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Molar Absorptivity and $A_{1\,cm}^{1\%}$ Values for Proteins at Selected Wavelengths of the Ultraviolet and Visible Regions. XXII.

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Abstract

The molar absorptivity and $A_{1cm}^{1\%}$ values for 150 proteins are reported. The conditions under which these values were obtained and citations to the sources of the data are also provided.

Index Entries: Proteins, molar absorptivity of; $A_{1cm}^{1\%}$ values, of proteins; molar absorptivity, of proteins; ultraviolet absorption, of proteins.

Introduction

The molar absorptivity and $A_{1cm}^{1\%}$ values for 150 proteins and the conditions under which these values were obtained are given in Table 1. The footnotes to Table 1 contain additional information. The method used to compile these data has been described (*1*).

This paper is part of a continuing compilation of absorption characteristics of proteins in the ultraviolet and visible regions (*2*).

References

1. Kirschenbaum, D. M. (1980), *J. Chem. Info. Comput. Sci.* **20,** 152.
2. Kirschenbaum, D. M. (1982), *J. Quant. Spectrosc. Radiat. Transfer* **27,** 23; **27,** 39.

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Table 1
Molar Absorption Coefficients, ϵ_M, and $A_{1cm}^{1\%}$ Values for Proteins

Protein, source	$\epsilon_M^a \times 10^{-4}$	$A_{1cm}^{1\% \, b}$	nm[c]	Ref.	Comments[d]
Pantetheinase					
Horse kidney		15.2	280	*1*	
Papain					
Papaya	0.1220		335	*2*	0.2 *M* NaOH, deaerated
	1.0100		190	*3*	
Paracasein[e]					
Bovine milk		10.6	277	*4*	*M*/15 Ph, pH 6.8
		10.3	277	*4*	*M*/20 Borax, pH 9.2
		11.0	280	*4*	0.1 *N* NaOH
Parvalbumin					
Lungfish [*Protopterus dolloi*]					
III	0.1986		259	*5*	
IIIa	0.2540		259	*5*	
IV	0.2370		259	*5*	
V	0.2295		259	*5*	
Hake [*Merluccius merluccius*]		4.4	280	*6*	0.5% AmBi, pH 8. Data from Fig. 5
Perch [*Perca fluviatilis*]					
I		1.23	259	*7*	Dry wt
II		1.49	259	*7*	Dry wt
Penicillopepsin					
Penicillium janthinellum		13.5	280	*8*	
Pepsin					
Pig	0.0936		335	*2*	0.2 *M* NaOH, deaerated
		14.0	280	*8*	
Peroxidase, estrogen-binding					
Human fetus					
A	24.75	11.25	406	*9*	50 m*M* Tris-HCl, pH 7, with 0.6 *M* NaCl. mw = 220,000 (*9*)
	11.78	5.35	278	*9*	50 m*M* Tris-HCl, pH 7, with 0.6 *M* NaCl. mw = 220,000 (*9*)
B	18.98	11.16	406	*9*	50 m*M* Tris-HCl, pH 7, with 0.6 *M* NaCl. mw = 170,000 (*9*)
	10.59	6.23	278	*9*	50 m*M* Tris-HCl, pH 7, with 0.6 *M* NaCl. mw = 170,000 (*9*)

Table 1 (*continued*)

Protein, source	ϵ_M^a $\times 10^{-4}$	$A_{1cm}^{1\%\,b}$	nm[c]	Ref.	Comments[d]
Phenylalanine hydroxylase					
Rat liver		—[f]	280	*10*	
Phosphatase, acid					
Bovine liver		8.6	280	*11*	Dry wt
Phosphodiesterase–phosphomonoesterase					
Fusarium moniliforme		21	280	*12*	Protein part
		15	280	*12*	Protein plus carbohydrate; dry wt
Phosphoenolpyruvate: sugar phosphotransferase system					
Escherichia coli					
Enzyme I	2.9	4.4	280	*13*	AA; mw = 65,826 (*13*)
Phosphofructokinase					
Bacillus stearothermophilus					
S-Carboxymethyl derivative	3.4	10.3	280	*14*	mw = 33,000 (*14*)
Phosphoglycerate kinase					
Chicken muscle		5.7	280	*15*	
Thermus thermophilus	2.01	4.5	280	*16*	mw = 44,600 (*16*), dry wt
Rat muscle					
Young		5.2	280	*17*	10 m*M* Tris, 100 m*M* KCl, 10 m*M* ME, pH 7.0
		3.2	260	*17*	10 m*M* Tris, 100 m*M* KCl, 10 m*M* ME, pH 7.0
		4.0	291	*17*	10 m*M* Tris, 100 m*M* KCl, 10 m*M* ME, pH 7.0
Old		7.2	280	*17*	10 m*M* Tris, 100 m*M* KCl, 10 m*M* ME, pH 7.0
		4.8	260	*17*	10 m*M* Tris, 100 m*M* KCl, 10 m*M* ME, pH 7.0
		4.9	291	*17*	10 m*M* Tris, 100 m*M* KCl, 10 m*M* ME, pH 7.0

