     C      DOB = M(2, M)      OXYATM
15.     C      IF (M.EQ.LOCK) GO TO 5      OXYATM
16.     C      RING COMPONENT KI IS NOT AN OXYGEN (OR NITROGEN) ATOM.      OXYATM
17.     C      RING INDEX, M)      OXYATM
18.     C      IF (I(KI, 1) .NE. 5) GO TO 4      OXYATM
19.     C      RING COMPONENT KI CONTAINS C(=O) LINKAGE.      OXYATM
20.     C      NOXY=NOXY+1      OXYATM
21.     C      GO TO 23      OXYATM
22.     C
23.     C      CONTINUE      OXYATM
24.     C2.0      SET ITEST ACCORDING TO NUMBER OF C(=O) LINKAGES PRESENT.      OXYATM
25.     C      IF (NOXY .NE. 2) GO TO 18      OXYATM
26.     C      TWO C(=O) GROUPS PRESENT. ARE THEY ADJACENT TO THE OXYGEN      OXYATM
27.     C      OR NITROGEN ATOM LOCK      OXYATM
28.     C      J01=MR(2)-M(1)      OXYATM
29.     C      J02=ABS(LOCK-M(1))      OXYATM
30.     C      IF (J01 .NE. 2 .OR. J02 .NE. 1 .AND. J02 .NE. ITRING(R, 1)) GO TO 17      OXYATM
31.     C      YES. SET FLAG=2.      OXYATM
32.     C      V=TEST+2      OXYATM
33.     C      RETURN      OXYATM
34.     C3.0      IS THERE ONE C(=O) GROUP PRESENT. SET FLAG=1.      OXYATM
35.     C      ITEST=1      OXYATM
36.     C      RETURN      OXYATM
37.     C      NONE PRESENT. SET FLAG=0.      OXYATM
38.     C      ITEST=0      OXYATM
39.     C      RETURN      OXYATM
40.     C      END      OXYATM
41.     C

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PRINT1

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1. SUBROUTINE PRINT1 PRINT1
2. C THIS SUBROUTINE PRINTS OUT THE ATOMIC COMPOSITION, THE ASSIGNED PRINT1
3. C WEIGHTS, AND THE STRUCTURE AND COORDINATE ARRAY IX. IT ALSO PRINT1
4. C WILL OUTPUT, IF PRESENT, THE NUMBER OF COMPONENTS IN EACH RING PRINT1
5. C AND THEIR GROUP NUMBERS. PRINT1
6. INTEGER SYM(4),SYMBOL(9),GRID(50,50) PRINT1
7. INTEGER WEIGHT(9) PRINT1
8. COMMON/BLK1/NO,NOS,SYM,SYMBOL,NOVAL(9),GRID PRINT1
9. COMMON/BLK2/WEIGHT,WMGT(9),MOLWT(100),IX(100,5,6),NC(100),KCC PRINT1
10. COMMON/BLK3/IRING(40,30),IATX(50,50),AM(100),IBC(100),KONC(100), PRINT1
11. IIDER(100),IS(100,8),IRA,NOBR PRINT1
12. COMMON/BLK4/NBC(60,50),NBS(60,2),MBX(60,20),IRC,NOFUS,IR,TOT PRINT1
13. COMMON/BLK5/NDATA,NUMAT(5),MBC(50),MBS(2),JW,JY,LFLAG,LFLAGB PRINT1
14. C1.0 THIS SECTION PRINTS OUT THE ATOMIC COMPOSITION OF THE MOLECULE. PRINT1
15. WRITE(6,1) PRINT1
16. 1 FORMAT(// 'NO,4X,33HATOMIC COMPOSITION OF MOLECULE PRINT1
17. 1//NO,5X,4HATOM,8X,6HNUMBER) PRINT1
18. DO5 J=1,NDATA PRINT1
19. IF(NUMAT(J).EQ.0)GO TO 5 PRINT1
20. WRITE(4,3)SYMBOL(J),NUMAT(J) PRINT1
21. 3 FORMAT(1H ,57X,A4,5X,15) PRINT1
22. CONTINUE PRINT1
23. C2. THIS SECTION PRINTS OUT THE ASSIGNED WEIGHTS OF THE GROUPS PRINT1
24. C AND THE IX ARRAY. DESCRIPTION OF IX OUTPUT, IX(M,N,J) - PRINT1
25. C DATA FOR CORE ATOM(M) AT N=1 AND FOR LIGANDS AT N=2 TO N=5, PRINT1
26. C CONTENTS OF J COLUMN - J=1 CHEMICAL SYMBOL OF COMPONENT, PRINT1
27. C J=2 GRID ROW COORDINATE, J=3 GRID COLUMN COORDINATE, PRINT1
28. C J=4 DIRECTION OF LIGAND BOND, J=5 BOND TYPE, J=6 GROUP NUMBER PRINT1
29. C OF CORE ATOM. PRINT1
30. WRITE(4,9) PRINT1
31. 9 FORMAT(// 'NO,47X,34HGROUP STRUCTURE AND COMPOSITION PRINT1
32. 1//1H ,21X,65HGROUP GROUP CHEMICAL SYMBOL GRID ROW GRID CO PRINT1
33. 2LUMN BOND BOND GROUP NUMBER /1H ,21X,65HNUMBER PRINT1
34. 3WEIGHT OF COMPONENT COORDINATE COORDINATE VECTOR TYPE OF PRINT1
35. 4 CORE ATOM ) PRINT1
36. DO15 M=1,NCU PRINT1
37. L=IX(M,1,1) PRINT1
38. WRITE(6,11)M,MOLWT(M),SYMBOL(L),IX(M,1,2),IX(M,1,3),IX(M,1,6) PRINT1
39. 11 FORMAT(1H ,22X,13,5X,15,11X,A4,7X,15,7X,15,22X,15) PRINT1
40. NF=KONC(M)+1 PRINT1
41. DO15 N=2,NF PRINT1
42. L=IX(M,N,1) PRINT1
43. WRITE(6,13)SYMBOL(L),IX(M,N,2),J=2,6) PRINT1
44. 13 FORMAT(1H ,46X,A4,7X,15,7X,15,7X,15,3X,14,5X,15) PRINT1
45. CONTINUE PRINT1
46. WRITE(6,17) PRINT1
47. 17 FORMAT(1H ) PRINT1
48. CONTINUE PRINT1
49. C3.0 IF RING STRUCTURES ARE PRESENT, THIS SECTION PRINTS OUT THE PRINT1
50. C NUMBER OF COMPONENTS IN EACH RING AND THEIR GROUP NUMBERS. PRINT1
51. IF(IRC.EQ.0)RETURN PRINT1
52. DO27 J=1,IRC PRINT1
53. WRITE(6,31)J,IRING(J,1) PRINT1
54. 31 FORMAT(// '1H ,24X,11HRING NUMBER,15,4H 15,13,10H MEMBERED) PRINT1
55. NF=IRING(J,1)+1 PRINT1
56. WRITE(6,34)IRING(J,N),N=2,NF) PRINT1
57. 34 FORMAT(1H ,23X,39HGROUP NUMBERS OF RING CONSTITUENTS ' ,1015, PRINT1
58. 1H ,17(1H ,62X,1015,1H,13) PRINT1
59. CONTINUE PRINT1
60. RETURN PRINT1
61. END PRINT1
```

PPRINT2

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1. SUBROUTINE PRINT2(NTITLE) PRINT2
2. C THIS SUBROUTINE OUTPUTS THE TITLE PRECEDING THE PRINTOUT OF PRINT2
3. C RING, SECOND-ORDER INTERACTION, AND CERTAIN SYMMETRY PRINT2
4. C CORRECTIONS. THE FLAG NTITLE IS ALSO RESET TO 1 WHEN THIS PRINT2
5. C ROUTINE IS EXECUTED. PRINT2
6. NTITLE=1 PRINT2
7. WRITE(6,1) PRINT2
8. 1 FORMAT(//1H0,20X,73HNONGROUP INTERACTION AND INTERNAL ROTATION PRINT2
9. 1AL SYMMETRY CONTRIBUTIONS /1H0,6X,4HTYPE,11X,14HRING NUMBER 0 PRINT2
10. 2R,3X,6HAMOUNT,2X,17HHEAT OF FORMATION,3X,7HENTROPY,14X,26HHEAT CAP PRINT2
11. 3ACITY COEFFICIENTS /1X ,22X,12HGROUP NUMBER,17X,4HKCAL,10X, PRINT2
12. 49HCAL/DEG K,5X,9HCAL/DEG K,2X,12HCAL/DEG K**2,1X,12HCAL/DEG K**3, PRINT2
13. 51X,12HCAL/DEG K**4) PRINT2
14. RETURN PRINT2
15. END PRINT2
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RESETR

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1. SUBROUTINE RESETR(MDIF, LK) RESETR
2. C THIS SUBROUTINE SETS THE RING ARRAY IBC AND ALSO ADDS THE RESETR
3. C RESIDUAL NON-BRANCH RING ATOMS TO ALL THE CHAINS, IF THE FIRST RESETR
4. C CHAIN ATOM DEFINED WAS A NON-BRANCH RING ATOM AND NO TERMINAL RESETR
5. C CORE ATOMS ARE PRESENT IN THE MOLECULE. THESE RESIDUAL ATOMS RESETR
6. C WERE NOT PREVIOUSLY INCLUDED IN THE CHAIN DEFINITIONS. RESETR
7. INTEGER WEIGHT(9) RESETR
8. DIMENSION NRLOC(40) RESETR
9. COMMON/BLK2/WEIGHT, MWGT(9), MOLWT(100), IX(100, 5, 6), NC(100), KCC RESETR
10. COMMON/BLK3/IRING(40, 30), IMATX(50, 80), NM(100), IBC(100), KDM(100), RESETR
11. IDBR(100), IB(100, 8), IRG, NDBR RESETR
12. COMMON/BLK4/NBC(40, 50), NBS(60, 2), NBX(40, 20), IRC, NONFUS, IRCTOT RESETR
13. EQUIVALENCE (NRLOC(1), IMATX(3, 47)) RESETR
14. C1.0 SET RING ARRAY IBC. RESETR
15. DOJ K=1, IRC RESETR
16. LF=IRING(K, 1)+1 RESETR
17. DOJ L=2, LF RESETR
18. KC=IRING(K, L) RESETR
19. IBC(KC)=K RESETR
20. 3 CONTINUE RESETR
21. KC=NBC(1, 1) RESETR
22. IF(MDIF.EQ.0 OR IBC(KC).EQ.0 OR NC(KC).GT.2)RETURN RESETR
23. C2.0 FIRST ATOM ON FIRST CHAIN IS A RING SPECIES BUT NOT A CHAIN RESETR
24. C ATOM AND NO TERMINAL CORE ATOMS ARE CONTAINED IN MOLECULE. RESETR
25. C FIND CHAIN LXX THAT IDENTIFIES RING K. RESETR
26. K=IBC(KC) RESETR
27. LXX=NRLOC(K) RESETR
28. NBP=NBS(LXX, 2) RESETR
29. IF(NBP.EQ.0)RETURN RESETR
30. C3.0 CHAIN ATOMS EXIST IN RING. FIND NUMBER OF NON-BRANCH ATOMS RESETR
31. C JDIF TO BE ADDED TO ALL CHAINS (IF ANY). RESETR
32. JDIF=IRING(K, 1)-NBX(LXX, NBP) RESETR
33. IF(JDIF.LE.0)RETURN RESETR
34. C4.0 ADD THE JDIF NON-BRANCH RING ATOMS TO ALL CHAINS AND CHANGE RESETR
35. C NBS AND NBX ACCORDINGLY. RESETR
36. NZ=NBX(LXX, NBP)+1 RESETR
37. DOJJ L=1, LK RESETR
38. IF(L.NE.LXX)GO TO 6 RESETR
39. C CHAIN L IS RING IDENTIFIER CHAIN. MOVE THE FIRST MF ELEMENTS RESETR
40. C IN ARRAY NBC CORRESPONDING TO CHAIN L JDIF LOCATIONS. RESETR
41. MF=NBX(LXX, NBP) RESETR
42. MX=MF+1 RESETR
43. DOJ M=1, MF RESETR
44. MY=MX-1 RESETR
45. MY=MY+JDIF RESETR
46. NBC(L, MY)=NBC(L, MX) RESETR
47. 5 CONTINUE RESETR
48. GO TO 8 RESETR
49. C CHAIN L IS NOT RING IDENTIFIER CHAIN. MOVE ALL THE ELEMENTS RESETR
50. C IN ARRAY NBC CORRESPONDING TO CHAIN L JDIF LOCATIONS. RESETR
51. 6 MF=NBS(L, 1) RESETR
52. MX=MF+1 RESETR
53. DOJ M=1, MF RESETR
54. MY=MX-1 RESETR
55. MY=MY+JDIF RESETR
56. NBC(L, MY)=NBC(L, MX) RESETR
57. 7 CONTINUE RESETR
58. NBS(L, 1)=NBS(L, 1)+JDIF RESETR
59. C STORE THE ADDITIONAL (REMAINING) RING ELEMENTS IN THE FIRST RESETR
60. C JDIF LOCATIONS OF NBC CORRESPONDING TO CHAIN L. RESETR
61. 8 MX=NZ RESETR
62. DOJ M=1, JDIF RESETR
63. MY=MX+1 RESETR
64. NBC(L, MY)=IRING(K, MY) RESETR
65. 9 CONTINUE RESETR
66. NBP=NBS(L, 2) RESETR
67. DOJJ N=1, NBP RESETR
68. NBX(L, N)=NBX(L, N)+JDIF RESETR
69. 11 CONTINUE RESETR
70. RETURN RESETR
71. END RESETR

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RING

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1.      SUBROUTINE RING(LX, LM, KE, IERR)      RING
2.      C      THIS SUBROUTINE DETERMINES IF A SIMILAR RING WAS NOT PREVIOUSLY      RING
3.      C      IDENTIFIED. IF NOT, THE GROUP NUMBERS OF THE RING CONSTITUENTS      RING
4.      C      ARE STORED IN ARRAY IRING. IF RING IS A DUPLICATE, IT IS NOT      RING
5.      C      USED.
6.      C      DIMENSION NRLOC(40)
7.      C      COMMON/BLK1/IRING(40,30),IMATX(50,50),NW(100),IBC(100),KUN(100),      RING
8.      C      IIDBR(10),IRC(100,0),IRB,NORR      RING
9.      C      COMMON/BLK2/NBC(60,50),NBS(60,2),NBX(60,20),IRC,NONPUS,IRCTOT      RING
10.     C      EQUIVALENCE (NRLOC(1),IMATX(3,47))      RING
11.     C1.0  CHECK IF IDENTICAL RING HAS ALREADY BEEN IDENTIFIED AND STORED      RING
12.     C      IN IRING ARRAY. IF SO, DELETE RING AND IF THE CHAIN IS ALSO      RING
13.     C      EQUAL, DELETE CHAIN AS WELL.
14.     C      NALT=LM-KE      RING
15.     C      KP=NALT+1      RING
16.     C      IF(IRC.EQ.0)GO TO 9      RING
17.     C      DO7 LL=1,IRC      RING
18.     C      IF(IRING(LL,1).NE.NALT)GO TO 7      RING
19.     C      RING LL HAS SAME NUMBER OF RING MEMBERS. TEST IT.      RING
20.     C      KI=LM      RING
21.     C      ARE RING MEMBERS THE SAME EXCEPT POSITIONED IN REVERSE ORDER      RING
22.     C      DO9 K=2,KP      RING
23.     C      IF(IRING(LL,K).NE.NBC(LX,KI))GO TO 3      RING
24.     C      KI=KI-1      RING
25.     C      5 CONTINUE      RING
26.     C      YES. ARE THE TWO CHAINS THE SAME LENGTH      RING
27.     C      LXX=NRLOC(LL)      RING
28.     C      IF(NBS(LXX,1).NE.LM-1)RETURN      RING
29.     C      YES. IF THERE ARE NO CHAINS IN ADDITION TO THE RINGS, GO      RING
30.     C      TO 2. OTHERWISE, CONTINUE.      RING
31.     C      IF(NBS(LXX,1).EQ.IRING(LL,1))GO TO 2      RING
32.     C      KI=KP-1      RING
33.     C      ARE THE REMAINDER OF THE CHAIN COMPONENTS THE SAME      RING
34.     C      DO4 J=1,KI      RING
35.     C      IF(NBC(LX,J).NE.NBC(LXX,J))RETURN      RING
36.     C      4 CONTINUE      RING
37.     C      YES. SET KE=-1 WHICH DELETES CHAIN FORMATION LX.      RING
38.     C      2 KE=-1      RING
39.     C      RETURN      RING
40.     C      NO. ARE THE RING COMPONENTS THE SAME EXCEPT FOR BEING      RING
41.     C      INVERTED AND DISPLACED BY ONE IN THEIR STORAGE ORDER      RING
42.     C      3 KI=LM-1      RING
43.     C      DO6 K=2,KP      RING
44.     C      IF(IMING(LL,K).NE.NBC(LX,KI))GO TO 7      RING
45.     C      KI=KI-1      RING
46.     C      6 CONTINUE      RING
47.     C      RETURN      RING
48.     C      7 CONTINUE      RING
49.     C2.0  RING IS NEW. STORE THE TOTAL NUMBER OF COMPONENTS (NALT) OF      RING
50.     C      RING IRC IN IRING(IRC,1) AND THE GROUP NUMBERS OF THESE      RING
51.     C      COMPONENTS IN IRING(IRC,K) FROM K=2 TO NALT+1.      RING
52.     C      9 IIRA=IRC+1      RING
53.     C      ARE THERE 00 MANY RINGS PRESENT      RING
54.     C      IF(IIRA.LE.50)GO TO 10      RING
55.     C      YES. DETERMINE IF SOME ARE NOT UNIQUE. IF SO, GO TO 10.      RING
56.     C      OTHERWISE, EXIT.      RING
57.     C      CALL LESSEN(IRC)      RING
58.     C      IF(IRC.LT.IRACH)GO TO 10      RING
59.     C      IERR=1      RING
60.     C      IRC=IRC+1      RING
61.     C      RETURN      RING
62.     C      STORE RING DATA IN IRING ARRAY.      RING
63.     C      10 IRC=IRC+1      RING
64.     C      KI=KE      RING
65.     C      IRING(IRC,1)=NALT      RING
66.     C      DO11 K=2,KP      RING
67.     C      IRING(IRC,K)=NBC(LX,KI)      RING
68.     C      KI=KI+1      RING
69.     C      NRLOC(IRC)=LX      RING
70.     C      RETURN      RING
71.     C      END

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SAME

1.		SUBROUTINE SAME(KC, K1, K2, K11, K22)	SAME
2.	C	THIS SUBROUTINE STORES ALL THE PERTINENT IDENTIFICATION	SAME
3.	C	VARIABLES FOR ANY TWO IDENTICAL LIGANDS. IF ONE OF THESE	SAME
4.	C	LIGANDS HAS BEEN IDENTIFIED PREVIOUSLY, IT IS BYPASSED AND	SAME
5.	C	ONLY THE VARIABLES FOR THE OTHER LIGAND ARE STORED.	SAME
6.		INTEGER SYM(4), SYMBOL(9), GRID(90,80)	SAME
7.		DIMENSION KCSAME(6,100), NOSAME(6,100), NTOTAL(3,100), HRST(6)	SAME
8.		COMMON/BLK1/ND, NOS, SYM, SYMBOL, NOVAL(9), GRID	SAME
9.		COMMON/BLK3/IRING(40,30), IMATX(50,80), MW(100), IBC(100), KDN(100),	SAME
10.		IJOB(100), IB(100,8), IRG, NDBR	SAME
11.		COMMON/BLK4/NBCC(60,30), NBS(40,2), NBR(60,20), IRC, NONFUS, IRCTOT	SAME
12.		EQUIVALENCE (KCSAME(1,1), GRID(4,42)), (NOSAME(1,1), GRID(3,34)),	SAME
13.		(NTOTAL(1,1), GRID(4,70)), (HRST(1), NBR(14,20))	SAME
14.	C1.0	SET KP	SAME
15.		KP=NOSAME(1,KC)	SAME
16.	C2.0	HAVE OTHER LIGANDS OF KC BEEN DETECTED WHICH ARE IDENTICAL	SAME
17.		IF(KP.EQ.0)GO TO 11	SAME
18.	C	YES DETERMINE IF K1 OR K2 IS AMONG THESE. DO SO BY CHECKING	SAME
19.	C	THE STORAGE SUBSCRIPTS FOR K1 AND K2, NAMELY K11 AND K22,	SAME
20.	C	VERSUS THE ARRAY CONTAINING THE STORAGE SUBSCRIPTS OF THE	SAME
21.	C	IDENTICAL LIGANDS WHICH WERE IDENTIFIED PREVIOUSLY.	SAME
22.		M1=0	SAME
23.		M2=0	SAME
24.		DO 9 K=1, KP	SAME
25.		IF(K11.NE.HRST(K))GO TO 3	SAME
26.		M1=K	SAME
27.		GO TO 5	SAME
28.	3	IF(K22.NE.HRST(K))GO TO 5	SAME
29.		M2=K	SAME
30.	5	CONTINUE	SAME
31.		IF(M1.GT.0)GO TO 7	SAME
32.		IF(M2.EQ.0)GO TO 11	SAME
33.	C	K2 IDENTIFIED PREVIOUSLY. SET DATA FOR K1.	SAME
34.		KCSAME(KF+1,KC)=K1	SAME
35.		HRST(KF+1)=K11	SAME
36.		KK=K2	SAME
37.		GO TO 8	SAME
38.	7	IF(M2.GT.0)RETURN	SAME
39.	C	K1 IDENTIFIED PREVIOUSLY. SET DATA FOR K2.	SAME
40.		KCSAME(KF+1,KC)=K2	SAME
41.		HRST(KF+1)=K22	SAME
42.		KK=K1	SAME
43.	8	NOSAME(1,KC)=KF+1	SAME
44.	C	FIND LOCATION OF PREVIOUSLY IDENTIFIED ATOM IN KCSAME ARRAY	SAME
45.		DO 9 J=1, KP	SAME
46.		IF(KK.EQ.KCSAME(J,KC))GO TO 10	SAME
47.	9	CONTINUE	SAME
48.	C	STORE REMAINDER OF VARIABLES.	SAME
49.	10	II=NOSAME(J+2,KC)	SAME
50.		NOSAME(KF+3,KC)=II	SAME
51.		NTOTAL(II,KC)=NTOTAL(II,KC)+1	SAME
52.		RETURN	SAME
53.	C	NO K1 AND K2 WERE NOT IDENTIFIED PREVIOUSLY AS IDENTICAL	SAME
54.	C	LIGANDS. STORE THEIR IDENTIFICATION VARIABLES.	SAME
55.	11	NOSAME(1,KC)=KF+2	SAME
56.		NOSAME(2,KC)=NOSAME(2,KC)+1	SAME
57.		II=NOSAME(2,KC)	SAME
58.		NOSAME(KF+3,KC)=II	SAME
59.		NOSAME(KF+4,KC)=II	SAME
60.		KCSAME(KF+3,KC)=K1	SAME
61.		KCSAME(KF+2,KC)=K2	SAME
62.		HRST(KF+3)=K11	SAME
63.		HRST(KF+2)=K22	SAME
64.		NTOTAL(II,KC)=NTOTAL(II,KC)+2	SAME
65.		RETURN	SAME
66.		END	SAME

SCAN

```

1. SUBROUTINE SCAN(KT, MR, NR, NUM, K, L, IERR) SCAN
2. C THIS SUBROUTINE LOCATES AND IDENTIFIES ALL ATOMS BONDED TO THE SCAN
3. C CORE ATOM OF GROUP KT WHICH HAVE NOT YET BEEN SCANNED AND SCAN
4. C STORES PERTINENT DATA OF EACH OF THESE LIGANDS IN IX ARRAY. IT SCAN
5. C ALSO REARRANGES DATA OF GROUP KT IN IX ARRAY SO THAT DATA OF SCAN
6. C CORE SPECIES ARE STORED FIRST, FOLLOWED BY THE DATA OF NON-CORE SCAN
7. C SPECIES. SCAN
8. C INTEGER SYM(4), SYMBOL(9), GRID(50, 00) SCAN
9. C INTEGER WEIGHT(9) SCAN
10. C COMMON/BLK1/ND, NDS, SYM, SYMBOL, NOVAL(9), GRID SCAN
11. C COMMON/BLK2/WEIGHT, HWGT(9), MDLUT(100), IX(100, 5, 6), NCC(100), KCC SCAN
12. C COMMON/BLK3/IKING(40, 30), IMATX(50, 80), NM(100), IBC(100), RDN(100), SCAN
13. C ITOBR(100), IBC(100, 0), IRG, NOBR SCAN
14. C COMMON/BLK5/NDATA, NUMAT(9), ABC(50), ABS(2), JM, JY, LFLAGS, LFLAGE SCAN
15. C1.0 INITIALIZE NS AND FIND BOND DIRECTION FROM CORE ATOM KT TO SCAN
16. C PARENT ATOM. SCAN
17. C NS=0 SCAN
18. C NZ=NUM-4 SCAN
19. C IF(NZ.GT.4)NZ=NZ-8 SCAN
20. C2.0 START SEARCH AND IDENTIFICATION CYCLE. SCAN
21. C DO1 JM=1, 7 SCAN
22. C FIND TEST BOND DIRECTION. SCAN
23. C NX=NZ+J SCAN
24. C IF(NX.GT.8)NIX=NIX-8 SCAN
25. C FIND TRANSFORMATION COORDINATES FOR THIS BOND DIRECTION. SCAN
26. C CALL ASSIGN(NX, K, L, KD, LD, JI, JF) SCAN
27. C IF(JI.GT.JF)GO TO 1 SCAN
28. C KX=KD SCAN
29. C LX=LD SCAN
30. C IF(GRID(KX, LX).EQ.SYM(4))GO TO 1 SCAN
31. C TEST LOCATION IS NOT BLANK. SCAN
32. C IF(MR.LE.9)GO TO 4 SCAN
33. C EXCESSIVE LIGANDS PRESENT IN GROUP. PRINT ERROR MESSAGE, SCAN
34. C SET ERROR FLAG, AND EXIT. SCAN
35. C WRITE(6, 3)KT SCAN
36. C3 FORMAT(//1H0, 31X, 43H EXCESSIVE NUMBER OF LIGANDS ABOUT CORE ATOM, SCAN
37. C14, 19H. CASE TERMINATED.) SCAN
38. C IERR=1 SCAN
39. C RETURN SCAN
40. C LOCATE AND IDENTIFY NON-BOND SYMBOL. SCAN
41. C4 CALL BOND(KX, LX, KD, LD, JI, JF, ICKT, MR, 5, IERR) SCAN
42. C IF(IERR.EQ.1)RETURN SCAN
43. C CALL IDENT(NX, KX, LX, M, IERR) SCAN
44. C IF(IERR.EQ.1)RETURN SCAN
45. C STORE DATA OF LIGAND IN ARRAY IX. SCAN
46. C ICKT, MR, 1)=M SCAN
47. C ICKT, MR, 2)=M SCAN
48. C ICKT, MR, 3)=LX SCAN
49. C ICKT, MR, 4)=NIX SCAN
50. C IS LIGAND ALSO A CORE ATOM SCAN
51. C NMU=ICKT, MR, 4) SCAN
52. C CALL NUMBER(NMU, NJ, KX, LX, MP, KX, LX, KD, LD, JI, JF) SCAN
53. C IF(MP.EQ.0)GO TO 2 SCAN
54. C5 YES, IT IS. INCREMENT NC AND NS. SCAN
55. C NCC(KT)=NCC(KT)+1 SCAN
56. C NS=NS+1 SCAN
57. C HAS LIGAND BEEN SCANNED PREVIOUSLY, THAT IS, IS LIGAND PART SCAN
58. C OF RING SYSTEM SCAN
59. C IF(IMATX(KX, LX).EQ.0)GO TO 11 SCAN
60. C YES, IT IS. OBTAIN REQUIRED DATA FROM IMATX. SCAN
61. C ICKT, MR, 6)=IMATX(KX, LX) SCAN
62. C IBC(KT, NS)=IMATX(KX, LX) SCAN
63. C DELETE ATOM(S) IN SYMBOL ICKT, MR, 1) FROM NUMATA. SCAN
64. C CALL SUMATX(ICKT, MR, 1), -1, NUMATA) SCAN
65. C INCREMENT IRG AND CONTINUE. SCAN
66. C IRG=IRG+1 SCAN
67. C GO TO 2 SCAN
68. C LIGAND NOT PART OF RING SYSTEM. ASSIGN NEW GROUP SCAN
69. C NUMBER(RCC) TO IT AND STORE DATA FOR THIS GROUP IN IX. SCAN
70. C SET IMATX. SCAN
71. C11 NCC=NCC+1 SCAN
72. C IF(RCC.LE.100)GO TO 12 SCAN
73. C WRITE(6, 110) SCAN
74. C110 FORMAT(//1H0, 36, 56H NUMBER OF ALLOWED CORE ATOMS EXCEEDED. CASE T SCAN

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75.	TERMINATED. 1	SCAN
76.	TERM=1	SCAN
77.	RETURN	SCAN
78.	12 IX(KT, NR, 6)=KCC	SCAN
79.	DO 13 N=1, 3	SCAN
80.	IX(KCC, 1, N)=IX(KT, NR, N)	SCAN
81.	13 IX(KCC, 2, N)=IX(KT, 1, N)	SCAN
82.	IX(KCC, 1, 4)=NR	SCAN
83.	IX(KCC, 1, 6)=IX(KT, NR, 6)	SCAN
84.	IX(KCC, 2, 4)=NRU	SCAN
85.	IX(KCC, 2, 5)=IX(KT, NR, 5)	SCAN
86.	IX(KCC, 3, 6)=IX(KT, 1, 6)	SCAN
87.	IB(KT, NS)=KCC	SCAN
88.	IMATX(KN, LK)=KCC	SCAN
89.	C INCREMENT NR AND CONTINUE.	SCAN
90.	2 NR=NR+1	SCAN
91.	1 CONTINUE	SCAN
92.	C2.0 REARRANGE DATA IN IX ARRAY (IF NECESSARY) SO THAT DATA FOR	SCAN
93.	C CORE ATOMS ARE STORED IN THE FIRST LOCATIONS OF J INDEX	SCAN
94.	C FOLLOWED BY DATA OF NON-CORE SPECIES.	SCAN
95.	DO 9 J=NR, 5	SCAN
96.	J1=J	SCAN
97.	J2=J	SCAN
98.	IF(IX(KT, J, 6).EQ.0)GO TO 9	SCAN
99.	5 J1=J1-1	SCAN
100.	IF(J1.LT.NR)GO TO 9	SCAN
101.	IF(IX(KT, J1, 6).NE.0)GO TO 9	SCAN
102.	DO 7 N=1, 6	SCAN
103.	ITEM=IX(KT, J1, N)	SCAN
104.	IX(KT, J1, N)=IX(KT, J2, N)	SCAN
105.	7 IX(KT, J2, N)=ITEM	SCAN
106.	J2=J2-1	SCAN
107.	GO TO 9	SCAN
108.	9 CONTINUE	SCAN
109.	C3.0 SCAN OF GROUP NY HAS BEEN COMPLETED HENCE IX(KT, 1, 5) IS SET	SCAN
110.	C TO 1000.	SCAN
111.	IX(KT, 1, 5)=1000	SCAN
112.	RETURN	SCAN
113.	END	SCAN

SCANBR

1.		SUBROUTINE SCANBR(KCNERT,KAFTR)	SCANBR
2.	C	THIS SUBROUTINE COMPUTES THE ATOMIC COMPOSITION OF ALL LIGANDS	SCANBR
3.	C	BONDED TO BRANCH ATOM KCNERT AND ESTABLISHES THE SIMILARITIES	SCANBR
4.	C	OF THESE LIGANDS PROVIDING KCNERT IS NOT A RING ATOM.	SCANBR
5.		INTEGER WEIGHT(9)	SCANBR
6.		INTEGER PERTK(4,100),PERLIG(4,100)	SCANBR
7.		DIMENSION KTOT(5),JBR(100),LIGAND(5,4,100)	SCANBR
8.		COMMON/BLK2/WEIGHT,MMBY(9),MOLWT(100),IX(100,5,4),NC(100),KCC	SCANBR
9.		COMMON/BLK3/RING(40,30),IMATX(50,50),NMC(100),IBC(100),KON(100),	SCANBR
10.		LIDBR(100),IW(100,8),IRG,NBR	SCANBR
11.		COMMON/BLK4/MSC(60,50),MBS(60,2),NBR(60,20),IRC,NMPLUS,IRCTOT	SCANBR
12.		COMMON/BLK5/NDATA,MUMAT(5),MBC(50),MBS(2),JM,JY,LFLAG,LPLAGG	SCANBR
13.		EQUIVALENCE (KTOT(1),IBC(2,0)),(JBR(1),IMATX(2,43)),	SCANBR
14.		(LIGAND(1,1),IMATX(2,1)),(PERTK(1,1),NBR(2,5)),(PERLIG(1,1),	SCANBR
15.		ZNBR(42,1))	SCANBR
16.	C1.0	INITIALIZE VARIABLES.	SCANBR
17.		DO1 J=1,NDATA	SCANBR
18.		KTOT(J)=0	SCANBR
19.	1	CONTINUE	SCANBR
20.		KSUB=JBR(KCNERT)	SCANBR
21.		IF(KSUB.LT.P)GO TO 5	SCANBR
22.	C2.0	STORE SUM TOTAL OF THE ATOMIC COMPOSITIONS OF THE KCNERT	SCANBR
23.	C	LIGANDS IDENTIFIED THUS FAR IN KTOT.	SCANBR
24.		DO2 LX=2,KSUB	SCANBR
25.		DO3 J=1,NDATA	SCANBR
26.		KTOT(J)=KTOT(J)+LIGAND(J,LX,KCNERT)	SCANBR
27.	3	CONTINUE	SCANBR
28.	5	IF(NC(KCNERT).EQ.KON(KCNERT))GO TO 9	SCANBR
29.	C3.0	KCNERT HAS NON-CORE ATOM LIGANDS. COMPUTE THEIR ATOMIC	SCANBR
30.	C	COMPOSITIONS.	SCANBR
31.		LS=NC(KCNERT)+2	SCANBR
32.		LF=KON(KCNERT)+1	SCANBR
33.		DO7 LX=LS,LF	SCANBR
34.		KSUB=KSUB+1	SCANBR
35.		PERTK(KSUB,KCNERT)=IX(KCNERT,LX,1)	SCANBR
36.		CALL SUMATM(IX(KCNERT,LX,1),1,LIGAND(1,KSUB,KCNERT))	SCANBR
37.		CALL SUMATM(IX(KCNERT,LX,1),1,KTOT(1))	SCANBR
38.	7	CONTINUE	SCANBR
39.	9	IF(KAFTR.EQ.100)GO TO 12	SCANBR
40.	C4.0	KAFTR IS NOT THE FIRST BRANCH ATOM IDENTIFIED. FIND ITS ATOMIC	SCANBR
41.	C	COMPOSITION.	SCANBR
42.		CALL SUMATM(IX(KCNERT,1,1),1,KTOT(1))	SCANBR
43.		DO1 J=1,NDATA	SCANBR
44.		LIGAND(J,1,KCNERT)=MUMAT(J)-KTOT(J)	SCANBR
45.	11	CONTINUE	SCANBR
46.		PERTK(1,KCNERT)=KAFTR	SCANBR
47.	C5.0	SET VARIABLES JBR AND PERLIG.	SCANBR
48.	12	JBR(KCNERT)=KSUB	SCANBR
49.		DO13 J=1,KSUB	SCANBR
50.	13	PERLIG(J,KCNERT)=J	SCANBR
51.	CA.0	IF KCNERT IS NOT A RING ATOM, DETERMINE WHICH OF ITS LIGANDS	SCANBR
52.	C	ARE IDENTICAL TO WHICH (IF ANY).	SCANBR
53.		IF(/RC(KCNERT).EQ.0)CALL SETUP(KCNERT,KCNERT,1,1,0,JBR(KCNERT)-1,	SCANBR
54.		LIGAND(J,1))	SCANBR
55.		RETURN	SCANBR
56.		END	SCANBR

