

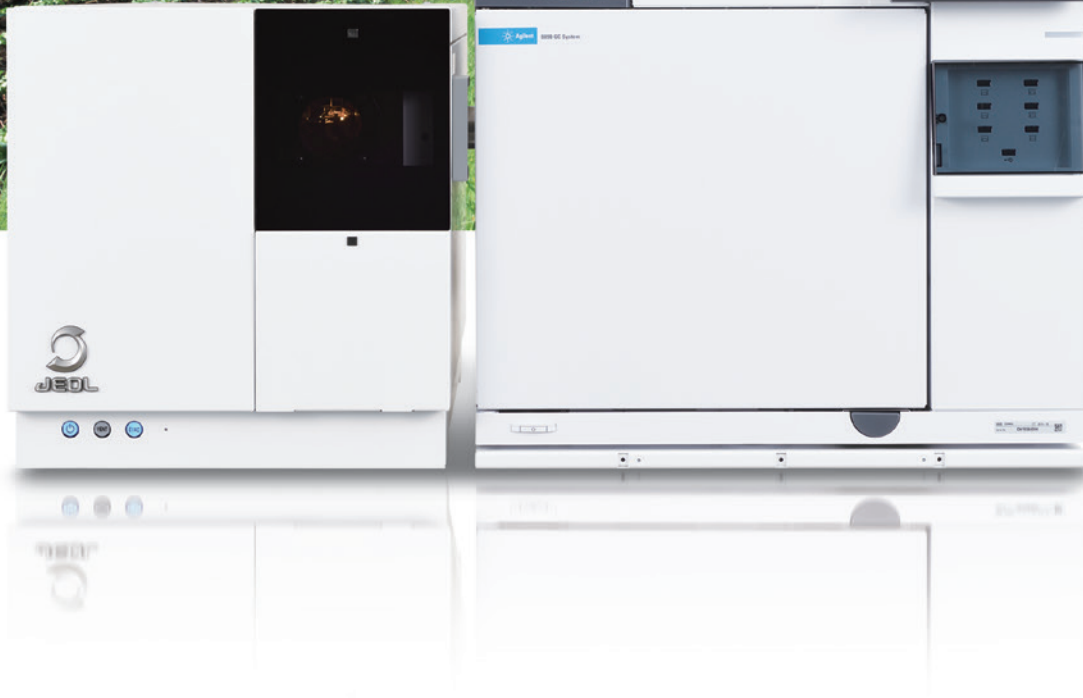


Scientific / Metrology Instruments
GC Triple Quadrupole Mass Spectrometer

Solutions for Innovation

JMS-TQ4000GC for Dioxins

Dedicated SIM/SRM data quantitative analysis software for Dioxins



JEOL Ltd.

