

Experimental methods in protein sequence analysis

Edman sequencing was performed on the isolated peptide fragments of the protein. The peptides that were sequenced correspond to their tryptic peptide numbers in the tryptic map above. PTH-amino acids that are in parentheses indicate ambiguous amino acid assignments; the yields of those PTH-amino acids were very low and likely were at the level of detection as the background peaks.

Microsequence analysis of tryptic peptides

Cycle	Amino acid (pmol)													
	T2	T3	T6a	T6b	T6c	T8	T14	T15	T18	T19	T23	T24	T25	
1	Cys (227)	Ala (329)	Cys (86)	Lys (111)	Val (313)	Gly (221)	Thr (100)	Ile (543)	Ser (103)	Ser (36)	Glu (184)	Ser (194)	Leu (170)	
2	Asn (262)	Glu (275)	Asn (132)	Val (238)	Ile (300)	Leu (197)	Pro (151)	Thr (111)	Ile (62)	Ile (68)	Pro (122)	Val (416)	Ser (84)	
3	Asn (246)	Glu (380)	Asn (159)	Ile (273)	Phe (289)	Cys (294)	Glu (264)	Gly (876)	Gly (159)	Gly (81)	Asp (197)	His (192)	Pro (149)	
4	—	His (84)	—	Phe (203)	Cys (194)	Leu (192)	Asp (122)	Leu (948)	Ile (38)	Ile (81)	Ser (68)	Leu (270)	Asp (119)	
5	Gly (122)	Tyr (203)	Gly (84)	Cys (140)	Ser (122)	Ser (151)	Thr (73)	Asp (1080)	Glu (184)	Glu (111)	Asn (262)	Phe (535)	Asp (173)	
6	Tyr (138)	Pro (125)	Tyr (95)	Ser (39)	(Arg) (22)	Cys (159)	Ala (248)	Pro (764)	Lys (127)	Lys (108)	Val (103)	Ile (297)	Ala (138)	
7	Glu (122)	Val (289)	Glu (79)	Arg (14)	—	Arg (51)	Glu (122)	Ala (659)	Pro (135)	Pro (73)	Ile (70)	Asp (286)	Asp (138)	
8	Ile (122)	Ser (167)	Ile (59)	—	—	—	Asp (78)	Gly (386)	Val (97)	Val (143)	Val (68)	Ser (97)	Phe (59)	
9	Asn (103)	Ala (148)	Asn (76)	—	—	—	Asp (103)	Pro (348)	Gly (135)	Gly (70)	Val (81)	Leu (186)	Val (84)	
10	Lys (20)	Gly (86)	Lys (22)	—	—	—	Cys (303)	Asn (564)	His (154)	His (43)	Asp (130)	Leu (394)	Asp (97)	
11	—	Tyr (103)	—	—	—	—	(His) (23)	Phe (370)	Val (100)	Val (149)	Trp (89)	Asn (265)	Val (111)	
12	—	(Thr)	—	—	—	—	Leu (57)	Glu (446)	Asp (176)	Asp (81)	Leu (65)	Glu (157)	Leu (95)	
13	—	(Lys)	—	—	—	—	Ile (38)	Tyr (356)	Ile (49)	Ile (73)	Ser (14)	Glu (132)	His (59)	
14	—	—	—	—	—	—	Pro (86)	Ala (389)	Tyr (132)	Tyr (51)	Tyr (22)	Asn (159)	Thr (24)	
15	—	—	—	—	—	—	Gly (46)	Glu (324)	Pro (105)	Pro (35)	(Lys) (22)	Pro (103)	Phe (46)	
16	—	—	—	—	—	—	(Val)	Ala (346)	Asn (24)	Asn (35)	—	Ser (16)	(Thr)	
17	—	—	—	—	—	—	(Val)	Pro (219)	Gly (14)	Gly (24)	—	(Lys) (65)	(Arg)	
18	—	—	—	—	—	—	(Glu)	(Ser)	(Gly)	(Gly)	—	—	—	
19	—	—	—	—	—	—	—	(Arg)	—	—	—	—	—	

4. Peptide T24 has an amino-terminal Ser (serine) residue as indicated by the detection of PTH-Ser as the first cycle of Edman sequencing of that peptide. Why is the yield of the PTH-Ser lower than the succeeding PTH-amino acids identified in the sequence?

5. In the actual protein, peptide T15 C-terminal Arg is in a peptide bond with the N-terminal Leu of peptide T25. The two peptides are contiguous such that the full-length sequence of T15-T25 would show an N-terminal Ile (isoleucine) amino acid and a C-terminal Arg (arginine) amino acid. This alignment of these two tryptic peptides, T15 and T25, were deduced from sequence homology to another similar protein whose sequence was already known.

If sequence homology data were not available, how might you experimentally determine the alignment of peptides T15 and T25 that reveals this contiguous (T15-T25) amino acid sequence? [Remember that Edman sequencing of the intact protein could only identify residues 1 through residue 19 so one cannot perform Edman amino acid sequence determination on the full-length protein.]

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This book includes selected papers presented at World Conference on Information Systems for Business Management ISBM 2024 held in Bangkok Thailand during September 12 13 2024 It covers up to date cutting edge research on data science information systems infrastructure and computational systems engineering systems business information systems and smart secure systems **Methods in Protein Sequence Analysis** Marshall Elzinga,2012-12-06
Methods in Protein Sequence Analysis contains an intensely practical account of all the new methodology available to scientists carrying out protein and peptide sequencing studies Many of the striking advances in fields as diverse as immunology cell motility and neurochemistry have in fact been fueled by our ever more powerful ability to determine the sequences and structures of key proteins and peptides It is our hope that the rich array of techniques and methods for sequencing proteins discussed in this volume methods that generate much of the information crucial to progress in modern biology will now become accessible to all who can benefit from them The papers of the present volume constitute the Proceedings of the IVth International Conference on Methods in Protein Sequence Analysis which was held at Brookhaven National Laboratory Upton NY September 21 25 1981 It was the most recent in a series of biennial conferences the previous one having been held in Heidelberg GFR in 1979 The series was originated by Richard Laursen and initially dealt with one aspect of the field solid phase sequencing The scope of the meeting was very broad and among the many aspects of protein sequencing discussed were instrumentation strategy chemicals mass spectrometry cleavage of proteins and separation of peptides and solid liquid manual and even gas phase sequencing Current Catalog ,1988 First multi year cumulation covers six years 1965 70 **Methods in protein sequence analysis** ,1987 **Scientific and Technical Books and Serials in Print** ,1989 Books in Print Supplement ,1985

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