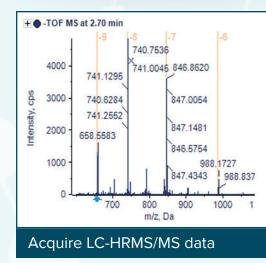


Achieve better insights on biotransformation and impurities



Accurate and flexible workflow





Report	Peak ID	Name	Formula	Neutral Mass	Average Mass	m/z	Charge
	M16-3	5'(n-2) [M-6H]6-	C208H301N56O113P15S15	6335.13	6339.30	1054.8474	-6
	M27-3	Desulfurization [M-7H]7-	C234H340N61O129P17S16	7106.29	7110.98	1014.1770	-7
	M4-3	5'(n-3) [M-6H]6-	C195H283N51O107P14S14	5932.08	5935.87	987.6720	-6
	M16-2	5'(n-2) [M-7H]7-	C208H301N56O113P15S15	6335.14	6339.22	904.0120	.7
		Parent [M-8H]8-	C234H340N61O128P17S17	7122.29	7126.95	889.2784	-8
	M23-1	Di-Desulfurization [M-8H]8-	C234H340N61O130P17S15	7090.32	7095.05	885.2822	-8
		Parent [M-9H]9-	C234H340N61O128P17S17	7122.29	7127.13	790.3580	-9
	M29	5'(n-3) [M-8H]8-	C195H283N51O107P14S14	5932.07	5935.85	740.5014	-8
	M27-1	Desulfurization [M-10H]10-	C234H340N61O129P17S16	7106.30	7110.96	709.6230	-10
0	M16	5'(n-2) [M-9H]9-	C208H301N56O113P15S15	6335.15	6339.20	702.8984	-9
I 🗌	M4	5'(n-3) [M-9H]9-	C195H283N51O107P14S14	5932.08	5935.89	658.1124	-9
2	M16-1	5'(n-2) [M-10H]10-	C208H301N56O113P15S15	6335.13	6339.21	632.5059	-10
3	M27	Desulfurization [M-9H]9-	C234H340N61O129P17S16	7106.31	7110.84	788.5831	-9
•		Parent [M-7H]7-	C234H340N61O128P17S17	7122.29	7127.02	1016.4631	-7
5		Parent [M-9H]9-	C234H340N61O128P17S17	7122.31	7127.07	790.3601	-9
6		Parent [M-8H]8-	C234H340N61O128P17S17	7122.27	7126.99	889.2770	-8

Identify potential metabolite based on TOF-MS

7	Groups	of 27 Potential	Metabolite Peak	Analog	g Integratio	
	Group ID	Name	Formula	Neutral Mass	Charge	
1	G1	Parent	C234H340N61O128P17S17	7122.30	From -6 To -10	
2	G2	Desulfurization	C234H340N61O129P17S16	7106.31	From -6 To -10	
3	G3	5'(n-1)	C221H321N59O120P16S16	6728.21	From -6 To -10	
4	G4	5'(n-3)	C195H283N51O107P14S14	5932.08	From -6 To -9	
5	G5	5'(n-2)	C208H301N56O113P15S15	6335.14	From -6 To -10	
6	G6	5'(n-3)+Desulfurization	C195H283N51O108P14S13	5916.07	From -7 To -8	
7	G7	5'(n-1)+Desulfurization	C221H321N59O121P16S15	6712.19	From -8 To -9	

Group charge states for relative quantification

						_
-1	TOF MS	S/MS of	658.	1, b	ackgr	oun
Intensity, cps	4000 - 3000 - 2000 -	150.041 206.9		356	392.0 401.56 .9736 : .0852	28 x

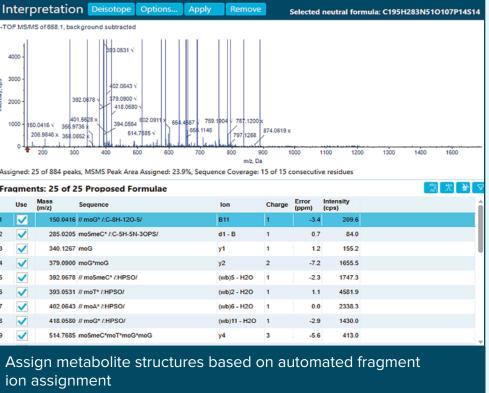
Interpretation

200

Fragments: 25 of 25 Proposed Formulae

	Use	Mass (m/z)	Seque
1	\checkmark	150.0416	// moG
2	✓	285.0205	mo5m
3	\checkmark	340.1267	moG
4	\checkmark	379.0900	moG*r
5	\checkmark	392.0678	// mo5
6	<	393.0531	// moT
7	\checkmark	402.0643	// moA
8	\checkmark	418.0580	// moG
9	\checkmark	514.7685	mo5m
	Assi	gn me	tak

Molecule Profiler software delivers highly accurate and flexible workflows for determining impurities and biotransformations for a wide variety of therapeutic molecules.