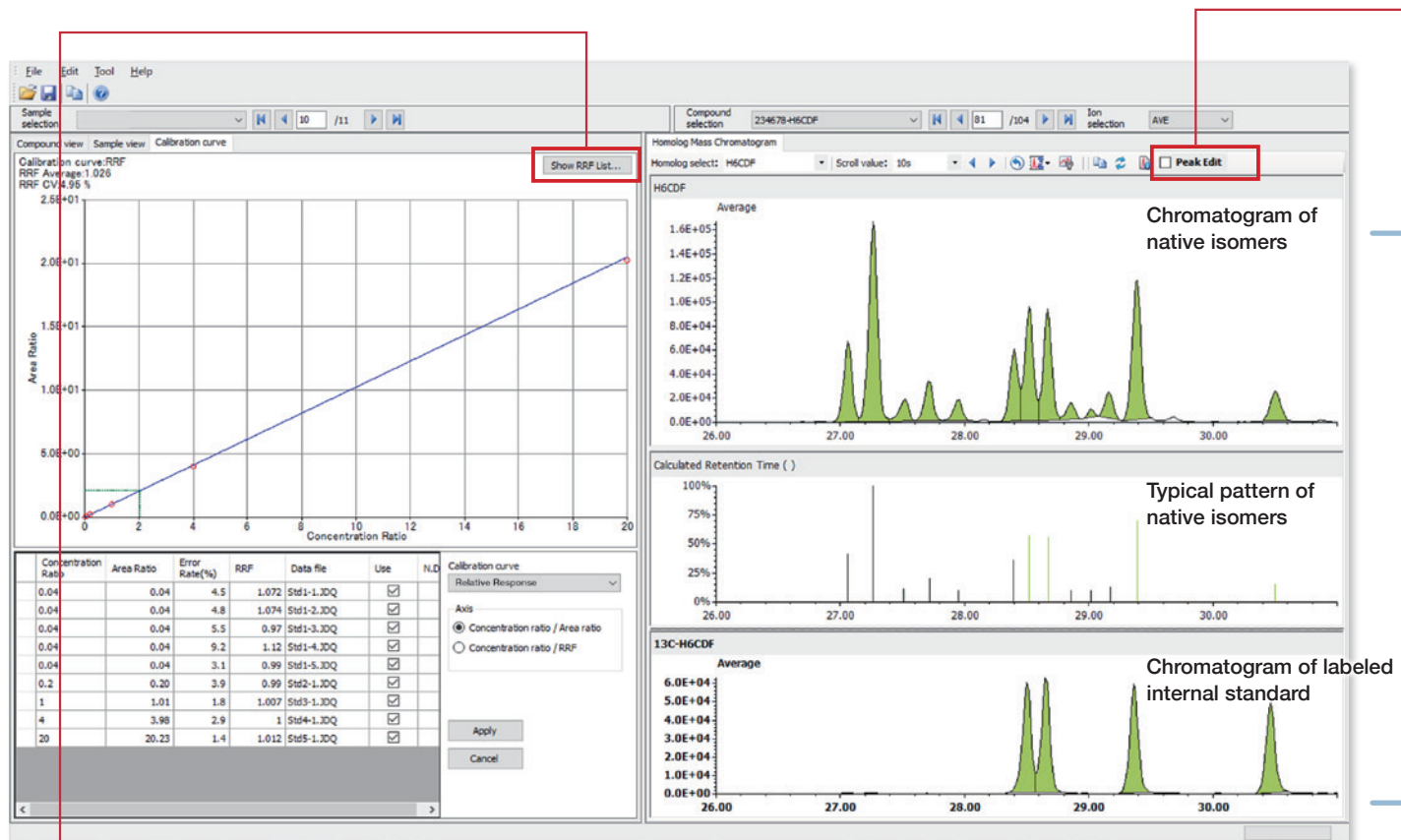
Dedicated quantitative analysis software for Dioxins "TQ-DioK^{*}"

^{*}Triple Quad DioK

TQ-DioK is a software dedicated for the quantitative processing, which requires simultaneous quantification of many isomers such as Dioxins and PCBs, and which requires the quantitative calculation using internal standard substances labeled with ¹³C isotopes. TQ-DioK has a unique GUI and functionalities that are useful for such quantitative processing.

■ Possible to automatically assign peaks for each isomer

The retention times of all native compounds are corrected based on the deviation of the retention times of the ¹³C labeled internal standard compounds, and all peaks of not only 2,3,7,8-substituted dioxins/furans but also non-2,3,7,8-substituted dioxins/furans are automatically assigned.



■ Capable of displaying all calibration curve information in a list

Calibration curve (RR) information and individual peak information can also be displayed in GUI.

