

USER GUIDE

Can You Complete An Amino Acid Analysis In **15:00 Minutes**? ...now you can!



Amino acid analysis kits for:

- Sample Prep
- Derivatization
- GC or LC Analysis



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Amino Acid Sample Prep and Analysis in 15 Minutes

guarantee



Evaluate an EZ:faast kit in your lab for 30 days. If you are not completely satisfied with the performance, return it for a full refund.

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EZ:faast kits provide reagents and supplies for sample preparation, derivatization and GC/FID, GC/NPD, GC/MS and LC/MS analysis of over 50 amino acids and di-peptides in complex matrices and protein hydrolysates. Additionally the EZ:faast method offers:

- A standard 8 minute procedure for sample preparation and derivatization
- Elimination of labor-intensive protein and urea removal procedures
- Excellent method reproducibility (RSD <1%) and quantitation down to 1nmol/mL

Established methods for amino acid analysis in serum, urine, beer, wine, feeds, fermentation broths, foodstuffs and protein hydrolysates



Obstacles in Current Amino Acid Protocols

Ion-exchange chromatography using ninhydrin derivatization or reversed phase chromatography have traditionally been used on dedicated instruments for amino acid analysis. Current ion-exchange methods originated in the late 1940s and are known for lengthy 60-180 minute runtimes along with extensive sample preparation to remove interfering components (such as proteins or urea). Ion-exchange methods typically use expensive, dedicated instruments that are difficult to maintain and operate. Other methods, relying on reversed-phase HPLC, have been developed that can be run on any HPLC system saving the expense of purchasing and maintaining a dedicated amino acid analyzer. However, reversed phase HPLC methods can suffer from numerous deficiencies including: long analysis times, laborious sample preparation protocols, poor peak resolution, marginal quantification, and limited stability of derivatized amino acids. Laboratories needing a rapid and simple method to process high volumes of samples may find traditional amino acid analysis laborious and costly. EZ:faast Amino Acid analysis kits has been developed to overcome these obstacles with a simple kit containing reagents and supplies to perform sample preparation, derivatization and improved quantitation using any GC/FID, GC/NPD, or GC/MS system in 15 minutes or by LC/MS in 24 minutes.

Economical, Hassle-Free Amino Acid Analysis

Free (Physiological) Amino Acids

Free amino acids are routinely analyzed in physiological fluids, feeds, fermentation broths and other sources for basic research, nutritional labeling and more recently for patient diagnosis. Metabolic deficiencies are diagnosed based on the levels of particular amino acids in body fluids. While some protocols may provide adequate chromatographic methods and derivatization procedures, sample throughput remains slow due to lengthy sample cleanup and preparation requirements. Using the EZ:faast Free (Physiological) Amino Acid GC and LC/MS kits, sample preparation time is only 7 minutes regardless of sample matrix. Blood, plasma, urine, cerebral spinal fluid, wine or grain samples contain interfering proteins, urea and other impurities that can lead to poor chromatographic results. In 7 minutes, EZ:faast can remove interfering components leaving a highly pure and derivatized amino acid sample ready for injection. Analysis time is dramatically reduced and quantitation significantly improved over traditional methods; this makes for a rapid and sensitive method for any lab (Figure 1). For labs with a large number of samples, EZ:faast truly provides rapid throughput. Without the need for lengthy sample preparation, labor cost is dramatically decreased, making EZ:faast a much more economical method.

Protein and Peptide Hydrolysates

Numerous labs perform quality control assays of both natural and synthetic proteins and peptides by quantifying the hydrolyzed amino acid composition of their final protein product. Protein core labs will find the EZ:faast kits excellent for confirming protein identity and purity quickly. Using an EZ:faast GC kit, results are obtainable in about 15 minutes and in 24 minutes when using the EZ:faast LC/MS kit. For labs analyzing large number of samples the short analysis time dramatically increases productivity and reduces the cost of sample analysis.

Proteins are long linear strings of amino acids connected to each other by peptide bonds. Hydrolysis of the peptide bonds releases the individual amino acids. The EZ:faast system allows rapid purification and derivatization of the released amino acids. Composition and quantity of hydrolyzed amino acids can then be determined quickly and accurately (Figure 2). The overall system provides both a rapid and simple sample preparation and analysis procedure, and is amenable to limited automation. More samples can now be analyzed over a given amount of time for less money as labor cost is dramatically decreased by this simple and rapid procedure.