(*continued*)

Table 1 (*continued*)

Protein, source	$\epsilon_M^a \times 10^{-4}$	$A_{1cm}^{1\%\,b}$	nm[c]	Ref.	Comments[d]
Young		4.9	280	*17*	50 m*M* Ph, pH 7.0
		2.8	260	*17*	50 m*M* Ph, pH 7.0
		2.91	291	*17*	50 m*M* Ph, pH 7.0
Old		6.2	280	*17*	50 m*M* Ph, pH 7.0
		3.9	260	*17*	50 m*M* Ph, pH 7.0
		4.0	291	*17*	50 m*M* Ph, pH 7.0
Young		5.0	280	*17*	10 m*M* Tris, pH 7.0.
		2.96	260	*17*	10 m*M* Tris, pH 7.0.
		3.54	291	*17*	10 m*M* Tris, pH 7.0.
Old		7.7	280	*17*	10 m*M* Tris, pH 7.0.
		5.36	260	*17*	10 m*M* Tris, pH 7.0.
		5.3	291	*17*	10 m*M* Tris, pH 7.0.
Young and old		8.4	280	*17*	0.2 *M* Tris, and 0.02 *M* EDTA, pH 8.2
		5.4	260	*17*	0.2 *M* Tris, and 0.02 *M* EDTA, pH 8.2
		5.8	291	*17*	0.2 *M* Tris, and 0.02 *M* EDTA, pH 8.2
		6.9	280	*17*	10 m*M* Tris, and 6 *M* GCl, pH 7.0
		4.6	260	*17*	10 m*M* Tris, and 6 *M* GCl, pH 7.0
		5.0	291	*17*	10 m*M* Tris, and 6 *M* GCl, pH 7.0
Phospholipase A					
Habu snake [*Trimeresurus flavoviridis*]					
Venom	3.58	25.6	280	*18*	mw = 14,000 (*18*)
Sea snake [*Enhydrina schistosa*]					
Venom	1.36	10.1	270	*19*	mw = 13,500 (*19*)
	1.69	13	276	*19*	mw = 13,500 (*19*)
PPB[g] derivative	3.46		270		
Phospholipase A2					
Cobra venom		22.0	278	*20*	
Pig pancreas		13.0	280	*21*	
Photoreaction center					
Rhodospirillum rubrum	14.3		868	*22*	
C-Phycocyanin					
Agmenellum quadruplicatum	9.44		662	*23*	Acid urea
Pili					
Pseudomonas aeruginosa K		7.8	280	*24*	

Table 1 (*continued*)

Protein, source	$\epsilon_M^a \times 10^{-4}$	$A_{1cm}^{1\%\,b}$	nm[c]	Ref.	Comments[d]
Plastocyanain					
Enteromorpha prolifera	0.47		597	*25*	
	0.61		277	*25*	
Poly[ADP-ribose] synthetase					
Calf thymus	9.73	8.85	280	*26*	Data from Fig. 5; 50 m*M* Tris-Cl, pH 8.0, cont. 10% glycerol, 0.2 *M* NaCl, and 10 m*M* ME. mw = 110,000 (*26*)
Polyamine oxidase					
Aspergillus terreus	26	20	280	*27*	0.05 *M* KPh, pH 5.5; mw = 130,000 (*27*)
	1.5	1.16	457	*27*	0.05 *M* KPh, pH 5.5; mw = 130,000 (*27*)
Penicillium chrysogenum	36.8	22.97	280	*28*	0.1 *M* NaAc, pH 3.8; mw = 160,000 (*28*)
	2.6	1.6	457	*28*	0.1 *M* NaAc, pH 3.8; mw = 160,000 (*28*), dry wt
Polypeptide					
Bovine epidermis		4.8	nc[h]	*29*	
Chalmydomonas reinhardtii					
Thylakoid membrane					
29 K peptide		13.9	280	*30*	
26 K peptide		14.2	280	*30*	
Porin					
Salmonella typhimurium					
Outer membrane					
SH 5551	7.28	18.3	277	*31*	mw = 39,800 (*31*)
SH 6377	8.23	20.9	277	*31*	mw = 39,300 (*31*)
SH 6017	6.84	18.0	277	*31*	mw = 38,000 (*31*)
Prekallikrein [Fletcher Factor]					
Bovine plasma	8.9	10.9	280	*32*	mw = 82,000 (*32*); int.