Standard Samples RRF List

	No.	Type	Compound	Isomer	Av-RRF	SD	%RSD	OK	Std1-1.JDQ		Std1-2.JDQ		Std1-3.JDQ		Std1-4.JDQ		Std1-5.JDQ	
									RRF	Error	RRF	Error	RRF	Error	RRF	Error	RRF	Error
▶	1	QNT	T4CDD	2378-T4CDD	1.1366	0.0451	4.0	OK(10)	1.1176	-0.0191	1.2043	0.0677	1.1692	0.0326	1.1847	0.0481	1.1527	0.0161
	2	QNT	P5CDD	12378-P5CDD	1.0075	0.0633	6.3	OK(10)	1.1494	0.1419	1.0302	0.0227	0.9292	-0.0784	0.9585	-0.0491	0.9553	-0.0522
	3	QNT	H6CDD	123478-H6...	1.1578	0.1090	9.4	OK(10)	1.2723	0.1144	1.0625	-0.0953	1.0675	-0.0904	1.3305	0.1727	1.2745	0.1167
	4	QNT	H6CDD	123678-H6...	1.0952	0.0921	8.4	OK(10)	0.9830	-0.1122	1.1527	0.0574	0.9165	-0.1787	1.1843	0.0891	1.1649	0.0698
	5	QNT	H6CDD	123789-H6...	1.0729	0.0805	7.5	OK(10)	1.2190	0.1460	0.9814	-0.0916	1.1657	0.0928	0.9993	-0.0737	1.0903	0.0172
	6	QNT	H7CDD	1234678-H7...	1.3383	0.1197	8.9	OK(10)	1.5185	0.1802	1.3599	0.0216	1.5441	0.2058	1.3218	-0.0165	1.2383	-0.1000
	7	QNT	O8CDD	12346789-O...	1.1529	0.0945	8.2	OK(10)	1.2461	0.0932	1.1384	-0.0145	1.1690	0.0160	1.0946	-0.0584	1.1006	-0.0523
	8	QNT	T4CDF	2378, 2347, ...	1.0287	0.0439	4.3	OK(10)	1.1060	0.0774	0.9889	-0.0397	1.0738	0.0451	0.9806	-0.0481	1.0499	0.0212
	9	QNT	P5CDF	12378-P5CDF	1.0271	0.0507	4.9	OK(10)	0.9938	-0.0333	0.9627	-0.0645	1.0987	0.0716	1.0951	0.0680	1.0463	0.0192
	10	QNT	P5CDF	23478, 2346...	1.0146	0.0605	6.0	OK(10)	1.1175	0.1029	1.0500	0.0354	1.0267	0.0121	0.9179	-0.0967	1.0383	0.0237
	11	QNT	H6CDF	123478-H6...	1.0809	0.0579	5.4	OK(10)	1.1730	0.0921	1.0392	-0.0418	1.1073	0.0263	1.1668	0.0858	1.0827	0.0016
	12	QNT	H6CDF	123678-H6...	1.0445	0.0697	6.7	OK(10)	1.0925	0.0480	1.1285	0.0841	1.1430	0.0985	1.0952	0.0507	0.9590	-0.0854
	13	QNT	H6CDF	234678-H6...	1.0255	0.0508	5.0	OK(10)	1.0718	0.0463	1.0745	0.0489	0.9695	-0.0560	1.1201	0.0945	0.9936	-0.0315
	14	QNT	H6CDF	123789, 123...	1.0442	0.0525	5.0	OK(10)	1.1062	0.0620	1.0286	-0.0156	0.9869	-0.0573	1.0333	-0.0109	1.1536	0.1094
	15	QNT	H7CDF	1234678-H7...	1.3563	0.0852	6.3	OK(10)	1.2830	-0.0733	1.2851	-0.0712	1.3406	-0.0157	1.4893	0.1330	1.4927	0.1364
	16	QNT	H7CDF	1234789-H7...	1.2306	0.0871	7.1	OK(10)	1.3045	0.0739	1.1659	-0.0647	1.1870	-0.0437	1.3770	0.1463	1.2883	0.0577
	17	QNT	O8CDF	12346789-O...	1.1547	0.0797	6.9	OK(10)	1.3249	0.1702	1.1142	-0.0405	1.1404	-0.0143	1.1495	-0.0052	1.1950	0.0403