Figure 1

Free Amino Acid Standards Analyzed by EZ:Faast

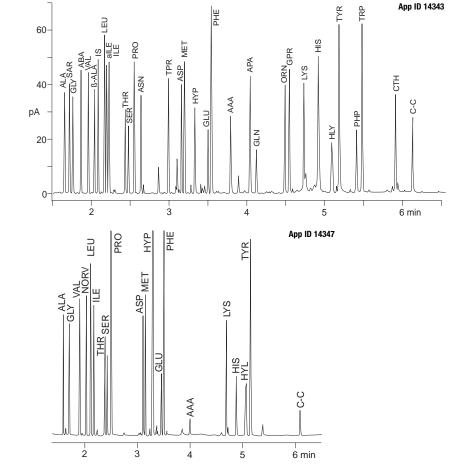


Figure 2

Protein Amino Acids Standards Analyzed by EZ:faast

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Table 1

Analyze Over 50 Amino Acids	Anal	yze	Over	50	Amino	Acid	S
------------------------------------	------	-----	-------------	----	-------	------	---

Allalyze V		U ACIUS	
Abbreviation	Alt. Abbreviation:	Chemical Name	SIM
ALA	A	Alanine	130, 70
SAR	SA	Sarcosine	130, 58
GLY	G	Glycine	116, 74
ABA	0	α -Aminobutyric acid	144, 102
VAL	V	Valine	158, 72
ß-ALA	•	ß-Alanine	217, 129, 116
ß-AIB	BAIBA	ß-Aminoisobutyric acid	172, 143, 84
ß-ABA	Brabra	ß-Amino-n-butyric acid	216, 172, 144
NORV		Norvaline	158, 72
LEU	L	Leucine	172, 86
ILE	-	Isoleucine	172, 130
alLE		Allo-Isoleucine	172, 130
pGLU		Pyroglutamic acid	84
HSER		Homoserine	101, 128, 143
NLE		Norleucine	172, 86
THR	Т	Threonine	160, 101
SER	S	Serine	146, 203
PRO	Р	Proline	156, 243
GABA		γ-Amino-n-butyric acid	130, 144, 17
ASN	Ν	Asparagine	155, 69
TPR		Thiaproline	174, 147
ASP	D	Aspartic acid	216, 130
MET	М	Methionine	203, 277
SME		Seleno-L-Methionine	230, 188, 142
HYP	OHPro	4-Hydroxyproline	172, 86
GLU	E	Glutamic acid	230, 170
PHE	F	Phenylalanine	206, 190
AAA		α-Aminoadipic acid	244, 98
CAD		Cadaverine (1,5 Diaminopentane)	116, 170, 215
CYS	С	Cysteine	248, 162, 206
PABA		4-Aminobenzoic acid	265, 206, 163
HCYS		Homocysteine	142, 203
APA		α-Aminopimelic acid	198, 258, 286
HA		Histamine	180, 168, 94
GLN	Q	Glutamine	84, 187
DABA		2,4-Diamino-n-butyric acid	203, 142, 245
GLY-GLY		Glycine-glycine (dipeptide)	117, 144, 201
ORN	0	Ornithine	156, 70
GPR		Glycine-proline (dipeptide)	70, 300
LYS	К	Lysine	170, 128
THR-ASP		Threonine-aspartic acid (dipeptide)	218, 360, 130
HIS	H	Histidine	282, 168
HLY	OHLys	Hydroxylysine (2 isomers)	129, 169
TYR	Y	Tyrosine	206, 107
DAP		Diaminopimelic acid	256, 168, 196
PHP		Proline-hydroxyproline (dipeptide)	156, 114
TRP	W	Tryptophan	130
LYS-ALA		Lysine-alanine (dipeptide)	170, 224, 153
DA		Dopamine	179, 136, 123
CTH		Cystathionine	203, 272
DOPA C-C	(Cys)2	3,4-Dihydroxyphenylalanine	222, 123
		Cystine	248, 216
HC-HC ARG-SUC	(Hcys)2	Homocystine	230, 188, 128
		Arginino-succinic acid	441, 326
Et(OH)NH2		Ethanolamine	116, 117
ETH SRO		Ethionine	203, 291, 143
SKU		Serotonin	146, 159, 232

50 Amino Acids & Related Compounds Quantified in 15 Minutes

The EZ:faast method is currently designed to analyze over 50 amino acids and related compounds (Table 1). All peaks can be accurately and reproducibly quantified. Additional amino acids can be analyzed with little to no modification of the standard methodology. Please contact Phenomenex for additional amino acids analyzed using the EZ:faast method.