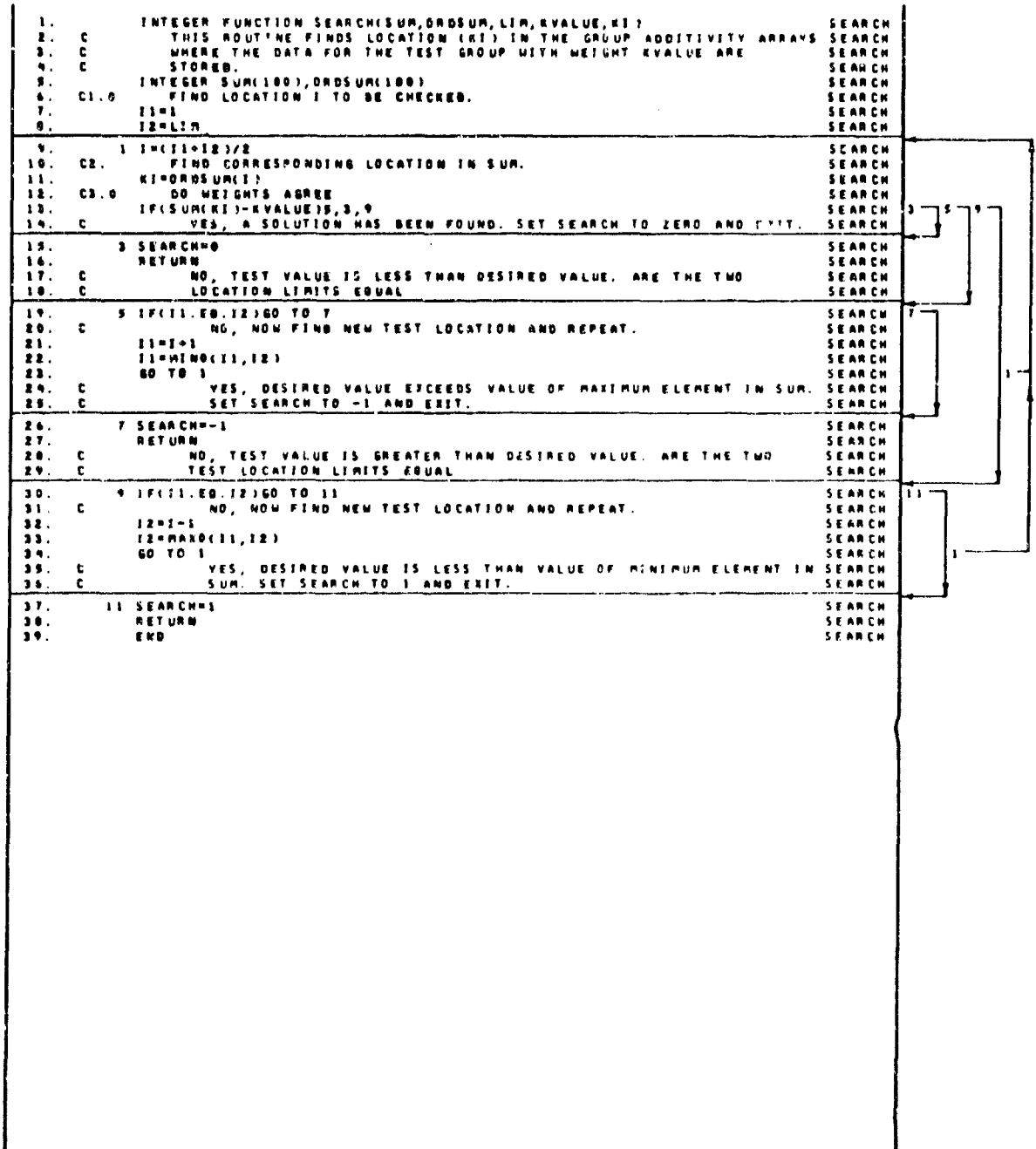
SCANCH

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1. SUBROUTINE SCANCH(KCBEF,KC,KCNEXT) SCANCH
2. C THIS SUBROUTINE COMPUTES THE ATOMIC COMPOSITION OF ALL LIGANDS SCANCH
3. C BONDED TO CHAIN ATOM KC AND ESTABLISHES THE SIMILARITIES OF SCANCH
4. C THESE LIGANDS PROVIDING KC IS NOT A RING ATOM. SCANCH
5. INTEGER WEIGHT(9) SCANCH
6. INTEGER PERTK(4,100),PERLIG(4,100) SCANCH
7. DIMENSION KTOT(5),JBR(100),LIGAND(5,4,100) SCANCH
8. COMMON/BLK2/WEIGHT,MWGT(9),MOLWT(100),IX(100,5,4),NC(100),KCC SCANCH
9. COMMON/BLK3/IRING(40,30),IMATX(50,80),MW(100),IBC(100),KOH(100), SCANCH
10. IJBR(100),IR(100,8),IRG,NDBR SCANCH
11. COMMON/BLK4/NBC(60,50),NBS(40,2),NBX(60,20),IRC,NONFUS,IRCTOT SCANCH
12. COMMON/BLK5/NDATM,NUMATM(5),MBC(50),MBS(2),JM,JY,LFLAG5,LFLAG6 SCANCH
13. EQUIVALENCE (KTOT(1),IBC(42,0)),(LIGAND(1,1,1),IMATX(2,1)), SCANCH
14. (JBR(1),IMATX(2,43)),(PERTK(1,1),NBX(2,5)),(PERLIG(1,1), SCANCH
15. NDBR(42,1))
16. C1.0 INITIALIZE VARIABLES. IF KCNEXT DOES NOT EXIST, SET IN=0. SCANCH
17. IN=1 SCANCH
18. IF(KCNEXT.EQ.1000)IN=0 SCANCH
19. IF(KCNEXT.EQ.1000)GO TO 3 SCANCH
20. C2.0 KC IS NOT THE FIRST ELEMENT IN THE CHAIN. THEREFORE KCBEF SCANCH
21. C EXISTS. COMPUTE ATOMIC COMPOSITION OF LIGAND KCBEF. SCANCH
22. IN=IN+1 SCANCH
23. DO1 J=1,NDATM SCANCH
24. LIGAND(J,IN,KC)=KTOT(J) SCANCH
25. CONTINUE SCANCH
26. PERTK(IN,KC)=KCBEF SCANCH
27. 3 IF(NC(KC).EQ.KON(KC))GO TO 7 SCANCH
28. C3.0 KC HAS NON-CORE ATOM LIGANDS. COMPUTE THEIR ATOMIC COMPOSITIONS SCANCH
29. LS=NC(KC)+2 SCANCH
30. LF=KON(KC)+1 SCANCH
31. DO5 LY=LS,LF SCANCH
32. IN=IN+1 SCANCH
33. PERTK(IN,KC)=IX(KC,LY,1) SCANCH
34. CALL SUMATM(IX(KC,LY,1),1,LIGAND(1,IN,KC)) SCANCH
35. CALL SUMATM(IX(KC,LY,1),1,KTOT(1)) SCANCH
36. CONTINUE SCANCH
37. C4.0 STORE ATOMIC COMPOSITION OF ATOM KC IN KTOT SCANCH
38. 7 CALL SUMATM(IX(KC,1,1),1,KTOT(1)) SCANCH
39. IF(KCNEXT.EQ.1000)GO TO 11 SCANCH
40. C5.0 KCNEXT EXISTS. COMPUTE ITS ATOMIC COMPOSITION. SCANCH
41. DO9 J=1,NDATM SCANCH
42. LIGAND(J,1,KC)=NUMATM(J)-KTOT(J) SCANCH
43. CONTINUE SCANCH
44. PERTK(1,KC)=KCNEXT SCANCH
45. C6.0 SET VARIABLES JBR AND PERLIG. SCANCH
46. 11 JBR(KC)=IN SCANCH
47. DO13 J=1,IN SCANCH
48. PERLIG(J,KC)=J SCANCH
49. C7.0 IF KC IS NOT RING ATOM, DETERMINE WHICH OF ITS LIGANDS ARE SCANCH
50. C IDENTICAL TO WHICH (IF ANY). SCANCH
51. IF(IBC(KC).EQ.0)CALL SETUP(KC,KC,1,1,0,JBR(KC)-1,JBR(KC),1) SCANCH
52. RETURN SCANCH
53. END SCANCH

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SEARCH



SETUP

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1. SUBROUTINE SETUP(KCX001,KCX002,N0001,N0002,MULT1,LF,KF,MULT2) SETUP
2. C THIS SUBROUTINE PROCESSES THE COMPARISON OF LIGANDS BONDED TO SETUP
3. C THE SAME OR DIFFERENT CENTRAL CORE ATOMS BY FIRST COMPARING SETUP
4. C THEIR ATOMIC COMPOSITIONS. IF (1) THE LATTER ARE IDENTICAL AND SETUP
5. C (2) THE LIGANDS ARE BOTH NON-CORE TYPES, THE LIGANDS ARE SETUP
6. C IDENTICAL. IF (1) IS TRUE, BUT THE LIGANDS ARE CORE ATOMS SETUP
7. C THEIR IDENTITY MUST BE CHECKED FURTHER. SETUP
8. C INTEGER SYMX(4),SYMBOL(9),GRID(50,80) SETUP
9. C INTEGER WEIGHT(9) SETUP
10. C INTEGER PERTKC(4,100),PERLIB(4,100) SETUP
11. C DIMENSION KCX001(3),KCX002(3),KNAME(4,3,2),LIGAND(5,4,100), SETUP
12. C IARR(100),NOSAME(8,100),NTOTAL(3,100),MRS1(4),MRS2(4) SETUP
13. C COMMON/BLK1/NO,NOS,SYMX,SYMBOL,NOVAL(9),GRID SETUP
14. C COMMON/BLK2/WEIGHT,MWGT(9),MOLWT(100),I(100,5,6),KCC(100),KCC SETUP
15. C COMMON/BLK3/IRING(40,36),IMATX(50,80),NMC(100),IB(100),KOM(100), SETUP
16. C IIDBR(100),ID(100,8),IRG,NDBR SETUP
17. C COMMON/BLK4/NBC(60,50),NBS(60,2),NBX(60,20),IRC,NONFUS,INCTOT SETUP
18. C COMMON/BLK5/NOATA,NUMATM(5),MBC(50),MBS(2),JM,JV,LFLAG5,LFLAG6 SETUP
19. C EQUIVALENCE (KNAME(1,1,1),IB(14,1)),(LIGAND(1,1,1),IMATX(2,1)), SETUP
20. C I(PERTKC(1,1),NBX(2,5)),(PERLIB(1,1),NBX(42,11)),(MRS(1),IB(62,3)), SETUP
21. C Z(NOSAME(1,1),GRID(4,54)),(NTOTAL(1,1),GRID(4,70)),(MRS1(1), SETUP
22. C 3NBX(20,20)),(MRS2(1),NBX(24,20)) SETUP
23. C1.0 INITIALIZE VARIABLES. SETUP
24. C KCX=KCX001(1) SETUP
25. C DO1 K=1,3 SETUP
26. C NOSAME(K,KCX)=0 SETUP
27. C NTOTAL(K,KCX)=0 SETUP
28. C DO1 J=1,4 SETUP
29. C KNAME(J,K,1)=0 SETUP
30. C KNAME(J,K,2)=0 SETUP
31. C 1 CONTINUE SETUP
32. C DO100 K=1,KCC SETUP
33. C MRS(K)=0 SETUP
34. C2.0 ARE LIGANDS TO BE COMPARED BONDED TO SAME OR DIFFERENT CORE SETUP
35. C ATOMS SETUP
36. C IF(KCX001(1).EQ.KCX002(1))GO TO 3 SETUP
37. C DIFFERENT. SET ARRAYS ACCORDINGLY. SETUP
38. C DO2 K=1,4 SETUP
39. C MRS1(K)=K SETUP
40. C MRS2(K)=K+4 SETUP
41. C 2 CONTINUE SETUP
42. C GO TO 5 SETUP
43. C SAME. SET ARRAYS ACCORDINGLY. SETUP
44. C 3 DO4 K=1,4 SETUP
45. C MRS1(K)=K SETUP
46. C MRS2(K)=K SETUP
47. C 4 CONTINUE SETUP
48. C 5 KY=0 SETUP
49. C II=1 SETUP
50. C3.0 START EXECUTION OF CYCLE THAT ESTABLISHES THE SIMILARITIES OF SETUP
51. C THE VARIOUS LIGANDS. SETUP
52. C DO27 M=1,N0001 SETUP
53. C KC1=KCX001(M) SETUP
54. C NI=1+MULT1*M SETUP
55. C DO27 N=N1,N0002 SETUP
56. C KC2=KCX002(N) SETUP
57. C DO23 L=1,LF SETUP
58. C LG1=PERLIB(L,KC1) SETUP
59. C K1 IS A LIGAND BONDED TO KC1. SETUP
60. C K1=PERTKC(LG1,KC1) SETUP
61. C K1=1+MULT2*L SETUP
62. C DO23 K=K1,KF SETUP
63. C LG2=PERLIB(K,KC2) SETUP
64. C K2 IS A LIGAND BONDED TO KC2. SETUP
65. C K2=PERTKC(LG2,KC2) SETUP
66. C IF(K1.EQ.KC2.OR.K2.EQ.KC1)GO TO 23 SETUP
67. C NEITHER K1 NOR K2 ARE EQUAL TO THE CORE ATOM TO WHICH THE SETUP
68. C OTHER IS BONDED. SETUP
69. C KEQUAL=0 SETUP
70. C CHECK WHETHER THE ATOMIC COMPOSITIONS OF LIGANDS K1 AND K2 SETUP
71. C ARE EQUAL. SETUP
72. C DO7 J=1,NOATA SETUP
73. C IF(LIGAND(J,LG1,KC1).NE.LIGAND(J,LG2,KC2))GO TO 7 SETUP
74. C KEQUAL=KEQUAL+1 SETUP

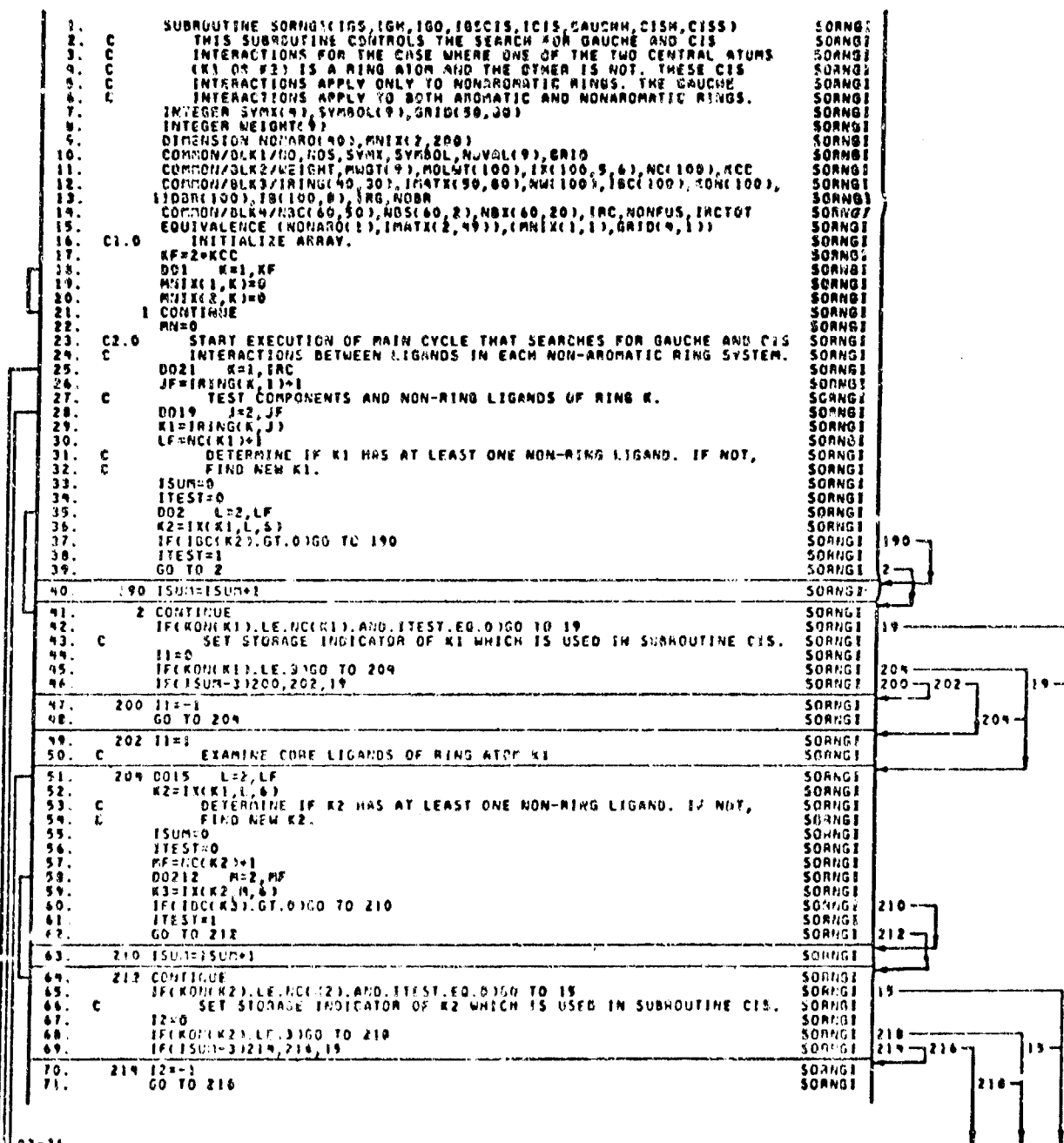
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75.	7	CONTINUE	SETUP	
76.		IF(KEQUAL.NE.5)GO TO 23	SETUP	23
77.	C	YES THEY ARE.	SETUP	
78.		IF(NOD02.EQ.1)GO TO 8	SETUP	8
79.	C	TWO OR MORE CENTRAL ATOMS OF TYPE KC2 ARE BEING USED.	SETUP	
80.		J1=N	SETUP	
81.		J2=N	SETUP	
82.		GO TO 9	SETUP	9
83.	C	ONLY ONE CENTRAL ATOM OF TYPE KC2 IS BEING USED.	SETUP	
84.	8	J1=L	SETUP	
85.		J2=K	SETUP	
86.	9	IF(K1.GT.0.AND.K2.GT.0)GO TO 11	SETUP	11
87.	C	K1 AND K2 ARE NOT BOTH CORE ATOMS.	SETUP	
88.		IF(K1+K2.EQ.0.OR.K1.NE.K2)GO TO 23	SETUP	23
89.	C	K1 AND K2 ARE BOTH IDENTICAL NON-CORE ATOMS. VERIFY THEIR	SETUP	
90.	C	SINGULARITY AND STORE THEIR IDENTIFICATION VARIABLES.	SETUP	
91.		CALL SAME(KC1,K1,K2,MRS1(J1),MRS2(J2))	SETUP	
92.		GO TO 23	SETUP	23
93.	C	K1 AND K2 ARE LIGANDS WITH COMPLEX STRUCTURES. TO WHICH	SETUP	
94.	C	IDENTITY SET DO K1 AND K2 BELONG	SETUP	
95.	11	IF(MRM(K1).EQ.0)GO TO 13	SETUP	13
96.	C	K1 FOUND IDENTICAL PREVIOUSLY. RETRIEVE ITS IDENTITY SET	SETUP	
97.	C	NUMBER.	SETUP	
98.		I1=MRM(K1)	SETUP	
99.		GO TO 19	SETUP	19
100.	13	IF(MRM(K2).EQ.0)GO TO 15	SETUP	15
101.	C	K2 FOUND IDENTICAL PREVIOUSLY. RETRIEVE ITS IDENTITY SET	SETUP	
102.	C	NUMBER.	SETUP	
103.		I1=MRM(K2)	SETUP	
104.		GO TO 17	SETUP	17
105.	C	NEITHER K1 NOR K2 WERE FOUND IDENTICAL PREVIOUSLY. ASSIGN	SETUP	
106.	C	THEM A NEW IDENTITY SET NUMBER = KV.	SETUP	
107.	15	KV=KV+1	SETUP	
108.		I1=KV	SETUP	
109.	17	MRM(K1)=I1	SETUP	
110.	19	MRM(K2)=I1	SETUP	
111.		KSAME(J1,I1,1)=1	SETUP	
112.		KSAME(J2,I1,2)=1	SETUP	
113.	23	CONTINUE	SETUP	
114.	27	CONTINUE	SETUP	
115.	C4.0	DETERMINE WHETHER COMPLEX LIGANDS ON KC1 AND KC2 ARE IDENTICAL.	SETUP	
116.		IF(KV.GT.0)CALL EQUAL(KCX001,KCX002,NOD01,NOD02,MULT1,LF,KF,	SETUP	
117.		MULT2,KV,0)	SETUP	
118.		RETURN	SETUP	
119.		END	SETUP	

SHIFT

1.		SUBROUTINE SHIFT(JC,KC,MFLAG)	SHIFT
2.	C	THIS SUBROUTINE SWITCHES DATA OF LIGAND CONTAINED IN COLUMN	SHIFT
3.	C	J=2 OF IX(JC,J,1) WITH DATA OF LIGAND CORRESPONDING TO CORE	SHIFT
4.	C	ATOM KC.	SHIFT
5.		INTEGER WEIGHT(4)	SHIFT
6.		COMMON/BLK2/WEIGHT,MWGT(9),MOLWT(100),IX(100,5,6),NC(100),KCC	SHIFT
7.		COMMON/BLK3/IRING(40,30),IMATX(50,80),NW(100),IBC(100),KON(100),	SHIFT
8.		I/OBR(100),IB(100,8),IHB,MOBR	SHIFT
9.	C1.0	SET IX(JC,1,4) EQUAL TO NEW PARENT CORE ATOM.	SHIFT
10.		IX(JC,1,4)=IX(KC,1,6)	SHIFT
11.	C2.0	FIND LOCATION J IN IX(JC,J,1) CONTAINING CORE ATOM DATA. THEN	SHIFT
12.	C	SHIFT DATA FROM COLUMN J=2 TO J.	SHIFT
13.		DO33 J=3,5	SHIFT
14.		IF(IX(JC,J,6).NE.IX(JC,1,4))GO TO 33	SHIFT
15.		DO32 LL=1,6	SHIFT
16.		IX(JC,J,LL)=IX(JC,2,LL)	SHIFT
17.		32 CONTINUE	SHIFT
18.		GO TO 39	SHIFT
19.		33 CONTINUE	SHIFT
20.	C3.0	NOW STORE DATA FOR CORE ATOM IX(KC,1,6) INTO J=2 COLUMN	SHIFT
21.	C	OF IX(JC,J,1). IN SO DOING, MAKE APPROPRIATE CHANGES FOR	SHIFT
22.	C	VECTOR DIRECTION.	SHIFT
23.		39 DO34 J=1,3	SHIFT
24.		34 IX(JC,2,J)=IX(KC ,1,J)	SHIFT
25.		KS=IX(JC,1,2)	SHIFT
26.		LS=IX(JC,1,3)	SHIFT
27.		DO36 L=3,5	SHIFT
28.		IF(IX(KC ,L,2).EQ.KS.AND.IX(KC ,L,3).EQ.LS)GO TO 38	SHIFT
29.		36 CONTINUE	SHIFT
30.		38 IX(JC,2,4)=IX(KC ,L,4) + 4	SHIFT
31.		IF(IX(JC,2,4).GT.8)IX(JC,2,4)=IX(JC,2,4)-8	SHIFT
32.		IX(JC,2,5)=IX(KC ,L,5)	SHIFT
33.		IX(JC,2,6)=IX(KC ,1,6)	SHIFT
34.	C4.0	RESET VALUES OF IB PERTAINING TO JC IF MFLAG IS NOT ZERO.	SHIFT
35.	C	MFLAG IS NOT ZERO IN FIRST SECTION OF PROGRAM.	SHIFT
36.		IF(MFLAG.EQ.0)RETURN	SHIFT
37.		IB(JC,1)=IX(JC,3,6)	SHIFT
38.		IB(JC,2)=IX(JC,4,6)	SHIFT
39.		IB(JC,3)=IX(JC,5,6)	SHIFT
40.		RETURN	SHIFT
41.		END	SHIFT

SORNGI



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72.	216 12=1		SORNGI
73.	C	HAS THE BOND PAIR K1 AND K2 BEEN TESTED PREVIOUSLY	SORNGI
74.	218	IF(MN.EQ.0)GO TO 5	SORNGI
75.		DO3 LL=1,MN	SORNGI
76.		IF(MNIX(1,LL).EQ.K1.AND.MNIX(2,LL).EQ.K2.OR.MNIX(1,LL).EQ.K2.AND.	SORNGI
77.		MNIX(2,LL).EQ.K1)GO TO 19	SORNGI
78.		3 CONTINUE	SORNGI
79.	C	PAIR HAS NOT YET BEEN TESTED. SET ARRAY INDICATORS.	SORNGI
80.	5	MN=MN+1	SORNGI
81.		MNIX(1,MN)=K1	SORNGI
82.		MNIX(2,MN)=K2	SORNGI
83.	C	IS K2 A RING ATOM	SORNGI
84.		IF(JBC(K2).GT.0)GO TO 13	SORNGI
85.	C	NO. IS BOND BETWEEN K1 AND K2 SINGLE OR DOUBLE	SORNGI
86.		IF(CIX(K1,L,5)-2)7,13,15	SORNGI
87.	C	SINGLE. SEARCH FOR GAUCHE INTERACTIONS.	SORNGI
88.	7	CALL GAUCHE(K1,K2,I65,I6M,I6O,GAUCHN)	SORNGI
90.		GO TO 19	SORNGI
91.	C	DOUBLE. SEARCH FOR CIS INTERACTIONS.	SORNGI
92.	C	YES, SEARCH FOR CIS INTERACTIONS IF RING IS NONAROMATIC.	SORNGI
93.	13	IF(NONAROM(K).EQ.0)GO TO 19	SORNGI
94.		CALL CISCOR(K1,K2,I1,I2,I65,I6SCIS,ICIS,CISM,CISS)	SORNGI
95.	15	CONTINUE	SORNGI
96.	19	CONTINUE	SORNGI
97.	21	CONTINUE	SORNGI
98.		RETURN	SORNGI
99.		END	SORNGI

STAND

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1. SUBROUTINE STANDISERR)
2. C THIS SUBROUTINE IS THE CONTROL ELEMENT FOR SECTION ONE OF THE STAND
3. C PROGRAM. THIS SECTION IDENTIFIES THE GROUPS AND GROUP STAND
4. C COMPONENTS OF THE MOLECULE AS WELL AS THE ATOMIC COORDINATES, STAND
5. C BOND VECTORS AND BOND TYPES. THE GROUP WEIGHTS ARE ALSO STAND
6. C ASSIGNED. FOR SOME UNSATURATED RING COMPOUNDS THE LATTER IS STAND
7. C ALTERED IN SECTION THREE OF THE PROGRAM. STAND
8. C INTEGER SYM(4), SYMBOL(9), GRID(50,50) STAND
9. C INTEGER WEIGHT(9) STAND
10. C DIMENSION MNC(100,2), ICN(100) STAND
11. C COMMON/BL1/ND, NDS, SYM, SYMBOL, NOVAL(9), GRID STAND
12. C COMMON/BL2/WEIGHT, WGT(9), MOLWT(100), IX(100,5,4), NC(100), KCC STAND
13. C COMMON/BL3/TRING(40,30), IMATX(50,80), NM(100), IRL(100), ROK(100), STAND
14. C IORR(100), IRL(100,8), IRL NDBA STAND
15. C COMMON/BL4/NDCL(40,50), NDS(40,2), NBR(40,20), IRC, NONFUS, IRECTO STAND
16. C COMMON/BL5/NDPTM, NUMATM(5), NBC(50), MBS(2), JM, JY, LFLAG, LFLAGB STAND
17. C EQUIVALENCE (MBS, NBC(3,1)), (MNC(1,1), NBC(4,1)), (LSUB, NBC(2,7)), STAND
18. C (ICN(1), NBC(3,7)) STAND
19. C1.0 INITIALIZE VARIABLES. STAND
20. C MRM=0 STAND
21. C IRG=0 STAND
22. C ITZ=0 STAND
23. C CONTENTS OF IX ARRAY (IX(M,N,J)) CONTAINS GRID DATA FOR CORE STAND
24. C ATOM(M) AT M=1 AND FOR LIGANDS AT M=2 TO M=5. CONTENTS OF STAND
25. C J COLUMN - J=1 CHEMICAL SYMBOL OF COMPONENT, J=2 GRID ROW STAND
26. C COORDINATE, J=3 GRID COLUMN COORDINATE, M=1 AND J=4 GROUP STAND
27. C NUMBER OF PARENT CORE ATOM, M NOT 1 AND J=4 DIRECTION OF STAND
28. C BOND FROM CORE ATOM TO LIGAND, J=5 BOND TYPE, J=6 GROUP STAND
29. C NUMBER OF CORE ATOM. STAND
30. C DO5 M=1,100 STAND
31. C DO1 M=1,5 STAND
32. C DO1 J=1,6 STAND
33. C 1 IX(M,N,J)=0 STAND
34. C DO3 J=1,8 STAND
35. C 3 JG(M,J)=0 STAND
36. C MOLWT(0)=0 STAND
37. C NCM(0)=0 STAND
38. C 5 CONTINUE STAND
39. C DO7 L=1,80 STAND
40. C DO7 K=1,50 STAND
41. C 7 IMATX(K,L)=0 STAND
42. C DO9 L=1,9 STAND
43. C NUMATM(L)=0 STAND
44. C 9 CONTINUE STAND
45. C IRC=0 STAND
46. C2.0 FIND FIRST NON-BLANK CHARACTER ON INPUT CARD. PROCEED TO 17. STAND
47. C DO11 L=1,99 STAND
48. C DO11 K=1,90 STAND
49. C IF(GRID(L,K).NE.SYM(0))GO TO 17 STAND
50. C 11 CONTINUE STAND
51. C PRINT ERROR MESSAGE, SET ERROR FLAG, AND TERMINATE CASE STAND
52. C CALCULATION. STAND
53. C 12 WRITE(6,13) STAND
54. C 13 FORMAT(// 1NO,394,50)STRUCTURE INPUT ARRAY INCORRECT CASE TERMIN STAND
55. C TATED. ) STAND
56. C 15 IERR=1 STAND
57. C RETURN STAND
58. C3.0 IS CHARACTER A CHEMICAL SYMBOL STAND
59. C 17 DO23 L=1,8 STAND
60. C IF(GRID(L,LI-SYM(0)))23,19,23 STAND
61. C NO, MOLECULE IS A FREE RADICAL. PRINT OUT ERROR MESSAGE STAND
62. C 19 WRITE(6,21)A,L STAND
63. C 21 FORMAT(// 1NO,438,32)FREE RADICAL AT GRID COORDINATES,14,14,14, STAND
64. C 13N. ) STAND
65. C GO TO 18 STAND
66. C 23 CONTINUE STAND
67. C YES, CHARACTER IS A CHEMICAL SYMBOL. NOW IDENTIFY IT. STAND
68. C NUM=0 STAND
69. C CALL IDENT(NUM,K,L,M,IERR) STAND
70. C IF(IERR.EQ.1)RETURN STAND
71. C K=3 STAND
72. C KCC=0 STAND
73. C MRM=0 STAND

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74 4.0 DETERMINE IF FIRST CHEMICAL SYMBOL IS A CORE ATOM. IF NOT, FIND STANB
75 C CORE SYMBOLS. STANB
76 CALL FINDNCL,2,L,R,HNA,NA,ZERR) STANB
77 IF ZERR,GO TO RETURN STANB
78 C SET VARIABLES IN AREA. STANB
79 IXC(1,1)=R STANB
80 IXC(1,2)=H STANB
81 IXC(1,3)=L STANB
82 IXC(1,4)=NA STANB
83 IXC(1,5)=ZERR STANB
84 IXC(1,6)=R STANB
85 IXC(1,7)=H STANB
86 IXC(1,8)=L STANB
87 US.0 IDENTIFY LIGANDS BONDED TO CORE ATOM JC. STANB
88 CALL SCANJC,NA,NA,NUM,K,L,ZERR) STANB
89 IF ZERR,GO TO RETURN STANB
90 IXC(1,9)=IXC(2,1) STANB
91 IXC(1,10)=IXC(2,2) STANB
92 IXC(1,11)=IXC(2,3) STANB
93 IXC(1,12)=IXC(2,4) STANB
94 IXC(1,13)=IXC(2,5) STANB
95 IXC(1,14)=IXC(2,6) STANB
96 IXC(1,15)=IXC(2,7) STANB
97 IXC(1,16)=IXC(2,8) STANB
98 IXC(1,17)=IXC(2,9) STANB
99 IXC(1,18)=IXC(2,10) STANB
100 IXC(1,19)=IXC(2,11) STANB
101 IXC(1,20)=IXC(2,12) STANB
102 IXC(1,21)=IXC(2,13) STANB
103 IXC(1,22)=IXC(2,14) STANB
104 IXC(1,23)=IXC(2,15) STANB
105 IXC(1,24)=IXC(2,16) STANB
106 IXC(1,25)=IXC(2,17) STANB
107 IXC(1,26)=IXC(2,18) STANB
108 IXC(1,27)=IXC(2,19) STANB
109 IXC(1,28)=IXC(2,20) STANB
110 IXC(1,29)=IXC(2,21) STANB
111 IXC(1,30)=IXC(2,22) STANB
112 IXC(1,31)=IXC(2,23) STANB
113 IXC(1,32)=IXC(2,24) STANB
114 IXC(1,33)=IXC(2,25) STANB
115 IXC(1,34)=IXC(2,26) STANB
116 IXC(1,35)=IXC(2,27) STANB
117 IXC(1,36)=IXC(2,28) STANB
118 IXC(1,37)=IXC(2,29) STANB
119 IXC(1,38)=IXC(2,30) STANB
120 IXC(1,39)=IXC(2,31) STANB
121 IXC(1,40)=IXC(2,32) STANB
122 IXC(1,41)=IXC(2,33) STANB
123 IXC(1,42)=IXC(2,34) STANB
124 IXC(1,43)=IXC(2,35) STANB
125 IXC(1,44)=IXC(2,36) STANB
126 IXC(1,45)=IXC(2,37) STANB
127 IXC(1,46)=IXC(2,38) STANB
128 IXC(1,47)=IXC(2,39) STANB
129 IXC(1,48)=IXC(2,40) STANB
130 IXC(1,49)=IXC(2,41) STANB
131 IXC(1,50)=IXC(2,42) STANB
132 IXC(1,51)=IXC(2,43) STANB
133 IXC(1,52)=IXC(2,44) STANB
134 IXC(1,53)=IXC(2,45) STANB
135 IXC(1,54)=IXC(2,46) STANB
136 IXC(1,55)=IXC(2,47) STANB
137 IXC(1,56)=IXC(2,48) STANB
138 IXC(1,57)=IXC(2,49) STANB
139 IXC(1,58)=IXC(2,50) STANB
140 IXC(1,59)=IXC(2,51) STANB
141 IXC(1,60)=IXC(2,52) STANB
142 IXC(1,61)=IXC(2,53) STANB
143 IXC(1,62)=IXC(2,54) STANB
144 IXC(1,63)=IXC(2,55) STANB