Show: O Results O Interpretation

Formula

C194H247N70O120P19

C194H247N70O120P19

C194H247N70O120P19

C194H247N70O120P19

Group

Assigned Neutral Mass

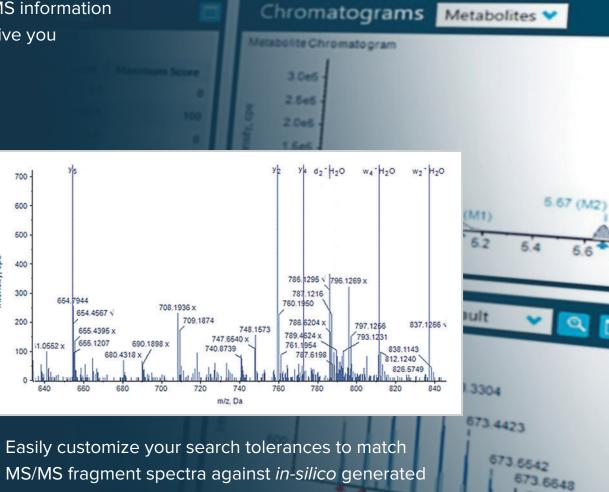
673.8849

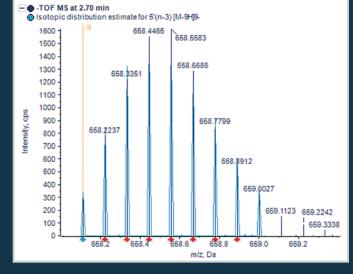
m/z. Da

Confidence through MS/MS

Many impurities and biotransformations result in isoelemental species that an MS-only workflow just cannot solve.

Molecule Profiler incorporates UV, MS and MS/MS information to provide clear and unambiguous results that give you complete confidence.



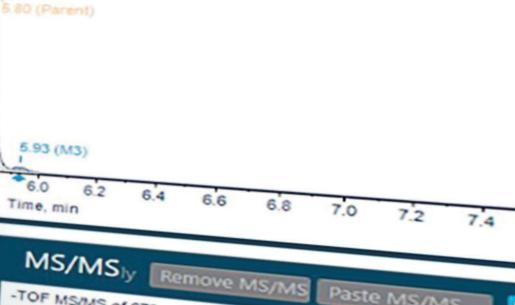


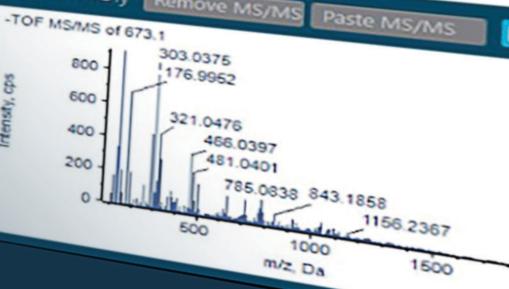
Use a variety of tools for identification at the MS level including mass accuracy and isotope ratio matching.

MS/MS fragment spectra against *in-silico* generated full-length, impurity or metabolite spectra.

	Assign ID	Add	MS/MS.	. Analog	ntegrat	10
			And the second se	Peak Index	the second s	R.T.
	Average Mass 6067.58	1009.8293	-6	2	-3.3	
6065.02			-8	2	-2.4	
6065.02	6067.59	757.1208	-0			
6065.03	6067.62	672.8847	-9	2	-1.9	
6065.04	6067.65	605.4966	-10	2	0.0	
						Þ