Additional Amino Acids analyzed by the EZ:faast LC/MS kit

Abbreviation	Alt. Abbreviation:	Chemical Name	SIM
ARG		Arginine	303
CIT		Citrulline	287
1MHIS		1-Methyl-histidine	298
3MHIS		3-Methyl-histidine	298



Steps N

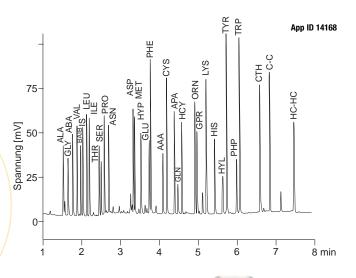
Colors added for illustration purposes only.



Step 1. 0 min Pipette sample and combine internal standard (yellow). S T E P 00:01:00

Step 2. 1 min Pipette sample through SPE sorbent tip. Advantage: No lengthy protein or urea removal.

8 Simple Steps



00:15:00

Step 8. 15 min Analyze the chromatogram Advantage: Full resolution of over 50 amino acids and related compounds in a 7 minute GC run.

* 15 minute sample prep and analysis time applies to GC kits only. Sample prep and analysis time by LC/MS is 24 minutes.

> **Step 7.** 7 min Sample preparation complete – inject onto GC/FID, GC/NPD or GC/MS system. Advantage: Very stable derivatized sample reduces losses due to degradation.

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Step 3. 2 min Draw wash solution (blue) through SPE sorbent tip. Advantage: Outstanding sample purity for less contamination and better quantitation.

in 15 Minutes!

The EZ:faast procedure's greatest benefit is the rapid sample preparation and derivatization method. For complex matrices like plasma, urine, fermentation broths or feeds this procedure can provide results equal to traditional protein and urea removal methods in less time. Even for relatively clean samples like protein hydrolysates, this method shows improvement in quantitation due to cleaner samples and more stable amino acid derivatives. Shorter sample preparation times cut labor time and cost, making this a highly cost effective assay for amino acid analysis (less than \$4 a sample). Below is a simplified diagram illustrating each of the major steps within the EZ:faast protocol.

Step 4. 3 min

S T E P

Expel amino acids (blue) with SPE sorbent from tip with Eluting Medium (clear). Advantage: Almost no loss of amino acids.

00:04:00

Add organic derivatizing reagent (orange). Advantage: Derivatization is complete in 1 min and can be done in aqueous phase.

Step 5. 4 min



Step 6. 6 min

Extract amino acid derivatives from aqueous layer (light green) into organic layer (orange). Advantage: Additional purification step. thethod

8 minutes of Sample Prep

No Protein or Urea Removal Required

The analysis of free amino acids in physiological fluids, grains, fermentation broths and other complex matrices differs from the analysis of protein hydrolysates due to the high concentration of interfering compounds. A relatively large amount of proteins, peptides, urea and other matrix components have to be removed prior to free amino acid analysis by GC or HPLC, otherwise columns deteriorate rapidly, quantitation is poor, and analysis results are not reproducible. Current procedures for de-proteinization and urea removal are labor intensive and recoveries are low for some amino acids. Also, reagents used for de-proteinization can interfere in the amino acid profile. The EZ:faast method, however, does not require traditional de-proteinization or urea removal methods to be followed; proteins are excluded from the sample as it is passes through an SPE sorbent tip. The SPE sorbent binds amino acids while proteins and urea are washed away leaving only the free amino acids. A comparison of the EZ:faast method to other common de-proteinization methods shows as good or better results using the EZ:faast method.

EZ:faast translates into major cost and time savings. Hydrolyzed protein samples are often in a clean sample matrix. Hydrolysis under strong acidic conditions at elevated temperatures causes proteins and peptides to breakdown into their component amino acids. Other components like hydrolyzed carbohydrates and lipids, are excluded from the sample as it passes through the SPE sorbent tip. With purer samples and better derivative stability – quantitation and method reproducibility can be improved.

Table 2: Data representing a series of comparative tests on the same plasma sample with and without protein removal; analysis of all samples was performed using the EZ:faast kit. The data represents the calculated amino acid concentration in μ mol/L after the sample has undergone three common de-proteinization procedures (SSA = sulfosalicylic acid; TCA = trichloroacetic acid; ORG = acetonitrile:ethanol 2:1) compared to the EZ:faast procedure. The comparative data (mean values for 12 measurements) is presented in the table below. Results for amino acid content show no significant difference between samples with or without protein removal.