(*continued*)

Table 1 (*continued*)

Protein, source	$\epsilon_M^a \times 10^{-4}$	$A_{1cm}^{1\%\ b}$	nm[c]	Ref.	Comments[d]
Prenyltransferase [E.C. 2.5.1.1]					
Chicken liver	8.84	10.3	nc[h]	*33*	
Procarboxypeptidase A					
Pig pancreas					
Form I		20.7	281.5	*34*	
Form II		15.55	278	*34*	
Profilactin					
Calf thymus and brain		11.0	280	*35*	
Profilin					
Calf spleen	1.98	13	280	*36*	mw = 15,220 (*36*)
Prolactin					
Bovine and ovine					
Nitrophenylsulfonyl-		24.1	280	*37*	LS
Prostatein					
Rat ventral prostate		9.3	280	*38*	
Protease					
Proteinase A					
Yeast	0.496		280	*39*	
	0.525		276	*39*	
Aspartyl proteinase					
Penicillium roqueforti		13.1	280	*8*	
Metalloprotease					
Serratia maracescens		12.4	280	*40*	0.1 *M* AmBi
Neutral protease					
Tricholoma columbetta		7.20	280	*41*	
Serine protease					
Morris					
hepatoma 8999		10.5	280	*42*	0.25 *M* KPh, pH 7.5; dry wt
Protein					
Japanese eel [*Anguilla japonica*]					
Egg yolk		7.60	280	*43*	0.1 *N* NaOH; dry wt
Serum [Vitellogenin]		9.04	280	*43*	0.1 *N* NaOH; dry wt
Human placenta tissue					
PP8-3.7S form		8.1	280	*44*	
PP10-3.8S form		10.9	280	*44*	
Hyalophora cecropia					
Inducible bacteriocidal proteins					
P7		26	280	*45*	Lowry
P9A		30	280	*45*	Lowry
P9B		16	280	*45*	Lowry

Table 1 (*continued*)

Protein, source	ϵ_M^a $\times 10^{-4}$	$A_{1cm}^{1\%\,b}$	nm[c]	Ref.	Comments[d]
Desulfovibrio gigas, cobalt-containing protein					
Sulfate reducer	2.2		588	*46*	
	0.8835		550	*46*	
	4.628		420	*46*	
	1.4900		278	*46*	
Soybean seeds [*Glycine max* var. Yagishirahana]					
α2		9.08	280	*47*	
α3		8.08	280	*47*	
α4		7.97	280	*47*	
Human plasma					
Protein C	8.99	14.5	280	*48*	AA
Human serum					
Vitamin D binding protein		9.12	280	*49*	
Human eosinophil					
Basic protein		26.7	277	*50*	
Human myelin					
Total myelin protein		11.1	280	*51*	Calc. from AA
Human urine					
Melanoma-specific protein		11.0	280	*52*	0.05 *M* NaCl; dry wt
		179.0	210	*52*	0.05 *M* NaCl; dry wt
Lymphocyte surface protein found in human urine		2.08	278	*53*	Refr.; dry wt
Bovine heart muscle					
Mitochondria		1.225[i]	275	*54*	
Bovine brain					
Modulator binding protein	8.2	9.8	278	*55*	Interf.; mw = 84,000 (*55*)
Bovine white matter					
Folch-Pi apoprotein	3.17	13.5	278	*56*	mw = 23,500 (*56*)
Bovine brain					
Acidic protein		6	280	*57*	Interf.
Bovine retina					
11-*cis*-Retinol-binding					
Apoprotein	3.2	9.7	278	*58*	mw = 32,000 (*58*)
Holoprotein	4.2		278	*58*	