Show controls





C	Confider	nce thr	ough	NS	/MS	5	Formula C194H247N70O120P19 C194H247N70O120P19 C194H247N70O120P19	Assigned	Neutra
Р	Potential Metabolites: 16 of 16	peaks		Update Tab	le Update Results a	and Close Cancel	Interpretation Deisotope	Options Apply	Remove
24 25 26 27 28 29 30 31 32 33 33	5 Parent [M-10H] 10- 6 Parent [M-3H] 3- 9 Parent [M-6H] 6- 6 Parent [M-8H] 8- 9 Parent [M-5H] 5- 9 Parent [M-4H] 4- 9 Parent [M-7H] 7- 10 S'(n+dA) [M-4H] 4- 11 S'(n+dA) [M-3H] 3-	C194H247N700 672.8847 C194H247N700 605.4966 C194H247N700 2020.6551 C194H247N700 1009.8293 C194H247N700 1009.8293 C194H247N700 757.1208 C194H247N700 1515.2426 C194H247N700 1515.2426 C194H247N700 865.4217 C204H259N750 1593.5116 C204H259N750 2125.0185	5 0.0 5.80 2.03E+ 1 -8.6 5.79 2.23E+ 3 -3.3 5.80 6.55E+ 8 -2.4 5.80 1.11E+ 4 -5.1 5.79 1.34E+ 5 -6.5 5.79 1.84E+ -5.9 5.80 5.26E+ 3 -3.3 5.93 1.14E+ 5 -3.1 5.93 1.90E+	05 14.68 66.7 05 16.14 100.0 04 4.74 66.7 05 8.04 100.0 05 9.68 100.0 05 9.68 100.0 05 13.35 100.0 04 3.81 100.0 04 3.81 100.0 04 3.81 100.0 04 3.81 100.0	9 03E+03 7 96E+03 8 75E+03 2 57E+03 4 36E+03 5 25E+03 7 24E+03 2 07E+03 5 55E+03	7.93 6.99 7.69 2.26 3.83 4.61 6.36 1.81 4.87	-TOF MS/MS of 790.4, background subt 10000 8000 8000 540.7475 548.5787 54 2000 10000 540.7475 548.5787 54 540.545 55 Assigned: 47 of 3094 peaks, MSMS P	555.1322 55.8878 2.0940 555.64014 559.0400 559.0400 559.0400 559.0400 559.0400 559.0400	568.1233 570.8810 555 570 n/z, Da
	hromatograms alog Sample,20201126_IDA_Impurity_10pc Spike_0	1.wiff,10% Spike - IDATop 3 35eV - XA1 19	Show controls	Baseline Subtract	R.T. Offset: 0	Coptions	Fragments: 47 of 47 Propos	ed Formulae	
Intensity			5.75 (Parent)		0 <u>1</u>	12	Use Mass (m/z) Sequence 6 ✓ 418.0582 // moG* /:HP. 3 ✓ 392.0696 // moSmeC* // 5 ✓ 402.0652 // moA* /:HP. 4 ✓ 393.0546 // moT* /:HP. 37 ✓ 1011.3764 moT*moSme 11 ✓ 565.1284 moT*moSme	(wb)2 - H2O 1 (wb)3 - H2O 1 (wb)5 - H2O 1 (wb)5 - H2O 1 (wb)5 - H2O 5 (wb)5 - H2O 1	rge Error (ppm) Inte (ppm) -2.3 2.3 2.3 4.9 -5.5 3.9
sity, cps SI	S Sample, Sum XIC of M0 (from 672.8629 to 672.907) 764 664 564 464	8), M+1 (from 672.9740 to 673.0189), M+2 (f	(fro3 (from 673.1962 to 673.24 6.80 (Parent)	1), M+4 (from 673.3073 to (573.3522), M+5 (from 6	73.4184 to 673.4633)	16 ✓ 680.1348 moT*mo5me 33 ✓ 940.6926 moT*mo5me 12 ✓ 584.1126 moT*mo5me 40 ✓ 1137.7234 moT*mo5me	a5 2 a5 - B 3	2.3 -8.4 1.5 -6.2
Intens	3e4 2e4 1e4 0e0 1 2	3 4 5	6 7 8 Time, min	9 1	0 11	12	40 ✓ 1137.7234 mo1*mo5me 30 ✓ 889.4973 moT*mo5me 20 ✓ 765.1454 moT*mo5me 38 ✓ 1020.5254 moT*mo5me	a7 3 a8 4	-6.2 -8.2 -0.2 -4.4

Molecule Profiler software gives you the flexibility to incorporate UV, MS or MS/MS data into your interrogation of metabolites or impurities.

detailed information on your fragment ion spectra.