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148.		TSUB=SUB+1	STAND
149.	C	SET VARIABLES DEPENDING UPON BONDING PROPERTIES OF UC.	STAND
147.		IF(NC=1) 147, 55, 55	STAND
148.	C	UC IS BRANCH ATOM.	STAND
149.		53 IF(NC=1)	STAND
150.		MM(C=MM, 1)=MM(C)-1	STAND
151.		MM(C=MM, 2)=MC	STAND
152.	C	UC IS CORE ATOM. RESTART CYCLE.	STAND
153.		55 ICM(SUB)=MC	STAND
154.		60 TO 51	STAND
155.	C	UC IS TERMINAL CORE ATOM.	STAND
156.		57 IF(UTZ.EQ.0) 50 TO 61	STAND
157.		ITZ=0	STAND
158.		IF(UTZ.C, 1, 4) NE. I(UCPV, 1, 5) CALL SHPTICC, 4LP, 1)	STAND
159.		60 TO 55	STAND
160.		61 ICM(SUB)=MC	STAND
161.	C11.0	FIND NEW BRANCH ATOM.	STAND
162.	C	IF NO BRANCH ATOM PRESENT, GO TO 81	STAND
163.		63 IF(ARM.EQ.0) 50 TO 65	STAND
164.	C	FIND POTENTIAL BRANCH ATOM. IF NONE PRESENT, GO TO 65	STAND
165.		65 DO 67 J=1, NR	STAND
166.		IF(NC=C, 1, 2) NE. 0) 50 TO 69	STAND
167.		67 CONTINUE	STAND
168.		60 TO 55	STAND
169.		69 MM(C, 1)=MM(C, 1)-1	STAND
170.		MM(C, 2)=R	STAND
171.		MC=MC	STAND
172.	C	FIND CORE ATOM BONDED TO BRANCH ATOM WHICH HAS NOT YET	STAND
173.	C	BEEN SCANNED AND TRANSFER TO 51. IF NONE, FIND OTHER	STAND
174.	C	BRANCH ATOM.	STAND
175.		IF(NC=C)	STAND
176.		DO 74 J=1, NR	STAND
177.		IF(NC=C, 1, 2) NE. 0) 50 TO 74	STAND
178.		74 CONTINUE	STAND
179.		IF(NC.C, 2) NE. 0) 50 TO 74	STAND
180.		72 CONTINUE	STAND
181.		IF(NC.EQ.0) 50 TO 65	STAND
182.		60 TO 51	STAND
183.		74 CONTINUE	STAND
184.		60 TO 65	STAND
185.	C12.0	SET AC AND NM COUNTER ARRAYS AND WEIGHT CONNECTIONS TO CORE	STAND
186.	C	ATOMS. CHECK VALENCE OF ALL ATOMS.	STAND
187.		85 DO 93 K=1, MCC	STAND
188.		MM(C)=0	STAND
189.		MM(C)=0	STAND
190.		MM(C)=0	STAND
191.		MM(C)=0	STAND
192.		IF(NC=C, 1, 2) NE. 0) 50 TO 64	STAND
193.		MM(C)=MM(C)+1	STAND
194.		60 TO 51	STAND
195.		86 IF(NC=C, 1, 2) NE. 0) 50 TO 91	STAND
196.		IF(NC=C, 1, 2) NE. 0) 50 TO 91	STAND
197.		IF(NC=C, 1, 2) NE. 0) 50 TO 91	STAND
198.	C	NON-CORE ATOM BONDED TO MC HAS CORRECT VALENCE.	STAND
199.		87 MM(C)=1	STAND
200.		89 CONTINUE	STAND
201.		91 IF(NC=C, 1, 2) NE. 0) 50 TO 91	STAND
202.		IF(NC=C, 1, 2) NE. 0) 50 TO 91	STAND
203.	C	CORE ATOM MC HAS CORRECT VALENCE.	STAND
204.		MM(C)=MM(C)	STAND
205.		IF(NC=C, 1, 2) NE. 0) 50 TO 91	STAND
206.		MM(C)=1	STAND
207.		MM(C)=MM(C)+MM(C)	STAND
208.		MM(C)=1, 5)=0	STAND
209.		93 CONTINUE	STAND
210.	C13.0	STORE GROUP NUMBER OF BRANCH CORE ATOMS IN ICMR AND TOTAL	STAND
211.	C	NUMBER OF ENTRIES IN NOBA.	STAND
212.		JJ=0	STAND
213.		IF(NC.EQ.0) 50 TO 97	STAND

214.	LL=1	STAND
215.	IF(MNC(1,2).EQ.1.AND.MC(1).LE.2)LL=2	STAND
216.	DO 95 L=LL,MRM	STAND
217.	JJ=JJ+1	STAND
218.	TDNR(JJ)=MNC(L,2)	STAND
219.	95 CONTINUE	STAND
220.	97 NOBR=JJ	STAND
221.	RETURN	STAND
222.	END	STAND

SURATM

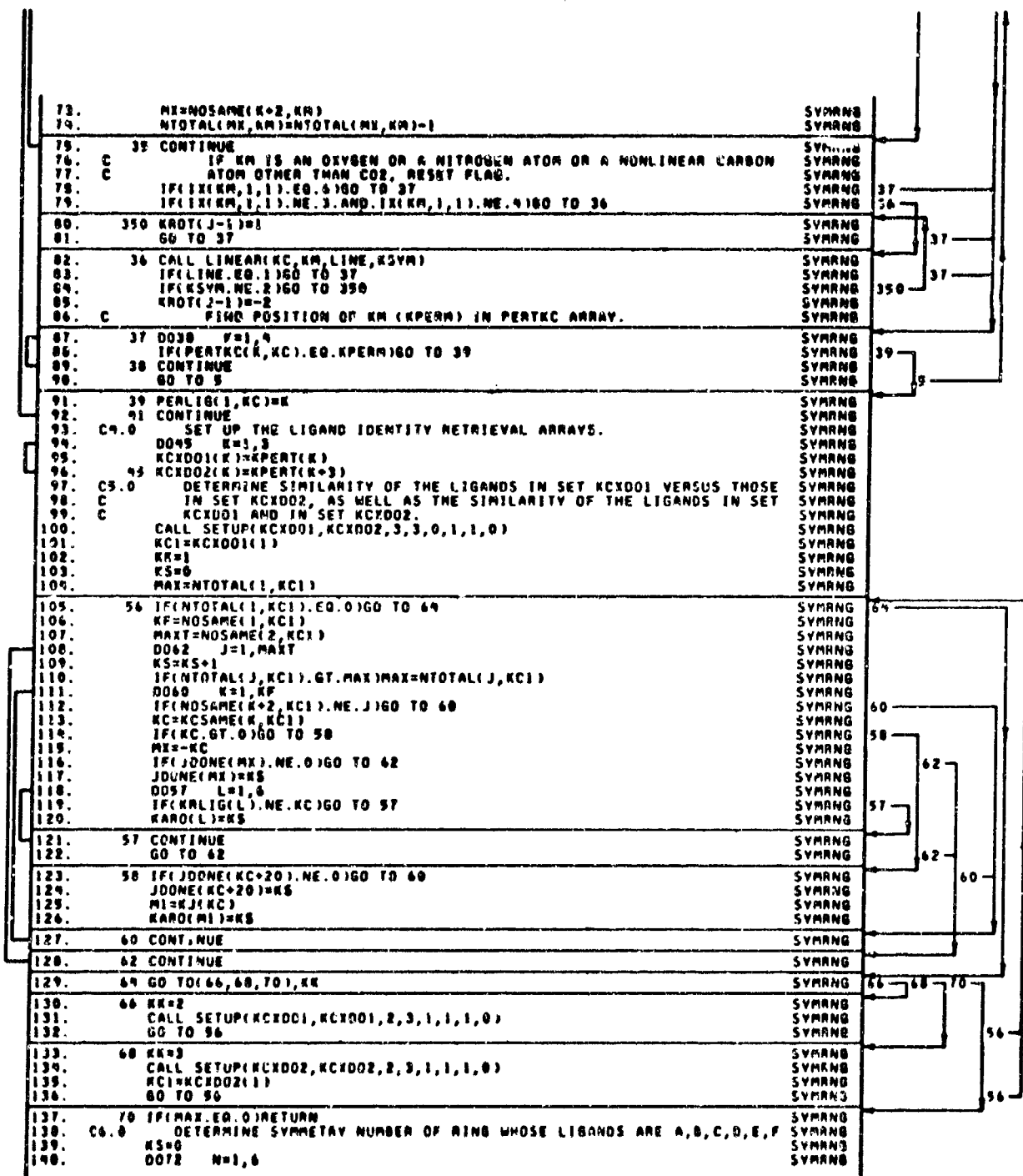
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1.      SUBROUTINE SURATM(M, KP, NUMATM)
2.      C      THIS SUBROUTINE ADDS OR SUBTRACTS (WHEN KP=1 OR -1) THE NUMBER
3.      C      OF EACH ELEMENT PRESENT IN THE CHEMICAL SYMBOL REPRESENTED BY
4.      C      M TO (FROM) THE LOCATION ASSIGNED THAT PARTICULAR ELEMENT IN
5.      C      ARRAY NUMATM.
6.      C      DIMENSION NUMATM(8)
7.      C      COMMON/BLK6/NUMFR(24)
8.      C      TEST SYMBOL CODE
9.      C      IF (M.LT.6) GO TO 4
10.     C      SYMBOL CODE IS 6 OR GREATER, HENCE IT REPRESENTS MULTI-
11.     C      CHARACTER SPECIES. FIND THE NUMBER OF EACH ELEMENT IT
12.     C      CONTAINS AND ADD (OR SUBTRACT) TO (FROM) CORRESPONDING
13.     C      LOCATION IN NUMATM DEPENDING ON VALUE OF KP.
14.     C      NI=1+(M-6)*6
15.     C      DO2   J=1,9,2
16.     C      NI=NI+J-1
17.     C      NV=NUMFR(NI)
18.     C      NUMATM(NV)=NUMATM(NV)+NUMFR(NI)*KP
19.     C      2 CONTINUE
20.     C      RETURN
21.     C      SYMBOL REPRESENTS A SINGLE ELEMENT. ADD KP (EQUAL TO +1 OR
22.     C      -1) TO LOCATION OF NUMATM THAT CORRESPONDS TO THIS ELEMENT.
23.     C      4 NUMATM(M)=NUMATM(M)+KP
24.     C      RETURN
25.     C      END

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SYMRNG

1.		SUBROUTINE SYMRNG(KCX,NOSHC)	SYMRNG
2.	C	THIS SUBROUTINE COMPUTES THE EXTERNAL ROTATIONAL SYMMETRY	SYMRNG
3.	C	NUMBER OF AROMATIC, MONOCYCLIC BENZENE-TYPE STRUCTURES.	SYMRNG
4.		INTEGER SYMX(4),SYMBOL(9),GRID(50,50)	SYMRNG
5.		INTEGER WEIGHT(9)	SYMRNG
6.		INTEGER PERTKC(4,100),PERLIG(4,100)	SYMRNG
7.		DIMENSION KBENZ(50),KCSAME(6,100),NOSAME(8,100),NTOTAL(3,100),	SYMRNG
8.		IKJ(100),KPERT(6),KCIDO(3),KCRD(2,3),KROT(6),MATRIX(6,3),KARO(6),	SYMRNG
9.		ZKZERO(6),KSET(3),JDONE(120),KRLIG(6)	SYMRNG
10.		COMMON/BLK1/NO,NOS,SYMX,SYMBOL,NOVAL(9),GRID	SYMRNG
11.		COMMON/BLK2/WEIGHT,MMGT(9),MOLWT(100),IX(100,5,6),NC(100),KCC	SYMRNG
12.		COMMON/BLK3/IRING(40,30),IMATX(50,50),MM(100),IBC(100),KON(100),	SYMRNG
13.		1IDBR(100),IB(100,8),IAB,NDBR	SYMRNG
14.		COMMON/BLK4/NBC(60,50),NBS(60,2),NBX(60,20),IRC,NONFUS,IRCTOT	SYMRNG
15.		COMMON/BLK5/NDATM,NUMATM(5),NBC(50),MBS(2),JU,JV,LFLAG5,LFLAG6	SYMRNG
16.		EQUIVALENCE (NBENZ,IR(10,1)),(KBENZ(1),IB(53,1)),(KCSAME(1,1),	SYMRNG
17.		IGRID(4,42)),(NOSAME(1,1),GRID(4,54)),(NTOTAL(1,1),GRID(4,70)),	SYMRNG
18.		ZI(PERTKC(1,1),NBX(2,5)),(PERLIG(1,1),NBX(42,11)),(KRUT(1),	SYMRNG
19.		3NBX(2,20)),(KPERT(1),NBX(8,20)),(MATRIX(1,1),NBX(30,20)),(KARO(1),	SYMRNG
20.		4NBX(40,20)),(KZERO(1),NBX(54,20)),(KJ(1),NBC(1,45)),(JDONE(1),	SYMRNG
21.		5NBC(1,48)),(KSET(1),IB(72,6)),(KRLIG(1),NBC(1,47))	SYMRNG
22.	C1.0	ESTABLISH THE RING PROPERTIES.	SYMRNG
23.		IF(IBC(KCX).LE.IRC.AND.NBENZ.EQ.1)GO TO 7	SYMRNG
24.	C	RING IS FUSED OR/AND BENZENE-TYPE RINGS ARE NOT PRESENT.	SYMRNG
25.	5	JW=9	SYMRNG
26.		RETURN	SYMRNG
27.	C	RING IS NOT FUSED AND BENZENE-TYPE RINGS ARE PRESENT.	SYMRNG
28.	7	KW=IBC(KCX)	SYMRNG
29.	C	DETERMINE IF ATOM KCX IS A COMPONENT OF ONE OF THE BENZENE-	SYMRNG
30.	C	TYPE RINGS. IF NOT, RETURN TO 5.	SYMRNG
31.		DO9 N=1,NBENZ	SYMRNG
32.		IF(KBENZ(N).EQ.KW)GO TO 13	SYMRNG
33.		CONTINUE	SYMRNG
34.		GO TO 5	SYMRNG
35.	C	ATOM KCX IS A COMPONENT OF A BENZENE-TYPE RING (KW).	SYMRNG
36.	C2.0	INITIALIZE VARIABLES.	SYMRNG
37.	13	DO14 N=1,6	SYMRNG
38.		KRLIG(N)=0	SYMRNG
39.		KARO(N)=0	SYMRNG
40.	14	KROT(N)=2	SYMRNG
41.		NF=KCC+20	SYMRNG
42.		DO15 N=1,NF	SYMRNG
43.	15	JDONE(N)=0	SYMRNG
44.		DO16 N=1,3	SYMRNG
45.	16	KSET(N)=0	SYMRNG
46.		KS=0	SYMRNG
47.	C3.0	EXECUTE RING CLASSIFICATION CYCLE.	SYMRNG
48.		DO4 J=2,7	SYMRNG
49.		KC=IRING(KW,J)	SYMRNG
50.		KS=KS+1	SYMRNG
51.		KPERT(KS)=KC	SYMRNG
52.		IF(NC(KC)-3)17,21,5	SYMRNG
53.	C	NON-RING ATOM BONDED TO RING ATOM KC IS A NON-CORE ATOM.	SYMRNG
54.	C	RESET FLAG IF LIGAND IS NO.	SYMRNG
55.	17	KPERM=-IX(KC,4,1)	SYMRNG
56.		KRLIG(J-1)=KPERM	SYMRNG
57.		IF(IX(KC,4,1).EQ.0)KROT(J-1)=1	SYMRNG
58.		GO TO 37	SYMRNG
59.	C	NON-RING ATOM BONDED TO RING ATOM KC IS A CORE ATOM. FIND	SYMRNG
60.	C	THIS CORE ATOM (KM) IN IX ARRAY.	SYMRNG
61.	21	NF=NC(KC)+1	SYMRNG
62.		DO27 K=2,NF	SYMRNG
63.		KM=IX(KC,K,6)	SYMRNG
64.		IF(IBC(KM).EQ.0)GO TO 33	SYMRNG
65.	27	CONTINUE	SYMRNG
66.	33	KPERM=KM	SYMRNG
67.		KJ(KM)=J-1	SYMRNG
68.		KRLIG(J-1)=KM	SYMRNG
69.	C	IF KC IS ONE OF THE IDENTICAL LIGANDS OF ATOM KM, REDUCE THE	SYMRNG
70.	C	TOTAL NUMBER OF IDENTICAL LIGANDS OF KM BY ONE.	SYMRNG
71.		DO35 N=1,6	SYMRNG
72.		IF(KCSAME(K,M).NF.KC)GO TO 35	SYMRNG



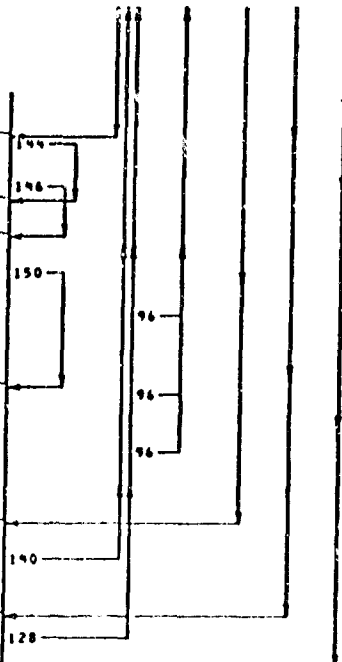
191.	IF(KARDI).NE.0)GO TO 72	SYMRNG	72
192.	N=KS+1	SYMRNG	
193.	RZERO(KS)=N	SYMRNG	
194.	72 CONTINUE	SYMRNG	
195.	C FIND NUMBER OF SETS OF EQUAL LIGANDS, NUMBER OF LIGANDS IN	SYMRNG	
196.	C EACH SET, AND LOCATION OF EACH LIGAND IN RING.	SYMRNG	
197.	NUM=0	SYMRNG	
198.	DO76 J=1,6	SYMRNG	
199.	KS=0	SYMRNG	
200.	IF(KARD(J).EQ.0.OR.J.EJ.0)GO TO 76	SYMRNG	76
201.	NUM=NUM+1	SYMRNG	
202.	KS=KS+1	SYMRNG	
203.	MATRIX(KS,NUM)=J	SYMRNG	
204.	K1=J+1	SYMRNG	
205.	DO74 K=K1,6	SYMRNG	
206.	IF(KARD(K).NE.KARD(J))GO TO 74	SYMRNG	74
207.	KS=KS+1	SYMRNG	
208.	MATRIX(KS,NUM)=K	SYMRNG	
209.	KARD(K)=0	SYMRNG	
210.	74 CONTINUE	SYMRNG	
211.	RSETI(NUM)=KS	SYMRNG	
212.	76 CONTINUE	SYMRNG	
213.	C ARRANGE ELEMENTS IN ARRAY MATRIX(J,K) IN ORDER OF INCREASING	SYMRNG	
214.	C MAGNITUDE.	SYMRNG	
215.	DO78 K=1,NUM	SYMRNG	
216.	NF=RSETI(K)-1	SYMRNG	
217.	DO78 N=1,NF	SYMRNG	
218.	J1=N	SYMRNG	
219.	J2=N+1	SYMRNG	
220.	77 IF(J2.EQ.1)GO TO 78	SYMRNG	78
221.	IF(MATRIX(J1,K).LE.MATRIX(J2,K))GO TO 78	SYMRNG	78
222.	MX=MATRIX(J1,K)	SYMRNG	
223.	MATRIX(J1,K)=MATRIX(J2,K)	SYMRNG	
224.	MATRIX(J2,K)=MX	SYMRNG	
225.	J1=J1+1	SYMRNG	
226.	J2=J2+1	SYMRNG	
227.	GO TO 77	SYMRNG	77
228.	78 CONTINUE	SYMRNG	
229.	GO TO(170,80,104,136,156,160),MAX	SYMRNG	80 104 136 156 160 170
230.	C MAXIMUM NUMBER OF EQUAL LIGANDS IN A GIVEN SET =2.	SYMRNG	
231.	80 IF(NUM-2)170,82,86	SYMRNG	82 86
232.	C TWO SETS OF EQUAL LIGANDS. TEST FOR A=C, F=D, B AND E HAVE	SYMRNG	
233.	C THOIFOLD ROTATIONAL SYMMETRY ABOUT PLANE OF RING.	SYMRNG	
234.	82 IF(RSETI(1).NE.2.OR.MATRIX(2,1)-MATRIX(1,1).NE.2.AND.MATRIX(2,1)-	SYMRNG	
235.	MATRIX(1,1).NE.2)RETURN	SYMRNG	
236.	IF(RSETI(2).NE.2.OR.MATRIX(2,2)-MATRIX(1,2).NE.2.AND.MATRIX(2,2)-	SYMRNG	
237.	MATRIX(1,2).NE.2)RETURN	SYMRNG	
238.	J1=RZRO(1)	SYMRNG	
239.	J2=RZRO(2)	SYMRNG	
240.	84 IF(RZRO(J1).EQ.1.OR.RZRO(J2).EQ.1.OR.J2-J1.NE.3)RETURN	SYMRNG	
241.	RZRO=2	SYMRNG	
242.	RETURN	SYMRNG	
243.	C THREE SETS OF EQUAL LIGANDS. TEST FOR A=B, F=D, B=E.	SYMRNG	
244.	C DETERMINE IF B HAS 120FOLD ROTATIONAL SYMMETRY ABOUT THE	SYMRNG	
245.	C PLANE OF THE RING.	SYMRNG	
246.	86 KS=0	SYMRNG	
247.	J1=0	SYMRNG	
248.	DO90 J=1,3	SYMRNG	
249.	IF(MATRIX(1,J)-MATRIX(1,J1).NE.2.AND.MATRIX(2,J)-MATRIX(1,J1).NE.1)	SYMRNG	88
250.	GO TO 88	SYMRNG	
251.	KS=KS+1	SYMRNG	90
252.	GO TO 90	SYMRNG	
253.	88 IF(MATRIX(2,J1)-MATRIX(1,J1).NE.3)GO TO 92	SYMRNG	92
254.	J1=MATRIX(1,J1)	SYMRNG	
255.	J2=MATRIX(2,J1)	SYMRNG	
256.	90 CONTINUE	SYMRNG	
257.	IF(KS.EQ.2.AND.J1.NE.0)GO TO 84	SYMRNG	84
258.	C TEST FOR A=D, D=E, C=F.	SYMRNG	
259.	92 DO94 J=1,3	SYMRNG	

210.	IF(MATRIX(2,J)-MATRIX(1,J).NE.0) GO 98	SYNRNG	98
211.	94 CONTINUE	SYNRNG	
212.	96 NOSNCZ	SYNRNG	
213.	RETURN	SYNRNG	
214.	98 KS=0	SYNRNG	
215.	J1=0	SYNRNG	
216.	DD102 J=1,3	SYNRNG	
217.	IF(MATRIX(2,J)-MATRIX(1,J).NE.1.AND.MATRIX(2,J)-MATRIX(1,J).NE.5)	SYNRNG	100
218.	GO TO 100	SYNRNG	
219.	KS=KS+1	SYNRNG	
220.	GO TO 102	SYNRNG	102
221.	100 IF(MATRIX(2,J)-MATRIX(1,J).NE.3)RETURN	SYNRNG	
222.	J1=1	SYNRNG	
223.	102 CONTINUE	SYNRNG	
224.	IF(KS.EQ.2.AND.J1.EQ.3)GO TO 96	SYNRNG	
225.	RETURN	SYNRNG	
226.	C MAXIMUM NUMBER OF EQUAL LIGANDS IN A GIVEN SET =3.	SYNRNG	94
227.	104 IF(NUM.NE.2)RETURN	SYNRNG	
228.	C TWO SETS OF EQUAL LIGANDS. FIND SET WITH TWO EQUAL LIGANDS	SYNRNG	
229.	C (IF ANY).	SYNRNG	
230.	IF(KSET(1).NE.3)GO TO 108	SYNRNG	108
231.	M1=1	SYNRNG	
232.	IF(KSET(2).NE.2)GO TO 120	SYNRNG	120
233.	M2=2	SYNRNG	
234.	GO TO 112	SYNRNG	112
235.	105 IF(KSET(1).NE.2)RETURN	SYNRNG	
236.	M2=1	SYNRNG	
237.	IF(KSET(2).NE.3)RETURN	SYNRNG	
238.	M1=2	SYNRNG	
239.	C TEST FOR A=BC, F=D, B AND E HAVE TWOFOLD ROTATIONAL	SYNRNG	
240.	C SYMMETRY ABOUT PLANE OF RING.	SYNRNG	
241.	112 J2=KTE(01)	SYNRNG	
242.	IF(MATRIX(2,M2)-MATRIX(1,M2).EQ.2.AND.J2-MATRIX(1,M2).EQ.1)GO	SYNRNG	118
243.	TO 110	SYNRNG	
244.	IF(MATRIX(2,M2)-MATRIX(1,M2).NE.4)RETURN	SYNRNG	
245.	IF(MATRIX(1,M2).EQ.1.AND.J2-MATRIX(2,M2).EQ.1)GO TO 118	SYNRNG	118
246.	IF(MATRIX(1,M2).EQ.2.OR.MATRIX(1,M2)-J2.NE.1)RETURN	SYNRNG	
247.	118 J1=MATRIX(2,M1)	SYNRNG	
248.	IF(KROT(J1).NE.1.AND.KROT(J2).NE.1)GO TO 96	SYNRNG	96
249.	RETURN	SYNRNG	
250.	120 IF(KSET(2).NE.3)RETURN	SYNRNG	
251.	C TEST FOR A=BC, D=E=F, B AND E HAVE TWOFOLD ROTATIONAL	SYNRNG	
252.	C SYMMETRY ABOUT PLANE OF RING.	SYNRNG	
253.	M2=2	SYNRNG	
254.	IF(MATRIX(2,M1)-MATRIX(1,M1).EQ.1.OR.MATRIX(3,M1)-MATRIX(2,M1).	SYNRNG	124
255.	NE.1).AND.(MATRIX(2,M1)-MATRIX(1,M1).EQ.1.OR.MATRIX(3,M1)-	SYNRNG	
256.	MATRIX(2,M1).EQ.4).AND.(MATRIX(2,M1)-MATRIX(1,M1).NE.4).OR.	SYNRNG	
257.	MATRIX(3,M1)-MATRIX(2,M1).NE.1)GO TO 124	SYNRNG	
258.	J2=MATRIX(2,M2)	SYNRNG	
259.	GO TO 118	SYNRNG	118
260.	C TEST FOR A=C AND B=D=F.	SYNRNG	
261.	124 IF(MATRIX(2,M1)-MATRIX(1,M1).NE.2.OR.MATRIX(3,M1)-MATRIX(2,M1).	SYNRNG	
262.	NE.2)RETURN	SYNRNG	
263.	J1=MATRIX(2,M1)	SYNRNG	
264.	J2=MATRIX(2,M2)	SYNRNG	
265.	IF(KROT(J1).NE.2.OR.KROT(J2).NE.2)GO TO 130	SYNRNG	130
266.	128 KOST=C-6	SYNRNG	
267.	RETURN	SYNRNG	
268.	130 KOST=C-3	SYNRNG	
269.	RETURN	SYNRNG	
270.	C PARTIAL NUMBER OF EQUAL LIGANDS IN A GIVEN SET =4.	SYNRNG	
271.	136 IF(NUM=1)GO TO 133,142	SYNRNG	142
272.	C ONE SET OF EQUAL LIGANDS. TEST FOR A=BCDE, F AND C WITH	SYNRNG	
273.	C TWOFOLD ROTATIONAL SYMMETRY ABOUT PLANE OF RING.	SYNRNG	
274.	133 J1=KTE(01)	SYNRNG	
275.	J2=KTE(02)	SYNRNG	
276.	IF(J2-J1.NE.1)RETURN	SYNRNG	
277.	140 IF(KROT(J1).EQ.2.AND.KROT(J2).EQ.2)GO TO 96	SYNRNG	96

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270. RETURN TWO SETS OF EQUAL LIGANDS. FIND SET WITH TWO EQUAL LIGANDS. SYMRNG
279. C SYMRNG
280. 142 IF(ASET(1).NE.2)GO TO 144 SYMRNG
281. M1=2 SYMRNG
282. M2=1 SYMRNG
283. GO TO 146 SYMRNG
284. 144 M1=1 SYMRNG
285. M2=2 SYMRNG
286. 146 J1=MATRIX(1,M2) SYMRNG
287. J2=MATRIX(2,M2) SYMRNG
288. IF(J2-J1.NE.3)GO TO 150 SYMRNG
289. C TEST FOR A=B=D+E AND F=C. IF F DOES NOT HAVE TWOFOLD SYMRNG
290. C ROTATIONAL SYMMETRY ABOUT PLANE OF RING, GO TO 96. SYMRNG
291. IF(KROT(J1).NE.2)GO TO 96 SYMRNG
292. C F HAS TWOFOLD SYMMETRY ABOUT PLANE OF RING. SYMRNG
293. NOSNC=4 SYMRNG
294. RETURN SYMRNG
295. C TEST FOR A=B=C+D AND E=F. SYMRNG
296. 150 IF(J2-J1.EQ.1 OR J2-J1.EQ.5)GO TO 96 SYMRNG
297. C TEST FOR A=B=C+D AND F=D. SYMRNG
298. IF(J2-J1.NE.2 AND J2-J1.NE.4)RETURN SYMRNG
299. J2=MATRIX(1,M1) SYMRNG
300. IF(KROT(J2).EQ.2)GO TO 96 SYMRNG
301. RETURN SYMRNG
302. C MAXIMUM NUMBER OF LIGANDS IN A GIVEN SET #5. A=B=C+D+E. SYMRNG
303. C DETERMINE IF C, F HAVE TWOFOLD ROTATIONAL SYMMETRY ABOUT SYMRNG
304. C PLANE OF RING. SYMRNG
305. 156 J1=KZERO(1) SYMRNG
306. J2=MATRIX(3,1) SYMRNG
307. GO TO 140 SYMRNG
308. C MAXIMUM NUMBER OF LIGANDS IN A GIVEN SET #6. A=B=C+D+E+F. SYMRNG
309. C DETERMINE IF A HAS TWOFOLD ROTATIONAL SYMMETRY ABOUT SYMRNG
310. C PLANE OF RING. SYMRNG
311. 160 J1=MATRIX(1,1) SYMRNG
312. IF(KROT(J1).NE.2)GO TO 128 SYMRNG
313. NOSNC=12 SYMRNG
314. 170 RETURN SYMRNG
315. END SYMRNG

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SYTRY

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1.      SUBROUTINE SYTRY(LI)
2.      C      THIS SUBROUTINE CONTROLS THE OPERATION WHICH FINDS THE ATOMIC
3.      C      COMPOSITION OF EACH LIGAND OF EACH CORE ATOM KC IN THE
4.      C      MOLECULE. IF KC IS NOT A BRANCH ATOM, THE ROUTINE DETERMINES
5.      C      WHETHER KC POSSESSES IDENTICAL LIGANDS. KC MAY HAVE MORE THAN
6.      C      ONE SET OF IDENTICAL LIGANDS.
7.      INTEGER SYMX(4),SYMBOL(9),GRID(50,50)
8.      INTEGER WEIGHT(9)
9.      INTEGER PERTKC(4,100)
10.     DIMENSION NTOT(5),LDDNE(100),JBR(100),LIGAND(5,4,100),MKT(40),
11.     I MER(3,40),NV(100),MVC(100),I BA(100),KCSAME(8,100),NOSAME(8,100),
12.     ZNTOTAL(3,100)
13.     COMMON/BLK1/NO,NDS,SYMX,SYMBOL,NOVAL(9),GRID
14.     COMMON/BLK2/WEIGHT,MWGT(9),MOLWT(100),IX(100,9,6),NC(100),KCC
15.     COMMON/BLK3/IRING(40,30),IMATX(50,50),NM(100),ZBC(100),RON(100),
16.     I IDBR(100),IB(100,8),IRG,NOBR
17.     COMMON/BLK4/NBC(60,50),NBS(60,2),NBX(60,20),IRC,NONFUS,INCTD
18.     COMMON/BLK5/NDATM,HUMATM(S),MBC(50),MBS(2),JM,JV,LFLAG,LFLAGG
19.     EQUIVALENCE (NTOT(1),IB(62,8)),(LDDNE(1),IMATX(2,41)),(JBR(1),
20.     IMATX(2,43)),(LIGAND(1,1,1),IMATX(2,1)),(PERTKC(1,1),NBX(2,5)),
21.     2(NCV,IB(97,8)),(MKT(1),IB(35,2)),(MER(1,1),GRID(1,37)),
22.     3(NV(1),GRID(1,29)),(MVC(1),GRID(1,31)),(I BA(1),GRID(1,40)),
23.     4(KCSAME(1,1),GRID(4,42)),(NOSAME(1,1),GRID(4,54)),(ZNTOTAL(1,1),
24.     ZGRID(4,78))
25.     C1.0 INITIALIZE VARIABLES USED HERE AND IN SUBSEQUENT SUBROUTINES.
26.     DD1 I=1,NDATM
27.     NTOT(I)=0
28.     1 CONTINUE
29.     DD3 I=1,KCC
30.     JBR(I)=0
31.     I BA(I)=0
32.     LDDNE(I)=0
33.     NV(I)=NC(I)
34.     MVC(I)=0
35.     KCSAME(1,I)=0
36.     DD2 K=1,9
37.     PERTKC(K,I)=0
38.     DD2 J=1,NDATM
39.     LIGAND(J,R,I)=0
40.     2 CONTINUE
41.     DD3 L=1,3
42.     KCSAME(L,I)=0
43.     ZNTOTAL(L,I)=0
44.     3 CONTINUE
45.     KCV=0
46.     DD4 K=1,40
47.     MKT(K)=0
48.     DD4 J=1,3
49.     MER(J,K)=0
50.     4 CONTINUE
51.     C2.0 EVALUATE THE ATOMIC COMPOSITION AND SYMMETRY OF THE LIGANDS
52.     C      UNTIL A BRANCH ATOM IS REACHED OR ALL CORE ATOMS HAVE BEEN
53.     C      PROCESSED.
54.     LXX=1
55.     LMM=1
56.     KCDEF=1000
57.     6 LMM=LMM+1
58.     KCNEXT=MBC(LXX,LMM)
59.     7 KC=NBC(LXX,LMM)
60.     C      COMPUTE ATOMIC COMPOSITION AND CHECK SIMILARITY OF LIGANDS
61.     C      OF CORE ATOM KC.
62.     CALL SCAN(KCDEF,KC,KCNEXT)
63.     LDDNE(KC)=1
64.     IF(KCNEXT.EQ.1000)GO TO 140
65.     IF(KCNEXT.GE.3)GO TO 8
66.     C      CORE ATOM KCNEXT IS NOT A BRANCH ATOM RESET VARIABLES AND
67.     C      REPEAT CYCLE.
68.     KCDEF=KC
69.     LMM=LMM+1
70.     IF(LMM.LT.MBS(LXX,1))GO TO 6
71.     KCNEXT=1000
72.     GO TO 7
73.     C      KCNEXT IS A BRANCH ATOM STORE COMPOSITION OF LIGAND.
74.     8 NFIRST=KCNEXT

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75.	KSUB=JBR(KCNEXT)	SYNTRY	
76.	DO 9 J=1,NDATM	SYNTRY	
77.	LIGAND(J,KSUB,KCNEXT)=KTOT(J)	SYNTRY	
78.	CONTINUE	SYNTRY	
79.	PERTK(KSUB,KCNEXT)=KC	SYNTRY	
80.	C3.0 CONTINUE THE EVALUATION OF THE ATOMIC COMPOSITION AND SYMMETRY	SYNTRY	
81.	C OF THE LIGANDS OF THE CHAIN, BRANCH, OR TERMINAL CORE ATOMS.	SYNTRY	
82.	LIMIT=LN	SYNTRY	
83.	11 LM=HBS(LXX,1)	SYNTRY	
84.	LMM=LX	SYNTRY	
85.	DO 13 J=1,NDATM	SYNTRY	
86.	KTOT(J)=0	SYNTRY	
87.	13 CONTINUE	SYNTRY	
88.	15 IF(LMM.GE.LIMIT)GO TO 17	SYNTRY	17
89.	C SCAN HAS BEEN COMPLETED. PRINT OUT THE ATOMIC COMPOSITION	SYNTRY	
90.	C OF THE LIGANDS AND EXIT.	SYNTRY	
91.	140 WRITE(6,150)	SYNTRY	
92.	150 FORMAT(/,1H0,31X,44HATOMIC COMPOSITION OF CORE ATOM AND LIG	SYNTRY	
93.	ANDS IN EACH GROUP/1H0,40X,12HGROUP NUMBER,5X,8HSUBGROUP,5X,	SYNTRY	
94.	21H1,5X,1HC,5X,1H0,5X,1H1)	SYNTRY	
95.	DD156 KC=1,KCC	SYNTRY	
96.	KSUB=JBR(KC)	SYNTRY	
97.	DD151 J=1,4	SYNTRY	
98.	151 KTOT(J)=0	SYNTRY	
99.	CALL SUMATM(X(KC,1,1),1,KTOT(1))	SYNTRY	
100.	WRITE(6,152)KC,(KTOT(J),J=1,4)	SYNTRY	
101.	152 FORMAT(1H,42X,15,12X,6HCORE,416)	SYNTRY	
102.	WRITE(6,154)((LIGAND(J,1,KC),J=1,4),1=1,KSUB)	SYNTRY	
103.	154 FORMAT(1H,50X,7HLIGAND,416)	SYNTRY	
104.	156 CONTINUE	SYNTRY	
105.	RETURN	SYNTRY	
106.	17 KCBF=KC	SYNTRY	
107.	KC=NBC(LXX,LMM)	SYNTRY	
108.	C HAVE ALL LIGANDS OF KC BEEN IDENTIFIED	SYNTRY	
109.	IF(LDONE(KC).EQ.0)GO TO 19	SYNTRY	19
110.	D YES. REPEAT CYCLE WITH THE NEXT ELEMENT UP CHAIN LXX.	SYNTRY	
111.	LMM=LMM+1	SYNTRY	
112.	GO TO 15	SYNTRY	
113.	C NO. HOW MANY CORE LIGANDS DOES KC HAVE	SYNTRY	
114.	19 IF(NC(KC).LT.3)GO TO 21	SYNTRY	21
115.	C IT IS A BRANCH ATOM. SET VARIABLES.	SYNTRY	
116.	KCNEXT=KC	SYNTRY	
117.	LMM=LMM+1	SYNTRY	
118.	KC=NBC(LXX,LMM)	SYNTRY	
119.	GO TO 27	SYNTRY	27
120.	C IT IS A CHAIN OR TERMINAL ATOM.	SYNTRY	
121.	21 IF(LMM.EQ.LM)GO TO 25	SYNTRY	25
122.	C CORE ATOM KC IS THE LAST ELEMENT IN CHAIN LXX. SET KCBF	SYNTRY	
123.	C ACCORDINGLY.	SYNTRY	
124.	KCBF=1000	SYNTRY	
125.	25 KCNEXT=NBC(LXX,LMM-1)	SYNTRY	
126.	C COMPUTE ATOMIC COMPOSITION AND SYMMETRY OF LIGANDS OF KC	SYNTRY	
127.	CALL SEARCH(KCBF,KC,KCNEXT)	SYNTRY	
128.	LDONE(KC)=1	SYNTRY	
129.	LMM=LMM-1	SYNTRY	
130.	C IF CORE LIGAND KCNEXT IS NOT A BRANCH ATOM, GO TO 17. IF	SYNTRY	
131.	C IT IS, CONTINUE.	SYNTRY	
132.	IF(NC(KCNEXT).LT.3)GO TO 19	SYNTRY	19
133.	C HAVE ALL LIGANDS OF BRANCH ATOM KCNEXT BEEN IDENTIFIED	SYNTRY	
134.	27 IF(LDONE(KCNEXT).EQ.0)GO TO 29	SYNTRY	29
135.	C YES. REPEAT CYCLE WITH THE NEXT ELEMENT OF CHAIN LXX.	SYNTRY	
136.	LMM=LMM-1	SYNTRY	
137.	GO TO 19	SYNTRY	19
138.	C NO. CONTINUE.	SYNTRY	
139.	29 IF(IBC(KCNEXT).EQ.0)GO TO 33	SYNTRY	33
140.	C KCNEXT IS A RING ATOM.	SYNTRY	
141.	IF(LMM.EQ.LM)GO TO 39	SYNTRY	39
142.	C KCNEXT IS NOT THE LAST ELEMENT IN CHAIN LXX. KC IS THE	SYNTRY	
143.	C ELEMENT BELOW KCNEXT IN CHAIN LXX.	SYNTRY	
144.	IF(IBC(KC).EQ.0)GO TO 33	SYNTRY	33
145.	C KC IS ALSO A RING ATOM.	SYNTRY	