Table 2

	Without De-proteinization (Standard EZ:faast method)	SSA (Recommended for OPA derivatized samples)	ТСА	ORG (Recommended for PITC derivatized samples)
Procedure Time	: 7 minutes	≥3 hours	≥3 hours	≥3 hours
GLY	290 (286-293)	288 (282-293)	259 (238-280)	261 (251-270)
ALA	421 (415-427)	422 (417-427)	380 (357-402)	393 (365-421)
ABA	23 (22-24)	23 (20-26)	22 (21-22)	22 (21-23)
LEU	165 (162-168)	164 (162-166)	162 (158-165)	163 (155-170)
ILE	74 (72-75)	70 (69-72)	71 (69-72)	73 (72-73)
MET	30 (29-30)	32 (31-33)	31 (30-31)	30 (29-30
PRO	209 (207-211)	207 (204-210)	212 (208-215)	206 (197-214)
ASP	18 (17-19)	16 (15-17)	16 (14-17)	19 (18-20)
GLU	40 (38-41)	35 (25-44)	35 (29-40)	35 (30-39)
THR	176 (170-181)	166 (161-171)	153 (145-161)	177 (168-186)
SER	142 (136-147)	133 (129-136)	129 (121-137)	136 (122-150)
НҮР	14 (13-14)	12 (11-12)	13 (12-13)	
ASN	34 (32-35)	34 (33-35)	31 (27-34)	31 (28-33)
GLN	540 (495-584)	588 (561-615)	553 (514-592)	569 (554-584)
C-C	41 (39-42)	41 (39-42)	45 (41-49)	30 (21-39)
PHE	58 (56-60)	58 (56-59)	63 (59-67)	60 (57-63)
TYR	62 (59-64)	62 (58-66)	63 (59-66)	60 (57-63)
TRP	48 (46-49)	44 (41-47)	45 (42-48)	50 (43-56)
ORN	60 (58-61)	68 (62-73)	64 (60-67)	46 (43-49)
LYS	179 (172-185)	200 (178-222)	184 (162-205)	118 (108-127)
HIS	84 (78-89)	89 (82-96)	90 (85-95)	82 (73-91)



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Derivatization Simplified

After the very short sample cleanup procedure, the amino acids are quickly derivatized at room temperature with the addition of two reagents. The proprietary reagents modify both the carboxyl and amino groups of the amino acids forming derivatives stable at room temperature for several hours and stable at 4°C for several days. With good derivative stability, amino acid quantitation is more accurate and reliable; almost no amino acid sample is lost in sample preparation or through sample degradation. Reagents and supplies for sample preparation allow for the analysis of 384 samples per kit. Reagents, when stored according to label directions, are guaranteed for up to 12 months.

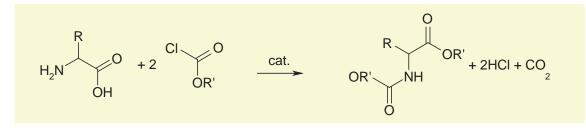
Rapid Chromatographic Analysis

Traditional ion exchange and reversed phase methods for the analysis of amino acids utilize long 45-180 minute runtimes. The EZ:faast method takes advantage of the fast separation capability and high resolution of GC/FID, GC/NPD, GC/MS to analyze over 50 amino acids in about 8 minutes. The LC/MS chromatographic runtime is a quick 12 minutes. High column efficiencies and resolution provides complete baseline separation for easy quantitation. Interfering compounds such as drug metabolites, proteins and urea that can be present in the sample matrix have been removed during sample preparation. With traditional methods, a large number of potential interfering compounds, like drugs and drug metabolites may co-migrate with amino acids thus affecting quatitation.

The high resolution GC method also allows for additional rare amino acids not listed in Table 1 to be analyzed without compromising throughput or resolution of other amino acids. In traditional HPLC based methods, rare amino acids may be analyzed but often results in a substantial increase of the analysis times – this is not the case with EZ:faast. The GC protocol allows for adjustments in carrier gas flow, oven temperature and the temperature gradient to ensure for the analysis of additional amino acids with a minor increase to the very short analysis time. High separation power and speed of the GC protocol also ensures method flexibility for the rapid analysis of additional amino acids with only slight (<5 min) increases in runtime.



Figure 3 Simplified diagram illustrating EZ:faast derivatization reactions





quantitation

EZ:faast kits provide reliable and accurate quantitation of over 50 fully baseline resolved amino acids. The lower limit of detection for EZ:faast is 1 nmol/mL and the precision in quantitation is <10% for most amino acids (a few amino acids show precisions in quantitation of +/- 15%). Sample loss and method precision is illustrated in the comparison of 5 injections of free amino acids extracted from plasma by a traditional ion exchange (IEX) method run on a dedicated amino acid analyzer and by the EZ:faast method (Table 3). EZ:faast provides improved quantitation due to several factors. Both sensitivity and reproducibility are improved with EZ:faast. Full baseline resolution accounts for some of the improvement, and the sample preparation procedure insures nearly all interfering compounds are removed without sacrificing amino acid recovery. Once derivatized, amino acids are stable for several hours at room temperature and for several days if refrigerated, preventing sample loss by degradation.