miz, Da

3.6648

673 8849

6065.02

6065.02

6065.03

570.8816

Intensity

2.3 16752.6 4.9 35979.8

6491.5

8596.2

497.8

197.9

354.5

1497.0

858.2

528.5

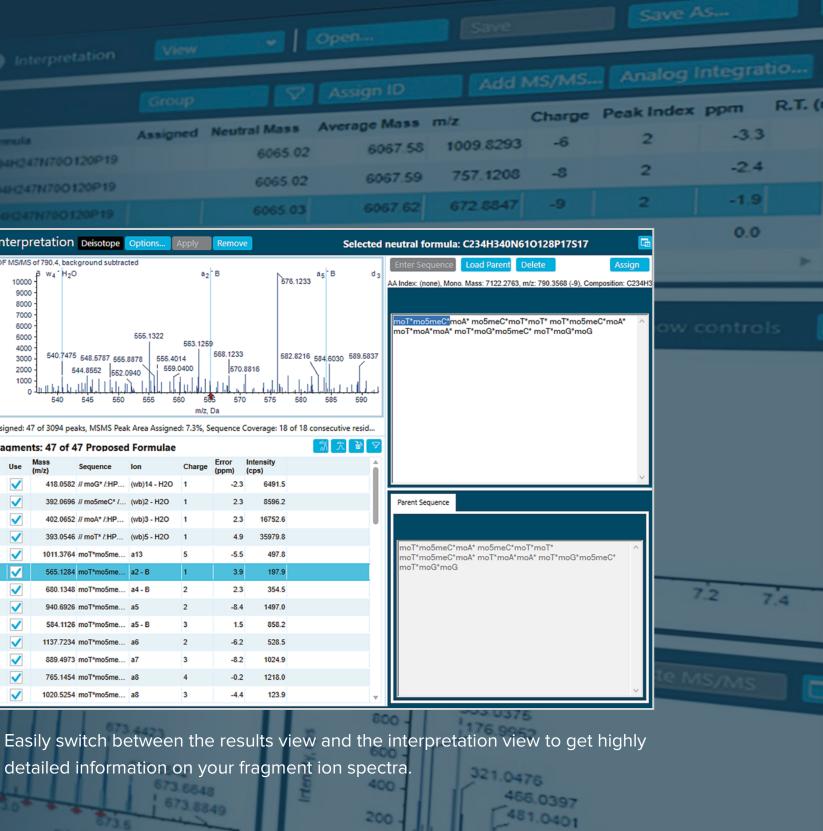
1024.9

1218.0

123.9

(cps)