146.	C	IF FIRST TIME THROUGH FOR ATOM KCNEXT, TRANSFER TO 33.	SYNTRV
147.	C	OTHERWISE, STORE ATOMIC COMPOSITION DATA IN SAME LOCATION	SYNTRV
148.	C	IN ARRAY LIGAND.	SYNTRV
149.	C	TS=KCNEXT)I=JBR(KCNEXT)+1	SYNTRV
150.	C	IF(LIGAND(KCNEXT).KB.1)GO TO 33	SYNTRV
151.	C	KSUB=JBR(KCNEXT)	SYNTRV
152.	C	DO37 J=1,NDATA	SYNTRV
153.	C	LIGAND(J,KSUB,KCNEXT)=LIGAND(J,KSUB,KCNEXT)+RTOT(J)	SYNTRV
154.	C	33 CONTINUE	SYNTRV
155.	C	GO TO 39	SYNTRV
156.	C	INCREMENT COUNTER ARRAY JBR.	SYNTRV
157.	C	33 JBR(KCNEXT)=JBR(KCNEXT)+1	SYNTRV
158.	C	KSUB=JBR(KCNEXT)	SYNTRV
159.	C	GO TO 36	SYNTRV
160.	C	STORE DATA IN LIGAND IN LOCATION SPECIFIED BY JBR.	SYNTRV
161.	C	35 JBR(KCNEXT)=JBR(KCNEXT)+1	SYNTRV
162.	C	KSUB=JBR(KCNEXT)	SYNTRV
163.	C	PERT=KSUB,KCNEXT)=KCNEXT	SYNTRV
164.	C	36 DO37 J=1,NDATA	SYNTRV
165.	C	LIGAND(J,KSUB,KCNEXT)=RTOT(J)	SYNTRV
166.	C	37 CONTINUE	SYNTRV
167.	C	INCREMENT CHAIN COUNTER LXX.	SYNTRV
168.	C	39 LXX=LXX+1	SYNTRV
169.	C	IF NUMBER OF BRANCHES IS NOT EXCEEDED AND LOCATION LMM IS	SYNTRV
170.	C	NOT GREATER THAN LENGTH OF NEW BRANCH AND KCNEXT IS	SYNTRV
171.	C	IDENTICAL TO THE ATOM LOCATED IN THE SAME POSITION AS	SYNTRV
172.	C	KCNEXT IN THE NEW CHAIN LXX, GO TO 11. OTHERWISE CONTINUE.	SYNTRV
173.	C	IF(LXX.LE.LR.AND.LMM.LE.NB(LXX,1).AND.NBC(LXX,LMM).EQ.KCNEXT)GO	SYNTRV
174.	C	TO 11	SYNTRV
175.	C	LMM=LMM+1	SYNTRV
176.	C	LXX=LXX+1	SYNTRV
177.	C	KNTER=NBC(LXX,LMM)	SYNTRV
178.	C	IF(KCNEXT.EQ.KFIRST)KAPTEC=1000	SYNTRV
179.	C	LDOHE(KCNEXT)=1	SYNTRV
180.	C	FIND ATOMIC COMPOSITION OF REMAINING LIGANDS OF KCNEXT AND	SYNTRV
181.	C	SYMMETRIES.	SYNTRV
182.	C	CALL SCANBR(KCNEXT,KAFTYR)	SYNTRV
183.	C	KCNEXT	SYNTRV
184.	C	REPEAT CYCLE AS BEFORE.	SYNTRV
185.	C	GO TO 15	SYNTRV
186.	C	END	SYNTRV

Appendix C
GLOSSARY OF PROGRAM VARIABLES

The following glossary contains definitions and cross references of all the FORTRAN symbols used in TGAP. The columns entitled "LOC" and "U" require some explanation. The symbols that appear in column LOC (location) have the following significance:

- Number - Location within a common block where the variable is stored.
If the variable is an array, it represents the storage location of the first element of the array.
- * - Variable is a local variable to the routine specified in column BLOCK.
- \$ - Defines a subprogram either of TGAP or the System's Library.

The letters that appear in column U (usage) have the following significance:

- A - Arithmetic statement function.
- C - Constant found in a data statement and on the right side of an arithmetic statement.
- D - Variable found in a data statement.
- E - Entry point.
- F - Function reference.
- I - Variable found in common or in the argument list and used only on the right side of an arithmetic statement.
- M - Variable found in common or in the argument list and used on both sides of an arithmetic statement (i. e., modified).
- O - Variable found in common or in the argument list and used only on the left side of an arithmetic statement.

- S - Subroutine call.
- W - Working variable found on the left side and then right side of an arithmetic statement which is not in common or in the argument list but is a local variable.

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
AA	(1)	Contains error printout information.	/CHAINM/1*		CHAINM	C	REAL	AA (4)
AFREQ		Reduction factor for the symmetry used when meso structures occur.	/ENTSYM/1*		ENTSYM	M	REAL	AFREQ
ALOG		Natural logarithm function routine (external routine of system).	/ALOG /10		ENTSYM	F		ALOG ALOG
ALTER	(i,j)	j = 1 contains weight of group i which lacks thermochemical data. j = 2 contains weight of group whose data will be utilized for group i.	/TGAP /1*		TGAP	C	INTE	ALTER (20,2)
ASSIGN		Establishes the change in coordinates required to scan about indexed core atom. Eight directions are possible. The desired direction is defined by calling subroutine. The lower and upper limits for the bond termination loop of subroutine BOND are also set.	/ASSIGN/1*		ASSIGN	E		ASSIGN IDENT S NUMBER S SCAN S ASSIGN ASSIGN
ASYMC		Determines the number of asymmetric carbon atoms present in the molecule.	/ASYMC /1*		ASYMC	E		ASYMC CORCIG S ASYMC
A1	(1)	Ring correction data for cyclopropane.	/CORCIG/1*		CORCIG	D	REAL	A1 (6)
A10	(1)	Ring correction data for cyclohexadiene 1,3.	/CORCIG/1*		CORCIG	D	REAL	A10 (6)
A11	(1)	Ring correction data for cyclohexadiene 1,4.	/CORCIG/1*		CORCIG	D	REAL	A11 (6)
A12	(1)	Ring correction data for cycloheptane.	/CORCIG/1*		CORCIG	D	REAL	A12 (6)
A13	(1)	Ring correction data for cycloheptene.	/CORCIG/1*		CORCIG	D	REAL	A13 (6)
A14	(1)	Ring correction data for cycloheptadiene 1,3.	/CORCIG/1*		CORCIG	D	REAL	A14 (6)
A15	(1)	Ring correction data for cycloheptatriene 1,3,5.	/CORCIG/1*		CORCIG	D	REAL	A15 (6)
A16	(1)	Ring correction data for cyclooctane.	/CORCIG/1*		CORCIG	D	REAL	A16 (6)
A17	(1)	Ring correction data for cis-cyclooctene.	/CORCIG/1*		CORCIG	D	REAL	A17 (6)
A18	(1)	Ring correction data for trans-cyclooctene.	/CORCIG/1*		CORCIG	D	REAL	A18 (6)
A19	(1)	Ring correction data for cyclooctatriene 1,3,5.	/CORCIG/1*		CORCIG	D	REAL	A19 (6)

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SCBA	D TYPE	VAN	DTM
A2	(1)	Ring correction data for cyclopropene.	/CORCIG/1*)	CORCIG D REAL	A2	(6)
A20	(1)	Ring correction data for cyclooctatetraene	/CORCIG/1*)	CORCIG D REAL	A20	(6)
A21	(1)	Ring correction data for cyclononane.	/CORCIG/1*)	CORCIG D REAL	A21	(6)
A22	(1)	Ring correction data for cis- cyclononane.	/CORCIG/1*)	CORCIG D REAL	A22	(6)
A23	(1)	Ring correction data for trans- cyclononane.	/CORCIG/1*)	CORCIG D REAL	A23	(6)
A24	(1)	Ring correction data for spiro-pentane.	/CORCIG/1*)	CORCIG D REAL	A24	(6)
A25	(1)	Ring correction data for bicyclobutane.	/CORCIG/1*)	CORCIG D REAL	A25	(6)
A26	(1)	Ring correction data for bicyclopentane.	/CORCIG/1*)	CORCIG D REAL	A26	(6)
A27	(1)	Ring correction data for bicyclohexane.	/CORCIG/1*)	CORCIG D REAL	A27	(6)
A28	(1)	Ring correction data for bicycloheptane.	/CORCIG/1*)	CORCIG D REAL	A28	(6)
A29	(1)	Ring correction data for bicyclooctane.	/CORCIG/1*)	CORCIG D REAL	A29	(6)
A3	(1)	Ring correction data for cyclobutane.	/CORCIG/1*)	CORCIG D REAL	A3	(6)
A30	(1)	Ring correction data for bicyclononane.	/CORCIG/1*)	CORCIG D REAL	A30	(6)
A31	(1)	This array and all arrays up to array A44 contain the thermochemical corrections for the oxygen- containing rings.	/CORCIG/1*)	CORCIG D REAL	A31	(6)
A32		Description not input	/CORCIG/1*)	CORCIG D REAL	A32	(6)
A33		Description not input	/CORCIG/1*)	CORCIG D REAL	A33	(6)
A34		Description not input	/CORCIG/1*)	CORCIG D REAL	A34	(6)
A35		Description not input	/CORCIG/1*)	CORCIG D REAL	A35	(6)
A36		Description not input	/CORCIG/1*)	CORCIG D REAL	A36	(6)

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
A37		Description not input	/CORCIG/1*) CORCIG	D	REAL	A37 (6)
A38		Description not input	/CORCIG/1*) CORCIG	D	REAL	A38 (6)
A39		Description not input	/CORCIG/1*) CORCIG	D	REAL	A39 (6)
A4	(1)	Ring correction data for cyclobutene.	/CORCIG/1*) CORCIG	D	REAL	A4 (6)
A40		Description not input	/CORCIG/1*) CORCIG	D	REAL	A40 (6)
A41		Description not input	/CORCIG/1*) CORCIG	D	REAL	A41 (6)
A42		Description not input	/CORCIG/1*) CORCIG	D	REAL	A42 (6)
A43		Description not input	/CORCIG/1*) CORCIG	D	REAL	A43 (6)
A44		Description not input	/CORCIG/1*) CORCIG	D	REAL	A44 (6)
A45	(1)	This array and all arrays up to array A50 contain the thermochemical corrections for the nitrogen-containing rings.	/CORCIG/1*) CORCIG	D	REAL	A45 (6)
A46		Description not input	/CORCIG/1*) CORCIG	D	REAL	A46 (6)
A47		Description not input	/CORCIG/1*) CORCIG	D	REAL	A47 (6)
A48		Description not input	/CORCIG/1*) CORCIG	D	REAL	A48 (6)
A49		Description not input	/CORCIG/1*) CORCIG	D	REAL	A49 (6)
A5	(1)	Ring correction data for cyclopentane.	/CORCIG/1*) CORCIG	D	REAL	A5 (6)
A50		Description not input	/CORCIG/1*) CORCIG	D	REAL	A50 (6)
A6	(1)	Ring correction data for cyclopentene.	/CORCIG/1*) CORCIG	D	REAL	A6 (6)
A7	(1)	Ring correction data for cyclopentadiene.	/CORCIG/1*) CORCIG	D	REAL	A7 (6)
A8	(1)	Ring correction data for cyclohexane.	/CORCIG/1*) CORCIG	D	REAL	A8 (6)

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE			USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR	DTM
AD	(1)	Ring correction data for cyclohexene.	/CORCIG/1*) CORCIG	D	REAL	AD	(6)
BLANK			/TGAP	/1*) TGAP	C	INTE	BLANK	
BOND		Determines bond type present at specified direction of indexed core atom. It also scans symbol input array along this direction until a symbol unequal to the designated bond is detected.	/BOND	/1*) BOND	E		BOND	
						FIND	S	BOND	
						SCAN	S	BOND	
CASE		Case number.	/TGAP	/1*) TGAP	M	INTE	CASE	
CHAINM		Control routine for section 2 of the program. This section identifies the chain formations present in the molecule as well as the number of unique rings and the ring components.	/CHAINM/1*) CHAINM	E		CHAINM	
						TGAP	S	CHAINM	
CHANGE		Redefines all chains in array NBC if a chain exists that has only one branch atom and an upper residual (I2) that is greater than the lower residual (I1). If more than one such chain exists, the chain with the maximum I2 - I1 is chosen as reference.	/CHANGE/1*) CHAINM	S		CHANGE	
						CHANGE	E	CHANGE	
CIS		Identifies each pair of ligands cis to the linkage C=C, where both carbon atoms (K1 and K2) have a connectivity of three.	/CIS	/1*) CIS	E		CIS	
						CISCOR	S	CIS	
						CYCORR	S	CIS	
						EXTROT	S	CIS	
CISCOR		Determines whether ligands of K1 and K2 exhibit a cis interaction. If so, it establishes the number, type, and magnitude of the correction.	/CISCOR/1*) CISCOR	E		CISCOR	
						CORCIG	S	CISCOR	
						SORNGI	S	CISCOR	
CISM		Sum of all cis contributions to the heat of formation.	/CISCOR/1*) CISCOR	M	REAL	CISM	
CISM		Sum of all cis contributions to the heat of formation.	/CORCIG/1*) CORCIG	M	REAL	CISM	
CISM		Sum of all cis corrections to the heat of formation.	/SORNGI/1*) SORNGI	I	REAL	CISM	
CISS		Sum of all cis contributions to the entropy.	/CISCOR/1*) CISCOR	M	REAL	CISS	
CISS		Sum of all cis contributions to the entropy.	/CORCIG/1*) CORCIG	M	REAL	CISS	
CISS		Sum of all cis corrections to the entropy.	/SORNGI/1*) SORNGI	I	REAL	CISS	

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SOBJ	D TYPE	VAR	DIR
CORCIG		Control routine for section 3 of the program. This section finds all second-order interaction and ring corrections as well as contributions due internal and external rotational symmetry and optical isomerism.	/CORCIG/18) CORCIG	E		CORCIG CORCIG
CP	(1)	Heat capacity coefficients of molecule.	/TGAP	/(*) TGAP	M	REAL	CP (4)
CPALT	(1)	Values of the heat capacity coefficients for a particular second-order interaction.	/BLK3	/ (639)) CORCIG	M	REAL	CPALT (4)
CPCIS	(1)	Heat capacity coefficients for cis corrections	/CORCIG/(*) CORCIG	C	REAL	CPCIS (4)
CPSYM	(1)	Total contribution to the heat capacity coefficients from second-order interactions and ring corrections.	/CORCIS/(*) CORCIG	M	REAL	CPSYM (4)
CPSYM	(1)	Total contribution to the heat capacity coefficients from second-order interactions and ring corrections.	/CRINGS/(*) CRINGS	M	REAL	CPSYM (4)
CPSYM	(1)	Total contribution to the heat capacity coefficients from second-order interactions and ring corrections.	/HEXGON/(*) HEXGON	M	REAL	CPSYM (4)
CPSYM	(1)	Total contribution to the heat capacity coefficients from second-order interactions and ring corrections.	/NRINGS/(*) NRINGS	M	REAL	CPSYM (4)
CPSYM	(1)	Sum total of corrections to the heat capacity coefficients derived from section 3 of the program.	/TGAP	/(*) TGAP	I	REAL	CPSYM (4)
CPT	(1)	Heat capacity of molecule for temperatures specified in TARRAY.	/BLK3	/ (1205)) TGAP	M	REAL	CPT (14)
CPX	(1, j)	Contains the four heat capacity arrays CP1, CP2, CP3, and CP4. [cal-deg ⁻¹ -mole ⁻¹]	/BLK7	/ (541)) DATA	D	REAL	CP1 (180) GADATA I REAL CP1 (180) TGAP I REAL CPX (180,4)
CP1	(1, j)	Contains the four heat capacity arrays CP1, CP2, CP3, and CP4.	/BLK7	/ (541)) DATA	D	REAL	CP1 (180) GADATA I REAL CP1 (180) TGAP I REAL CPX (180,4)
CP2	(1)	Coefficients for the temperature dependent term CP2·T of the fitted group additivity heat capacities. [cal-deg ⁻² -mole ⁻¹]	/BLK7	/ (721)) DAT:1	D	REAL	CP2 (180) GADATA I REAL CP2 (180)

FORTRAN SYMBOL	PATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIR
CP3	(1)	Coefficients for the temperature dependent term CP3-T ² of the fitted group additivity heat capacities. [cal-deg ⁻³ -mole ⁻¹]	/BLK7	/(901)	DATA1	D	REAL	CP3	(180)
					GADATA	I	REAL	CP3	(180)
CP4	(1)	Coefficients for the temperature dependent term CP4-T ³ of the fitted group additivity heat capacities. [cal-deg ⁻⁴ -mole ⁻¹]	/BLK7	/(1081)	DATA1	D	REAL	CP4	(180)
					GADATA	I	REAL	CP4	(180)
CRINGS		Searches for certain carbon fused ring systems and applies ring corrections if present.	/CRINGS/10) CORCIG	S		CRINGS	
					CRINGS	E		CRINGS	
CTWO		Checks for the presence of monocyclic aromatic rings and nitro groups which exhibit twofold internal rotational symmetry about an axis with a nonlinear configuration. If present, it stores the pertinent identification numbers and contributions to the entropy.	/CTWO	/10) CTWO	E		CTWO	
					INTROT	S		CTWO	
CYCORA		Determines the type of ring correction for a non-fused ring. Also sets various ring arrays and other indicators providing benzene- or pyridine-type rings are present.	/CYCORA/10) CORCIG	S		CYCORA	
					CYCORA	E		CYCORA	
DATCIS	(1,j)	Contains the heat of formation (i=1) and entropy (i=2) corrections for the second-order interaction j.	/BLK3	/(4451)	CISCOR	M	REAL	DATCIS(2,150)	
					CORCIG	M	REAL	DATCIS(2,150)	
					CTWO	D	REAL	DATCIS(2,150)	
					DITERE	M	REAL	DATCIS(2,150)	
					GAUCHE	M	REAL	DATCIS(2,150)	
					INTROT	M	REAL	DATCIS(2,150)	
DELETE		Disengages from use all the pairs of chain ring atoms and their non-ring ligands which have been found to be dissimilar by the comparison tests of subroutine EQUALR.	/DELETE/10) DELETE	E		DELETE	
					EQUALR	S		DELETE	
DELM		Heat of formation of molecule for 298°K. [kcal-mole ⁻¹]	/TGAP	/10) TGAP	M	REAL	DELM	
DELTA1		Determines that part of the group weight composed of the sum of the assigned weights of the group core atom and of the atomic constituents bonded to the core atom.	/DELTA1/10) DELTA1	E		DELTA1	
					STAND	S		DELTA1	
DELTA2		Adds all second-order multiple-bond contributions to the group weight value.	/DELTA2/10) DELTA2	E		DELTA2	
					STAND	S		DELTA2	

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIM
DITERE		Searches for ditertiary ether groups in molecule and applies the appropriate correction, if present.	/DITERE/18) CORCIG S DITERE E			DITERE DITERE
DORPAR		Ortho/para correction for pyridine-type structures.	/CORCIG/10) CORCIG C	REAL		DORPAR
DORPAR		Ortho/para correction for pyridine-type structures.	/HEXGON/10) HEXGON I	REAL		DORPAR
DORTHO	(1)	Ortho corrections for benzene-type structures.	/CORCIG/10) CORCIG C	REAL		DORTHO(6)
DORTHO	(1)	Ortho corrections for benzene-type structures.	/HEXGON/10) HEXGON I	REAL		DORTHO(6)
DTEM		Sum of all ditertiary ether corrections to the heat of formation.	/CORCIG/10) CORCIG W	REAL		DTEM
DTEM		Sum of all ditertiary ether corrections to the heat of formation.	/DITERE/10) DITERE M	REAL		DTEM
ENDCS1		First symbol of end of case test variable.	/TGAP /10) TGAP	C	INTE	ENDCS1
ENDCS2		Second symbol of end of case test variable.	/TGAP /10) TGAP	C	INTE	ENDCS2
ENDCS3		Third symbol of end of case test variable.	/TGAP /10) TGAP	C	INTE	ENDCS3
ENDRUN		End of run test variable.	/TGAP /10) TGAP	C	INTE	ENDRUN
ENTSYM		Computes entropy contributions from internal and external rotational symmetry and optical isomerism, as well as auxiliary properties such as the longest chain in the molecule.	/ENTSYM/10) CORCIG S ENTSYM E			ENTSYM ENTSYM
EQUAL		Processes the operation that determines whether two or more complex (core) ligands have identical structures.	/EQUAL /10) CTWD EQUAL SETUP	S E S		EQUAL EQUAL EQUAL
EQUALM		Determines whether the backbone structures of two rings, a and b, are the same. Non-ring ligands bonded to these rings are also classified and stored, but their symmetries are checked in subroutine EQUAL, not here.	/EQUALR/10) EQUAL EQUALR	S E		EQUALR EQUALM
EXTROT		Computes the external rotation symmetry number of the molecule.	/EXTROT/10) CORCIG S EXTROT E			EXTROT EXTROT

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
FIND		Determines whether the first atom to be indexed is a core atom or an univalent atom. If the latter, it determines the location of one of the core atoms that is bonded to this non-core and first-indexed atom. The data for this non-core atom are stored in IX.	/FIND	/18) FIND	E		FIND
					STAND	S		FIND
FIRSTR		Determines if the two ring atoms under comparison are part of two different fused ring systems. If so, it compares several of the composition and structural properties of the two fused ring systems for similarity. If the two rings are not fused, it compares their ring size.	/FIRSTR	/18) EQUALR	S		FIRSTR
					FIRSTR	E		FIRSTR
FT	(1)	Gibbs free energy of molecule for temperatures specified in TARKAY.	/BLK3	/1 (1247)	TGAP	M	REAL	FT (14)
FUSION		Identifies the set(s) of fused ring system(s) when present. [kcal-mole ⁻¹]	/FUSION	/18) CORCIG	S		FUSION
					FUSION	E		FUSION
GADATA		Prints out Bensen's tables of thermochemical group additivity data if requested by input data.	/GADATA	/18) GADATA	E		GADATA
					TGAP	S		GADATA
GAUCHE		Determines whether the ligands of the test core atoms K1 and K2 are gauche to each other. If so, it finds the number, type, and magnitude of the gauche correction.	/GAUCHE	/18) CORCIG	S		GAUCHE
					GAUCHE	E		GAUCHE
					SORNGI	S		GAUCHE
GAUCHM		Sum of all gauche contributions to the heat of formation.	/CORCIG	/18) CORCIG	M	REAL	GAUCHM
GAUCHM		Sum of all gauche contributions to the heat of formation.	/GAUCHE	/18) GAUCHE	M	REAL	GAUCHM
GAUCHM		Sum of all gauche corrections to the heat of formation.	/SORNGI	/18) SORNGI	I	REAL	GAUCHM
GRID	(I,J)	Input array containing two-dimensional structure of the molecule (required input).	/BLK1	/1 (25)	BOND	I	INTE	GRID (50,80)
					IOENT	M	INTE	GRID (50,80)
					NUMBER	I	INTE	GRID (50,80)
					SCAN	I	INTE	GRID (50,80)
					STAND	I	INTE	GRID (50,80)
					TGAP	M	INTE	GRID (50,80)
GROUP1	(1)	First part of the chemical symbol of each group in the data library.	/BLK4	/1 (2)	DATAL	D	INTE	GROUP1(180)
					GADATA	I	INTE	GROUP1(180)
GROUP2	(1)	Second part of the chemical symbol of each group in the data library.	/BLK4	/1 (62)	DATAL	D	INTE	GROUP2(180)
					GADATA	I	INTE	GROUP2(180)

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
GROUP3	(1)	Third part of the chemical symbol of each group in the data library.	/BLK4	/(1442)	DATA1	D	INTE	GROUP3(180) GADATA I INTE GROUP3(180)
HCONS		Enthalpy constant.	/TGAP	/(0) TGAP	M	REAL	HCONS
HEXGON		Assigns the necessary weight corrections to the groups of a fused ring system which form part of a benzene or pyridine-type structure (i.e. conjugated, six-membered rings) and/or to non-fused rings of similar structure and to all groups bonded to these ring structures.	/HEXGON/(8) CORCIG	S		HEXGON HEXGON E HEXGON
HF298	(1)	Heat of formation at 298°K of each group in the data library. [kcal-mole ⁻¹]	/BLK7	/(181)	DATA1	D	REAL	HF298 (180) GADATA I REAL HF298 (180) TGAP I REAL HF298 (180)
HRING		Total of ring contributions to the heat of formation.	/CORCIG/(+) CORCIG	M	REAL	HRING
HRING		Sum of ring contributions to the heat of formation.	/CRINGS/(+) CRINGS	M	REAL	HRING
HRING		Description not input	/HEXGON/(+) HEXGON	M	REAL	HRING
HRING		Sum of ring contributions to the heat of formation.	/NRINGS/(+) NRINGS	M	REAL	HRING
HSDT	(1)	Enthalpy of molecule at temperature T minus enthalpy at temperature 298°K for temperatures specified in TARRAY. [kcal-mole ⁻¹]	/BLK3	/(1261)	TGAP	M	REAL	HSDT (14)
HST	(1)	Enthalpy of molecule for temperatures specified in TARRAY. [kcal-mole ⁻¹]	/BLK3	/(1223)	TGAP	M	REAL	HST (14)
MSYM		Total contribution to the heat of formation from second-order interactions and ring corrections.	/CORCIG/(+) CORCIG	D	REAL	MSYM
MSYM		Sum total of corrections to the heat of formation at 298°K derived from section 3 of the program.	/TGAP	/(0) TGAP	I	REAL	MSYM
HTE	(1)	Total enthalpy of molecule (enthalpy + heat of formation at 298°K) for temperatures specified in TARRAY. [kcal-mole ⁻¹]	/BLK3	/(1275)	TGAP	M	REAL	HTE (14)
I		Subscript that designates bond type.	/BOND	/(0) BOND	M	INTE	I

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE			
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIR	
I		Subscript.	/CORCIB/	(*)	CORCIB	M	INTE	I	
I		Loop counter and subscript.	/CRINGS/	(*)	CRINGS	M	INTE	I	
I		Loop counter and subscript.	/CTWO	/	(*)	CTWO	M	INTE	I
I		Group number of nitrogen atom in ring K.	/CYCORR/	(*)	CYCORR	M	INTE	I	
I		Symbol code for element or radical in program library.	/DELTA1/	(*)	DELTA1	M	INTE	I	
I		Loop counter and subscript.	/HEXGON/	(*)	HEXGON	M	INTE	I	
I		Loop counter and subscript.	/LESSEN/	(*)	LESSEN	M	INTE	I	
I		Loop counter and subscript.	/MULTI	/	(*)	MULTI	M	INTE	I
I		Subscript.	/NRINGS/	(*)	NRINGS	M	INTE	I	
I		Actual location in array ORDSUM used in the calculation	/SEARCH/	(*)	SEARCH	M	INTE	I	
I		Loop counter and subscript.	/SYMTRY/	(*)	SYMTRY	M	INTE	I	
I		Loop counter and subscript.	/TGAP	/	(*)	TGAP	M	INTE	I
IA	(I)	Contains the size of each ring in the fused ring set B.	/BLK1	/	(1325)	FIRSTA	M	INTE	IA	(90)
IA	(I)	Array used for temporary storage	/BLK3	/	(6375)	EQUAL	M	INTE	IA	(9)
						EQUALA	M	INTE	IA	(9)
IA	(I)	Contains order elements of IB would have if arranged in order of increasing magnitude.	/ORDER	/	(*)	ORDER	M	INTE	IA	(180)
IATOM	(I)	Contains characters of multi-character chemical symbol.	/BLK4	/	(291)	IDENT	M	INTE	IATOM	(3)
IATOM	(I)	Contains characters of multi-word input symbol.	/MULTI	/	(*)	MULTI	I	INTE	IATOM	(3)
IB	(I,J)	Contains group numbers of all core atom ligands in group I except for that of the parent core atom (which has already been scanned).	/BLK3	/	(5601)	SCAN	G	INTE	IB	(100,0)
						SHIFT	O	INTE	IB	(100,0)
						STAND	M	INTE	IB	(100,0)
IB	(I)	Array the elements of which are to be checked for order of increasing magnitude.	/ORDER	/	(*)	ORDER	I	INTE	IB	(180)

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE			USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIM
IBA	(1)	Transfer flag. =0 ligand composition of core atom I stored in new location. >0 data stored in same location of array LIGAND.	/BLK1	/(1975)	SYMTRY	M	INTE	IBA	(100)
IBC	(1)	Location I contains the ring number of the ring of ring component I. If I is a non-ring atom, location I = 0.	/BLK3	/(5301)	ASYMC	I	INTE	IBC	(100)
					CHAINM	O	INTE	IBC	(100)
					CIS	I	INTE	IBC	(100)
					CISCGR	I	INTE	IBC	(100)
					CONCIG	I	INTE	IBC	(100)
					CTWO	I	INTE	IBC	(100)
					CYCORA	I	INTE	IBC	(100)
					EQUAL	I	INTE	IBC	(100)
					EQUALA	I	INTE	IBC	(100)
					EXTROT	I	INTE	IBC	(100)
					FIRSTR	I	INTE	IBC	(100)
					FUSION	O	INTE	IBC	(100)
					LINEAR	I	INTE	IBC	(100)
					RESETR	M	INTE	IBC	(100)
					SCANBR	I	INTE	IBC	(100)
					SCANCH	I	INTE	IBC	(100)
					SORING	I	INTE	IBC	(100)
					SYMRNG	I	INTE	IBC	(100)
					SYMTRY	I	INTE	IBC	(100)
IBND	(1)	Transfer flag array equal to 0 or 1 depending whether or not bond is adjacent to first character (I=1) or second character (I=2).	/BLK4	/(244)	IDENT	M	INTE	IBND	(2)
IBONDD	(1)	Contains ring locations of double bonds.	/BLK3	/(5851)	CYCORA	M	INTE	IBONDD(30)	
IBONDS	(1)	Contains ring locations of single bonds.	/BLK3	/(5821)	CYCORA	M	INTE	IBONDS(30)	
IBX		Temporary storage variable.	/CONCIG/(*)	CONCIG	M	INTE	IBX	
IBX		Subscript.	/DITERE/(*)	DITERE	M	INTE	IBX	
IBX		Transfer flag.	/EQUALA/(*)	EQUALA	M	INTE	IBX	
IC	(1)	Contains the number of nitrogen atoms in each ring in fused set B.	/BLK3	/(3802)	FIRSTR	M	INTE	IC	(40)
IC		Number of distinct fused ring sets in molecule.	/CRINGS/(*)	CRINGS	M	INTE	IC	
IC		Total number of fused ring sets.	/FUSION/(*)	FUSION	M	INTE	IC	
IC		Total number of fused ring sets.	/HEXGON/(*)	HEXGON	M	INTE	IC	
IC		Total number of fused ring sets.	/NRINGS/(*)	NRINGS	M	INTE	IC	

FORTRAN SYMBOL	DATA SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE USAGE				
			BLOCK	LOC	SUBR	TYPE	VAR	DIR	
ICC		Number of non-aromatic core atoms bonded to the central nitrogen atom.	/GAUCHE/1*			GAUCHE	M	INTE	ICC
ICF		Transfer flag.	/IDENT/1*			IDENT	M	INTE	ICF
ICMNR1		Group number of first core atom in ligand KC1.	/EQUAL/1*			EQUAL	M	INTE	ICMNR1
ICMNR2		Group number of first core atom in ligand KC2.	/EQUAL/1*			EQUAL	M	INTE	ICMNR2
ICIS		Sum total of all cis interactions.	/CISCOR/1*			CISCOR	M	INTE	ICIS
ICIS		Sum total of all cis interactions.	/CORCIS/1*			CORCIS	M	INTE	ICIS
ICIS		Sum total of all cis interactions.	/SORNGI/1*			SORNGI	I	INTE	ICIS
ICM	(I)	Contains group number of core atoms which have been topologically scanned and identified. For identification purpose, the number 10000 is stored prior to the group number of a terminal core atom.	/ALAY/1*	363		STAND	M	INTE	ICM (100)
ICT		Transfer flag.	/IDENT/1*			IDENT	M	INTE	ICT
ICI		Identification number of non-fused ring or of fused ring set A.	/FIRSTA/1*			FIRSTA	M	INTE	ICI
IC2		Denotes number of entries in array IC2A.	/BLK3/1*	5921		HEXDN	M	INTE	IC2
ICB		Identification number of non-fused ring or of fused ring set B.	/FIRSTB/1*			FIRSTB	M	INTE	ICB
IC2A	(I)	Contains the I.D. number of all fused ring sets composed of benzene and/or pyridine-type structures.	/BLK3/1*	5922		HEXDN	M	INTE	IC2A (10)
ID	(I)	Contains the number of double bonds in each ring in fused set B.	/BLK3/1*	3842		FIRSTB	M	INTE	ID (40)
ID		Direction of chemical bond.	/CIS/1*			CIS	M	INTE	ID
IDB		Number of double bonds in ring K.	/CYCORR/1*			CYCORR	M	INTE	IDB
IDBR	(I)	Group number of branch core atom I.	/BLK3/1*	5501		CHAINM	I	INTE	IDBR (100)
						STAND	O	INTE	IDBR (100)

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR	
IDENT		Identifies chemical symbol of indexed atom. If two or three characters are present in symbol these are packed into one word and the excess words occupied by these characters are replaced by a bond symbol or a blank, as required.	/IDENT	/10) FIND	S	IDENT		
					IDENT	E	IDENT		
					SCAN	S	IDENT		
					STAND	S	IDENT		
ID1		Direction of chemical bond between central test core atoms K1 and K2.	/CIS	/10) CIS	W	INTE	ID1	
IDIF		Number of ring locations between the last two double bonds in ring K.	/CYCORR/	/10) CYCORR	W	INTE	IDIF	
IDIF		Difference between size of test ring and the number of its components contained in the reference ring.	/LESSEN/	/10) LESSEN	W	INTE	IDIF	
IDIF1		Number of ring locations between the next to the last and second to the last double bonds in ring K.	/CYCORR/	/10) CYCORR	W	INTE	IDIF1	
IDTE		Counter that specifies the number of ditertiary ether groups present.	/CORCIG/	/10) CORCIG	W	INTE	IDTE	
IDTE		Counter that specifies the number of ditertiary ether groups present.	/DITERE/	/10) DITERE	W	INTE	IDTE	
IDP	(I, J)	Contains the group numbers (I=1 and 5) of a pair of atoms J, one from each branch, and the group numbers (I=2 to 4 and 6 to 8) of their ligands which are to be tested.	/BLK1	/1	27)	DELETE	I	INTE	IDP
					EQUAL	M	INTE	IDP	
					EQUALR	M	INTE	IDP	
IDX		Displacement between the first and third oxygen atoms in ring K.	/CYCORR/	/10) CYCORR	W	INTE	IDX	
IDXR	(I, J)	Contains the group numbers (I=1 and 5) of a pair of ring atoms J, one from each ring, and the group numbers (I=2 to 4 and 6 to 8) of their ligands which are to be tested.	/BLK1	/1	825)	EQUALR	M	INTE	IDXR
IDXR								(8,30)	
IDXR	(I)	Contains bond directions between atom KC1R and the ring atoms bonded to it, excluding atom KC1PR.	/BLK1	/1	822)	EQUALR	M	INTE	IDXR
IDXR								(3)	
ID12		Displacement between the first and second oxygen atoms in ring K.	/CYCORR/	/10) CYCORR	W	INTE	ID12	
IE	(I)	Contains the number of oxygen atoms in each ring in rused set B.	/BLK3	/1	5822)	FIRSTR	M	INTE	IE
IE								(40)	
IEND		End of run input symbol.	/TLAP	/10) TLAP	W	INTE	IEND	
IERR		Error flag =0 no error. =1 error present.	/BOND	/10) BOND	O	INTE	IERR	