(*continued*)

Table 1 (*continued*)

Protein, source	$\epsilon_M^a \times 10^{-4}$	$A_{1cm}^{1\%\ b}$	nm[c]	Ref.	Comments[d]
Bacteriophage T5					
Double-stranded DNA-binding protein					
Protein D5	2.4	8.4	280	*59*	mw = 28,600 (*59*)
Bacteriophage N4					
Protein subunits		7.2	280	*60*	0.1 Tris, pH 7.2
Bacteriophage T4D tail sheath					
Protein P18		8.9	278	*61*	Lowry
		9.0	278	*61*	Interf.
Bacteriophage λ					
Main shell protein, PE		12.5	280	*62*	
Outer shell protein, PD					
Mature phage		14.0	280	*62*	
E^- lysate		11.5	280	*62*	
Photobacterium phosphoreum					
Lumazine protein		7.5	274	*63*	Dry wt
Escherichia coli					
Ribonucleic acid synthesis termination protein					
Protein p	1.776	3.7	280	*64*	mw = 48,000 (*64*); 0.05 *M* TEAHCl, pH 8.0, 0.1 *M* KCl, 0.1 *M* EDTA, 0.1 *M* DTT, 50% glycerol, v/v
recA protein		5.16	280	*65*	
Ribosome					
Protein Sl	3.9[j]	6.0	280	*66*	Lowry
	4.9[k]	7.5	280	*67*	mw = 65,000 (*67*)
	6.9	9.8	280	*68*	mw = 70,000 (*68*)
Protein S4	1.42		284	*69*	10 m*M* Tris, 20 m*M* $MgCl_2$, 360 m*M* KCl, pH 7.6; N, LS
		8.7	278	*70*	0.1 *M* NaCl, 0.03 *M* NaPh, pH 7.0
Protein S3		8.9	280	*71*	Refr.; 15% HOAc
Protein S5		3.5	280	*71*	Refr.; 15% HOAc
Total protein		8.0	280	*71*	Refr.; 15% HOAc
Protein S4		12.0		*71*	0.03 *M* Tris, 0.02 *M* $MgCl_2$, 0.35 *M* KCl, pH 7.4
Protein S6		9.9		*71*	0.03 *M* Tris, 0.02 *M* $MgCl_2$, 0.35 *M* KCl, pH 7.4

Table 1 (*continued*)

Protein, source	$\epsilon_M^a \times 10^{-4}$	$A_{1cm}^{1\%\,b}$	nm[c]	Ref.	Comments[d]
Protein S20		2.8		*71*	0.03 *M* Tris, 0.02 *M* $MgCl_2$, 0.35 *M* KCl, pH 7.4
Protein S15		3.25	277	*72*	N; LS, pH 5.6–7
HeLa nuclei, adenovirus type 2					
Deoxyribonucleic acid binding protein		8.6	280	*73*	DB
Mustard proteins					
[*B. juncea*]		9.9	280	*74*	0.2 *M* Tris-glycine buffer, pH 8.3
Phytolacca americana					
Antiviral protein					
I		8.3	280	*75*	
II		9.1	280	*75*	
Porcine brain					
Acidic protein	1.63	2.8	280	*76*	mw = 58,000 (*76*)
Porcine pylorus					
Non-IF B_{12} binding		8.0	278	*77*	
Rat kidney					
Mercury binding protein					
Isoform 1	0.5900[l]	68.5[m]	250	*78*	0.01 *M* pH, pH 7.8
	0.2500[l]	36.7[m]	310	*78*	0.01 *M* pH, pH 7.8
Isoform 2	0.7200[l]	67[m]	250	*78*	0.01 *M* pH, pH 7.8
	0.2700[l]	32[m]	310	*78*	0.01 *M* pH, pH 7.8
Isoform 3	0.7100[l]	77[m]	250	*78*	0.01 *M* pH, pH 7.8
	0.2400[l]	30[m]	310	*78*	0.01 *M* pH, pH 7.8
Spinach chloroplasts					
33 Kilodalton protein	2.76	8.37	276	*79*	0.1 *M* NaCl, 0.1 *M* Ph, pH 7.6. Data from Fig. 3 (*79*); mw = 33,000 (*79*)
Tobacco mosaic virus grown in *Tabacum var Samsun*					
Coat protein		12.0[o]	280	*80*	
Protein kinase regulatory subunit					
Bovine skeletal muscle		7.4	278	*81*	Data from Fig. 2 (*81*)
		7.0[n]	280	*81*	Data from Fig. 2 (*81*)
Protocatechuate 3,4-dioxygenase [E.C. 1.13.1.3]					
Azotobacter vinelandii	77.9	16.2	280	*82*	mw = 480,000 (*82*)
	3.39	0.71	480	*82*	mw = 480,000 (*82*)