Con

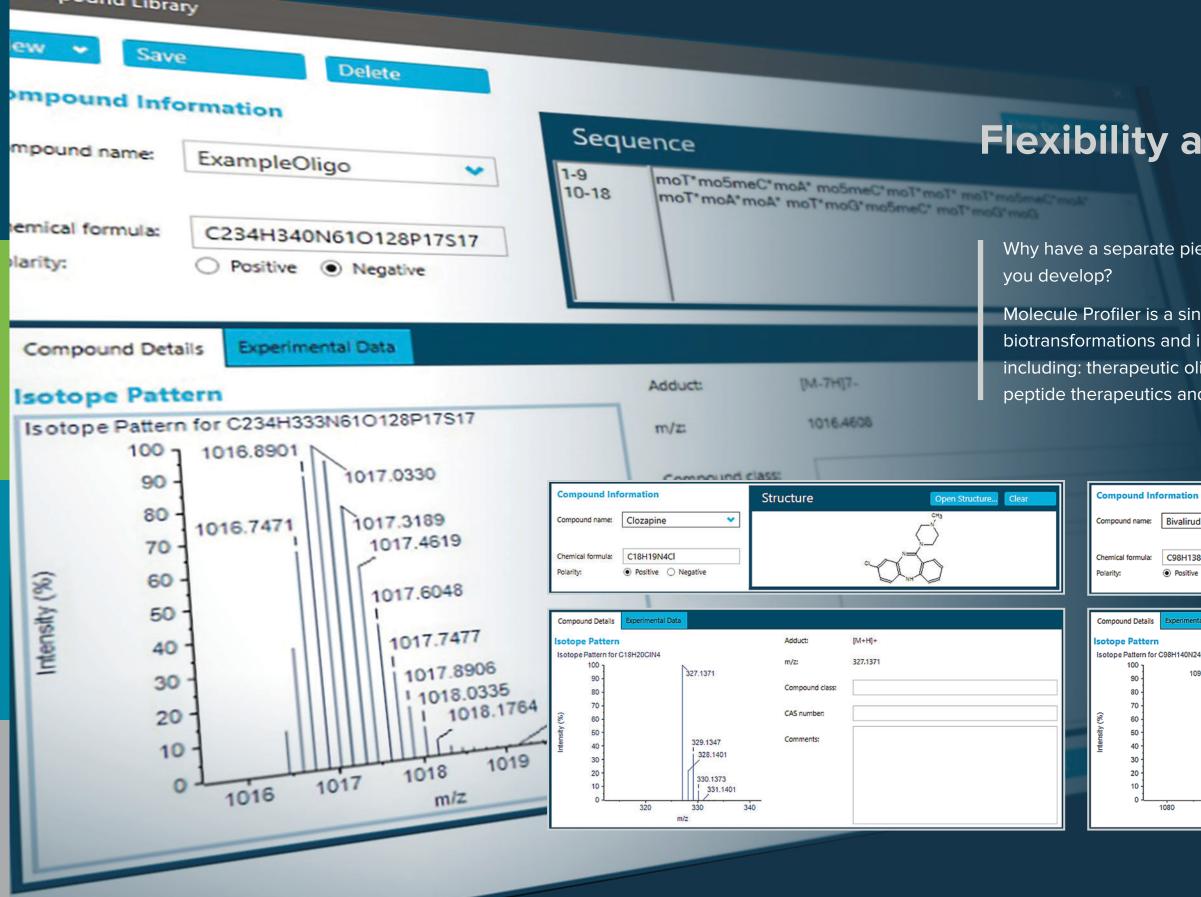


785.0838 843.1858 1000

m/z. Da

1500

1156 2367



Flexibility across molecule types

Why have a separate piece of software for every type of molecule

- Molecule Profiler is a single software to provide insights about
- biotransformations and impurities across molecular classes
- including: therapeutic oligonucleotides, small molecule drugs,
- peptide therapeutics and even antibody-drug conjugates.

n S	equence	
Idin ✔ 1-21 38N24O33 re ○ Negative) FPRPGGGGN	G DFEEIPEEYL
ntal Data		
24O33 090.5002 1091.0016 1091.5030 1092.0044 1092.5057 1093.0070 1101.0256 1090 1100 m/z	Adduct: m/z: Compound class: CAS number: Comments:	[M+2H]2+ 1090.5002

detabolites

ple/Controls	
MS Sample:	Entre Contraction of the
MyOligo Biotrans t=0	X Sample Default Predicted_a Get to an a
MS Sample:	
MyOligo Biotrans t=5	X Sample X Controls Predicted_a
MS Sample:	X Sample Larger and more comple
MyOligo Biotrans t=10	Controls
MS Sample:	X Sample Default Predicted a The powerful MS/MS en the time to an answer free
MyOligo Biotrans t=15	X Controls
MS Sample:	X Sample Default V Predicted a. V D Easily build processing of
MyOligo Biotrans t=20	Controls multiple processing met analysis can be complet
MS Sample:	X Sample Default Y Predicted_a Y
MyOligo Biotrans t=25	X Controls Predicted_a V
MS Sample:	X Sample Default
MyOligo Biotrans t=30	X Controls Predicted_a_ V D
MS Sample:	X Sample Default
MyOligo Biotrans t=35	Controls
	Sample Default
MS Sample:	Controls
MyOligo Biotrans t=40	
And Samples	

nswer, faster

ex therapeutics like oligonucleotides ice very complex MS/MS data.

ngine in Molecule Profiler can reduce om days down to hours.

queues with the ability to choose thods and controls. Each result ted in just a few minutes.