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIM
IERR		Error flag =0 no error. =1 error present.	/CHPIN/(*) CHAIM		INT	IERR	
IERR		Error flag =0 no error =1 error present	/FIND /(*) FIND		M	INT	IERR
IERR		Error flag =0 no error. =1 error present.	/IDENT /(*) IDENT		M	INT	IERR
IERR		Error flag =0 If multi-character input symbol is identified. =1 If multi-character input symbol is not identified.	/MULTI /(*) MULTI		O	INT	IERR
IERR		Error flag =0 no error. =1 error present.	/NEWCOL/(*) NEWCOL		O	INT	IERR
IERR		Error flag =0 no error. =1 error present.	/RING /(*) RING		O	INT	IERR
IERR		Error flag =0 no error. =1 error present.	/SCAN /(*) SCAN		M	INT	IERR
IERR		Error flag =0 no error. =1 error present.	/STAND /(*) STAND		M	INT	IERR
IERR		Error flag. If zero, no error. If non zero, input or computational error exists.	/TGAP /(*) TGAP		M	INT	IERR
IEXIT		Flag that causes an exit from calling subroutine.	/CIS /(*) CIS		O	INT	IEXIT
IEXIT		Exit flag. =0 conditions satisfied in subroutine CIS. Continue. =1 conditions not satisfied. Exit from subroutine CISCOR.	/CISCOR/(*) CISCOR		I	INT	IEXIT
IEXIT		Exit flag =0 subroutine CIS executed. =1 subroutine CIS not executed.	/CYCORR/(*) CYCORR		I	INT	IEXIT
IEXIT		Exit flag from subroutine CIS. =0 cis computation performed. =1 cis computation not performed.	/EXTROT/(*) EXTROT		I	INT	IEXIT

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	STOR	D TYPE	VAR	DTM	
IFIX	(I)	Identifies characters of a particular symbol in SYMBL which have been matched to characters of input symbol in IATOM.	/BLK4	/I	301	MULTI	M	INTE	IFIX (4)
IFLAG1		Transfer flag of subroutine NEWKC.	/CHAINM	/I				INTE	IFLAG1
IFLAG1		Transfer flag of subroutine NEWKC.	/NEWCOL	/I				INTE	IFLAG1
IFLAG1		Flag used to skip the intermediate test and search instructions.	/NEWKC	/I				INTE	IFLAG1
IFLAG2		Operation flag of subroutine NEWKC.	/CHAINM	/I				INTE	IFLAG2
IFLAG2		Operation flag of subroutine NEWKC =0 KC is the required branch junction atom. =1 KC is not the required branch atom junction.	/NEWCOL	/I				INTE	IFLAG2
IFLAG2		Operation flag =0 ligands of KC have all been processed. =1 unused ligands remain.	/NEWKC	/I				INTE	IFLAG2
IFUNCT		Function flag. =0 symmetry test is not for a single aromatic ring. =1 symmetry test is for a single aromatic ring. =2 aromatic ring has twofold internal rotational symmetry.	/CTWO	/I				INTE	IFUNCT
IFUNCT		Function flag. =0 symmetry test is not for a single aromatic ring. =1 symmetry test is for a single aromatic ring. =2 aromatic ring has twofold internal rotational symmetry.	/EQUAL	/I				INTE	IFUNCT
IFUNCT		Function flag. =0 symmetry test is not for a single aromatic ring. =1 symmetry test is for a single aromatic ring. =2 aromatic ring has twofold internal rotational symmetry.	/EQUALR	/I				INTE	IFUNCT
IGM		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit gauche interactions.	/CORCIG	/I				INTE	IGM

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
1GM		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit gauche interactions.	/GAUCHE/(*)	GAUCHE	M	INTE	1GM
1GM		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit gauche interactions.	/SORNGI/(*)	SORNGI	I	INTE	1GM
1GO		Counter that specifies the number of ether oxygen gauche interactions present in the molecule.	/CORCIG/(*)	CORCIG	M	INTE	1GO
1GO		Counter that specifies the number of ether oxygen gauche interactions present in the molecule.	/DITERE/(*)	DITERE	I	INTE	1GO
1GO		Counter that specifies the number of ether oxygen gauche interactions present in the molecule.	/GAUCHE/(*)	GAUCHE	M	INTE	1GO
1GO		Counter that specifies the number of ether oxygen gauche interactions present in the molecule.	/SORNGI/(*)	SORNGI	I	INTE	1GO
1GS		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit second-order interactions.	/DISCOR/(*)	DISCOR	M	INTE	1GS
1GS		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit second-order interactions.	/CORCIG/(*)	CORCIG	M	INTE	1GS
1GS		Counter that specifies the number of ring and second-order corrections.	/CRINGS/(*)	CRINGS	M	INTE	1GS
1GS		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit second-order interactions.	/CTWO /(*)	CTWO	M	INTE	1GS
1GS		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit second-order interactions.	/DITERE/(*)	DITERE	M	INTE	1GS
1GS		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit second-order interactions.	/GAUCHE/(*)	GAUCHE	M	INTE	1GS
1GS		Counter that specifies the number of ring and second-order corrections.	/HEXGON/(*)	HEXGON	M	INTE	1GS
1BS		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit second-order interactions.	/INTROT/(*)	INTROT	M	INTE	1BS

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
IGS		Counter that specifies the number of ring and second-order corrections.	/NRINGS/(*) NRINGS	M	INTE	IGS
IGS		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit second-order interactions.	/SORNGI/(*) SORNGI	I	INTE	IGS
IGSCIS		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit one or two cis interactions.	/CISCOR/(*) CISCOR	M	INTE	IGSCIS
IGSCIS		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit one or two cis interactions.	/CORCIG/(*) CORCIG	M	INTE	IGSCIS
IGSCIS		Counter that specifies the number of pairs of core atoms (K1 and K2) whose ligands exhibit one or two cis interactions.	/SORNGI/(*) SORNGI	I	INTE	IGSCIS
II		Storage flag for cis atoms.	/CIS	/(*) CIS	M	INTE	II
II		Loop counter and subscript.	/EQUAL	/(*) EQUAL	M	INTE	II
II		Loop counter and subscript.	/HEXCON/(*) HEXCON	M	INTE	II
II		Subscript for IBND array.	/IDENT	/(*) IDENT	M	INTE	II
II		Subscript.	/LESSEN/(*) LESSEN	M	INTE	II
II		Ordinal number assigned each of the identical ligands.	/SAME	/(*) SAME	M	INTE	II
II		Code number that distinguishes each type of identical ligand.	/SETUP	/(*) SETUP	M	INTE	II
IKC	(I)	Temporary storage array.	/BLK1	/(* 3925)	INTRD	M	INTE	IKC (100)
IM	(I)	Contains the order the subscripts of the second-order interaction data would have if the data were arranged in order of increasing numerical order.	/BLK3	/(* 4001)	CORCIG	I	INTE	IM (150)
					OTERE	I	INTE	IM (150)
IMATX	(I,J)	Contains the group number pertaining to a particular core atom in that location of IMATX that corresponds to the location in GRID containing the symbol for the core atom.	/BLK3	/(* 1201)	SCAN	M	INTE	IMATX (50,80)
					STAND	O	INTE	IMATX (50,80)
IN		Subscript of array LIGAND.	/SCANCH/(*) SCANCH	M	INTE	IN

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
INR		Counter that specifies the number of groups with internal rotational symmetry.	/CORCIG/	(+)	CORCIG	I	INTE	INR
INR		Counter that specifies the number of groups with internal rotational symmetry.	/CTWO	(+)	CTWO	M	INTE	INR
INR		Counter that specifies the number of groups with internal rotational symmetry.	/INTROT/	(+)	INTROT	M	INTE	INR
INTMIN		Number of entries in array KINT.	/BLK1	(/ 3778)	EXTROT	M	INTE	INTMIN INTROT I INTE INTMIN
INTROT		Searches for atoms which have three-fold rotational symmetry and which have not been included in the external rotational symmetry contribution. If present, the data are printed and the total internal contribution to the entropy is computed.	/INTROT/	(+)	CORCIG S INTROT E			INTROT INTROT
ID		Subscript.	/CTWO	(+)	CTWO	M	INTE	ID
IOPATH	(1)	Contains group numbers of asymmetric atoms.	/BLK3	(/ 3402)	ASYMC	0	INTE	IOPATH(100) ENTSYM I INTE IOPATH(100) MAXCHW I INTE IOPATH(100)
IORD	(1)	Contains the order that the I subscripts of the data in JRC(I,J) would have if said data were arranged in increasing numerical order.	/BLK2	(/ 3353)	LESSEN	I	INTE	IORD (40)
IORPAR		Counter that specifies the number of ortho and para pyridine corrections.	/CORCIG/	(+)	CORCIG	M	INTE	IORPAR
IORPAR		Counter that specifies the number of ortho and para pyridine corrections.	/HEXGON/	(+)	HEXGON	M	INTE	IORPAR
IORTHO		Counter that specifies the number of ortho benzene corrections.	/CORCIG/	(+)	CORCIG	M	INTE	IORTHO
IORTHO		Counter that specifies the number of ortho benzene corrections.	/HEXGON/	(+)	HEXGON	M	INTE	IORTHO

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
IPRINT		Printout options flag (OJK). K=1 print data library. K=0 do not print data library. J=0 print heading and case number. J=1 do not print heading and case number. J=2 print heading but not case number. J=3 print case number but not heading.	/TGAP	/(+)	TGAP	M	INTE	IPRINT
IRA		Temporary variable equal to total number of rings identified thus far.	/RING	/(+)	RING	M	INTE	IRA
IRC		Denotes total number of rings in molecule.	/BLK4	/(4321)	CHAINM	I	INTE	IRC
					CORCIG	I	INTE	IRC
					FUSION	I	INTE	IRC
					HEXGON	I	INTE	IRC
					LESSEN	M	INTE	IRC
					PRINT1	I	INTE	IRC
					RESETA	I	INTE	IRC
					RING	M	INTE	IRC
					SORNGI	I	INTE	IRC
					STAND	O	INTE	IRC
					SYMRNG	I	INTE	IRC
IRCMD		Net number of ring corrections.	/CORCIG	/(+)	CORCIG	M	INTE	IRCMD
IACFOT		Total number of fused and non-fused ring sets in molecule.	/BLK4	/(4323)	FUSION	O	INTE	IACFOT
IRCX		Value of IRC entered in subroutine LESSEN.	/CHAINM	/(+)	CHAINM	I	INTE	IRCX
IRCX		Computed value for the total number of rings entered into subroutine LESSEN.	/LESSEN	/(+)	LESSEN	M	INTE	IRCX
IRCX		Value of IRC entered in subroutine LESSEN.	/RING	/(+)	RING	I	INTE	IRCX
IRDD	(1)	Contains the order the subscripts of the data in array IDYRD would have if said data were arranged in numerical order.	/BLK1	/(2075)	EQUALR	I	INTE	IRDD (3)
IRG		Ring Indicator =0 ring(s) not present in molecule >0 ring(s) present in the molecule.	/BLK3	/(6401)	CHAINM	I	INTE	IRG
					JCAN	M	INTE	IRG
					STAND	O	INTE	IRG

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE			USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIR
IRING	(I,J)	Contains ring size in j=1 and group numbers of ring components in j>1 of ring number I.	/BLK3 /(+		1)	CRINGS	I	INTE	IRING (40,30)
						CTWO	I	INTE	IRING (40,30)
						CYCORR	I	INTE	IRING (40,30)
						FIRSTR	I	INTE	IRING (40,30)
						FUSION	I	INTE	IRING (40,30)
						HEXGON	I	INTE	IRING (40,30)
						LESSEN	M	INTE	IRING (40,30)
						NRINGS	I	INTE	IRING (40,30)
						OXYATM	I	INTE	IRING (40,30)
						PRINTI	I	INTE	IRING (40,30)
						RESETR	I	INTE	IRING (40,30)
						RING	M	INTE	IRING (40,30)
						SORNGI	I	INTE	IRING (40,30)
						SYMRNG	I	INTE	IRING (40,30)
IRK		Ring number of ring forming part of ring pair KSUB.	/FUSION/(+)	FUSION	M	INTE	IRK
IRNG2		Counter that specifies the number of fused carbon-ring corrections.	/CORCIG/(+)	CORCIG	M	INTE	IRNG2
IRNG2		Counter that specifies the number of fused carbon-ring corrections.	/CRINGS/(+)	CRINGS	M	INTE	IRNG2
IRNG3		Counter that specifies the number of fused nitrogen-containing-ring corrections.	/CORCIG/(+)	CORCIG	M	INTE	IRNG3
IRNG3		Counter that specifies the number of fused nitrogen-containing-ring corrections.	/NRINGS/(+)	NRINGS	M	INTE	IRNG3
IRR		Description not input	/GAUCHE/(+)	GAUCHE	M	INTE	IRR
ISB		Number of single bonds in ring K.	/CYCORR/(+)	CYCORR	M	INTE	ISB
ISB		Number of pairs of non-ring branch atoms found to be equal.	/EQUAL /(+)	EQUAL	M	INTE	ISB
ISB		Number of pairs of non-ring branch atoms found to be equal.	/EQUALR/(+)	EQUALR	I	INTE	ISB
ISBE		Number of pairs of non-ring atoms forming part of a pair of ligands bonded to two separate rings and which have been found to be equal.	/DELETE/(+)	DELETE	M	INTE	ISBE
ISBE		Number of pairs of non-ring atoms forming part of a pair of ligands bonded to two separate rings and which have been found to be equal.	/EQUALR/(+)	EQUALR	M	INTE	ISBE
ISBR		Number of pairs of ring atoms found to be equal.	/EQUALR/(+)	EQUALR	M	INTE	ISBR
ISER		Equivalent to integer function SEARCH.	/TGAP /(+)	TGAP	M	INTE	ISER

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U TYPE	VAR	DIM	
ISET	(1)	Denotes the locations in the reference ring where the ring atoms are identical to atoms in those test rings that are estimated to be completely contained in the reference ring.	/BLK3	/(3253)	LESSEN	M	INTE	ISET (30)	
ISETX	(1)	Denotes the locations in the reference ring where the ring atoms are identical to atoms in those test rings that are estimated to be partially contained in the reference ring.	/BLK3	/(3453)	LESSEN	M	INTE	ISETX (30)	
ISUB		Number of entries in array ICN.	/BLK4	/(362)	STAND	M	INTE	ISUB	
ISUM		Number of atoms bonded to a particular ring which are also ring atoms.	/SORNGI/(*)	SORNGI	M	INTE	ISUM	
IT		Location in data arrays containing thermochemical data for group k.	/TGAP	/(*)	TGAP	I	INTE	IT
ITAG1		Transfer flag.	/CIS	/(*)	CIS	M	INTE	ITAG1
ITAG2		Transfer flag.	/CIS	/(*)	CIS	M	INTE	ITAG2
ITEM		Variable used for temporary storage.	/SCAN	/(*)	SCAN	M	INTE	ITEM
ITEMP		Variable used for temporary storage in exchange of location operation.	/NEWKC	/(*)	NEWKC	M	INTE	ITEMP
ITEST		Number of CO groups in ring adjacent to ring atom LOCX.	/OXYATM/(*)	OXYATM	O	INTE	ITEST	
ITEST		Flag set to one if non-ring ligands are bonded to the ring. Otherwise equal to zero.	/SORNGI/(*)	SORNGI	M	INTE	ITEST	
ITEST2		Specifies the number of CO atoms adjacent to a designated ring atom.	/CYCORR/(*)	CYCORR	I	INTE	ITEST2	
ITZ		Flag: =0 no ring present in molecule. =1 ring present in molecule.	/STAND	/(*)	STAND	M	INTE	ITZ

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U	TYPE	VAR	DTM
1X	(1,j,k)	Contains structural data for core atom 1 at j=1 and for ligands at j=2 to j=5. Contents of column k k=1 chemical symbol of component, k=2 row coordinate of species (from input structural grid), k=3 column coordinate, j=1 and k=4 group number of parent core atom, j not 1 and k=4 direction of ligand bond, j=5 bond type and j=6 group number of core atom.	/BLK2	/(119)	ASVMC	I	INTE	IX	(100,5,6)
					CHAINM	I	INTE	IX	(100,5,6)
					CIS	I	INTE	IX	(100,5,6)
					CISCOR	I	INTE	IX	(100,5,6)
					CORCIG	I	INTE	IX	(100,5,6)
					CTWO	I	INTE	II	(100,5,6)
					CYCORR	I	INTE	IX	(100,5,6)
					DELTA1	I	INTE	IX	(100,5,6)
					DELTA2	I	INTE	IX	(100,5,6)
					DITERE	I	INTE	IX	(100,5,6)
					EQUAL	I	INTE	IX	(100,5,6)
					EQUALM	I	INTE	IX	(100,5,6)
					EXTROT	I	INTE	IX	(100,5,6)
					FIND	M	INTE	IX	(100,5,6)
					GAUCHE	I	INTE	IX	(100,5,6)
					HEXGON	I	INTE	IX	(100,5,6)
					INTROT	I	INTE	IX	(100,5,6)
					LINEAR	I	INTE	IX	(100,5,6)
					NRINGS	I	INTE	IX	(100,5,6)
					OXYTM	I	INTE	IX	(100,5,6)
					PRINT1	I	INTE	IX	(100,5,6)
					SCAN	M	INTE	IX	(100,5,6)
					SCANBR	I	INTE	IX	(100,5,6)
					SCANCB	I	INTE	IX	(100,5,6)
					SHIFT	M	INTE	IX	(100,5,6)
					SORNG1	I	INTE	IX	(100,5,6)
					STAMP	M	INTE	IX	(100,5,6)
					SYMRNG	I	INTE	IX	(100,5,6)
					SYMTRY	I	INTE	IX	(100,5,6)
1Z		Location j in NBC(1,j) of uppermost branch atom in previous chain.	/CHAINM/(*)	CHAINM	I	INTE	IZ	
1Z		Location j in NBC(1,j) of uppermost branch atom in new or previous chain.	/NEWCOL/(*)	NEWCOL	O	INTE	IZ	
11		Number of chain elements from the start of the chain up to but excluding the branch atom.	/CHANGE/(*)	CHANGE	M	INTE	11	
11		Storage flag for ligand bonded to atom K1. =-1 ligand is not stored and used in the cis test. =0 ligand is stored and used in the cis test. =1 ligand is stored and used in the cis test but 11 is reset to -1.	/CIS	/(*)	CIS	I	INTE	11
11		Storage flag for K1 ligands used in subroutine CIS.	/CISCOR/(*)	CISCOR	I	INTE	11	
11		Bond type flag of first central test core atom.	/GAUCHE/(*)	GAUCHE	M	INTE	11	
11		Lower limit of location in ORDSUM used in the calculation.	/SEARCH/(*)	SEARCH	M	INTE	11	
11		Storage flag for K1 ligands used in subroutine CIS.	/SORNG1/(*)	SORNG1	M	INTE	11	

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE			USAGE	
			BLCK	LOC	SUBR	U	TYPE	VAR	DIM
12		Number of chain elements one location above the branch atom to the end of the chain. (upper residual).	/CHANGE/	(*)	CHANGE	W	INTE	12
12		Storage flag for ligand bonded to atom K2. Conditions are the same as for flag I1.	/CIS	/(*)	CIS		INTE	12
12		Storage flag for K2 ligands used in subroutine CIS.	/CISCOR/	(*)	CISCOR	1	INTE	12
12		Bond type flag of second central test core atom.	/GAUCHE/	(*)	GAUCHE	W	INTE	12
12		Upper limit of location in ORDSUM used in the calculation.	/SEARCH/	(*)	SEARCH	W	INTE	12
12		Storage flag for K2 ligands used in subroutine CIS.	/SORNGI/	(*)	SORNGI	W	INTE	12
J		Loop counter and subscript.	/CHAINM/	(*)	CHAINM	W	INTE	J
J		Loop counter and subscript.	/CHANGE/	(*)	CHANGE	W	INTE	J
J		Loop counter and subscript.	/CORCIG/	(*)	CORCIG	W	INTE	J
J		Loop counter and subscript.	/CTWO	/(*)	CTWO	W	INTE	J
J		Loop counter and subscript.	/CYCORR/	(*)	CYCORR	W	INTE	J
J		Loop counter and subscript.	/EQUAL	/(*)	EQUAL	W	INTE	J
J		Loop counter and subscript.	/EQUALR/	(*)	EQUALR	W	INTE	J
J		Loop counter and subscript.	/EXTROT/	(*)	EXTROT	W	INTE	J
J		Loop counter and subscript.	/FIRSTR/	(*)	FIRSTR	W	INTE	J
J		Loop counter and subscript.	/FUSION/	(*)	FUSION	W	INTE	J
J		Loop counter and subscript.	/HEXGON/	(*)	HEXGON	W	INTE	J
J		Loop counter and subscript.	/IDENT	/(*)	IDENT	W	INTE	J
J		Loop counter and subscript.	/LESSEN/	(*)	LESSEN	W	INTE	J

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE			USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIM
J		Loop counter and subscript.	/MULTI	/(*)	MULTI	M	INTE	J
J		Loop counter and subscript.	/NEWCOL	/(*)	NEWCOL	M	INTE	J
J		Loop counter and subscript.	/NEWRC	/(*)	NEWRC	M	INTE	J
J		Loop counter and subscript.	/NRINGS	/(*)	NRINGS	M	INTE	J
J		Loop counter and subscript.	/NUMBER	/(*)	NUMBER	M	INTE	J
J		Loop counter and subscript.	/ORDER	/(*)	ORDER	M	INTE	J
J		Loop counter and subscript.	/PRINT1	/(*)	PRINT1	M	INTE	J
J		Loop counter and subscript.	/RING	/(*)	RING	M	INTE	J
J		Loop counter and subscript.	/SAME	/(*)	SAME	M	INTE	J
J		Loop counter and subscript.	/SCAN	/(*)	SCAN	M	INTE	J
J		Loop counter and subscript.	/SCANB	/(*)	SCANB	M	INTE	J
J		Loop counter and subscript.	/SCANCH	/(*)	SCANCH	M	INTE	J
J		Loop counter and subscript.	/SETUP	/(*)	SETUP	M	INTE	J
J		Loop counter and subscript.	/SHIFT	/(*)	SHIFT	M	INTE	J
J		Loop counter and subscript.	/SORNGI	/(*)	SORNGI	M	INTE	J
J		Loop counter and subscript.	/STAND	/(*)	STAND	M	INTE	J
J		Loop counter and subscript.	/SUMATH	/(*)	SUMATH	M	INTE	J
J		Loop counter and subscript.	/SYMRNG	/(*)	SYMRNG	M	INTE	J
J		Loop counter and subscript.	/SYMTRY	/(*)	SYMTRY	M	INTE	J
J		Loop counter and subscript.	/TGAP	/(*)	TGAP	M	INTE	J

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	BIT
JA		Loop counter and subscript.	/STAND	/(+)	STAND	W	INTE	JA
JBOND	(I)	Contains ring core atom to which heavy ligand is bonded.	/BLK3	/(3701)	HEXGOM	M	INTE	JBOND (100)
JBR	(I)	Counter designating the location in array LIGAND where the composition data of a particular ligand of core atom I are stored.	/BLK3	/(3302)	ASYMC	I	INTE	JBR (100)
					EXTRAT	I	INTE	JBR (100)
					SCANDR	M	INTE	JBR (100)
					SCANCM	M	INTE	JBR (100)
					SYMBRY	R	INTE	JBR (100)
JC		Counter limit and subscript.	/MULTI	/(+)	MULTI	W	INTE	JC
JC		Identification number of group whose ligand data storage position is to be altered.	/SHIFT	/(+)	SHIFT	I	INTE	JC
JC		Group number of core atom bonded to core atom KC whose ligands are identified and classified in the scan operation.	/STAND	/(+)	STAND	W	INTE	JC
JDIF		Number of residual ring atoms which are to be added to all the chains.	/RESETR	/(+)	RESETR	W	INTE	JDIF
JDL		Counter denoting number of test rings partially contained in reference ring.	/LESSEN	/(+)	LESSEN	W	INTE	JDL
JDONE	(I)	Location I is set equal to 1 if the ring atom of group number I has been tested. Otherwise, it equals 0.	/BLK3	/(3502)	DELETE	O	INTE	JDONE (100)
					EQUALR	M	INTE	JDONE (100)
JDONE	(I)	Aromatic ring flag =0 ring I is a benzene or pyridine-type ring forming part of a fused ring set.	/BLK3	/(5881)	HEXGOM	M	INTE	JDONE (40)
JDONE	(I)	Identifies ring ligands which have (1) or have not (0) been checked against other ligands for similarity.	/BLK4	/(2821)	SYMRNG	M	INTE	JDONE (120)
JDT		Counter denoting number of test rings completely contained in reference ring.	/LESSEN	/(+)	LESSEN	W	INTE	JDT
JDI		Temporary storage variable.	/CYCORR	/(+)	CYCORR	W	INTE	JDI
JDI		Displacement between the first and second CO groups in ring K.	/OXYATM	/(+)	OXYATM	W	INTE	JDI
JDJ		Temporary storage variable.	/CYCORR	/(+)	CYCORR	W	INTE	JDJ
JDJ		Displacement between atom LOCX and the first CO group in ring K.	/OXYATM	/(+)	OXYATM	W	INTE	JDJ

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FORTRAN SYMBOL	DATA SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLDGR	LOC	SUBR	U	TYPE	VAR
JF		Upper limit for bond termination loop in subroutine BOND.	/ASSIGN/	1*) ASSIGN	0	INTE	JF
JF		Upper limit for bond termination loop.	/BOND	1*) BOND	1	INTE	JF
JF		Upper limit of loop counter.	/CHAINM/	1*) CHAINM	W	INTE	JF
JF		Upper limit of loop counter.	/CHANGE/	1*) CHANGE	W	INTE	JF
JF		Upper limit of loop counter.	/CORCIG/	1*) CORCIG	W	INTE	JF
JF		Upper limit of loop counter.	/CTWO	1*) CTWO	W	INTE	JF
JF		Upper limit of bond termination loop of indexed atom number 1 ligand.	/FIND	1*) FIND	1	INTE	JF
JF		Upper limit of loop counter.	/FUSION/	1*) FUSION	W	INTE	JF
JF		Upper limit of loop counter.	/HEXGON/	1*) HEXGON	W	INTE	JF
JF		Upper limit for bond termination loop in subroutine BOND.	/IDENT	1*) IDENT	1	INTE	JF
JF		Upper limit of loop counter.	/LESSEN/	1*) LESSEN	W	INTE	JF
JF		Upper limit of loop counter.	/NEWRC	1*) NEWRC	W	INTE	JF
JF		Upper limit of bond termination loop.	/NUMBER/	1*) NUMBER	1	INTE	JF
JF		Upper limit of loop counter.	/ORDER	1*) ORDER	W	INTE	JF
JF		Upper limit for bond termination loop.	/SCAN	1*) SCAN	1	INTE	JF
JF		Upper limit of loop counter.	/SORNGI/	1*) SORNGI	U	INTE	JF
JF		Upper limit of cycle counter.	/STAND	1*) STAND	W	INTE	JF
JFF		Upper limit of bond termination loop for ligand one.	/NUMBER/	1*) NUMBER	0	INTE	JFF
JJ		Lower limit of bond termination loop in subroutine BOND.	/ASSIGN/	1*) ASSIGN	0	INTE	JJ
JJ		Lower limit of bond termination loop.	/BOND	1*) BOND	1	INTE	JJ

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			LOC	LOC	U	TYPE	VAR	DIM
J1		Lower limit of loop counter.	/CTWO	/C*) CTWO	M	INTE	J1
J1		Lower limit of bond termination loop of indexed atom number 1 ligand.	/FIND	/C*) FIND	I	INTE	J1
J1		Lower limit of bond termination loop in subroutine BOND.	/IDENT	/C*) IDENT	I	INTE	J1
J1		Lower limit of bond termination loop.	/NUMBER	/C*) NUMBER	I	INTE	J1
J1		Lower limit of bond termination loop.	/SCAN	/C*) SCAN	I	INTE	J1
J11		Lower limit of bond termination loop for ligand one.	/NUMBER	/C*) NUMBER	O	INTE	J11
J2		Loop counter.	/BOND	/C*) BOND	O	INTE	J2
J2		Ring location para to nitrogen atom.	/CYCORR	/C*) CYCORR	M	INTE	J2
J2		Variable used for temporary storage.	/DITERE	/C*) DITERE	M	INTE	J2
J2		Loop counter.	/EQUAL	/C*) EQUAL	M	INTE	J2
J2		Loop counter and subscript.	/FUSION	/C*) FUSION	M	INTE	J2
J2		Ring number.	/HEXGON	/C*) HEXGON	M	INTE	J2
J2		Identification number of test ring.	/LESSEN	/C*) LESSEN	M	INTE	J2
J2		Counter ultimately equal to NOBR.	/STAND	/C*) STAND	M	INTE	J2
JK		Ring number or non-ring ligand weight identifier.	/HEXGON	/C*) HEXGON	M	INTE	JK
JOR		Number of entries in array JBOND.	/HEXGON	/C*) HEXGON	M	INTE	JOR
JORD	(I)	Contains subscripts of IRING data arranged in order of increasing ring size.	/BOND	/C(3053)) LESSEN	I	INTE	JORD (40)
JPRINT		Equal to digit K of IPRINT (OJK).	/IGAP	/C*) IGAP	M	INTE	JPRINT
JRC	(I,J)	Contains Incompstability factors and ring numbers of JRING data pertaining to test rings that are partially contained in the reference ring.	/BOND	/C(3153)) LESSEN	M	INTE	JRC (40,2)

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
JRDIF	(I)	Contains the computed differences between the ring size and the number of atoms of the test rings that are also contained in the reference ring. Referred to as incompatibility factor.	/BLK3	/(3103)	LESSEN	M	INTE	JRDIF (40)
JRING	(I,J)	Contains the negative group number of test ring atoms not contained in reference ring or the ring locations in the reference ring where the test ring atoms are located. The value is stored in location j which corresponds to the location of the test ring atom.	/BLK3	/(1855)	LESSEN	M	INTE	JRING (40,30)
JS		Lower limit of character search cycle counter.	/IDENT	/(+)	IDENT	M	INTE	JS
JSCAN	(I)	Scan flag =0 ring I has not been tested. =1 ring I has been tested.	/BLK3	/(3561)	FUSION	M	INTE	JSCAN (40)
JSTOP		I location in arrays IRING(i,j) and NRLOC(i) to which ring data are shifted when one or more rings are discarded.	/LESSEN/(+)		LESSEN	M	INTE	JSTOP
JSTORE	(I)	Contains ring numbers of six-membered rings composed of 4 carbon and 2 nitrogen atoms and devoid of double bonds.	/BLK3	/(6398)	NRINGS	M	INTE	JSTORE(3)
JSUM		Counter denoting number of atoms of a particular test ring that are also present in the reference ring.	/LESSEN/(+)		LESSEN	M	INTE	JSUM
JT		Identification number of group to be tested for second-order multiple-bond weight contributions. If present, these are added to group weight of XT.	/DELTA2/(+)		DELTA2	I	INTE	JT
JUNCT	(I,J)	Contains group number of core atom ligand i bonded to branch atom j where j is also the group number of the branch atom.	/BLK3	/(1203)	CHAINM	O	INTE	JUNCT (5,100)
JW		Subscript for printout legend. Setting denotes whether the external symmetry number can be computed.	/BLK5	/(59)	CORCIG	O	INTE	JW
					ENTSYM	I	INTE	JW
					EXTROT	O	INTE	JW
					FIRSTM	O	INTE	JW
					LINEAR	O	INTE	JW
					SYMMG	O	INTE	JW
JX		Subscript.	/FIRST/(+)		FIRST	M	INTE	JX

FORTRAN SYMBOL	NAYN SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUCH	U TYPE	VAR	DIM
JX		Subscript.	/LESSEN/(*) LESSEN	M	INTE	JX
JX		Temporary storage variable.	/ORDER /(*) ORDER	M	INTE	JX
JY		Subscript for printout legend. Setting denotes whether the number of enantiomers and meso compounds can be computed in total.	/BLFS /(*	(0)	COARCIG	O	INTE	JY
					ENTSYN	I	INTE	JY
					FIRSTA	O	INTE	JY
					MAICMN	O	INTE	JY
J1		Subscript of one of the two ligands under comparison.	/EQUAL /(*) EQUAL	M	INTE	J1
J1		Flag which is activated if character symbol is not found in cycle.	/IDENT /(*) IDENT	M	INTE	J1
J1		Location in IX of data of non-core ligand.	/SCAN /(*) SCAN	M	INTE	J1
J1		Subscript of array KSAME.	/SETUP /(*) SETUP	M	INTE	J1
J1		Subscript and flag.	/SYMRNG/(*) SYMRNG	M	INTE	J1
J2		Subscript of one of the two ligands under comparison.	/EQUAL /(*) EQUAL	M	INTE	J2
J2		Flag which is activated if character symbol is found in cycle.	/IDENT /(*) IDENT	M	INTE	J2
J2		Subscript.	/LESSEN/(*) LESSEN	M	INTE	J2
J2		Location in IX of data of core ligand.	/SCAN /(*) SCAN	M	INTE	J2
J2		Subscript of array KSAME.	/SETUP /(*) SETUP	M	INTE	J2
J2		Subscript.	/SYMRNG/(*) SYMRNG	M	INTE	J2
K		Row coordinate of indexed core atom.	/ASSIGN/(*) ASSIGN	I	INTE	K
K		Loop counter and subscript.	/ASYNC /(*) ASYNC	M	INTE	K
K		Loop counter and subscript.	/CISCOR/(*) CISCOR	M	INTE	K
K		Loop counter and subscript. Also i.e. number of ring examined in subroutine CYCORR.	/FORCIG/(*) COARCIG	M	INTE	K
K		Identification number of ring.	/CTWO /(*) CTWO	M	INTE	K

FORTRAN SYMBOL	MAYM SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
K		Identification number of ring.	/CYCORR/10) CYCORR	I	INTE	K
K		Loop counter and subscript.	/DELETE/10) DELETE	O	INTE	K
K		Loop counter and subscript.	/ENTSYM/10) ENTSYM	M	INTE	K
K		Loop counter and subscript.	/EQUAL //10) EQUAL	M	INTE	K
K		Loop counter and subscript.	/EQUALR/10) EQUALR	M	INTE	K
K		Loop counter and subscript.	/EXTROY/10) EXTROY	M	INTE	K
K		Entry value: row coordinate of indexed atom. Exit value: row coordinate of core atom.	/FIND //10) FIND	N	INTE	K
K		Loop counter and subscript.	/FIRSTA/10) FIRSTA	M	INTE	K
K		Loop counter and subscript.	/FUSION/10) FUSION	M	INTE	K
K		Loop counter and subscript.	/HEXGON/10) HEXGON	M	INTE	K
K		Row coordinate of first character of symbol.	/IDENT //10) IDENT	N	INTE	K
K		Loop counter and subscript.	/INTROT/10) INTROT	M	INTE	K
K		Identification number of reference ring.	/LESSEN/10) LESSEN	M	INTE	K
K		Loop counter and subscript.	/LINEAR/10) LINEAR	M	INTE	K
K		Loop counter and subscript.	/MAXCHN/10) MAXCHN	M	INTE	K
K		Loop counter and subscript.	/MULTI //10) MULTI	M	INTE	K
K		Loop counter and subscript.	/NRINGS/10) NRINGS	M	INTE	K
K		Row coordinate of indexed core atom.	/NUMBER/10) NUMBER	I	INTE	K
K		Ring number of ring under inspection.	/OXYATR/10) OXYATR	I	INTE	K
K		Loop counter and subscript, also ring number.	/RESETR/10) RESETR	M	INTE	K