(*continued*)

Table 1 (*continued*)

Protein, source	ϵ_M^a $\times 10^{-4}$	$A_{1cm}^{1\% \, b}$	nm[c]	Ref.	Comments[d]
Protoxin, entomocidal					
Bacillus thuringiensis		9.1	280	*83*	Lowry
Pyrocatechase					
Pseudomonas					
arvilla C-1	6.1	9.73	280	*84*	pH 7.5; dry wt; mw = 63,000 (*84*)
Pyrophosphatase, inorganic [EC 3.6.1.1]					
B. stearothermophilus		10.8	280	*85*	20 m*M* Tris-SO_4, pH 7.8, containing 0.1 *M* EDTA
	15.4	11.0	280	*86*	mw = 140,000 (*86*)
Bacterium PS-3		10.8	280	*85*	20 m*M* Tris-SO_4, pH 7.8, containing 0.1 m*M* EDTA
Pyruvate:ferredoxin oxidoreductase					
Halobacterium					
halobium	24.7	9.65	280	*87*	Data from Fig. 8 (*87*); mw = 256,000 (*87*)
Pyruvate transaminase, ω-amino acid					
Pseudomonas sp.					
Tetramer	6.64[p]		280	*88*	Data from Fig. 1 (*88*)
	0.88[p]		340	*88*	Data from Fig. 1 (*88*)
Quinolinate phosphoribosyltransferase					
Alcaligenes eutrophus subsp.					
quinolinicus		3.54	280	*89*	
Porcine kidney	18.11	8.23	280	*90*	pH 7.0; mw = 220,000 (*90*)
Rhodopsin					
Bovine	4.0600		498	*91*	
	1.0340[q]		350	*91*	
	451.0000[q]		191	*91*	
Todarodes					
pacificus	3.4000		480	*92*	
Watasenia					
scintillans	3.4000		482	*92*	
Riboflavin-binding protein					
Duck [*Anas platyrhynchos*]					
Egg white	4.75	13.2	280	*93*	mw = 36,000[r] (*93*)
Riboflavin synthase					
Bacillus subtilis					
Light	2.1	3.0	280	*94*	mw = 70,000 (*94*)
Heavy	70.0	7.0	280	*94*	mw = 1,000,000 (*94*)

Table 1 (*continued*)

Protein, source	$\epsilon_M^a \times 10^{-4}$	$A_{1cm}^{1\%\,b}$	nm[c]	Ref.	Comments[d]
Ribonuclease					
Aspergillus clavatus	3.1600		281	*95*	pH 4.7
Bacillus intermedius 7P	2.2	18	280	*96*	0.1 *M* NaCl, pH 7; mw = 12,257 (*96*); dry wt
Ribonuclease A					
Bovine pancreas	0.1712		335	2	0.2 *M* NaOH
		36.9	235	*97*	
		9.27	280	*97*	
	0.9640		190	*98*	
Ribonuclease Uc					
Human urine		6.5	280	*99*	
Ribonuclease Us		10.7	280	*99*	
Ribonucleic acid polymerase [RNA polymerase], DNA-dependent					
Thermus thermophilus					
Core enzyme		6.8	280	*100*	
Holoenzyme		7.5	280	*100*	
Escherichia coli					
α Subunit	1.4	3.7	280	*101*	0.05 *M* NaPh, pH 8, 0.45 *M* NaCl, 0.1 *M* DTT; N; LS
β Subunit	8.1	5.2	280	*101*	0.05 *M* NaPh, pH 8, 0.45 *M* NaCl, 0.1 *M* DTT; N; LS
β1 Subunit	10.2	6.2	280	*101*	0.05 *M* NaPh, pH 8, 0.45 *M* NaCl, 0.1 *M* DTT; N; LS
α2β	10.7	4.7	280	*101*	0.05 *M* NaPh, pH 8, 0.45 *M* NaCl, 0.1 *M* DTT; N; LS
α2ββ1	22.8	5.8	280	*101*	0.05 *M* NaPh, pH 8, 0.45 *M* NaCl, 0.1 *M* DTT; N; LS
α2ββ1σ	32.1	6.7	280	*101*	0.05 *M* NaPh, pH 8, 0.45 *M* NaCl, 0.1 *M* DTT; N; LS
σ Subunit	10.0	11.6	280	*101*	0.05 *M* NaPh, pH 8, 0.45 *M* NaCl, 0.1 *M* DTT; N; LS