Table 3. Comparative data for the analysis of plasma free amino acids by ion exchange chromatography (on a dedicated amino acid analyzer with ninhydrin detection), and by GC/FID (EZ:faast). Concentrations are given in nmol/mL (statistical evaluation by Horn). P_L stands for mean, L_L is lower limit; L_U is upper limit; IEX is ion exchange chromatography.

Table 3

	GLY	ALA	ABA	VAL	LEU	ILE	MET	PRO
	IEX EZ:faast	IEX EZ:faast	IEX EZ:faast	IEX EZ:faast	IEX EZ:faast	IEX EZ:faast	IEX EZ:faast	IEX EZ:faast
PL	270.0 230.5	530.5 471.5	29.0 20.0	316.5 281.5	167.5 152.5	77.5 75.5	44.5 39.0	197.0 165.0
L	265.8 194.9	515.8 406.6	24.8 7.4	272.5 254.3	119.3 104.3	54.5 44.1	38.2 30.6	37.9 160.8
LU	274.2 266.1	545.2 536.4	33.2 32.6	360.5 308.7	215.7 200.7	100.5 106.9	50.8 47.4	356.1 169.2
	297 222	645 453	28 17	330 275	156 132	62 67	41 37	235 164
	270 264	529 487	32 16	307 315	224 173	72 87	46 43	241 186
	271 218	534 456	25 23	327 288	159 164	81 83	47 39	159 166
	257 239	511 505	30 19	288 280	151 141	83 70	43 41	151 164
	269 235	527 468	30 23	306 270	179 143	90 68	44 31	228 165

	THR	SER	ASP	GLU	GLN	C-C	PHE	TYR
	IEX EZ:faast							
PL	175.0 163.5	117.5 91.0	33.5 17.0	147.5 142.0	622.5 575.0	28.0 23.5	76.5 74.0	82 97.5
L	145.7 136.3	94.5 70.1	10.5 4.4	91.0 116.9	566.0 453.5	23.8 17.2	61.8 69.8	104.0 82.8
LU	204.3 190.7	140.5 111.9	56.5 29.6	204.0 167.1	679.0 696.5	32.2 29.8	91.2 78.2	91.4 112.2
	209 146	123 81	43 14	114 136	739 493	44 23	84 83	82 94
	179 165	119 107	35 14	163 128	636 563	29 25	73 74	107 101
	182 170	123 96	39 24	161 148	636 604	21 31	76 73	106 107
	168 157	112 86	28 18	152 137	609 546	27 22	80 66	108 91
	159 179	99 94	19 20	134 157	596 624	27 20	66 75	101 96

	TRP		OF	RN	L	/S	H	IS
	IEX	EZ:faast	IEX E	Z:faast	IEX	EZ:faast	IEX E	Z:faast
PL	-	57.5	87.0	58.0	185.0	153.5	118.0	106.0
L	-	34.5	74.4	37.1	159.0	130.5	270.0	59.9
LU	-	80.5	99.6	78.9	210.0	176.5	270.0	152.1
		63	81	53	198.0	159	114	92
		52	89	78	182.0	167	122	118
		57	100	57	191.0	158	127	112
		67	84	51	170.0	144	114	95
		41	90	63	179.0	148	115	117

Accuracy and Precision

Detection Limit	1nmol/mL by GC/FID
	1nmol/mL by GC/MS
Precision in Quantitation, %RSD	+/-15% (<10% for most amino acids)
Reproducibility of Retention Time, % RSD	<1%

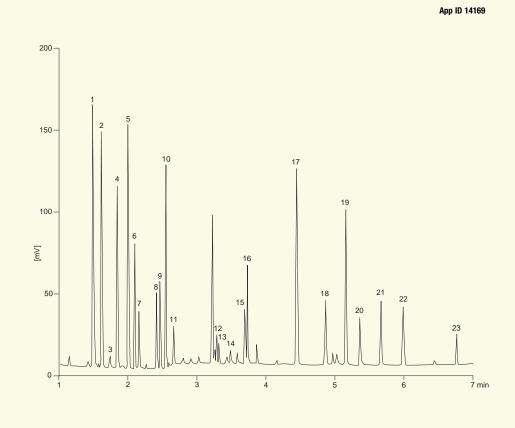
Sample:

Derivatized amino acids in human serum (0.1mL), Norvaline is the internal standard added at a concentration of 200 µmol/L

- 1. Alanine 9. Serine 2. Glycine 10. Proline 3. α -Aminobutyric acid 11. Asparagine Aspartic Acid 4. Valine 12. 5. Norvaline (IS) 13. 6. Leucine 14. 7. Isoleucine 15. Glutamic Acid 8. Threonine 16. Phenylalanine
 - Methionine 4-Hydroxyproline
- 17. Glutamine
- 18. Ornithine
- 19. Lysine
 - 20. Histidine
 - 21. Tyrosine
 - 22. Tryptophan
 - 23. Cystine