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			D LCR	LOC	SOBR	U TYPE	VAN	DTA
K		Loop counter and subscript.	/RING	/I*	1 RING	M	INTE	K
K		Loop counter and subscript.	/SAME	/I*	2 SAME	M	INTE	K
X		Row coordinate of core atom in array GRID.	/SCAN	/I*	1 SCAN	I	INTE	K
K		Loop counter and subscript.	/SETUP	/I*	1 SETUP	M	INTE	K
X		Loop counter and subscript.	/SORNGI	/I*	1 SORNGI	M	INTE	K
X		Row grid coordinate of core atom.	/STAND	/I*	1 STAND	M	INTE	K
A		Loop counter and subscript.	/SYBRNG	/I*	1 SYBRNG	M	INTE	R
K		Loop counter and subscript.	/SYMTRY	/I*	1 SYMTRY	M	INTE	R
K		Loop counter and subscript.	/TGAP	/I*	1 TGAP	M	INTE	K
KAFTR		Transfer flag which prevents storage of the ligand data already defined at the start of the atomic composition evaluation cycle.	/SCANBR	/I*	1 SCANBR	I	INTE	KAFTR
KAFTR		Transfer flag which prevents storage of the ligand data already defined at the start of the atomic composition evaluation cycle.	/SYMTRY	/I*	1 SYMTRY	M	INTE	KAFTR
KANE		Denotes which of the two central atoms has no unsaturated bonds.	/GAUCHI	/I*	1 GAUCHI	M	INTE	KANE
KARD	(1)	Ring locations (1) containing identical ligands are assigned the same identifiers (KS) in this array.	/RKN	/I(4308)	1 SYBRNG	M	INTE	KARD (6)
KB		Value of KY at the beginning of the cycle.	/FUSION	/I*	1 FUSION	M	INTE	KB
KBENZ	(1)	Contains the ring numbers of the benzene type rings present in the molecule.	/BRZ	/I(5453)	1 CYCORR 1 HEXON 1 SYBRNG	O I I	INTE	KBENZ (40) KBENZ (40) KBENZ (40)
KBU		Counter that specifies whether one or both ligands in the cis position are carbon atoms with a connectivity of four and bonded to only one heavy atom.	/CICORR	/I*	1 CICORR	M	INTE	KBU
KC		Group number of chain atom being processed.	/CHAINM	/I*	1 CHAINM	M	INTE	KC

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIM
KC		Group number of core atom bonded to ring atom K1.	/CTWO	/1*) CTWO	W	INTE	KC
KC		Group number of atom whose ligands are being compared.	/EQUALR/	/1*) EQUALR	I	INTE	KC
KC		Group number.	/FIND	/1*) FIND	I	INTE	KC
KC		Group number of atom whose ligands are being compared.	/FIRSTR/	/1*) FIRSTR	I	INTE	KC
KC		Group number of ligand bonded to saturated central atom.	/GAUCHE/	/1*) GAUCHE	W	INTE	KC
KC		Loop counter and subscript.	/HEXGON/	/1*) HEXGON	W	INTE	KC
KC		Group number of atom whose ligand is to be tested for linearity and rotational symmetry.	/LINEAR/	/1*) LINEAR	I	INTE	KC
KC		Test branch atom in chain LX which may serve as the junction for the new chain.	/NEWCOL/	/1*) NEWCOL	M	INTE	KC
KC		Group number of chain atom being processed.	/NEWKC	/1*) NLWKC	M	INTE	KC
KC		Group number of ring component.	/RESETR/	/1*) RESETR	W	INTE	KC
KC		Group number of core atom under which the data are stored in each of the symmetry identification arrays.	/SAME	/1*) SAME	I	INTE	KC
KC		Group number of chain atom currently being processed by SCANCH.	/SCANCH/	/1*) SCANCH	I	INTE	KC
KC		Identification number of core atom whose data are to be stored in j=2 of core atom j=JC.	/SHIFT	/1*) SHIFT	I	INTE	KC
KC		Group number. Also designates core atom of group.	/STAND	/1*) STAND	W	INTE	KC
KC		Group number of ring component.	/SYMRNG/	/1*) SYMRNG	W	INTE	KC
KC		Group number of atom under inspection.	/SYMTRY/	/1*) SYMTRY	W	INTE	KC
KCANE		Group number of central atom devoid of unsaturated bonds.	/GAUCHE/	/1*) GAUCHE	W	INTE	KCANE
KCBEF		Group number of atom processed immediately prior to atom KC.	/SCANCH/	/1*) SCANCH	I	INTE	KCBEF
KCBEF		Group number of chain atom previously processed. If none, it is set to 1000.	/SYMTRY/	/1*) SYMTRY	W	INTE	KCBEF

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLK#	LOC	SUBR	U	TYPE	VAR	DIM
KCC		Total number of core atoms in molecular structure.	/BLK2	/(3219)	ASYMC	I	INTE	KCC	
					CHAINM	I	INTE	KCC	
					CRICIG	I	INTE	KCC	
					CTWO	I	INTE	KCC	
					EQUAL	I	INTE	KCC	
					EQUALR	I	INTE	KCC	
					HEXGON	I	INTE	KCC	
					INTROT	I	INTE	KCC	
					PRINTI	I	INTE	KCC	
					SCAN	M	INTE	KCC	
					SETUP	I	INTE	KCC	
					SORNGI	I	INTE	KCC	
					STAND	M	INTE	KCC	
					SYMRNG	I	INTE	KCC	
					SYMTRY	I	INTE	KCC	
					TGAP	I	INTE	KCC	
KCCR	(I,J)	Contains the group numbers I of each pair J of ring atoms, one from each ring, which have been tested.	/BLK1	/(1125)	DELETE	I	INTE	KCCR	(2,30)
					EQUALR	O	INTE	KCCR	(2,30)
KCENE		Group number of central atom containing an unsaturated bond.	/GAUCHE/	(*)	GAUCHE	M	INTE	KCENE
KCGAUS	(I,J)	Contains the group numbers I of the central atoms associated with the second-order interaction J.	/BLK3	/(4751)	CISCOR	O	INTE	KCGAUS	(3,150)
					CRICIG	M	INTE	KCGAUS	(3,150)
					CRINGS	O	INTE	KCGAUS	(3,150)
					CTWO	O	INTE	KCGAUS	(3,150)
					DITERE	M	INTE	KCGAUS	(3,150)
					GAUCHE	O	INTE	KCGAUS	(3,150)
					HEXGON	O	INTE	KCGAUS	(3,150)
					INTROT	M	INTE	KCGAUS	(3,150)
					CRINGS	O	INTE	KCGAUS	(3,150)
KCIS		Number of cis interactions (1 or 2) exhibited by a particular pair of test core atoms.	/CISCOR/	(*)	CISCOR	M	INTE	KCIS
KCL		Counter that specifies whether the atom one removed from the first central test core atom is a carbon atom.	/CISCOR/	(*)	CISCOR	M	INTE	KCL
KCNEXT		Group number of atom adjacent to atom KC1.	/EXTROT/	(*)	EXTROT	M	INTE	KCNEXT
KCNEXT		Group number of atom in ligand to be tested which is bonded to atom KC.	/LINEAR/	(*)	LINEAR	I	INTE	KCNEXT
KCNEXT		Group number of branch atom currently being processed by SCANBR.	/SCANBR/	(*)	SCANBR	I	INTE	KCNEXT
KCNEXT		Group number of atom to be processed immediately after atom KC.	/SEARCH/	(*)	SEARCH	I	INTE	KCNEXT
KCNEXT		Group number of next atom down the chain.	/SYMTRY/	(*)	SYMTRY	M	INTE	KCNEXT
KCPV		Group number of chain atom preceding atom KC.	/CHAINM/	(*)	CHAINM	M	INTE	KCPV

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U	TYPE	VAR	DTM
KCPV		Chain atom preceding atom KC.	/NEWCOL/(*)	NEWCOL	R	INTE	KCPV
KCPV		Group number of chain atom preceding atom KC.	/NEWKC /(*)	NEWKC	R	INTE	KCPV
KCPV		Group number of parent core atom, namely, core atom processed immediately prior to KC.	/STAND /(*)	STAND	M	INTE	KCPV
KCR		Counter that specifies whether the atom one removed from the second central test core atom is a carbon atom.	/CISCOR/(*)	CISCOR	M	INTE	KCR
KCSAME	(I,J)	Group number of identical ligand I associated with core atom J.	/BLK1 /(*	2078)		ASYMC	I	INTE	KCSAME(6,100)
						EXTROY	I	INTE	KCSAME(6,100)
						LINEAR	I	INTE	KCSAME(6,100)
						SAME	M	INTE	KCSAME(6,100)
						SYMRNG	I	INTE	KCSAME(6,100)
						SYMTRY	O	INTE	KCSAME(6,100)
KCSUDA		Group number of pseudoasymmetric atom.	/CORCIG/(*)	CORCIG	I	INTE	KCSUDA
KCSUDA		Group number of pseudoasymmetric atom.	/ENTSYM/(*)	ENTSYM	I	INTE	KCSUDA
KCSUDA		Group number of pseudoasymmetric atom.	/EXTROT/(*)	EXTROT	O	INTE	KCSUDA
KCY		Variable equal to the number of atoms in common between ring pair KSUB.	/FUSION/(*)	FUSION	M	INTE	KCY
KCX		Subscript.	/CISCOR/(*)	CISCOR	M	INTE	KCX
KCX		Variable used for temporary storage.	/NEWCOL/(*)	NEWCOL	M	INTE	KCX
KCX		Group number denoting the location in the arrays where the data are to be stored in subroutine SOME.	/SETUP /(*)	SETUP	M	INTE	KCX
KCX		Group number of ring atom.	/SYMRNG/(*)	SYMRNG	I	INTE	KCX
KCX001	(I)	Group number information input to subroutine EQUAL. I=1 KC or 1000. I=2 KI.	/CTWO /(*)	CTWO	M	INTE	KCX001(3)
KCX001	(I)	Contain the group number(s) (set A) of the core atom(s) whose ligands are to be compared structurewise with those of set B.	/EQUAL /(*)	EQUAL	I	INTE	KCX001(3)

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIR
KCX001	(I)	Contains the group number(s) (set A) of the core atom(s) whose ligands are to be compared structurewise with those of set B.	/SETUP	/(*)	SETUP	I	INTE	KCX001(3)
KCX001	(I)	Contains the group numbers of the first three ring components.	/SYMRNG	/(*)	SYMRNG	W	INTE	KCX001(3)
KCX002		Same as KCX001(1).	/CTWO	/(*)	CTWO	W	INTE	KCX002
KCX002	(I)	Contains the group number(s) (set B) of the core atom(s) whose ligands are to be compared structurewise with those of set A.	/EQUAL	/(*)	EQUAL	I	INTE	KCX002(3)
KCX002	(I)	Contains the group number(s) (set B) of the core atom(s) whose ligands are to be compared structurewise with those of set A.	/SETUP	/(*)	SETUP	I	INTE	KCX002(3)
KCX002	(I)	Contains the group numbers of the last three ring components.	/SYMRNG	/(*)	SYMRNG	W	INTE	KCX002(3)
KCY		Ordinal number used to identify the non-ring ligand data of a pair of rings which has been tested for symmetry. Also number of entries in arrays RKT and MER.	/BLK3	/(*	6397)	EQUAL	M	INTE	KCY
						EQUALR	M	INTE	KCY
						SYMTRY	O	INTE	KCY
KC1		Group number of first carbon atom bonded to the oxygen atom.	/DITERE	/(*)	DITERE	W	INTE	KC1
KC1		Group number of atom contained in array KCX001 and whose ligands are being compared.	/EQUAL	/(*)	EQUAL	W	INTE	KC1
KC1		Group number of central atom in longest chain if chain is odd or one of the two central atoms if chain is even.	/EXTROT	/(*)	EXTROT	W	INTE	KC1
KC1		Group number of atom contained in array KCX001.	/SETUP	/(*)	SETUP	W	INTE	KC1
KC1		Group number under which the symmetry data of the ring are stored.	/SYMRNG	/(*)	SYMRNG	W	INTE	KC1
KCIALT	(I)	Temporary storage for original KCSAME data computed for KC1.	/BLK1	/(*	3883)	EXTROT	M	INTE	KCIALT(6)
KCIP		Group number of atom previous (parent) to atom K1.	/EQUAL	/(*)	EQUAL	W	INTE	KCIP
KCIP		Group number of atom previous to the entry ring atom K1.	/EQUALR	/(*)	EQUALR	I	INTE	KCIP
KCIPR		Group number of atom previous (parent) to atom K1R.	/EQUALR	/(*)	EQUALR	W	INTE	KCIPR

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SGR	U	TYPE	VAR
KC2		Group number of second carbon atom bonded to the oxygen atom.	/DITERE/	(+)	DITERE	W	INTE	KC2
KC2		Group number of atom contained in array KCXD02 and whose ligands are being compared.	/EQUAL	(+)	EQUAL	W	INTE	KC2
KC2		Group number of atom adjacent to atom KC1.	/EXTR0T/	(+)	EXTR0T	W	INTE	KC2
KC2		Group number of atom contained in array KCXD02.	/SETUP	(+)	SETUP	W	INTE	KC2
KC2ALT	(1)	Temporary storage for original KCSAME data computed for KC2.	/BLK1	(1 3889)	EXTR0T	W	INTE	KC2ALT(6)
KC2P		Group number of atom previous (parent) to atom K2.	/EQUAL	(+)	EQUAL	W	INTE	KC2P
KC2P		Group number of atom previous to the entry ring atom K2.	/EQUALR/	(+)	EQUALR	I	INTE	KC2P
KC2PR		Group number of atom previous (parent) to atom K2R.	/EQUALR/	(+)	EQUALR	W	INTE	KC2PR
KC3		Counter used in the search of 3-ene structures.	/DISCOM/	(+)	DISCOM	W	INTE	KC3
KC3		Group number of atom adjacent to atom KC1.	/EXTR0T/	(+)	EXTR0T	W	INTE	KC3
KD		Assigned change in row coordinate of symbol input array.	/ASSIGN/	(+)	ASSIGN	0	INTE	KD
KD		Change in row coordinate.	/BOND	(+)	BOND	I	INTE	KD
KD		Upper limit of loop counter.	/DELETE/	(+)	DELETE	W	INTE	KD
KD		Change in row coordinate for indexed atom number 1 ligand.	/FIND	(+)	FIND	I	INTE	KD
KD		Change in row coordinate	/IDENT	(+)	IDENT	W	INTE	KD
KD		Change in row coordinate of array GRID.	/NUMBER/	(+)	NUMBER	I	INTE	KD
KD		Change in row coordinate for transformation to NX.	/SCAN	(+)	SCAN	I	INTE	KD
KD0		Change in row coordinate of ligand one.	/NUMBER/	(+)	NUMBER	0	INTE	KD0
KD2		KD value of second character.	/IDENT	(+)	IDENT	W	INTE	KD2
KENE		Denotes which of the two central atoms has an unsaturated bond.	/GAUCHE/	(+)	GAUCHE	W	INTE	KENE

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
KEQUAL		Counter that specifies the number of different atoms which are contained in equal amounts by two ligands.	/SETUP	/(*) SETUP	W	INTE	KEQUAL
KF		Upper limit of loop counter.	/CIS	/(*) CIS	W	INTE	KF
KF		Upper limit of loop counter.	/CORCIG	/(*) CORCIG	W	INTE	KF
KF		Upper limit of loop counter that controls the selection of the test ligand from set B.	/EQUAL	/(*) EQUAL	I	INTE	KF
KF		Subscript corresponding to highest value of data in IDXR.	/EQUALR	/(*) EQUALR	W	INTE	KF
KF		Upper limit of loop counter.	/FIRSTR	/(*) FIRSTR	W	INTE	KF
KF		Upper limit of loop counter.	/FUSION	/(*) FUSION	W	INTE	KF
KF		Upper limit of loop counter.	/LINEAR	/(*) LINEAR	W	INTE	KF
KF		Upper limit of counter.	/RING	/(*) RING	W	INTE	KF
KF		Upper limit of loop counter.	/SAME	/(*) SAME	W	INTE	KF
KF		Upper limit of loop counter that controls the selection of the test ligand from set B.	/SETUP	/(*) SETUP	I	INTE	KF
KF		Upper limit of loop counter	/SOHNGI	/(*) SOHNGI	W	INTE	KF
KF		Description not input	/SYMRNG	/(*) SYMRNG	W	INTE	KF
KFGKUS	(I)	Frequency or number of corrections of the second-order interaction I. In CRINGS, it contains subscript of data array associated with ring correction.	/BLK3	/(* 400)	CISCOR O CORCIG M CRINGS O DITERE O GAUCHE R	O M O O R	INTE	KFGAUS(150)
KFIRST		Group number of first atom processed in composition cycle.	/SYNTRY	/(*) SYNTRY	W	INTE	KFIRST
KFLAG		Flag that denotes whether data in arrays NTOTAL, KCSAME, and NOSAME were (1) or were not (0) transferred to the temporary storage arrays.	/EXTRD	/(*) EXTRD	W	INTE	KFLAG
KFLAG		Flag that designates the weight correction for ring atoms.	/HEIGON	/(*) HEIGON	W	INTE	KFLAG
KGMAT	(I, J)	Contains alkane C-C gauche corrections.	/GAUCHE	/(*) GAUCHE	O	INTE	KGMAT (4,4)

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SCBA	U TYPE	VAR	DIM
KBO		Atom type flag. =1 one of the two central atoms is a nitrogen atom. =2 the two central atoms are carbon atoms.	/GAUCHE/1*) GAUCHE	M	INTE	KBO
KGRID	(1)	Contents of input card containing structure or label of molecule shifted and centered for printout purposes.	/BLK4	/(361)	TGAP	M	INTE	KGRID (103)
KHEAVY		Group number of carbon test core atom bonded to oxygen atom forming part of ether linkage.	/GAUCHE/1*) GAUCHE	M	INTE	KHEAVY
KI		Lower limit of loop counter.	/CORCIG/1*) CORCIG	M	INTE	KI
KI		Lower limit of loop counter that controls the selection of the test ligand from set B.	/EQUAL/1*) EQUAL	M	INTE	KI
KI		Subscript corresponding to lowest value of data in IDXRD.	/EQUALR/1*) EQUALR	M	INTE	KI
KI		Lower limit of loop counter.	/HEXGON/1*) HEXGON	M	INTE	KI
KI		Lower limit of loop counter.	/MAXCHN/1*) MAXCHN	M	INTE	KI
KI		Lower limit of loop counter.	/MULTI/1*) MULTI	M	INTE	KI
KI		Location in array SUM corresponding to location I in ORDSUM.	/SEARCH/1*) SEARCH	M	INTE	KI
KI		Lower limit of loop counter that controls the selection of the test ligand from set B.	/SETUP/1*) SETUP	M	INTE	KI
KI		Description not input	/SYMRNG/1*) SYMRNG	M	INTE	KI
KINT	(1)	Contains the group number of atoms whose internal rotational symmetry is included in the external rotational symmetry of the molecule.	/BLK1	/(3719)	EXTROT 0 INTROT 1		INTE	KINT (100) (100)
KJ	(1)	Contains the location of the ring atom bonded to the non-ring atom I.	/BLK4	/(2641)	SYMRNG	M	INTE	KJ (100)
KJ	(1)	Contains I.d. numbers of the two rings in the fused ring set.	/BLK4	/(9280)	CRINGS	M	INTE	KJ (2)
KJ		Group number of ring component.	/CYCORR/1*) CYCORR	M	INTE	KJ

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FORTRAN SYMBOL	CATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIM
KK		Counter of ring test cycle. Also denotes location in chain LX that contains the first atom of the ring.	/CHAINM/(*)	CHAINM	W	INTE	KK
KK		Loop counter and subscript.	/CIS /(*)	CIS	W	INTE	KK
KK		Temporary storage variable.	/CORCIG/(*)	CORCIG	W	INTE	KK
KK		Loop counter and subscript.	/CRINGS/(*)	CRINGS	W	INTE	KK
KK		Test standard for the locations of the double bonds in ring K.	/CYCORR/(*)	CYCORR	W	INTE	KK
KK		Subscript of array KCCR.	/DELETE/(*)	DELETE	W	INTE	KK
KK		Loop counter.	/EQUAL /(*)	EQUAL	W	INTE	KK
KK		Loop counter and subscript.	/FUSION/(*)	FUSION	W	INTE	KK
KK		Loop counter and subscript.	/HEXGON/(*)	HEXGON	W	INTE	KK
KK		Subscript.	/LESSEN/(*)	LESSEN	W	INTE	KK
KK		Loop counter and subscript.	/NRINGS/(*)	NRINGS	W	INTE	KK
KK		Location j in NBC(I,j) where first atom of ring is located. Also used as a deletion flag if identical chain formations have been defined.	/RING /(*)	RING	W	INTE	KK
KK		Transfer flag.	/SYMRNG/(*)	SYMRNG	W	INTE	KK
KL		Number of heavy atoms bonded to the first central test core atom K1 that are capable of exhibiting a gauche interaction.	/GAUCHE/(*)	GAUCHE	W	INTE	KL
KLH		Counter that specifies whether two ligands cis to each other are both hydrogen atoms.	/CISCOR/(*)	CISCOR	W	INTE	KLH
KM		Loop counter and subscript.	/DELTA1/(*)	DELTA1	W	INTE	KM
KM		Loop counter and subscript.	/DELTA2/(*)	DELTA2	W	INTE	KM
KN		Group number of atom bonded to ring atom KC.	/SYMRNG/(*)	SYMRNG	W	INTE	KN

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	UTM
KMAX		Number of core atom constituents of longest chain.	/MAXCHN/1*					MAXCHN W INTE KMAX
KNBENZ	(I)	Contains ring numbers of pyridine-type ring structures.	/BLK1	(1 3976)	CYCORR	U	INTE	KNBENZ(40, HEXGON I INTE KNBENZ(40)
KNRAT	(I,J)	Contains alkane c-n corrections.	/GAUCHE/1*					GAUCHE C INTE KNRAT (4,5)
KNO		Number of characters in multi-word input symbol.	/MULTI	/1*				MULTI I INTE KNO
KNT	(I,J)	Contains the locations I in array IDX where the group numbers of the test ligands associated with the branch pair J are found.	/BLK1	(1 1625)	EQUAL	M	INTE	KNT (2,99) EQUALR O INTE KNT (2,99)
KNTR	(I,J)	Contains the locations I in array IDX where the group numbers of the test ligands associated with the ring pair J are found.	/BLK1	(1 1065)	EQUALR	M	INTE	TR M (2,30)
KOMB	(I,J)	Contains the ring number (I) of the ring component in fused ring set (J).	/BLK3	(1 5962)	CRIMP	I	INTE	KOM (10,10) CRIMP I INTE KOM (10,10) FUSION M INTE KOM (10,10) HEXGON I INTE KOM (40,10) NRINGS I INTE KOM (40,10)
KOMMON	(I,J,K)	Multi-storage array j=1,2 ring numbers of fused ring pair I in fused ring set K. j=3 number of atoms which ring pair has in common. j>3 group numbers of these atoms.	/BLK1	(1 26)	FUSION	M	INTE	KOMMON(40,9,10)
KON	(I)	Number of ligands bonded to core atom I.	/BLK3	(1 5401)	LIS	I	INTE	KON (100) CYCORR I INTE KON (100) CYCORR I INTE KON (100) EQUAL I INTE KON (100) EQUALR I INTE KON (100) EXTROT I INTE KON (100) GAUCHE I INTE KON (100) INTROT I INTE KON (100) LINEAR I INTE KON (100) PRINT I INTE KON (100) SCANBR I INTE KON (100) SCANCH I INTE KON (100) SORNGI I INTE KON (100) STAND O INTE KON (100)
KONF		Connectivity of atom KCI plus one	/EXTROT/1*					EXTROT W INTE KONF
KOMMR		Upper limit of loop counter.	/CYCORR/1*					CYCORR W INTE KOMMR

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE							
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIR					
KONT		Upper limit of loop counter.	/EQUAL	/I*) EQUAL	W	INTE	KONT						
KONT		Upper limit of loop counter.	/EQUALR	/I*) EQUALR	W	INTE	KONT						
KOP		Number of asymmetric atoms present in a particular chain.	/MAXCHN	/I*) MAXCHN	W	INTE	KOP						
KOPMAX		Greatest number of asymmetric atoms present in a particular chain.	/MAXCHN	/I*) MAXCHN	W	INTE	KOPMAX						
KORD	(1)	Contains the order that the subscripts of the data in KREM would have if said data were arranged in increasing numerical order.	/BLK3	/I (3553)) LESSEN	W	INTE	KORD (40)						
KOXY		Group number of oxygen test core atom.	/GAUCHE	/I*) GAUCHE	W	INTE	KOXY						
KP		Addition or subtraction operation flag.	/IDENT	/I*) IDENT	W	INTE	KP						
KP		Integer equal to ±1.	/SUMATN	/I*) SUMATN	I	INTE	KP						
KPERM		Group number of non-ring ligands bonded to ring atom KC.	/SYMRNG	/I*) SYMRNG	W	INTE	KPERM						
KPERT	(1)	Contains the group numbers of the ring components.	/BLK4	/I (4268)) SYMRNG	W	INTE	KPERT (6)						
KPRINT		Equal to digit J of IPRINT (QJK).	/TGAP	/I*) TGAP	W	INTE	KPRINT						
KR		Number of heavy atoms bonded to the second central test core atom K2 or possible of exhibiting a the interaction.	/GAUCHE	/I*) GAUCHE	W	INTE	KR						
KR		Subscript of array KREM.	/LESSEN	/I*) LESSEN	W	INTE	KR						
KRCNOR	(1)	This array applies only to rings containing one nitrogen atom in the ring structure. Locations I=K1 and I=K2 contains the group number j of the nitrogen atom which is adjacent to the carbon atoms X1 and K2. Location I=K3, where K3 is the group number of the ring atom para to the nitrogen atom, contains -j.	/BLK1	/I (3775)) CORCIG	Q	INTE	KRCNOR(100) CYCORR	Q	INTE	KRCNOR(100) HEXGON	I	INTE	KRCNOR(100)
KRCNMT	(1)	Contains flags that govern the type of identifying weight correction to be applied to ring atom I.	/BLK1	/I (3875)) CORCIG	Q	INTE	KRCNMT(100) CYCORR	Q	INTE	KRCNMT(100) HEXGON	I	INTE	KRCNMT(100)

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DTM
KRER	(1)	Contains the ring number of the rings that are not mutually exclusive and hence are to be discarded.	/BLK3	/C 1303	LESSEN	M	INTE	KRER (40)
KRING1		Ring comparison flag. =0 the two ring-containing ligands are not equal. =1 they are equal.	/EQUAL	/C*	EQUAL	I	INTE	KRING1
KRING1		Ring comparison flag. =0 the two ring-containing ligands are not equal. =1 they are equal.	/EQUALR	/C*	EQUALR	O	INTE	KRING1
KRING2		Preliminary ring comparison tests flag. =0 Initial comparison tests of two rings negative. =1 Initial comparison tests of two rings positive.	/EQUALR	/C*	EQUALR	I	INTE	KRING2
KRING2		Preliminary ring comparison tests flag. =0 Initial comparison tests of two rings negative. =1 Initial comparison tests of two rings positive.	/FIRSTR	/C*	FIRSTR	O	INTE	KRING2
KRLIG	(1)	Contains I.d. number of non-core ligand of ring location I.	/BLK4	/C 2763	SYMRNG	M	INTE	KRLIG (4)
KRO	(1)	Indicates whether ligand I has (2) or does not have (1) twofold rotational symmetry about plane of ring.	/BLK4	/C 4262	SYMRNG	M	INTE	KRO1 (4)
KRPROP	(1, J)	Multi-variable array I=1 number of oxygen atoms in ring k. I=2 ring location of first oxygen atom. I=3 number of nitrogen atoms in ring k. I=4 ring location of first nitrogen atom. I=5 number of double bonds in ring k. I=6 ring location of first double bond.	/BLK4	/C 3122	CRINGS	I	INTE	KRPROP(6,40) CYCGAR M INTE KRPROP(6,40) FIRSTR I INTE KRPROP(6,40) NRINGS I INTE KRPROP(6,40)
KB		Transfer variable.	/CISCOM	/C*	CISCOM	M	INTE	KB
KB		Group number of ring ligand, also a subscript.	/EQUALR	/C*	EQUALR	M	INTE	KB
KB		Entry value of IGS.	/ENTR	/C*	ENTR	M	INTE	KB

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIM
KS		Row coordinate of core atom JC.	/SMIFT/(*)	SMIFT	W	INTE	KS
KS		Identifier stored in array KARO or variable counter.	/SYMRNG/(*)	SYMRNG	W	INTE	KS
KSAME	(I,J,K)	The array location corresponding to ligand I of type J in set K is set equal to one if ligand I is equal to another ligand.	/BLK3 / (5614)	EQUAL	I	INTE	KSAME (4,3,2)	
				SETUP	0	INTE	KSAME (4,3,2)	
KSAME		Denotes the number of chains of maximum length in the molecule.	/MAXCHN/(*)	MAXCHN	W	INTE	KSAME
KSET	(I)	Contains the number of identical ring ligands in set I.	/BLK3 / (6372)	SYMRNG	M	INTE	KSET (3)	
SIX	(I)	Contains the ring numbers of the six-membered rings with two or more double bonds in their structure.	/BLK3 / (5781)	CYCORA	0	INTE	KSIX (40)	
				HEXON	1	INTE	KSIX (40)	
KSTORE	(I)	Contains identification number of rings which have some but not all of their atoms in common with the reference ring.	/BLK3 / (3403)	LESSEN	M	INTE	KSTORE(40)	
KSUB		Number of ring pairs.	/FUSION/(*)	FUSION	W	INTE	KSUB
KSUB		Total number of ligands of a particular atom processed to this point.	/SCANBR/(*)	SCANBR	W	INTE	KSUB
KSUB		Storage location in array LIGAND for the composition data of a particular ligand.	/SYMTRV/(*)	SYMTRV	W	INTE	KSUB
KSUM		Transfer variable.	/CISCOR/(*)	CISCOR	W	INTE	KSUM
KSUM		Total number of second order interactions and ring corrections.	/EORCIG/(*)	EORCIG	W	INTE	KSUM
KSUM		Sum total of various ring properties.	/CRINGS/(*)	CRINGS	W	INTE	KSUM
KSUM		Denotes presence of allene structure when equal to 2.	/DELTA1/(*)	DELTA1	W	INTE	KSUM
KSYM	(I)	Contain internal rotational symmetry of ligand I.	/DLK1 / (3881)	EXTROY	M	INTE	KSYM (2)	
KSYM		Denotes whether ligand is (1) or is not (0) linear.	/CTWO /(*)	CTWO	I	INTE	KSYM
KSYM		Denotes the rotational symmetry of the ligand.	/EQUALR/(*)	EQUALR	I	INTE	KSYM
KSYM		Denotes the rotational symmetry of the ligand.	/LINEAR/(*)	LINEAR	0	INTE	KSYM

FORTRAN SYMBOL	PARAM SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
KSYM		Description not input	/SYMRNG/	(+)	SYMRNG	I	INTE	KSYM
KT		Group number of carbon atom adjacent to nitrogen atom in ring K.	/CYCORR/	(+)	CYCORR	M	INTE	KT
KT		Identification number of group whose first-order contributions to the group weight are to be calculated.	/DELTA1/	(+)	DELTA1	I	INTE	KT
KT		Identification number of group whose second-order multiple-bond weight contributions are to be calculated.	/DELTA2/	(+)	DELTA2	I	INTE	KT
KT		Subscript.	/HEXGON/	(+)	HEXGON	M	INTE	KT
KT		Group number. Also used to refer to core atom of group.	/SCAN	/(+)	SCAN	I	INTE	KT
KTGENZ	(1)	Ring numbers of benzene- and pyridine-type rings.	/BLK1	/ (1365)	CTWO	I	INTE	KTGENZ(40)
					HEXGON	M	INTE	KTGENZ(40)
KTBL		Counter that specifies whether ligand bonded to first central core K1 is a tertiary carbon atom.	/CISCOR/	(+)	CISCOR	M	INTE	KTBL
KTBL		Flag set equal to 1 when KTBL is incremented. Serves to indicate when tertiary carbon groups are cis to each other.	/CISCOR/	(+)	CISCOR	M	INTE	KTBL
KTBR		Counter that specifies whether ligand bonded to second central core atom K2 is a tertiary carbon atom.	/CISCOR/	(+)	CISCOR	M	INTE	KTBR
KTEMP	(1)	Used to distinguish between cis and trans ring configurations.	/BLK3	/ (5693)	CYCORR	M	INTE	KTEMP (12)
KTEST		Ring pair detection flag. =0 ring pair was not detected by test cycle. >0 ring pair(s) detected by test cycle.	/FUJION/	(+)	FUJION	M	INTE	KTEST
KTETRA		Counter that specifies whether two groups cis to each other are both tertiary butyl groups, that is, carbon atoms bonded to four heavy atoms.	/CISCOR/	(+)	CISCOR	M	INTE	KTETRA
KTGAUS	(1)	Denotes the type of the second-order interaction I.	/BLK3	/ (4191)	CISCOR	O	INTE	KTGAUS(150)
					CORCIS	M	INTE	KTGAUS(150)
					CRINGS	O	INTE	KTGAUS(150)
					CTWO	O	INTE	KTGAUS(150)
					UIERE	O	INTE	KTGAUS(150)
					GAUCHE	O	INTE	KTGAUS(150)
					HEXGON	O	INTE	KTGAUS(150)
					INTRD	O	INTE	KTGAUS(150)
					WRINGS	O	INTE	KTGAUS(150)

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
KTOT	(I)	Number of atoms of type I in ligand.	/BLK3	/I 6362	SCANRR	M	INTE	KTOT (9)
					SCANCH	I	INTE	KTOT (9)
					SYMTKY	M	INTE	KTOT (9)
KTY		Number of atom pair entries in array KCCR.	/DELETE/	/I*	DELETE	M	INTE	KTY
KTY		Number of atom pair entries in array KCCR.	/EQUALR/	/I*	EQUALM	M	INTE	KTY
KV		Location of data in group JT associated with ligand KT.	/DELTA2/	/I*	DELTA2	M	INTE	KV
KV		Row coordinate of current character.	/IDENT	/I*	IDENT	M	INTE	KV
KVALUE		Identification weight of data for which a match is sought in group additivity arrays.	/SEARCH/	/I*	SEARCH	I	INTE	KVALUE
KW		Identification number of the ring.	/SYMRNG/	/I*	SYMRNG	M	INTE	KW
KX		Row coordinate of initial bond location and of non-bond symbol.	/BOND	/I*	BOND	M	INTE	KX
KX		Subscript.	/EQUAL	/I*	EQUAL	M	INTE	KX
KX		Row coordinate of indexed atom number 1 ligand.	/FIND	/I*	FIND	I	INTE	KX
KX		Test row coordinate.	/IDENT	/I*	IDENT	M	INTE	KX
KX		Subscript.	/LESSEN/	/I*	LESSEN	M	INTE	KX
KX		Row coordinate of first location along NX in array GRID.	/NUMBER/	/I*	NUMBER	M	INTE	KX
KX		Group number of previously identified atom.	/SAME	/I*	SAME	M	INTE	KX
KX		Row coordinate of first location along NX in array GRID.	/SCAN	/I*	SCAN	M	INTE	KX
KX1		Row coordinate of ligand one.	/NUMBER/	/I*	NUMBER	O	INTE	KX1
KX2		Row coordinate of first atom bonded to ligand.	/SCAN	/I*	SCAN	I	INTE	KX2
KX2		Row coordinate of second character.	/IDENT	/I*	IDENT	M	INTE	KX2
KY		Subscript that defines bond direction between atoms K1 and K2.	/CIS	/I*	CIS	M	INTE	KY

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
KV		Number of different types of identical atoms in ligand sets A and B.	/EQUAL	/I*) EQUAL	I	INTE	KV
KV		Number of rings in fused ring set A.	/FIRSTA	/I*) FIRSTA	M	INTE	KV
KV		Number of rings in a particular fused ring set.	/FUSION	/I*) FUSION	M	INTE	KV
KV		Number of rings in a particular fused ring set.	/HEXGON	/I*) HEXGON	M	INTE	KV
KV		Number of rings in a particular fused ring set.	/NRINGS	/I*) NRINGS	M	INTE	KV
KV		Subscript that defines the identity type number of a ligand the first time said ligand is processed.	/SETUP	/I*) SETUP	M	INTE	KV
KZ		Group number of core atom whose cis ligands are to be identified.	/CIS	/I*) CIS	M	INTC	KZ
KZ		Row coordinate of first location beyond KX,LX along the radial direction.	/IDENT	/I*) IDENT	M	INTE	KZ
KZERO	()	Contains locations in ring which have unique ligands.	/BLK	/I (4319)) SYMRG	M	INTE	KZERO (6)
KZZ		Identification number of core atom.	/CIS	/I*) CIS	M	INTC	KZZ
K1		Group number of first central test core atom.	/CIS	/I*) CIS	I	INTE	K1
K1		Group number of first central test core atom.	/CISCOR	/I*) CISCOR	I	INTE	K1
K1		Group number of first central test core atom.	/CORCIG	/I*) CORCIG	M	INTE	K1
K1		Identification number of ring one.	/CRINGS	/I*) CRINGS	M	INTE	K1
K1		Group number of ring component.	/CTWO	/I*) CTWO	M	INTE	K1
K1		Group number of ring component.	/CYCORR	/I*) CYCORR	M	INTE	K1
K1		Subscript of routine arrays.	/DELETE	/I*) DELETE	M	INTE	K1
K1		Group number of one of two ligand atoms currently under comparison.	/EQUAL	/I*) EQUAL	M	INTE	K1
K1		Group number of entry atom in ring A.	/EQUALR	/I*) EQUALR	I	INTE	K1