(*continued*)

Table 1 (*continued*)

Protein, source	ϵ_M^a $\times 10^{-4}$	$A_{1cm}^{1\%\ b}$	nm[c]	Ref.	Comments[d]
	6.89	8.4	280	*102*	5 m*M* KHPh, 0.1 *M* K_2SO_4, pH 7.0; mw = 82,000 (*102*)
Ribonucleoside diphosphate reductase					
Corynebacterium nephridii	51.4	26.2	280	*103*	mw = 196,000 (*103*)
Ribonucleotide reductase					
Calf thymus					
Protein M1		12.0	280	*104*	50 m*M* Tris-Cl, pH 7.6, 0.1 *M* KCl; dry wt
Escherichia coli					
Protein B2	0.8650		365	*105*	
	0.7500		360	*105*	Radical free form
Ribulose biphosphate carboxylase-oxygenase					
Synechococcus sp.		6.8	280	*106*	
D-Ribulose 5-phosphate 3-epimerase [EC 5.1.3.1]					
Calf liver		12.6	280	*107*	
Rubredoxin					
Desulfovibrio africanus	1.145		490	*108*	
	1.338		378	*108*	
	2.553		278	*108*	
Desulphovibrio salixigens	1.5980		280	*109*	AA
	0.7750		376	*109*	AA
	0.6250		493	*109*	AA
Clostridium thermoaceticum					
Rubredoxin 1	0.628		490	*110*	
	0.715		375	*110*	
	1.475		280	*110*	
Rubredoxin 2	0.515		490	*110*	
	0.599		375	*110*	
	1.670		280	*110*	
Saccharopine dehydrogenase [L-lysine forming] [EC 1.5.1.7]					
Bakers' yeast	1.45		280	*111*	Same value for reduced and native enzyme; 0.1 *M* KPh, pH 6.8
Sarcosine oxidase					
Cylindrocarpon didymum M.		26.4	280	*112*	Dry wt
		3.0	450	*112*	Dry wt

Table 1 (*continued*)

Protein, source	$\epsilon_M^a \times 10^{-4}$	$A_{1cm}^{1\%\,b}$	nm[c]	Ref.	Comments[d]
Serine hydroxymethyltransferase [EC 2.1.2.1]					
Bonnet monkeys					
Macaca radiata		2.9	420	*113*	Data from Fig. 5 (*113*)
Rabbit liver					
Mitochondria		1.29	425	*114*	10 m*M* KPh–200 m*M*; glycine, pH 6; data from Fig. 5 (*114*)
		1.17	425	*114*	10 m*M* KPh–200 m*M*; glycine, pH 8.6; data from Fig. 5 (*114*)
Siroheme sulfite reductase					
Thiobacillus					
denitrificans	28.0		273	*115*	50 m*M* KPh, pH 7.0
	18.1		393	*115*	50 m*M* KPh, pH 7.0
	6.0		594	*115*	50 m*M* KPh, pH 7.0
Spinae					
Bacterial		6.25	280	*116*	10 m*M* Ph, pH 6.8; AA, LS
Storage particle					
Xenopus laevis					
Oocytes					
Protein a		10	280	*117*	AA
		7	265	*117*	AA
Protein b		9.5	280	*117*	AA
		6.5	265	*117*	AA
Streptokinase					
β-Hemolytic streptococcus, Lancefield group C					
Strain H64	3.77	7.5	280	*118*	0.02 *M* Ph, pH 7.2; AA, Lowry, N; mw = 50,200 (*118*)
Squalene and sterol carrier protein					
Rat liver		3.4	280	*119*	AA
Subtilisin BPN′	0.8850		190	*98*	
Succinyl-CoA synthetase					
Rat liver	4	5	280	*120*	Refr.; mw = 80,000 (*120*)
S-Succinylglutathione hydrolase					
Human liver	3.8	21.2[s]	280	*121*	Biuret; mw = 18,000 (*121*)