Free Amino Acids in **Human Serum** by GC/FID

Kit: EZ:faast GC/FID Free (Physiological) Amino Acid Kit KG0-7165 Order No.: Split 1:15 @ 250°C, Injection: 2.5uL **Carrier Gas:** Helium 1.5mL/minute (60 kPa) @ 110°C 6 kPa/min Pressure Rise: 30°C/min from Oven Program: 110° to 320°C, hold at 320° for 1 minute Detector: FID @ 320°C



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Free Amino Acids in Human Urine by GC/FID

Sample:

Derivatized amino acids in human urine (0.1mL). Norvaline is the internal standard added at a concentration of 200 $\mu mol/L$

9. Serine

10. Proline

11. Asparagine

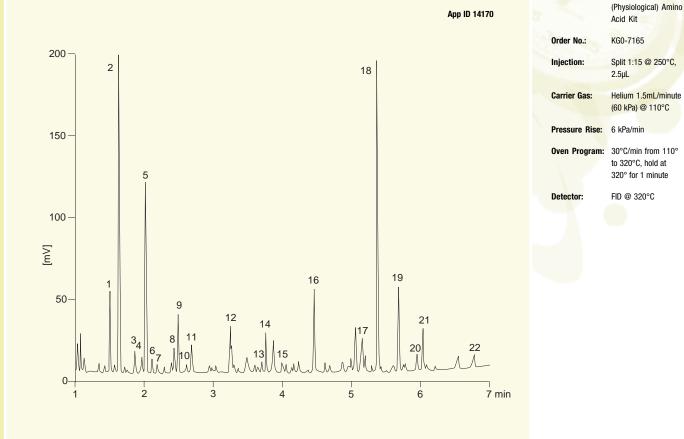
- 1. Alanine
- 2. Glycine
- 3. Valine
- 4. ß-Aminoisobutyric acid 12. Aspartic Acid
- 5. Norvaline (IS)
 - 13. Glutamic Acid 14. Phenylalanine
- 6. Leucine
 7. Isoleucine
- 8. Threonine
- 15. α-Aminoadipic acid
- 16. Glutamine

- 17. Lysine
- 18. Histidine
- 19. Tyrosine
- 20. Proline hydroxyproline (dipeptide)

EZ:faast GC/FID Free

Kit:

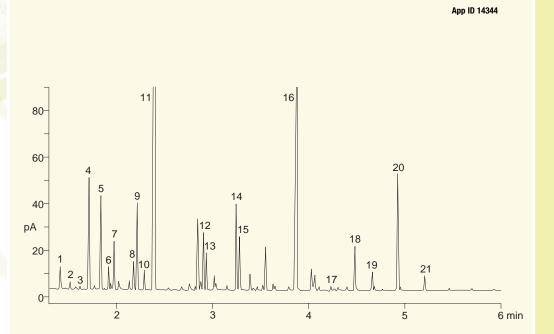
- 21. Tryptophan
- 22. Cystine



		EZ:faa
Sample: Derivatized amino acids in		
Norvaline is the internal sta	indard added at a concentration of 200 µmol/L	
1. Alanine	12. Aspartic Acid	
2. Glycine	13. Methionine	
3. α -Aminobutyric Acid	14. Glutamic Acid	
4. Valine	15. Phenylalanine	
5. Norvaline (IS)	16. Glutamine	
6. Leucine	17. Ornithine	
7. Isoleucine	18. Lysine	
8. Threonine	19. Histidine	
9. Serine	20. Tyrosine	
10. Proline	21. Tryptophan	

11. Asparagine

Kit:	EZ:faast GC/FID Free (Physiological) Amino Acid Kit
Order No.:	KG0-7165
Injection:	Split 1:15 @ 250°C, 2.5µL
Carrier Gas:	Helium 1.5mL/minute (60 kPa) @ 110°C
Pressure Rise:	Constant pressure
Oven Program:	30°C/min from 110° to 320°C, hold at 320° for 1 minute
Detector:	FID @ 320°C



by GC/FID

ast[®]

Free Amino

Potato Tissue

Acids in



Free Amino Acids in Corn Meal by GC/FID

Sample:

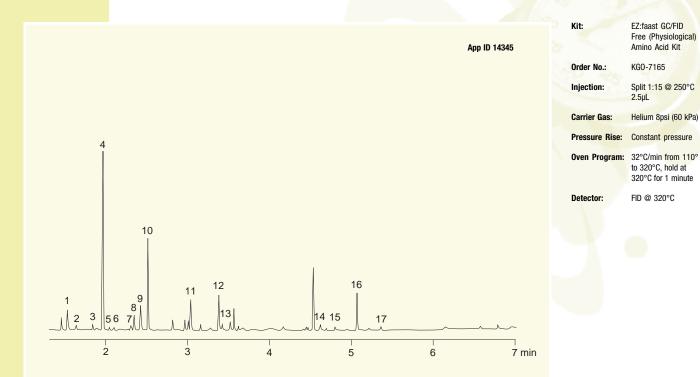
Derivatized amino acids in corn meal (0.1mL). Norvaline is the internal standard added at 200 $\mu \text{mol/L}$

- 1. Alanine 11. Aspartic Acid
- 2. Glycine
 - -/- !' - -
- 3. Valine
- 4. Norvaline (IS) 14. Lysine
- 5. Leucine
- 15. Histidine
- 16. Tyrosine

12. Glutamic Acid

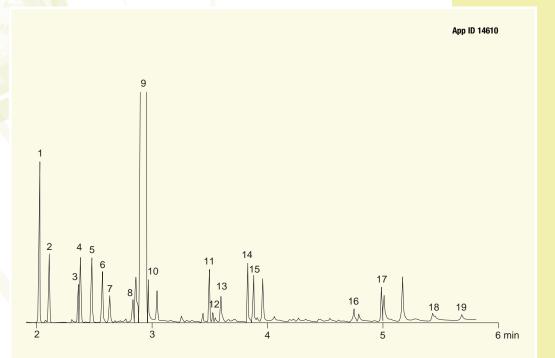
13. Phenylalanine

- 6. Isoleucine
 7. Threonine
- 17. Tryptophan
- 8. Serine
- 9. Proline
- 10. Asparagine



Der	imple: ivatized amino acids in winvaline is the internal stand	ne (0 lard a	1mL). dded at a concentration of 200 μmol/L	Free Amino Acids in Wine
1.	Alanine	11.	Aspartic Acid	by GC/MS
2.	Glycine	12.	Methionine	
3.	Valine	13.	4-Hydroxyproline	
4.	β-Aminoisobutyric acid	14.	Glutamic Acid	
5.	Norvaline (IS)	15.	Phenylalanine	
6.	Leucine	16.	Ornithine	
7.	Isoleucine	17.	Lysine	
8.	Threonine	18.	Tyrosine	
9.	Proline	19.	Tryptophan	
10.	Asparagine			

Kit:	EZ:faast GC/MS Free (Physiological) Amino Acid Kit
Order No.:	KG0-7166
Injection:	Split 1:15 @ 250°C, 2.5µL
Carrier Gas:	Helium 1.1mL/ minute@110°C
Pressure Rise:	6 kPa/min
Oven Program:	30°C/min from 110° to 320°C
Detector:	MS @ 300°C



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Free Amino Acids in Beer by GC/FID

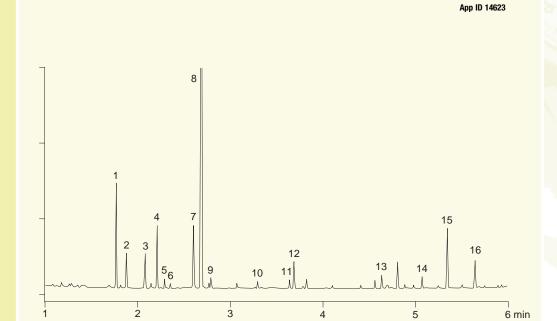
Sample:

7.

Serine

Derivatized amino acids in beer. Norvaline is the internal standard added at 200 $\mu mol/L$

- 9. Asparagine 1. Alanine 2. Glycine 10. Aspartic Acid 3. Valine 11. Glutamic Acid Phenylalanine 4. Norvaline (IS) 12. Leucine 13. Ornithine 5. 6. Isoleucine 14. Histidine
 - 15. Tyrosine
- 8. Proline 16. Tryptophan