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE USAGE				
			BLOCK	LOC	SUBR	U TYPE	VAR DIM		
K1		Group number of entry atom in ring A.	/FIRSTA/		1	FIRSTA	I	INTE	K1
K1		Group number of first central test core atom.	/GAUCHE/		1	GAUCHE	I	INTE	K1
K1		Group number of first of two central core atoms bonded to an ortho ligand.	/HEXGON/		1	HEXGON	W	INTE	K1
K1		Group number of atom previous to or parent to the atom tested.	/LINEAR/		1	LINEAR	W	INTE	K1
K1		Group number of atom common to 3 fused rings.	/NRINGS/		1	NRINGS	W	INTE	K1
K1		Location of element in IB whose weight is to be compared with that of element in location K2.	/ORDER /		1	ORDER	W	INTE	K1
K1		Group number of ring component.	/OXYATM/		1	OXYATM	W	INTE	K1
K1		Subscript and counter limit.	/RING /		1	RING	W	INTE	K1
K1		Group number of atom 1 in identical ligand 1.	/SAME /		1	SAME	I	INTE	K1
K1		Group number of ligand core atom bonded to atom K01.	/SETUP /		1	SETUP	W	INTE	K1
K1		Group number of first central test core atom.	/SORNGE/		1	SORNGE	W	INTE	K1
K10		Group number of one of two ring atoms currently under comparison.	/EQUALR/		1	EQUALR	W	INTE	K10
K10D		Group number of atom in ring branch set where the deletion stops.	/DELETE/		1	DELETE	I	INTE	K10D
K11		Ordinal number assigned ligand 1 for identification purposes.	/SAME /		1	SAME	I	INTE	K11
K2		Group number of second central test core atom.	/CIS /		1	CIS	I	INTE	K2
K2		Group, number of second central test core atom.	/CISCOR/		1	CISCOR	I	INTE	K2
K2		Group number of second central test core atom.	/CORCIG/		1	CORCIG	W	INTE	K2
K2		Identification number of ring two.	/BRINGS/		1	BRINGS	W	INTE	K2
K2		Group number of ring component.	/CYCORR/		1	CYCORR	W	INTE	K2
K2		Subscript of routine arrays.	/DELETE/		1	DELETE	W	INTE	K2

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE			USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR	DATA
K2		Group number of one of two ligand atoms currently under comparison.	/EQUAL	/1+)	EQUAL	M	INTE	K2
K2		Group number of entry atom in ring 8.	/EQUALR	/1+)	EQUALR	I	INTE	K2
K2		Group number of entry atom in ring B.	/FIRSTA	/1+)	FIRSTA	I	INTE	K2
K2		Group number of second central test core atom.	/GAUCHE	/1+)	GAUCHE	I	INTE	K2
K2		Group number of second of two central core atoms bonded to an ortho ligand.	/MEXGON	/1+)	MEXGON	M	INTE	K2
K2		Subscript.	/LESSEN	/1+)	LESSEN	M	INTE	K2
K2		Group number of the atom tested.	/LINEAR	/1+)	LINEAR	M	INTE	K2
K2		Group number of atom common to 3 fused rings.	/NRINGS	/1+)	NRINGS	M	INTE	K2
K2		Location of element in I5 whose weight is to be compared with that of element in location K1.	/ORDER	/1+)	ORDER	M	INTE	K2
K2		Group number of atom 1 in identical ligand 2.	/SAME	/1+)	SAME	I	INTE	K2
K2		Group number of ligand core atom bonded to atom KC2.	/SETUP	/1+)	SETUP	M	INTE	K2
K2		Group number of second central test core atom.	/SORNGI	/1+)	SORNGI	M	INTE	K2
K2R		Group number of one of two ring atoms currently under comparison.	/EQUALR	/1+)	EQUALR	M	INTE	K2R
K2SET		Storage location variable for KNTR.	/EQUALR	/1+)	EQUALR	M	INTE	K2SET
K22		Ordinal number assigned ligand 2 for identification purposes.	/SAME	/1+)	SAME	I	INTE	K22
K3		Group atom of nitrogen ring atom.	/NRINGS	/1+)	NRINGS	M	INTE	K3
K3		Lower element of array IA used in order check.	/ORDER	/1+)	ORDER	M	INTE	K3
K3		Identification number of core atom.	/SORNGI	/1+)	SORNGI	M	INTE	K3
K4		Upper element of array IA used in order check.	/ORDER	/1+)	ORDER	M	INTE	K4
L		Column coordinate of indexed core atom.	/ASSIGN	/1+)	ASSIGN	I	INTE	L

FORTRAN SYMBOL	MATN SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE			USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIM
L		Loop counter and subscript.	/CHAINR/	(+)	CHAINR	W	INTE	L	
L		Loop counter and subscript.	/CHANGE/	(+)	CHANGE	W	INTE	L	
L		Loop counter and subscript.	/CISCOR/	(+)	CISCOR	W	INTE	L	
L		Loop counter and subscript.	/CORCIG/	(+)	CORCIG	W	INTE	L	
L		Loop counter and subscript.	/CYCORR/	(+)	CYCORR	W	INTE	L	
L		Loop counter and subscript.	/DATA1 /	(+)	DATA1	W	INTE	L	
L		Loop counter and subscript.	/DITERE/	(+)	DITERE	W	INTE	L	
L		Loop counter and subscript.	/EXTROT/	(+)	EXTROT	W	INTE	L	
L		Entry value: column coordinate of Indexed atom. Exit value: column coordinate of core atom.	/FIND /	(+)	FIND	M	INTE	L	
L		Loop counter and subscript.	/FUSION/	(+)	FUSION	W	INTE	L	
L		Loop counter and subscript.	/GADATA/	(+)	GADATA	W	INTE	L	
L		Loop counter and subscript.	/GAUCHE/	(+)	GAUCHE	W	INTE	L	
L		Loop counter and subscript.	/HEXGON/	(+)	HEXGON	W	INTE	L	
L		Column coordinate of first character of symbol.	/IDENT /	(+)	IDENT	M	INTE	L	
L		Loop counter and subscript.	/INTROT/	(+)	INTROT	W	INTE	L	
L		Loop counter and subscript.	/LESSEN/	(+)	LESSEN	W	INTE	L	
L		Loop counter and subscript.	/MAXCHN/	(+)	MAXCHN	W	INTE	L	
L		Loop counter and subscript.	/MULTI /	(+)	MULTI	W	INTE	L	
L		Column coordinate of indexed core atom.	/NUMBER/	(+)	NUMBER	:	INTE	L	
L		Subscript of symbol array (SYMBOL).	/PRINTI/	(+)	PRINTI	W	INTE	L	

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLDCK	LOC	SUBR	U	TYPE	JAA
L		Loop counter and subscript.	/RESETR/	(+)	RESETR	M	INTE	L
L		Column coordinate of core atom in array GRID.	/SCAN	(+)	SCAN	I	INTE	L
L		Loop counter and subscript.	/SETUP	(+)	SETUP	M	INTE	L
L		Loop counter and subscript.	/SHIFT	(+)	SHIFT	M	INTE	L
L		Loop counter and subscript.	/SORNGI	(+)	SORNGI	M	INTE	L
L		Column grid coordinate of core atom.	/STAND	(+)	STAND	M	INTE	L
L		Description not input	/SYMRNG	(+)	SYMRNG	M	INTE	L
L		Loop counter and subscript.	/SYMTRY	(+)	SYMTRY	M	INTE	L
L		Loop counter and subscript.	/TGAP	(+)	TGAP	M	INTE	L
LABEL	()	Hollerith symbol for blank. Input array containing identification label for molecule (optional).	/BLKN	((288))	TGAP	M	INTE	LABEL (50)
LD		Assigned change in column coordinate of symbol input array.	/ASSIGN	(+)	ASSIGN	O	INTE	LD
LD		Change in column coordinate	/BOND	(+)	BOND	I	INTE	LD
LD		Change in row coordinate for indexed atom number 1 ligand.	/FIND	(+)	FIND	I	INTE	LD
LD		Change in column coordinate.	/IDENT	(+)	IDENT	M	INTE	LD
LD		Change in column coordinate of array GRID.	/NUMBER	(+)	NUMBER	I	INTE	LD
LD		Change in column coordinate for transformation to NX.	/SCAN	(+)	SCAN	I	INTE	LD
LOD		Change in column coordinate of ligand one.	/NUMBER	(+)	NUMBER	O	INTE	LOD
LOONE	()	Indicator array I=0 composition of all ligands of a core atom not yet found. I=1 all compositions have been found.	/BLK3	((3202))	SYMTRY	M	INTE	LOONE (100)

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIM
LDZ		LD value of second character.	/IDENT	/C*) IDENT	W	INTE	LDZ
LESSEW		Examines the uniqueness of the ring structures identified by the program. Any rings that are equal to other rings or composed of smaller rings are discarded.	/LESSEN	/C*) CHAINM LESSEN RING	S E S		LESSEM LESSEM LESSEM
LF		Upper limit of loop counter.	/DITERE	/C*) DITERE	W	INTE	LF
LF		Upper limit of loop counter that controls the selection of a test ligand from set A.	/EQUAL	/C*) EQUAL	I	INTE	LF
LF		Upper limit of loop counter.	/GAUCHE	/C*) GAUCHE	W	INTE	LF
LF		Upper limit of loop counter.	/LESSEN	/C*) LESSEN	W	INTE	LF
LF		Upper limit of loop counter.	/NEWCOL	/C*) NEWCOL	W	INTE	LF
LF		Upper limit of loop counter.	/RESETR	/C*) RESETR	W	INTE	LF
LF		Upper limit of loop counter.	/SCANBR	/C*) SCANBR	W	INTE	LF
LF		Upper limit of loop counter.	/SCANCH	/C*) SCANCH	W	INTE	LF
LF		Upper limit of loop counter that controls the selection of a test ligand from set A.	/SETUP	/C*) SETUP	I	INTE	LF
LF		Upper limit of loop counter.	/SORNGI	/C*) SORNGI	W	INTE	LF
LFLAG		Data flag =0 no group data are missing from data library. =1 one or more group data are missing from data library.	/BLKS	/C	62) TGAP	W	INTE	LFLAG
LFLAGS		Data flag =0 symmetry and optical contributions are computable. =1 symmetry and/or optical contributions noncomputable and data for their computation not input.	/BLKS	/C	61) ENT5VM TGAP	0 I	INTE	LFLAGS LFLAGS
LOI		Subscript of array PERTKC that assigns the group number of a ligand core atom bonded to atom KCI.	/EQUAL	/C*) EQUAL	W	INTE	LOI

FORTRAN SYMBOL	MAIN SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE USAGE				
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIM
L01		Subscript of array PERTKC that assigns the group number of a ligand core atom bonded to atom KC1.	/SETUP /(+)	SETUP	M	INTE	L01
L02		Subscript of array PERTKC that assigns the group number of a ligand core atom bonded to atom KC2.	/EQUAL /(+)	EQUAL	M	INTE	L02
L03		Subscript of array PERTKC that assigns the group number of a ligand core atom bonded to atom KC2.	/SETUP /(+)	SETUP	M	INTE	L03
L1		Lower limit of loop counter.	/DITERE/(+)	DITERE	M	INTE	L1
LIGAND	(I,J,K)	Contains atomic composition I of ligand J of core atom K.	/BLK3 /(+ 1202)			SCANBR	M	INTE	LIGAND(5,4,100)
						SCANCM	M	INTE	LIGAND(5,4,100)
						SETUP	I	INTE	LIGAND(5,4,100)
						SYMTRY	M	INTE	LIGAND(5,4,100)
LIM		Number of elements in array IA or IB.	/ORDER /(+)	ORDER	I	INTE	LIM
LIM		Dimension of array to be searched.	/SEARCH/(+)	SEARCH	I	INTE	LIM
LIMIT		Chain location occupied by atom at the start of the branch test cycle.	/SYMTRY/(+)	SYMTRY	M	INTE	LIMIT
LINE	(I)	Indicates whether ligand I is (1) or is not (0) linear.	/BLK1 /(+ 3879)			EXTROT	M	INTE	LINE (2)
LINE		Denotes the rotational symmetry of the ligand.	/CTWO /(+)	CTWO	I	INTE	LINE
LINE		Denotes whether ligand is (1) or is not (0) linear.	/EQUALR/(+)	EQUALR	I	INTE	LINE
LINE		Denotes whether ligand is (1) or is not (0) linear.	/LINEAR/(+)	LINEAR	O	INTE	LINE
LINE		Description not input	/SYMRNG/(+)	SYMRNG	I	INTE	LINE
LINEAR		Establishes the linearity and rotational symmetry of a particular ligand.	/LINEAR/(+)	CTWO	S		LINEAR
						EQUALR	S		LINEAR
						EXTROT	S		LINEAR
						LINEAR	E		LINEAR
						SYMRNG	S		LINEAR
LK		Upper limit of counter KK of ring test cycle.	/CHAINM/(+)	CHAINM	M	INTE	LK
LL		Loop counter and subscript.	/CORCIG/(+)	CORCIG	M	INTE	LL
LL		Subscript.	/GAUCHE/(+)	GAUCHE	M	INTE	LL

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			DLCK	LOC	SUBR	U	TYPE	VAR
LL		Loop counter and subscript.	/INTROT/	(*)	INTROT	W	INTE	LL
LL		Loop counter and subscript.	/NEWCOL/	(*)	NEWCOL	W	INTE	LL
LL		Loop counter and subscript.	/RING	(*)	RING	W	INTE	LL
LL		Loop counter and subscript.	/SHIFT	(*)	SHIFT	W	INTE	LL
LL		Loop counter and subscript.	/SORNGI/	(*)	SORNGI	W	INTE	LL
LL		Lower limit of cycle counter.	/STAND	(*)	STAND	W	INTE	LL
LL		Subscript.	/TGAP	(*)	TGAP	W	INTE	LL
LM		Number of atoms or links in chain.	/CHAINM/	(*)	CHAINM	W	INTE	LM
LM		Location j in NBC(i,j) of uppermost element in portion of new chain defined in subroutine NEWCOL.	/NEWCOL/	(*)	NEWCOL	W	INTE	LM
LM		Number of atoms in chain LX.	/RING	(*)	RING	I	INTE	LM
LM		Number of components of a particular chain.	/SYNTRY/	(*)	SYNTRY	W	INTE	LM
LMA		Chain location of atom below atom LMM.	/SYNTRY/	(*)	SYNTRY	W	INTE	LMA
LMM		Location in chain LXX of core atom under inspection.	/SYNTRY/	(*)	SYNTRY	W	INTE	LMM
LM		Chain location of next atom down the chain.	/SYNTRY/	(*)	SYNTRY	W	INTE	LM
LOCCO	(7)	Contains ring locations of CO atoms.	/BLK3	(1 344)	CYCOPR	O	INTE	LOCCO (30)
LOCN	(1)	Contains ring locations of nitrogen atoms.	/BLK3	(1 347)	CYCOPR	N	INTE	LOCN (30)
LOCO	(1)	Contains ring locations of oxygen atoms.	/BLK3	(1 350)	CYCOPR	O	INTE	LOCO (30)
LOCK		Ring atom which may be adjacent to one or two CO groups.	/OXYATH/	(*)	OXYATH	I	INTE	LOCK
LS		Lower limit of loop counter.	/SCANBR/	(*)	SCANBR	W	INTE	LS
LS		Lower limit of loop counter.	/SCANCH/	(*)	SCANCH	W	INTE	LS

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U	TYPE	VAN	DTM
LX		Column coordinate of core atom JC.	/SHIFT	/(*)	SHIFT	M	INTE	LX
LX		Start location in KGRID into which column of data from array GRID is to be transferred.	/TGAP	/(*)	TGAP	M	INTE	LX
LV		Column coordinate of current character.	/IDENT	/(*)	IDENT	M	INTE	LV
LX		Column coordinate of initial bond location and of non-bond symbol.	/BOND	/(*)	BOND	M	INTE	LX
LX		Computed number of chains in molecule.	/CHAINM	/(*)	CHAINM	M	INTE	LX
LX		Computed number of chains in molecule.	/CHANGE	/(*)	CHANGE	I	INTE	LX
LX		Computed number of chains in molecule.	/CORCIB	/(*)	CORCIB	I	INTE	LX
LX		Column coordinate of indexed atom number ; ligand.	/FIND	/(*)	FIND	I	INTE	LX
LX		Test column coordinate.	/IDENT	/(*)	IDENT	M	INTE	LX
LX		Subscript.	/LESSEN	/(*)	LESSEN	M	INTE	LX
LX		Computed number of chains in molecule.	/MAXCHN	/(*)	MAXCHN	I	INTE	LX
LX		Computed number of chains in molecule.	/NEWCOL	/(*)	NEWCOL	M	INTE	LX
LX		Column coordinate of first location along NX in array GRID.	/NUMBER	/(*)	NUMBER	M	INTE	LX
LX		Computed number of chains in molecule.	/RESETR	/(*)	RESETR	I	INTE	LX
LX		Computed number of chains in molecule. Refers also to the particular chain under investigation.	/RING	/(*)	RING	I	INTE	LX
LX		Column coordinate of first location along NX in array GRID.	/SCAN	/(*)	SCAN	M	INTE	LX
LX		Loop counter and subscript.	/SCANBR	/(*)	SCANBR	M	INTE	LX
LX		Loop counter and subscript.	/SCANCH	/(*)	SCANCH	M	INTE	LX
LX		Computed number of chains in molecule.	/SYMTIV	/(*)	SYMTIV	I	INTE	LX

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
LX		Number of chains in molecule.	/TGAP	(1)) TGAP	I	INTE	LX
LXL		Uppermost chain column used in the construction of the new chain.	/CHAINM	(1)) CHAINM	M	INTE	LXL
LXL		Last computed chain to be used in the calculation.	/NEWCOL	(1)) NEWCOL	I	INTE	LXL
LXX		Column coordinate of ligand one.	/NUMBEW	(1)) NUMBER	O	INTE	LXX
LXX		Number of chain that identifies ring K.	/RESETR	(1)) RESETR	M	INTE	LXX
LXX		Number of chain that contains ring LL.	/RING	(1)) RING	M	INTE	LXX
LXX		Column coordinate of first atom bonded to ligand.	/SCAN	(1)) SCAN	I	INTE	LXX
LXX		Number of the chain under inspection.	/SYMETRY	(1)) SYMETRY	M	INTE	LXX
LXZ		Column coordinate of second character.	/IDENT	(1)) IDENT	M	INTE	LXZ
LY		Chain number of longest chain computed thus far by routine MAXCHN.	/MAXCHN	(1)) MAXCHN	M	INTE	LY
LY		Used to denote location of KCPV element in chain as well as the new chain number.	/NEWCOL	(1)) NEWCOL	U	INTE	LY
LYP		Chain number of longest chain.	/MAXCHN	(1)) MAXCHN	M	INTE	LYP
LZ		Column coordinate of first location beyond KX,LX along the radial direction.	/IDENT	(1)) IDENT	M	INTE	LZ
L1		Group number of core atom bonded to first central atom and cis to L2.	/CISCOR	(1)) CISCOR	M	INTE	L1
L1		Location of data (subscript of RINGD) for the ring corrections of ring K.	/CORCIG	(1)) CORCIG	M	INTE	L1
L1		Location of ring correction data (subscript of RINGD) for ring K.	/CYCORR	(1)) CYCORR	O	INTE	L1
L2		Group number of core atom bonded to second central atom and cis to L1.	/CISCOR	(1)) CISCOR	M	INTE	L2
M		Amount by which bond direction is changed.	/CIS	(1)) CIS	M	INTE	M
M		Loop counter and subscript.	/CYCORR	(1)) CYCORR	M	INTE	M

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	BIT
M		Code symbol of indexed atom.	/FIND	/(*)	FIND	I	INTE	M
M		Subscript of SYMBOL array used for identification of input symbol.	/IDENT	/(*)	IDENT	M	INTE	M
M		Loop counter and subscript.	/INTROT	/(*)	INTROT	M	INTE	M
M		Loop counter and subscript.	/LESSEN	/(*)	LESSEN	M	INTE	M
M		Loop counter and subscript.	/MATCHM	/(*)	MATCHM	M	INTE	M
M		Subscript of program library symbol that corresponds to input symbol.	/MULTI	/(*)	MULTI	D	INTE	M
M		Loop counter and subscript.	/OXYATR	/(*)	OXYATR	M	INTE	M
M		Loop counter and subscript.	/PRINTI	/(*)	PRINTI	W	INTE	M
M		Loop counter and subscript.	/RESETR	/(*)	RESETR	M	INTE	M
M		Identifies type of ligand atom.	/SCAN	/(*)	SCAN	I	INTE	M
M		Loop counter and subscript.	/SETUP	/(*)	SETUP	W	INTE	M
M		Counter.	/SORNGI	/(*)	SORNGI	W	INTE	M
M		Subscript of array SYMBOL used to identify a chemical symbol.	/STAND	/(*)	STAND	W	INTE	M
M		Subscript of array SYMBOL which designates a particular chemical symbol.	/SUMATM	/(*)	SUMATM	I	INTE	M
MA	(I)	Contains location of CO group in ring K.	/BLK3	/ (3531)	OXYATR	M	INTE	MA (30)
MARD	(I)	Aromatic ring flag. I=1 core atom I is an aromatic benzene-type ring component. I=2 core atom I is an aromatic pyridine-type ring component. I=0 core atom I is not an aromatic ring component.	/BLK1	/ (1225)	CORCIC GAUCHE HEXGOM	O I O	INTE	MARD (100) MARD (100) MARD (100)
MATRIX	(I, J)	Contains ring locations (I) of all ligands belonging to set J of identical ligands.	/BLK4	/ (4290)	SYMRNG	M	INTE	MATRIX(6, 3)

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SURROUNTING		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DATA
MAX		Description not input	/SYMRNG/1*) SYMRNG	W	INTE	MAX
MAX		Location of last data group contained in Bensons tables.	/TGAP /1*) TGAP	W	INTE	MAX
MAXCHN		Finds the longest chain in the molecule and prints out the group numbers of the core atom constituents of the chain. If asymmetric atoms are present, it also determines if another chain of the same (maximum) length is present which contains more asymmetric atoms than the first maximum chain detected. If so, this chain becomes the new maximum chain.	/MAXCHN/1*) CORCIG S MAXCHN E			MAXCHN MAXCHN
MAXD		Maximum value of MDIF.	/CHANGE/1*) CHANGE	W	INTE	MAXD
MAXIZ		Location of branch atom in chain MAXL.	/CHANGE/1*) CHANGE	W	INTE	MAXIZ
MAXL		Chain number corresponding to MAXD.	/CHANGE/1*) CHANGE	W	INTE	MAXL
MAXT		Upper limit of loop counter.	/SYMRNG/1*) SYMRNG	W	INTE	MAXT
MBC	(1)	Contains group numbers of core atom constituents of longest chain.	/BLKS /1) EXTROT I MAXCHN M	INTE	MBC	(50) (50)
MBL		Left-most location of data in column j of array GRID or in array LABEL.	/TGAP /1*) TGAP	W	INTE	MBL
MBR		Right-most location of data in column j of array GRID or in array LABEL.	/TGAP /1*) TGAP	W	INTE	MBR
MBS	(1)	Properties of longest chain. i=1 number of atoms in longest chain. i=2 chain number of longest chain.	/BLKS /1) EXTROT I MAXCHN O	INTE	MBS	(2) (2)
MCV	(1)	Contains the ordinal ring number (KCY) of the test ring pair to one of which the non-ring core atom I is bonded.	/BLK1 /1	(1525)	EQUAL I EQUALR M SYMTRY O	INTE	MCV	(100) (100) (100)
MD		Total number of entries in array MDEL.	/BLK3 /1	(5612)	CORCIG M CRINGS M HEXGOM M	INTE	MD	MD MD MD

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
MDEL	(I)	Contains the ring number of the rings which form part of an aromatic fused ring system and whose ring corrections are not to be used in the calculation.	/BLK3	/(5633)	CORCIG	I	INTE	MDEL (40)
					CRINGS	0	INTE	MDEL (40)
					NERSON	0	INTE	MDEL (40)
MDIF		Terminal group flag. =0 terminal group is present in molecule. =1 terminal group is not present.	/CHAINM/	(+)	CHAINM	W	INTE	MDIF
MDIF		The difference I2 - I1.	/CHANGE/	(+)	CHANGE	W	INTE	MDIF
MDIF		Terminal group flag. =0 terminal group is present in molecule. =1 terminal group is not present.	/RESETR/	(+)	RESETR	I	INTE	MDIF
ME		Number of rings for which there are no ring corrections.	/CORCIG/	(+)	CORCIG	W	INTE	ME
MER	(I, J)	Multi-variable array I=1,2 group numbers of entry ring atoms in two test rings. I=3 number of non-ring ligands in two test rings.	/BLK1	/(1825)	EQUAL	I	INTE	MER (3,40)
					EQUALR	0	INTE	MER (3,40)
					SYMTAY	0	INTE	MER (3,40)
MESO		Input value for total number of meso structures of molecule (optional).	/CORCIG/	(+)	CORCIG	I	INTE	MESO
MESO		Input value for total number of meso structures of molecule (optional).	/ENTSYM/	(+)	ENTSYM	I	INTE	MESO
MESO		Input value for total number of meso structures of molecule (optional).	/TGAP	/(+)	TGAP	W	INTE	MESO
MESOC		Computed value for the number of meso structures.	/ENTSYM/	(+)	ENTSYM	W	INTE	MESOC
MP		Upper limit of loop counter.	/CYCORR/	(+)	CYCORR	W	INTE	MP
MP		Number of components in reference ring.	/LESSEN/	(+)	LESSEN	W	INTE	MP
MP		Upper limit of loop counter.	/OXYTM/	(+)	OXYTM	W	INTE	MP
MP		Upper limit of loop counter.	/RESETR/	(+)	RESETR	W	INTE	MP
MP		Upper limit of loop counter.	/SORH1/	(+)	SORH1	W	INTE	MP

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLK3	LOC	SUBR	U	TYPE	VAR	DIR
MFIX	(I)	Designates the weight correction to be applied to the non-ring core atoms bonded to the ring.	/BLK3	/(3001)	HEXGON	M	INTE	MFIX	(100)
MFLAG		Flag. If non zero, the elements of IB corresponding to JC are reset. Otherwise they are not.	/SHIFT	/(*	SHIFT	I	INTE	MFLAG	
MID2		Number of atoms contained in longest chain divided by 2.	/EXTROT	/(*	EXTROT	M	INTE	MID2	
MID2P		Atom position in longest chain equal to MID2 plus one.	/EXTROT	/(*	EXTROT	M	INTE	MID2P	
MJ		Group number of ring component.	/CYCORR	/(*	CYCORR	M	INTE	MJ	
MJ		Value of counter J.	/IDENT	/(*	IDENT	M	INTE	MJ	
MKJF		Upper limit of loop counter.	/CYCORR	/(*	CYCORR	M	INTE	MKJF	
MKT	(I)	Contains group numbers for cis ligand pairs. If the ligand is not a core atom, the group number is, of course, 0. Ligands I=1 and I=3 are cis to each other as well as ligands I=2 and I=4.	/BLK3	/(5606)	CIS	0	INTE	MKT	(4)
					CISCOR	I	INTE	MKT	(4)
					CYCORR	I	INTE	MKT	(4)
					EXTROT	M	INTE	MKT	(4)
MKT	(I)	Ring scan test indicator array. I=0 ring I has not been scanned in reverse direction. I=1 yes it has.	/BLK3	/(5735)	EQUAL	I	INTE	MKT	(40)
					EQUALR	M	INTE	MKT	(40)
					SYNTRY	0	INTE	MKT	(40)
MM		Loop counter and subscript.	/EQUAL	/(*	EQUAL	M	INTE	MM	
MM		Loop counter and subscript.	/LESSEN	/(*	LESSEN	M	INTE	MM	
MM		Value of j index in IX(I,j,k) where the search for the core atom data commences.	/SCAN	/(*	SCAN	I	INTE	MM	
MM		Value of j index in IX(I,j,k) where the search for the core atom data commences.	/STAND	/(*	STAND	M	INTE	MM	
MMF		Upper limit of loop counter.	/LESSEN	/(*	LESSEN	M	INTE	MMF	
MM		Number of atom pairs stored in array MNIX.	/CORCIG	/(*	CORCIG	M	INTE	MM	
MM		Number of atom pairs stored in array MNIX.	/SORNGI	/(*	SORNGI	M	INTE	MM	

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
MNC	(I, J)	Contains value of NC (j=1) and group number KC (j=2) of branch core atoms. The exception occurs with core atom one which is also included when it has only two core atom ligands.	/BLK4	/1	4)	STAND	M	INTE MNC (100,2)
MNIX	(I)	Indicator array that specifies whether core atom I has been processed. no if 0, yes if 1.	/BLK1	/1	20)	COARCIG	M	INTE MNIX (2,200)
						SOANGI	M	INTE MNIX (2,200)
MOLWT	(I)	Computed weight of each group in molecule.	/BLK2	/1	19)	DELTA1	M	INTE MOLWT (100)
						DELTA2	M	INTE MOLWT (100)
						HEXGON	M	INTE MOLWT (100)
						PRINT1	I	INTE MOLWT (100)
						STAND	M	INTE MOLWT (100)
						TGAP	I	INTE MOLWT (100)
MP		Number of ligands attached to indexed atom.	/FIND	/10	1)	FIND	I	INTE MP
MP		Number of ligands of indexed atom computed in subroutine NUMBER.	/NUMBER/10		1)	NUMBER	M	INTE MP
MP		Number of atoms bonded to ligand as computed in NUMBER.	/SCAN	/10	1)	SCAN	I	INTE MP
MPOS		Bond-type flag =0 ring does not have 3 double bonds. =1 ring has 3 double bonds.	/HEXGON/10		1)	HEXGON	M	INTE MPOS
MR		Column coordinate of IX where data of next ligand in group KC are to be stored.	/FIND	/10	1)	FIND	O	INTE MR
MR		Value of j index in IX(I, j, k) where the ligand data are stored.	/SCAN	/10	1)	SCAN	M	INTE MR
MR		Value of j index in IX(I, j, k) where the ligand data are stored.	/STAND	/10	1)	STAND	M	INTE MR
MRM	(I)	Contains number that denotes the identity type of the core ligand whose group number equals I.	/BLK3	/1	5862)	SETUP	M	INTE MRM (100)
MRM		Subscript I of array MNC(I, j) equal to the number of branch atoms in the molecule.	/BLK4	/1	3)	STAND	M	INTE MRM
MRST	(I)	Contains ordinal numbers of previously identified identical ligands of core atom KC.	/BLK4	/1	4274)	SAME	M	INTE MRST (6)
MR51	(I)	Contains ordinal identification numbers for ligands of atom in set A	/BLK4	/1	4280)	EQUAL SETUP	I M	INTE MR51 (4) INTE MR51 (4)
MR52	(I)	Contains ordinal identification numbers for ligands of atom in set B	/BLK4	/1	4284)	EQUAL SETUP	I M	INTE MR52 (4) INTE MR52 (4)

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
MS	(1)	Contains chemical symbols subscript codes for cis ligand pairs. Ligands l=1 and l=3 are cis to each other as well as ligands l=2 and l=4.	/BLK3	/(5602)	CIS	0	INTE MS	(4)
					CISCOR	1	INTE MS	(4)
					EXTROT	1	INTE MS	(4)
MS		Loop counter and subscript.	/IDENT	/(+)) IDENT	W	INTE MS	
MS		Subscript of array IB.	/SCAN	/(+)) SCAN	W	INTE MS	
HTEMP		Value of MD at start of cycle.	/HEXGON	/(+)) HEXGON	W	INTE HTEMP	
MULT1		Identifies a designated multi-character multi-word input symbol with the corresponding single word Hollerith program library symbol.	/MULT1	/(+)) IDENT	S	MULT1	MULT1
					MULT1	E	MULT1	MULT1
MULT1		Factor that determines the lower limit of a particular loop counter.	/EQUAL	/(+)) EQUAL	I	INTE MULT1	
MULT1		Factor that determines the lower limit of a particular loop counter.	/SETUP	/(+)) SETUP	I	INTE MULT1	
MULT2		Factor that determines the lower limit of a particular loop counter.	/EQUAL	/(+)) EQUAL	I	INTE MULT2	
MULT2		Factor that determines the lower limit of a particular loop counter.	/SETUP	/(+)) SETUP	I	INTE MULT2	
MVM	(1)	Ring location of bonds or group numbers of carbon atoms on either side of nitrogen atom in unsaturated nitrogen-containing rings.	/BLK1	/(3765)	CYCORR	M	INTE MVM	(2)
MWGT	(1)	Additional identification number added to original weight of an element or radical when present as the core atom of the group.	/BLK2	/(10)	STAND	1	INTE MWGT	(9)
					FGAP	0	INTE MWGT	(9)
MX		Subscript of array NBC.	/CHANGE	/(+)) CHANGE	W	INTE MX	
MX		Subscript that selects data of IDXR to be tested, also subscript of MCY.	/EQUALR	/(+)) EQUALR	W	INTE MX	
MX		Subscript. Also group number of atom adjacent to atom KC1.	/EXTROT	/(+)) EXTROT	W	INTE MX	
MX		Subscript of arrays NBC and IRING.	/RESETR	/(+)) RESETR	W	INTE MX	
MX		Subscript.	/STAND	/(+)) STAND	W	INTE MX	
MX		Initial value of subscript MZ.	/SUMATM	/(+)) SUMATM	W	INTE MX	
MX		Subscript.	/SYMRNG	/(+)) SYMRNG	W	INTE MX	

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIA
K1		Subscript of IDX governing the storage of the ligand data for K1.	/EQUAL	/(*) EQUAL	W	INTE	K1
K2		Subscript of IDX governing the storage of the ligand data for K2.	/EQUAL	/(*) EQUAL	W	INTE	K2
KV		Subscript and temporary storage variable.	/CHANGE	/(*) CHANGE	W	INTE	KV
KV		Subscript of array NBC.	/RESETR	/(*) RESETR	W	INTE	KV
KV		Number of particular element contained in species M.	/SUMATM	/(*) SUMATM	W	INTE	KV
MZ		Subscript.	/RESETR	/(*) RESETR	W	INTE	MZ
MZ		Location in NUMFRQ containing data for species M.	/SUMATM	/(*) SUMATM	W	INTE	MZ
M1		Indicates whether or not ligand 1 has already been found equal to another ligand.	/SAME	/(*) SAME	W	INTE	M1
M1		Subscript.	/SYMRNG	/(*) SYMRNG	W	INTE	M1
M2		Indicates whether or not ligand 2 has already been found equal to another ligand.	/SAME	/(*) SAME	W	INTE	M2
M2		Subscript.	/SYMRNG	/(*) SYMRNG	W	INTE	M2
N		Location where data are stored in arrays MS and MKT.	/CIS	/(*) CIS	W	INTE	N
N		Loop counter and subscript.	/CTWO	/(*) CTWO	W	INTE	N
N		Loop counter and subscript.	/CYCORR	/(*) CYCORR	W	INTE	N
N		Loop counter and subscript.	/EQUAL	/(*) EQUAL	W	INTE	N
N		Loop counter.	/LESSEN	/(*) LESSEN	O	INTE	N
N		Loop counter and subscript.	/MULTI	/(*) MULTI	W	INTE	N
N		Loop counter and subscript.	/PRINTI	/(*) PRINTI	W	INTE	N
N		Loop counter and subscript.	/RESETR	/(*) RESETR	W	INTE	N
N		Loop counter and subscript.	/SCAN	/(*) SCAN	W	INTE	N