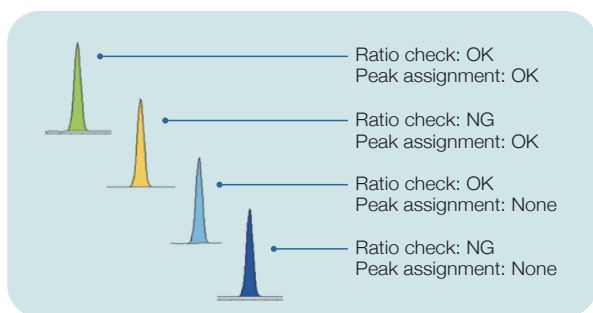
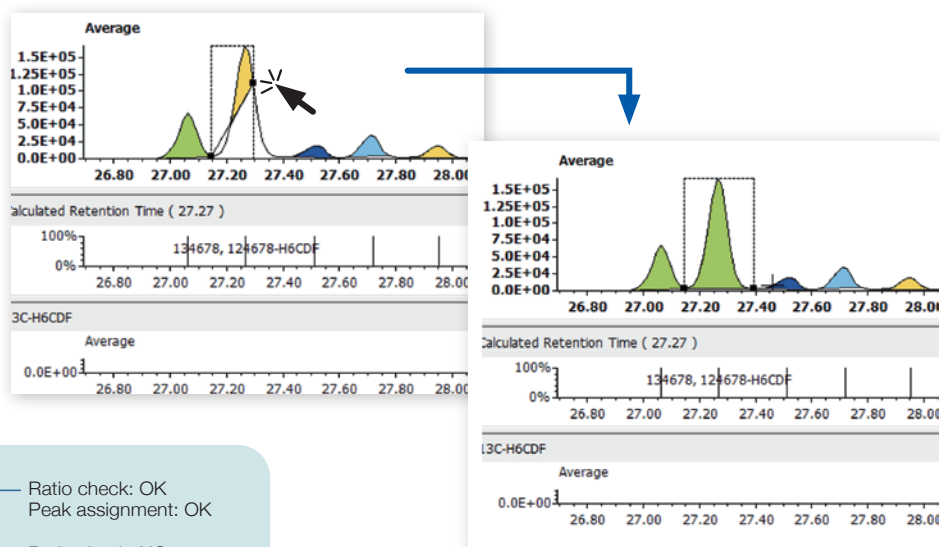
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Close

■ Easy manual integration and Judgment for each peak

The manual operation for setting peak baselines is the same as that of DioK. This makes it easy to identify each peak, and the coloring function allows the user to check the judgment status of that peak.



■ Possible to display native compounds and ¹³C-labeled compounds in the same window

In the "Three Layer Chromatogram Window", you can check the peak assignment status while comparing the measured chromatogram of the native compound, the corrected retention time order of each isomer in calculated retention time window, and the measured chromatogram of the ¹³C labeled internal standard substance.

■ Capable of exporting all values required for quantitative analysis as a CSV file

TQ-DioK can automatically calculate the values required for quantitative analysis and validation of 2,3,7,8-substituted dioxins/furans as well as non-2,3,7,8-substituted dioxins/furans.

All quantitative values, areas, S/N, RSD, etc. can be exported as a CSV file. The contents of this CSV file are compatible with those exported by DioK.

No.	Compound name	Group name	Retention time measured[Ave/Sum]	Height[Ave/Sum]	S/N (RMS)[Ave/Sum]	Area[Ave/Sum]	IQ ratio 1 (measured)	IQ1 Ratio OK
1	1368-T4CDD	T4CDD	19.16	561440.7	269363.8	5565417	0.97	OK
2	1379-T4CDD	T4CDD	19.36	142995.3	68709.2	1424635	1.03	OK
3	1369-T4CDD	T4CDD	19.57	12379.0	5948.1	122928	1.01	OK
4	1247, 1248, 137...	T4CDD	20.14	36475.3	17526.4	375565	1.06	OK
5	1246, 1249-T4CDD	T4CDD	20.27	36759.4	17662.9	396006	1.03	OK
6	1268-T4CDD	T4CDD	20.37	13584.4	6204.5	124382	1.02	OK
7	1478-T4CDD	T4CDD	20.50	1385.7	377.8	7884	0.94	OK
8	1279-T4CDD	T4CDD	20.65	16453.7	2068.1	171035	0.97	OK
9	1234, 1236, 126...	T4CDD	20.88	9519.2	1196.5	94970	1.00	OK
10	1237, 1238-T4CDD	T4CDD	21.13	34726.4	4364.7	432054	1.03	OK
11	2378-T4CDD	T4CDD	21.31	6319.8	31.5	70052	0.90	OK
12	1239-T4CDD	T4CDD	21.56	5426.6	824.7	70774	0.92	OK
13	1278-T4CDD	T4CDD	21.62	2692.0	409.1	13488	0.60	NG