Kit:EZ:faast GC/FID
Free (Physiological)
Amino Acid KitOrder No.:KG0-7165Injection:Split 1:15 @ 250°C
2.5µLCarrier Gas:Helium 8psi (60 kPa)Pressure Rise:Constant pressureOven Program:32°C/min from 110°
320°C for 1 minuteDetector:FID @ 320°C

ample	9:					Amino Acid
Derivatized amino acids from a corn meal hydrolysate sample. Norvaline is the internal standard added at 200 μmol/L						in Corn Mea Hydrolysate
1. Alanin	ne 10	0. Aspartic Acid				by GC/FID
2. Glycir	ne 1 ⁻	1. Methionine				
3. Valine	12	2. Hydroxyproline				
4. Norva	lline (IS) 13	3. Glutamic Acid				
5. Leucir	ne 14	4. Phenylalanine				
6. Isoleu	icine 1	5. Lysine				
7. Threo	nine 10	6. Histidine				
8. Serine	e 1	7. Tyrosine				
9. Prolin	e					
t	EZ:faast GC/FID Protein Hydrolysate Kit					App ID 14346
t: rder No.:	Protein					App ID 14346
der No.:	Protein Hydrolysate Kit					App ID 14346
der No.: jection:	Protein Hydrolysate Kit KG0-7167 Split 1:15 @ 250°C,	5				App ID 14346
der No.: jection: rrier Gas:	Protein Hydrolysate Kit KG0-7167 Split 1:15 @ 250°C, 2.5µL Helium 1.5mL/ minute (60 kPa) @ 110°C	5				App ID 14346
der No.: jection: urrier Gas: essure Rise:	Protein Hydrolysate Kit KG0-7167 Split 1:15 @ 250°C, 2.5µL Helium 1.5mL/ minute (60 kPa) @ 110°C	5 9				App ID 14346
rder No.: jection: arrier Gas: ressure Rise:	Protein Hydrolysate Kit KG0-7167 Split 1:15 @ 250°C, 2:5µL Helium 1.5mL/ minute (60 kPa) @ 110°C 6kPa/min : 30°C/min from 110° to 320°C, hold at		13			App ID 14346

USERGUIDE



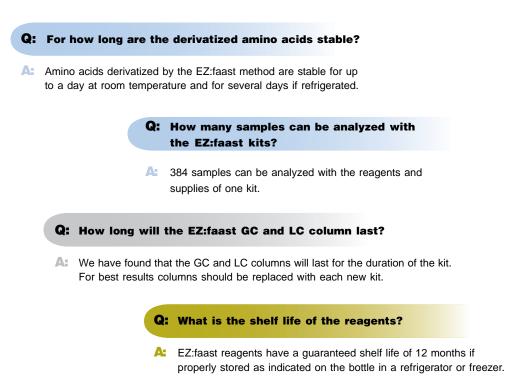




384 SPE Sorbent Tips SGE GC FocusLiners (Not Shown)

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Frequently Asked Questions



Q: What are the derivatization reagents and reaction?

The derivatization reagents and reaction are proprietary. The reaction derivatizes both the amine and carboxyl groups of the amino acids forming a highly stable derivative.

Amino Acid Analysis Kits

Each kit includes: ZB-AAA GC column, or AAA LC column, sample prep and derivatization reagents, sample prep vials, AA standards, SPE pipette tips, vial rack, and microdispenser.

Order No.	Description	Unit	Price
KG0-7165	GC/FID Free (Physiological) Amino Acid Analysis Kit	ea	\$1,500
KG0-7166	GC/MS Free (Physiological) Amino Acid Analysis Kit	ea	1,600
KG0-7167	GC/FID Protein Hydrolysate Kit	ea	1,600
KG0-7168	GC/MS Protein Hydrolysate Kit	ea	1,700
CG0-7169	ZB-AAA 10m x 0.25mm ID Amino Acid Analysis GC Column	ea	350
KH0-7337	LC/MS Free (Physiological) Amino Acids Kit with 250 x 2.0mm column	ea	1,600
KH0-7338	LC/MS Free (Physiological) Amino Acids Kit with 250 x 3.0mm column	ea	1,600
KH0-7339	LC/MS Protein Hydrolysates Kit with 250 x 2.0mm column	ea	1,700
KH0-7340	LC/MS Protein Hydrolysates Kit with 250 x 3.0mm column	ea	1,700
AG0-7184	Physiological Amino Acid Standards (SD1, 2, 3) 2mL/vial x 2	ea	52
AG0-7263	Protein Hydrolysate Standard (SD) 2mL/vial x 2	ea	25

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Can You Complete An Amino Acid Analysis In 15:00 Minutes? ...now you can!



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Canada 411 Madrid Ave. Torrance, CA 90501-1430 USA (800) 543-3681 (310) 328-7768 info@phenomenex.com

United Kingdom Queens Avenue, Hurdsfield Ind. Est., Macclesfield, Cheshire SK10 2BN, England 01625-501367 01625-501796 ukinfo@phenomenex.com

Germany Zeppelinstr. 5 63741 Aschaffenburg Deutschland 06021-58830-0 06021-58830-11

New Zealand P.O. Box 31-601 Milford Auckland New Zealand 09-4780951 09-4780952 anfrage@phenomenex.com info@phenomenex.co.nz

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