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE			
			BLOCK	LOC	SUBR	U TYPE	VAR	DTM		
N		Loop counter and subscript.	/SETUP	/(*) SETUP	M	INTE	N		
N		Loop counter and subscript.	/STAND	/(*) STAND	M	INTE	N		
N		Loop counter and subscript.	/SYMRNG	/(*) SYMRNG	M	INTE	N		
NAL		Number of groups for which there are no thermochemical group additivity values and which have been assigned the thermochemical properties of another similar group.	/TGAP	/(*) TGAP	C	INTE	NAL		
NALT		Number of atomic constituents that form the backbone of the ring.	/CHAINM	/(*) CHAINM	M	INTE	NALT		
NALT		Number of atomic constituents that form the backbone of the ring.	/RING	/(*) RING	M	INTE	NALT		
NASYMC		Number of asymmetric carbon atoms in molecule.	/ASYMC	/(*) ASYMC	M	INTE	NASYMC		
NASYMC		Number of asymmetric carbon atoms in molecule.	/CORCIG	/(*) CORCIG	I	INTE	NASYMC		
NASYMC		Number of asymmetric atoms in molecule.	/ENTSYM	/(*) ENTSYM	I	INTE	NASYMC		
NASYMC		Number of asymmetric carbon atoms in molecule.	/EXTROT	/(*) EXTROT	I	INTE	NASYMC		
NASYMC		Number of asymmetric atoms in molecule.	/MAXCHN	/(*) MAXCHN	I	INTE	NASYMC		
NBC	(i,j)	Contains group number of atom i in chain j.	/BLK4	/(*)	CHAINM	M	INTE	NBC	(60,50)
						CHANGE	M	INTE	NBC	(60,50)
						MAXCHN	I	INTE	NBC	(60,50)
						NEWCOL	M	INTE	NBC	(60,50)
						RESETR	M	INTE	NBC	(60,50)
						RING	I	INTE	NBC	(60,50)
						SYNTRY	I	INTE	NBC	(60,50)
NBENZ		Total number of benzene type rings present in molecule.	/BLK3	/(* 5610))	CORCIG	M	INTE	NBENZ	
						CYCORR	M	INTE	NBENZ	
						HEXGON	I	INTE	NBENZ	
						SYMRNG	I	INTE	NBENZ	
NBP		Number of branch points (atoms) in molecule.	/CHAINM	/(*) CHAINM	M	INTE	NBP		
NBP		Number of branch points (atoms) in molecule.	/NEWCOL	/(*) NEWCOL	M	INTE	NBP		
NBP		Number of branch atoms in chain LXX.	/RESETR	/(*) RESETR	M	INTE	NBP		
NBPA		Number of branch atoms in ring.	/RESETR	/(*) RESETR	M	INTE	NBPA		

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIR
NBS	(1, J)	Data pertaining to chain I J=1 number of atoms in chain. J=2 number of branch atoms in chain.	/BLK9	/(3001)	CHAINM	O	INTE	NBS (60, 2)	
					CHANGE	M	INTE	NBS (60, 2)	
					MAXCMN	I	INTE	NBS (60, 2)	
					NEWCOL	I	INTE	NBS (60, 2)	
					RESETR	M	INTE	NBS (60, 2)	
					RING	I	INTE	NBS (60, 2)	
					SYMTRY	I	INTE	NBS (60, 2)	
NBR	(1, J)	Location J in chain I (stored in arrayNBC) that contains a branch atom.	/BLK9	/(3121)	CHAINM	O	INTE	NBR (60, 20)	
					CHANGE	M	INTE	NBR (60, 20)	
					NEWCOL	M	INTE	NBR (60, 20)	
					RESETR	M	INTE	NBR (60, 20)	
NC	(1)	First section of the program: number of input core atoms bonded to core atom I excluding that of the parent core atom. At end of first section: total number of input core atoms bonded to core atom I.	/BLK2	/(3119)	CHAINM	I	INTE	NC (100)	
					CIS	I	INTE	NC (100)	
					CISCON	I	INTE	NC (100)	
					CORCIG	I	INTE	NC (100)	
					CTWD	I	INTE	NC (100)	
					CYCORR	I	INTE	NC (100)	
					EQUALA	I	INTE	NC (100)	
					EXTROT	I	INTE	NC (100)	
					GAUCHE	I	INTE	NC (100)	
					LINEAR	I	INTE	NC (100)	
					NEWKC	I	INTE	NC (100)	
					RESETR	I	INTE	NC (100)	
					SCAN	M	INTE	NC (100)	
					SCANBR	I	INTE	NC (100)	
					SCANCH	I	INTE	NC (100)	
					SORNGI	I	INTE	NC (100)	
					STAND	M	INTE	NC (100)	
					SYMHNG	I	INTE	NC (100)	
					SYMTRY	I	INTE	NC (100)	
NCF		Upper limit of loop counter.	/EXTROT/(*)	EXTROT	M	INTE	NCF	
NDATA		Number of elements used in the formation of the chemical groups.	/BLK5	/(1)	PRINTI	I	INTE	NDATA	
					SCANBR	I	INTE	NDATA	
					SCANCH	I	INTE	NDATA	
					SETUP	I	INTE	NDATA	
					SYMTRY	I	INTE	NDATA	
					TGAP	O	INTE	NDATA	
NDIF		Total number of rings which are part of the fused ring sets.	/FUSION/(*)	FUSION	M	INTE	NDIF	
NDONE	(1)	Designates that the ligand core atom I has been processed when I=1. Otherwise, I=0.	/BLK1	/(3929)	EQUAL	R	INTE	NDONE (100)	
NENAN		Input value for total number of enantiomeric configurations of molecule (optional).	/CORCIG/(*)	CORCIG	I	INTE	NENAN	
NENAN		Input value for total number of enantiomeric configurations of molecule (optional).	/ENTSYM/(*)	ENTSYM	I	INTE	NENAN	
NENAN		Input value for total number of enantiomeric configurations of molecule (optional).	/TGAP	/(*)	TGAP	M	INTE	NENAN

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIM
NEWANC		Computed value for the total number of enantiomers.	/ENTSYM/10) ENTSYM	W	INTE	NEWANC
NEWB		Number of 3-ene structures associated with pair of central core atoms.	/CISCON/10) CISCON	W	INTE	NEWB
NEWCOL		Defines the initial constituents of a new chain. The group numbers of the previous chain common to the new chain are stored in a new row of array NBC. The related array <i>branch</i> data for the new chain are stored in the NBX array.	/NEWCOL/10) CHAINM	S	NEWCOL	E NEWCOL
NEWKC		Finds the next chain atom when the last identified atom KC of the chain is a branch atom. The new chain atom is set equal to one of the unused core atom ligands of KC and is stored in KC. If all these ligands have already been incorporated in some chain link, the program exits from the subroutine unless the required storage order is not present.	/NEWKC/10) CHAINM	S	NEWCOL	S NEWKC
NF		Upper limit of loop counter N.	/LESSEN/10) LESSEN	W	INTE	NF
NF		Upper limit of loop counter.	/PRINT/10) PRINT	W	INTE	NF
NF		Upper limit of loop counter.	/SYMRNG/10) SYMRNG	W	INTE	NF
NI		Lower limit of loop counter.	/EQUAL/10) EQUAL	W	INTE	NI
NI		Lower limit of loop counter.	/SETUP/10) SETUP	W	INTE	NI
NJ		Bond direction from ligand to first atom bonded to ligand which is not KT.	/SCAN/10) SCAN	I	INTE	NJ
NMU		Bond direction from core atom to ligand.	/SCAN/10) SCAN	W	INTE	NMU
NN		Loop counter and subscript.	/EQUAL/10) EQUAL	W	INTE	NN
NN		Settings for array MARO. 1=benzene-type ring, 2=pyridine-type ring, 0=neither.	/HEXCON/10) HEXCON	W	INTE	NN
NN		Subscript of array JORD.	/LESSEN/10) LESSEN	W	INTE	NN

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUB OUTLINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
NN		Value of j subscript in IX(I,J,K) where data required for scan operation are located.	/STAND	/(+)	STAND	W	INTE	NN
NNBENZ		Number of pyridine-type ring structures.	/BLK1	/(3975)	CORCIG	M	INTE	NNBENZ
					CYCDRA	M	INTE	NNBENZ
					HEXGON	I	INTE	NNBENZ
NO		Number of cards used to input structure of molecule.	/BLK1	/()	ASSIGN	I	INTE	NO
					IDENT	I	INTE	NO
					STAND	I	INTE	NO
					TGAP	M	INTE	NO
NOBR		Number of branch core atoms present in molecule.	/BLK3	/(6402)	CHAINM	I	INTE	NOBR
					STAND	O	INTE	NOBR
NOBRD	(I)	Counter that denotes which ligand of the branch atom of group number I is to be added to the chain.	/BLK3	/(1703)	CHAINM	O	INTE	NOBRD (100)
					NEWCOL	O	INTE	NOBRD (100)
					NEWKC	M	INTE	NOBRD (100)
NOCAR		Denotes whether the carbon atom is the first or second central atom of the gauche interaction structure.	/GAUCHE	/(+)	GAUCHE	W	INTE	NOCAR
NODD1		Number of entries in array KCXD01.	/EQUAL	/(+)	EQUAL	I	INTE	NODD1
NODD1		Number of entries in array KCXD01.	/SETUP	/(+)	SETUP	I	INTE	NODD1
NODD2		Number of entries in array KCXD02.	/EQUAL	/(+)	EQUAL	I	INTE	NODD2
NODD2		Number of entries in array KCXD02.	/SETUP	/(+)	SETUP	I	INTE	NODD2
NOK	(I, J)	Multi-storage array I=1 number of ring pairs in fused ring set J. I=2 total number of atoms common to any ring pair in set. I=3 total number of atoms common to all ring pairs in set. I>3 group number of atoms comprising the total in I=3.	/BLK3	/(3901)	CRINGS	I	INTE	NOK (10,10)
					FIRSTA	I	INTE	NOK (10,10)
					FUSION	O	INTE	NOK (10,10)
					HEXGON	I	INTE	NOK (10,10)
					NRINGS	I	INTE	NOK (10,10)
NOKOMB	(I)	Contents of array. I=1 number of fused ring systems in molecule. I>1 number of rings in fused ring system I-1.	/BLK3	/(4380)	CORCIG	M	INTE	NOKOMB(11)
					CRINGS	I	INTE	NOKOMB(11)
					FIRSTA	I	INTE	NOKOMB(11)
					FUSION	M	INTE	NOKOMB(11)
					HEXGON	I	INTE	NOKOMB(11)
					NRINGS	I	INTE	NOKOMB(11)

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
NOMESO		Function type =0 no asymmetric atom or meso structures present. =1 asymmetric atom present. =2 meso structures present.	/CORCIG/(*)	CORCIG	I	INTE NOMESO
NOMESO		Function type =0 no asymmetric atom or meso structures present. =1 asymmetric atom present. =2 meso structures present. Are being compared. Are being compared.	/ENTSYM/(*)	ENTSYM	I	INTE NOMESO
NOMESO		Function type. =0 no asymmetric atom or meso structures present. =1 asymmetric atom present. =2 meso structures present.	/EXTROT/(*)	EXTROT	O	INTE NOMESO
NONARO	(I)	Array in which non-aromatic ring units (i) are set equal to 1 and aromatic units (i) are set equal to 0.	/BLK3	/I	3602)	CORCIG	O	INTE NONARO(40) HEXGON O INTE NONARO(40) SORANGI I INTE NONARO(40)
NONFUS		Total number of rings in molecule which are not part of any fused ring set.	/BLK4	/I	4322)	FUSION	M	INTE NONFUS
NONIT		Denotes whether the nitrogen atom is the first or second central atom of the gauche interaction structure.	/GAUCHE/(*)	GAUCHE	M	INTE NONIT
NOPTS		Total number of enantiomeric and meso forms computed from input data.	/ENTSYM/(*)	ENTSYM	M	INTE NOPTS
NOPTSC		Computed value for the total number of enantiomers and meso structures present.	/ENTSYM/(*)	ENTSYM	M	INTE NOPTSC
NOS		Number of elements plus radicals used in the formation of the chemical groups.	/BLK1	/I	2)	IDENT	I	INTE NOS TGAP O INTE NOS
NOSAME	(I, J)	Multi-variable array I=1 number of entries in array KCSAME for core atom j. I=2 number of different types of identical ligands in set. I>2 number of each type.	/BLK1	/I	2678)	EXTROT	I	INTE NOSAME(8,100) SAME M INTE NOSAME(8,100) SETUP O INTE NOSAME(8,100) SYMRNG I INTE NOSAME(8,100)
NOSIX		Total number of six-membered rings containing at least two double bonds.	/BLK3	/I	5611)	CORCIG	O	INTE NOSIX CYCORR M INTE NOSIX HEXGON I INTE NOSIX
NOSW		Input value for external symmetry number of molecule (optional).	/CORCIG/(*)	CORCIG	I	INTE NOSW

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	DCBR	U TYPE	VAR	DIR
NOSM		Input value for external symmetry number of molecule (optional).	/ENTSYM/	(+)	ENTSYM	I	INTE	NOSM
NOSN		Input value for external symmetry number of molecule (optional).	/TGAP	/	(+)	TGAP	M	INTE NOSM
NOSNC		Computed value for the external rotation symmetry number.	/CORCIG/	(+)	CORCIG	I	INTE	NOSNC
NOSNC		Computed value for the external rotation symmetry number.	/ENTSYM/	(+)	ENTSYM	I	INTE	NOSNC
NOSNC		Computed value for the external rotation symmetry number.	/EXTROT/	(+)	EXTROT	M	INTE	NOSNC
NOSNC		Computed value for the external rotation symmetry number.	/SYMANG/	(+)	SYMANG	O	INTE	NOSNC
NOVAL	(?)	Chemical valence of each element and radical. In the group additivity tables nitrogen always has a valence of three.	/BLK1	/	(16)	STAND	I	INTE NOVAL (9) TGAP O INTE NOVAL (9)
NOXY		Number of CO groups found in ring K.	/OXYATM/	(+)	OXYATA	M	INTE	NOXY
NOIALT	(1)	Temporary storage for original NOSAME data computed for KC1.	/BLK1	/	(3895)	EXTROT	M	INTE NOIALT(8)
NOZALT	(1)	Temporary storage for original NOSAME data computed for KC2.	/BLK1	/	(3903)	EXTROT	M	INTE NOZALT(8)
NPSUDA		Pseudoasymmetric atom flag =0 pseudoasymmetric atom not present. =1 pseudoasymmetric atom present.	/CORCIG/	(+)	CORCIG	I	INTE	NPSUDA
NPSUDA		Pseudoasymmetric atom flag =0 pseudoasymmetric atom not present. =1 pseudoasymmetric atom present.	/ENTSYM/	(+)	ENTSYM	I	INTE	NPSUDA
NPSUDA		Pseudoasymmetric atom flag. =0 pseudoasymmetric atom not present. =1 pseudoasymmetric atom present.	/EXTROT/	(+)	EXTROT	O	INTE	NPSUDA
NRING	(1)	Identifies nitrogen containing rings. Location 1 is set to 1 if ring 1 contains nitrogen and to 0 if it does not.	/BLK1	/	(3725)	CORCIG O CYCORR O MEXGON I	INTE	NRING (40) NRING (40) NRING (40)
NRINGS		Searches for a particular fused nitrogen-containing-ring molecule and applies ring correction if present.	/NRINGS/	(+)	CORCIG S NRINGS E			NRINGS NRINGS

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
NRLOC	(I)	The number of the chain that contains ring I is stored in location I.	/BLK3	/(3503)	LESSEN	M	INTE	NRLOC (40)
					RESETR	I	INTE	NRLOC (40)
					RING	M	INTE	NRLOC (40)
NS		Bond direction of second character.	/IDENT	/(*)	IDENT	W	INTE	NS
NTBENZ		Total number of benzene- and pyridine-type rings.	/BLK3	/(6396)	CORCIG	D	INTE	NTBENZ
					CTWO	I	INTE	NTBENZ
					HEXGON	M	INTE	NTBENZ
NTITLE		Title printout flag =0 title of interaction (ata not yet output. =1 title has been output.	/CORCIG/(*)		CORCIG	W	INTE	NTITLE
NTITLE		Title printout flag =0 title of interaction data not yet output. =1 title has been output.	/PRINTZ/(*)		PRINTZ	D	INTE	NTITLE
NTOTAL	(I, J)	Number of identical atoms I of a particular type that are associated with core atom J.	/BLK1	/(3478)	EXTROT	M	INTE	NTOTAL(3, 100)
					INTROT	I	INTE	NTOTAL(3, 150)
					LINEAR	I	INTE	NTOTAL(3, 100)
					SAME	M	INTE	NTOTAL(3, 100)
					SETUP	D	INTE	NTOTAL(3, 100)
					SVIRNG	M	INTE	NTOTAL(3, 100)
					SVNTRY	D	INTE	NTOTAL(3, 100)
NTIALT	(I)	Temporary storage for original NTOTAL data computed for KC1	/BLK1	/(3911)	EXTROT	M	INTE	NTIALT(3)
NTIX	(I)	Same as data in array NTIALT except that here the contribution from atom KC2 is deleted if present.	/BLK1	/(3917)	EXTROT	M	INTE	NTIX (3)
NT2ALT	(I)	Temporary storage for original NTOTAL data computed for KC2.	/BLK1	/(3914)	EXTROT	M	INTE	NT2ALT(3)
NT2X	(I)	Same as data in array NT2ALT except that here the contribution from atom KC1 is deleted if present.	/BLK1	/(3920)	EXTROT	M	INTE	NT2X (3)
NUM		Bond direction 1 = north 2 = northeast 3 = east 4 = southeast 5 = south 6 = southwest 7 = west 8 = northwest	/ASSIGN/(*)		ASSIGN	I	INTE	NUM
NUM		Number of ring components.	/CYCORR/(*)		CYCORR	W	INTE	NUM

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIR
NUM		Entry value: number used to compute initial bond scan direction. Exit value: bond direction from indexed atom to ligand core atom.	/FIND	/10	1	FIND	M	INTE NUM	
NUM		Number of atoms which ring pair KSUB has in common.	/FUSION	/10	1	FUSION	M	INTE NUM	
NUM		Bond direction from parent atom to indexed atom. Set to -3 initially prior to the identification of the first symbol of the molecule.	/IDENT	/10	1	IDENT	M	INTE NUM	
NUM		Bond direction. Entry value: from parent core atom to indexed core atom. Computed value: from indexed core atom to parent core atom.	/NUMBER	/10	1	NUMBER	M	INTE NUM	
NUM		Bond direction from parent atom to core atom.	/SCAN	/10	1	SCAN	I	INTE NUM	
NUM		Initial setting for the bond direction variable.	/STAND	/10	1	STAND	M	INTE NUM	
NUM		Number of sets of identical ligands on the ring.	/SYMRNG	/10	1	SYMRNG	M	INTE NUM	
NUMATM	(1)	Contains elemental composition of molecule.	/BLK5	/1	2	IDENT PRINT1 SCAN SCAI/R SCANCH STAND	I I I I I O	INTE INTE INTE INTE INTE INTE	NUMATM(5) NUMATM(5) NUMATM(5) NUMATM(5) NUMATM(5) NUMATM(5)
NUMATM	(1)	Contains elemental composition of molecule or ligand.	/SUMATM	/10	1	SUMATM	M	INTE	NUMATM(5)
NUMBER		This subroutine determines the number of ligands (MP) attached to core atom 1 or the number of ligands - 1 of any core atom whose group number exceeds 1.	/NUMBER	/10	1	FIND NUMBER SCAN	S E S	NUMBER NUMBER NUMBER	
NUMC		Number of carbon atoms in ring backbone.	/BLK3	/1 5776	1	CYCORR	M	INTE	NUMC
NUMCP		Number of CO atoms in ring backbone.	/BLK3	/1 5779	1	CYCORR	M	INTE	NUMCP
NUMFR0	(1)	Contains the subscript of array SYMBOL that identifies each element in a radical and the number of each element contained therein. Six locations per radical. Odd locations contain subscript, even locations the number.	/BLK6	/1	11	SUMATM TGAP	I O	INTE INTE	NUMFR0(24) NUMFR0(24)
NUMN		Number of nitrogen atoms in ring backbone.	/BLK3	/1 5778	1	CYCORR	M	INTE	NUMN

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U TYPE	VAR	DIM	
NUM0		Number of oxygen atoms in ring backbone.	/BLK3	/(5777)	CYCORR	M	INTE	NUM0	
NV	(I)	Number of core atoms bonded to atom I. If I is a ring atom, value is reset in subroutine EQUALR to the number of non-ring core atoms bonded to I plus one.	/BLK1	/(1425)	EQUAL	I	INTE	NV	(100)
					EQUALR	M	INTE	NV	(100)
					SYMTAY	O	INTE	NV	(100)
NVR	(I)	Number of ring atoms bonded to ring atom I.	/BLK4	/(4162)	EQUALR	M	INTE	NVR	(100)
NW	(I)	Number of actual core atoms bonded to core atom I, this includes the oxygen atom of the CO radical.	/BLK3	/(5201)	DITERE	I	INTE	NW	(100)
					GAUCHE	I	INTE	NW	(100)
					STAND	M	INTE	NW	(100)
NX		Redefinition value for bond direction if limit is exceeded.	/CIS	/(+)	CIS	M	INTE	NX	
NX		Flag that controls the transfer to the various ring correction sections in subroutine CYCORR.	/CYCORR	/(+)	CYCORR	M	INTE	NX	
NX		Sum of asymmetric and pseudoasymmetric atoms.	/ENTSYM	/(+)	ENTSYM	M	INTE	NX	
NX		Transfer flag to computation areas for diverse structural types.	/EXTROT	/(+)	EXTROT	M	INTE	NX	
NX		Bond direction from indexed atom to number 1 (core) ligand.	/FIND	/(+)	FIND	I	INTE	NX	
NX		Current test bond direction.	/IDENT	/(+)	IDENT	M	INTE	NX	
NX		Bond direction from core atom.	/NUMBER	/(+)	NUMBER	M	INTE	NX	
NX		Bond direction from core atom to test location.	/SCAN	/(+)	SCAN	M	INTE	NX	
NX2		Bond direction from indexed core atom to ligand one.	/NUMBER	/(+)	NUMBER	O	INTE	NX2	
NX3		Number of entries in array JSTORE.	/NRINGS	/(+)	NRINGS	M	INTE	NX3	
NV		Value outside range of bond direction.	/CIS	/(+)	CIS	M	INTE	NV	
NZ		Bond direction from number 1 (core) ligand to indexed atom.	/FIND	/(+)	FIND	M	INTE	NZ	
NZ		Initial test bond direction.	/IDENT	/(+)	IDENT	M	INTE	NZ	
NZ		Bond direction from core atom to parent atom. Inverse of NUM.	/SCAN	/(+)	SCAN	M	INTE	NZ	

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	OTA
N1		Ring number.	/CRINGS/	(+))	CRINGS	W	INTE N1
N1		Location in IDX where group number of ligand of KC1P is stored.	/EQUAL	/	(+))	EQUAL	W INTE N1
N1B		Direction of bond adjacent to bond between atoms K1R and KC1PR.	/EQUALR/	(+))	EQUALR	W INTE N1B	
N1E		Number of non-ring core atoms bonded to an atom in ring A.	/EQUALR/	(+))	EQUALR	W INTE N1E	
N1F		Upper limit of loop counter.	/EQUAL	/	(+))	EQUAL	W INTE N1F
N1R		Number of other ring atoms bonded to an atom in ring A.	/EQUALR/	(+))	EQUALR	W INTE N1R	
N2		Ring size.	/CRINGS/	(+))	CRINGS	W INTE N2	
N2		Location in IDX where group number of ligand of KC2P is stored.	/EQUAL	/	(+))	EQUAL	W INTE N2
N2E		Number of non-ring core atoms bonded to an atom in ring B.	/EQUALR/	(+))	EQUALR	W INTE N2E	
N2R		Number of other ring atoms bonded to an atom in ring B.	/EQUALR/	(+))	EQUALR	W INTE N2R	
N3		Ring correction indicator.	/CRINGS/	(+))	CRINGS	W INTE N3	
OPTS		Floating point equivalent of the total number of enantiomeric and meso structures.	/ENTSYM/	(+))	ENTSYM	W REAL	OPTS
ORDER		Stores in array IA the order that the elements in array IB would have if rearranged in numerical order.	/ORDER	/	(+))	COARCIB S EQUALR S LESSEN S ORDER E TGAP S	ORDER ORDER ORDER ORDER ORDER
ORDSUM	(1)	Contains order elements in array SUM would have if arranged in order of increasing magnitude.	/SEARCH/	(+))	SEARCH	I INTE	ORDSUM(100)
ORDSUM	(1)	Contains order elements in array SUM would have if arranged in order of increasing magnitude.	/TGAP	/	(+))	TGAP	I INTE ORDSUM(100)
OXYATM		Determines the number of CO atoms in a particular ring which are adjacent to another specific atom in the ring.	/OXYATM/	(+))	CYCORN S OXYATM E		OXYATM OXYATM

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
PERLIG	(I,J)	Ordinal number I of ligand bonded to atom J.	/BLK4	/(3762)	EQUAL	I	INTE	PERLIG(4,100)
					SCANBA	0	INTE	PERLIG(4,100)
					SCANCM	0	INTE	PERLIG(4,100)
					SETUP	I	INTE	PERLIG(4,100)
					SYMANG	0	INTE	PERLIG(4,100)
PERTKC	(I,J)	Group number of first atom in ligand I that is bonded to core atom J. If atom is non-core, the negative of the chemical symbol subscript of the atom is stored instead.	/BLK4	/(3362)	EQUAL	I	INTE	PERTKC(4,100)
					SCANBA	0	INTE	PERTKC(4,100)
					SCANCM	0	INTE	PERTKC(4,100)
					SETUP	I	INTE	PERTKC(4,100)
					SYMANG	I	INTE	PERTKC(4,100)
					SYMTRY	0	INTE	PERTKC(4,100)
PRINT1		Prints the atomic composition, the assigned weights, the structure and coordinate array IX, and (and if rings are present) the number of components in each ring and their group numbers.	/PRINT1/(6)	CORCIG	S		PRINT1
					HEXGON	S		PRINT1
					PRINT1	E		PRINT1
					TGAP	S		PRINT1
PRINT2		Prints the title preceding the printout of ring, second-order interaction, and internal rotational symmetry contributions.	/PRINT2/(6)	CORCIG	S		PRINT2
					PRINT2	E		PRINT2
RDATA	(I,J)	Thermodynamic corrections for certain fused carbon-ring systems.	/CRINGS/(4)	CRINGS	I	REAL	RDATA (6,F)
RDATA	(I)	Thermodynamic corrections for a particular fused nitrogen-containing-ring molecule.	/NRINGS/(4)	NRINGS	I	REAL	RDATA (6)
RESETR		Sets the ring array JBC and adds to all the chain columns the residual non-branch ring atoms, if the first chain atom defined was a non-branch ring atom. These residuals were not included when the chains were first constructed.	/RESETR/(6)	CHAINM	S		RESETR
					RESETR	E		RESETR
RING		Determines if similar ring was not previously identified. If not, the group numbers of the ring constituents are stored in IRING.	/RING	/(6)	CHAINM	S	RING
					RING	E		RING
RINGD	(I,J)	Array equivalenced to the entire set of arrays A1, A2 etc.	/CORCIG/(4)	CORCIG	I	REAL	RINGD (6,50)
RINGLI	(I)	Contains variable that designates the ring correction to be applied to ring I.	/BLK3	/(5695)	CORCIG	M	INTE	RINGLI(40)
ROTINS		Total contribution to the entropy due to internal rotational symmetry.	/CORCIG/(4)	CORCIG	I	REAL	ROTINS
ROTINS		Total contribution to the entropy due to internal rotational symmetry.	/INTROT/(4)	INTROT	M	REAL	ROTINS
S		Entropy of molecule for 298°K. (cal-deg ⁻¹ -mole ⁻¹)	/TGAP	/(4)	TGAP	M	REAL

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE			USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR	DIM
SAME		Stores all the pertinent identification variables for any two identical ligands. If one of these ligands has been thus identified previously, it is bypassed and only the variables for the other ligand are stored.	/SAME	/10) EQUAL	S			SAME
					SAME	E			SAME
					SETUP	S			SAME
SCAN		Locates and identifies all atoms bonded to core atom KT of group KT which have not yet been scanned and stores pertinent data of ligand in IX. It also rearranges data of group KT in IX such that data of core species are stored first followed by data of non-core species.	/SCAN	/10) SCAN	E			SCAN
					STAND	S			SCAN
SCANBR		Computes the atomic composition of all ligands bonded to a branch atom and establishes the similarities of said ligands providing the branch atom is not a ring atom.	/SCANBR/10) SCANBR	E			SCANBR
					SYNTAX	S			SCANBR
SCANCH		Computes atomic composition of all ligands bonded to a chain atom and establishes the similarities of these ligands providing said chain atom is not a ring atom.	/SCANCH/10) SCANCH	E			SCANCH
					SYNTAX	S			SCANCH
SCONS		Entropy constant.	/TGAP	/10) TGAP	M	REAL		SCONS
SEARCH		Integer function flag. =0 a data match for computed group weight MOLWT(k) has been found. =1 no match found, computed weight below range of data group weights. =-1 no match found, computed weight above range of data group weights.	/SEARCH/10) SEARCH	D			SEARCH
					TGAP	F			SEARCH
SETUP		Processes the comparison of ligands bonded to the same or to different core atoms by first comparing their atomic compositions. If the compositions are the same and both are non-core ligands, they are identical but if the ligands are non-core atoms, their identity must be checked further.	/SETUP	/10) EXTHOT	E			SETUP
					SCANBR	S			SETUP
					SCANCH	S			SETUP
					SETUP	E			SETUP
					SYNTAX	S			SETUP

FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U TYPE	VAR	DIR
SHIFT		Data contained in column j=2 of IX(JC,j,k) is switched with that of core atom KC.	/SHIFT	/10	1	CORCIG S EXTR0T S SHIFT E STAND S		SHIFT SHIFT SHIFT SHIFT
SN		Floating point equivalent for the symmetry number.	/ENTSYM	/10	1	ENTSYM W REAL SN		
SOPTS		Total contribution to the entropy due to optical isomerism.	/CORCIG	/10	1	CORCIG I REAL SOPTS		
SOPTS		Total contribution to the entropy due to optical isomerism.	/ENTSYM	/10	1	ENTSYM O REAL SOPTS		
SOPTSC		Computed value for the contribution to the entropy due to optical isomerism.	/ENTSYM	/10	1	ENTSYM W REAL SOPTSC		
SOPTSI		Entropy contribution due to optical isomerism computed from input data.	/ENTSYM	/10	1	ENTSYM W REAL SOPTSI		
SORNGI		Controls the search for gauche and cis interactions in which one or both of the central atoms are non-aromatic ring atoms and for their contributions if these interactions occur.	/SORNGI	/10	1	CORCIG S SORNGI E		SORNGI SORNGI
SRING		Total of ring contributions to the entropy.	/CORCIG	/10	1	CORCIG W REAL SRING		
SRING		Sum of ring contributions to the entropy.	/CRINGS	/10	1	CRINGS W REAL SRING		
SRING		Sum of ring contributions to the entropy.	/HEXGON	/10	1	HEXGON W REAL SRING		
SRING		Sum of ring contributions to the entropy.	/NRINGS	/10	1	NRINGS W REAL SRING		
SSN		Total contribution to the entropy due to external rotational symmetry.	/CORCIG	/10	1	CORCIG I REAL SSN		
SSN		Total contribution to the entropy due to external rotational symmetry.	/ENTSYM	/10	1	ENTSYM O REAL SSN		
SSNC		External rotational entropy contribution computed by program.	/ENTSYM	/10	1	ENTSYM W REAL SSNC		
SSNI		External rotational entropy contribution computed from input data.	/ENTSYM	/10	1	ENTSYM W REAL SSNI		
SSYM		Total contribution to the entropy from second-order interactions, ring corrections, symmetry and optical isomerism.	/CORCIG	/10	1	CORCIG O REAL SSYM		

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE		
			BLOCK	LOC	SUBR	U TYPE	VAR	DIM	
SSYM		Sum total of corrections to the entropy at 298°K derived from section 3 of the program.	/TGAP	/(+)	TGAP	I	REAL	SSYM	
ST	(1)	Entropy of molecule for temperatures specified in TARRAY. [cal-deg ⁻¹ -mole ⁻¹]	/BLK3	/(1219)	YGAP	M	REAL	ST	(14)
STAND		Control routine for section 1 of the program. this section identifies the groups and group components of the molecule as well as the atomic coordinates, bond vectors and bond types. The group weights are also assigned. For some unsaturated ring compounds the latter is altered in section 3 of the program. [cal-deg ⁻¹ -mole ⁻¹]	/STAND	/(+)	STAND TGAP	E S		STAND STAND	
SUM	(1)	Identification weight of each group in the data library.	/BLK7	/(1)	DAT1 GADATA TGAP	D I C	INTE INTE INTE	SUM SUM SUM	(100) (100) (100)
SUM		Identification weight of particular group contained in data library.	/SEARCH/	/(+)	SEARCH	I	INTE	SUM	(100)
SUMATM		Adds or subtracts (when KP= 1 or -1 respectively) the number of each element present in the chemical symbol represented by M to the location assigned that particular atom in array umatm.	/SUMATM/	(+)	IDENT SCANR SCANR SCANR SUMATM SYMTRY	S S S S E S		SUMATM SUMATM SUMATM SUMATM SUMATM SUMATM	
SUM1		Sum of symbol code numbers of carbon atoms one and two.	/DITERE/	/(+)	DITERE	M	INTE	SUM1	
SUM2		Sum total of core atoms bonded to carbon atoms one and two.	/DITERE/	/(+)	DITERE	M	INTE	SUM2	
SYMBL	(1,j)	Contains character 1 of multi-character program library symbol j. The description and order of these symbols correspond to those of the single word, multi-character Hollerith program library symbols.	/MULTI	/(+)	MULTI	C	INTE	SYMBL	(3,4)
SYMBOL	(1)	Chemical symbol for elements and radicals contained in the program.	/BLK1	/(1)	IDENT PRINT1 TGAP	I I D	INTE INTE INTE	SYMBOL(9) SYMBOL(9) SYMBOL(9)	
SYMANG		Computes the external rotation symmetry number of aromatic, monocyclic benzene-type structures.	/SYMANG/	(+)	EXTROY SYMANG	S E		SYMANG SYMANG	

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FORTRAN SYMBOL	NATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
SYNTRV		Controls the operation which finds the atomic composition of each ligand of each core atom in the molecule. If the core atom is not a ring atom, the routine determines whether it possesses identical ligands.	/SYNTRV/10		1	CORCIG S SYNTRV E		SYNTRV SYNTRV
SYMR	(1)	Contains symbols for bond types and blank.	/BLK1 /1		3)	BOND I INTE SYMR (4) IDENT I INTE SYMR (4) NUMBER I INTE SYMR (4) SCAN I INTE SYMR (4) STAND I INTE SYMR (4) TGAP D INTE SYMR (4)		
S298	(1)	Entropy at 298°K of each group in the data library. [cal-deg ⁻¹ -mole ⁻¹]	/BLK7 /1	361)		DATA1 D REAL S298 (100) GADATA I REAL S298 (100) TGAP I REAL S298 (100)		
TARRAY	(1)	Temperature values used to compute and output thermochemical data.	/TGAP /10		1	TGAP C REAL TARRAY(14)		
TCIS		Floating point equivalent of variable ICIS.	/CORCIG/10		1	CORCIG W REAL TCIS		
TGAP		Main or control unit of the thermochemical group additivity program. It prints out data library (optional), reads input data, prints out structural input data, transfers control to 3 main sections of the program, and computes and prints out thermochemical properties of molecule	/TGAP /10		1	TGAP E TGAP		
TOUT	(1)	Output legend that specifies whether property printed was input, computed, or is not computable.	/ENTSYM/10		1	ENTSYM C REAL TOUT (12)		
TYPE	(1,J)	Contains legends that describe the type of second-order interaction to be printed.	/CORCIG/10		1	CORCIG C REAL TYPE (4,8)		
WEIGHT	(1)	Identification number assigned each element and radical.	/BLK2 /1		1)	DELTA1 I INTE WEIGHT(9) TGAP D INTE WEIGHT(9)		
.UNOS.		Description not input	/.UNOS./10		1	TGAP I .UNOS.		

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FORTRAN SYMBOL	MATH SYMBOL	DESCRIPTION	STORAGE		SUBROUTINE		USAGE	
			BLOCK	LOC	SUBR	U	TYPE	VAR
.UN06.		Description not input	/.UN06./10					
					BOND	0		.UN06.
					CHAINM	0		.UN06.
					CORCIS	0		.UN06.
					DITERE	0		.UN06.
					ENTSY	0		.UN06.
					EQUAI	0		.UN06.
					FIND	0		.UN06.
					FIRS/R	0		.UN06.
					GADATA	0		.UN06.
					IDENT	0		.UN06.
					MAICMN	0		.UN06.
					PRINT1	0		.UN06.
					PRINT2	0		.UN06.
					SCAN	0		.UN06.
					STAND	0		.UN06.
					SYTRY	0		.UN06.
					TGAP	0		.UN06.

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