Integrated for ease

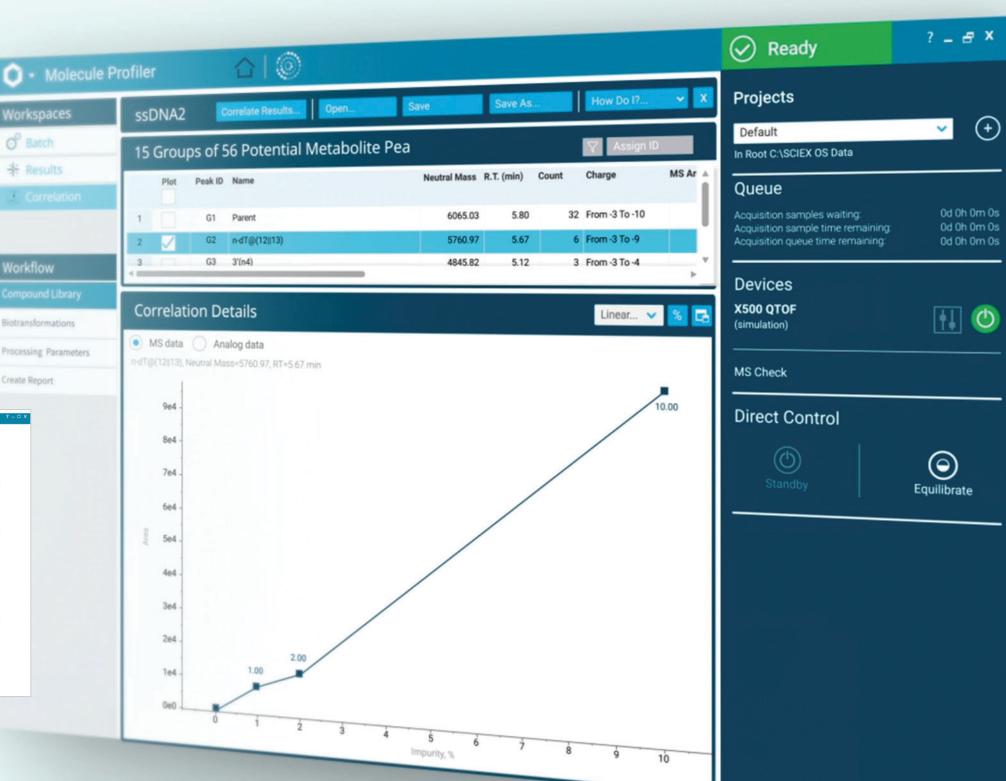
Having many different software products generally requires you to jump around from app to app.

Molecule Profiler is fully integrated as part of SCIEX OS, and has the same look and feel. Easily multitask with other functions in SCIEX OS. And, there is no need to move data around.

Molecule Profiler software is an application within SCIEX OS software. There is no need to move data files around since all acquired data are easily accessible within the SCIEX OS framework between different applications. It is also easy to navigate between the impurity and metabolite discovery functions of Molecule Profiler to the highly customizable

quantitative workflows of Analytics.

A 🕢 Ready SCIEX OS Acquisition Management Configuratio Â Library Batch Queue Explorer LC Method Analytics Event Log Audit Trail MS Tune Molecule Profiler MS Method



Complete coverage

Oligonucleotides, peptides and small molecules can have an enormous number of impurities and biotransformations.

Molecule Profiler has off-the-shelf libraries for oligonucleotides, peptides and small molecules with thousands of entries targeted to your molecule type.

SCIEX has also worked with our partners at IDT to create a comprehensive library especially for oligonucleotides. You can even create and edit your own biotransformation libraries.

You can customize the peak finding algorithm and library search algorithms to optimize your search for a particular molecule or molecule class.

mation origid INIGEO128F1 INIGEO128F1	1-12 13-18	moT*mo5meC*moA* moT*moG*mo5meC*	mo5meC*moT*moT* moT*moG*moG	*moT*mo5meC*moA* moT*moA*moA
tegy		pecific Parameters		
	Biotransformations Chromatogr		MS/MS Parameters	Confirmation Scoring
	Use this set: Oligonucleotide Con Biotransformations selected: 83 Name	prehensive		
	Loss of G + S to O		Mass Shift	Description
	Loss of G		-1	67.0266 -Guanine -H2O+ S to O
	Loss of A + S to O		-1	51.0494 -Guanine -H2O
6 14	Depunnation of G +S to O Loss of T + S to O		-1	51.0317 -Adening -H2O
	Loss of 5-Methylcytosine + S to O		-1-	51.0317 -Adenine - H2O + S to O 49.0160 -Guanine +S to O
	A MA		-14	42.0202 Thumas
	Depurination of G		-14	42.0202 -Thymine -H2O + S to O
	Depurination of A +S to O			41.0361 -SMeCytosine -H2O + S to O 35.0545 -Adenine -H2O
	costs of U + S to O		-13	33.0388 P. Con
	Loss of C + S to O Loss of T		-13	33.0388 R-C5N5OH4 to R-OH
			-12	27.0205 -Cytosine -H2O + S to O 26.0430 -Thymine -H2O













ZenoTOF 7600 system

This mass spectrometer gives richer, more comprehensive data with new innovations that have never been seen in an accurate mass system. EAD fragmentation and the Zeno trap pave the way for precise and accurate MS and MS/MS data.

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This high-performance accurate mass solution offers a combination of qualitative and quantitative analysis and advanced workflow capabilities. Optimized for large-scale quantitative mass spectrometry, the TripleTOF 6600+ system offers sensitive and robust performance.



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