JMS-TQ4000GC: High-throughput Triple QMS

SRM method for Dioxins

JEOL provides a measurement method that allows you to quickly prepare for measurements.

High sensitivity

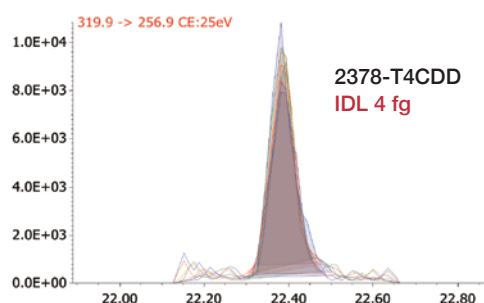
It has sufficient sensitivity for analysis of Dioxins.

High robustness

It is highly durable and provides stable measurement over a long period.

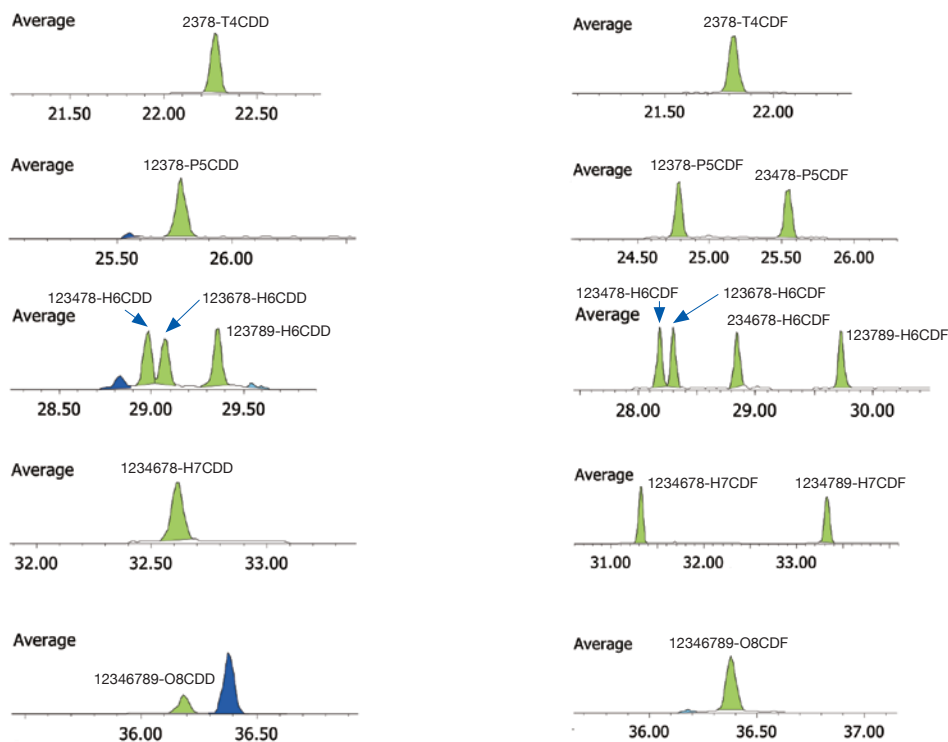
Easy maintenance

No tools are required to remove or insert the ion source chamber.



PCDDs / PCDFs

(T4-H7: 0.025 pg/μL, O8: 0.05 pg/μL)



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