(*continued*)

Table 1 (*continued*)

Protein, source	$\epsilon_M^a \times 10^{-4}$	$A_{1cm}^{1\%\,b}$	nm[c]	Ref.	Comments[d]
Sulfhydryl oxidase					
Rat seminal vessel secretion		22.4	275	*122*	0.02 *M* NaPh, pH 6.8; data from Fig. 1 (*122*)
Superoxide dismutase					
Bacillus stearothermophilus		13.2	280	*123*	
		14.1	280	*124*	Lowry
Brassica campestris	7.4	18.0	278	*125*	mw = 41,000 (*125*)
Desulfovibrio desulfuricans	8.6		280	*126*	
Drosophila melanogaster	1.32	4.1	258	*127*	mw = 32,000 (*127*)
Euglena gracilis					
Protein 1	6.11[t]	10.63[t]	275	*128*	mw = 57,500 (*128*)
Protein 2	0.6718[t]		380	*128*	mw = 57,500 (*128*)
Green pea	0.0250		680	*129*	
Human erythrocytes					
SOD I		8.19	266	*130*	Neutral pH
		1.84	320–323	*130*	Neutral pH
Apo-SOD I		6.56	270–275	*130*	Neutral pH
		1.65	322–324	*130*	Neutral pH
SOD II		6.26	270–272	*130*	Neutral pH
Apo-SOD II		5.31	279–280	*130*	Neutral pH
SOD I		6.47	274–277	*130*	Acid pH
Apo-SOD I		5.91	278–279	*130*	Acid pH
SOD II		5.32	276	*130*	Acid pH
Apo-SOD II		5.01	279	*130*	Acid pH
Human liver	19.7		283	*131*	
	0.2050		480	*131*	
Maize [*Zea mays*]					
SOD-2		6.6[u]	250	*132*	5 m*M* KPh, pH 7.0
SOD-3		5.2[u]	280	*132*	5 m*M* KPh, pH 7.0
SOD-4		3.9[u]	280	*132*	5 m*M* KPh, pH 7.0
Methanobacterium bryanti	19.0		280	*133*	
	1.1		350	*133*	
Pisum sativum L.	12.0		275	*134*	
Testosterone-binding globulin					
Canine serum	9.47	12.46	280	*135*	mw = 76,000 (*135*)

Table 1 (*continued*)

Protein, source	$\epsilon_M^a \times 10^{-4}$	$A_{1cm}^{1\%\,b}$	nm[c]	Ref.	Comments[d]
Thermitase		18.0	nc	*136*	
Thioredoxin					
Anabaena sp.	1.37		280	*137*	AA
Bacteriophage T4	0.63[v]	6.06	280	*138*	mw = 10,400 (*138*) Refr.
Threonine dehydrogenase					
Escherichia coli K-12	23.3	16.6	280	*139*	0.05 *M* Tris-HCl, pH 8.4, 1 m*M* ME; mw = 140,000 (*139*)
Threonyl tRNA synthetase					
Rat liver	23.8	14.0	280	*140*	50 m*M* Tris HCl, 0.1 m*M* DTT, 0.1 m*M* EDTA, 10% glycerol, pH 7.5
Thrombin					
Human		17.3[w]	280	*141*	0.21 *M* NaCl, 20 m*M* NaPh, pH 7.2
		17.4[w]	280	*141*	1.0 *M* HOAc
		18.3[w]	280	*141*	0.10 *M* NaOH
Thrombocytin					
Bothrops atrex, Venom	2.3	6.35	280	*142*	0.15 *M* NaCl, AA, Dry wt, mw = 36,000 (*142*)
Thrombospondin					
Human platelets		9.5	280	*143*	Lowry
		8.85	280	*143*	KN
Thy-1 glycoprotein					
Rat brain		2.5	278	*144*	
Thymidylate synthease					
Lactobacillus casei amethopterin resistant	10.5	15.0	280	*145*	
Thyroglobulin					
Normal thyroid and nodular euthyroid goiter		—[x]		*146*	
Toxin					
Scorpion [*Androctonus mauretanicus mauretanicus*] Venom		15.6	280	*147*	AA
Wilting toxin [*Ceratocystis ulmi*]		4.40	278	*148*	60% aqueous EtOH; data from Fig. 4 (*148*)

(*continued*)

Table 1 (*continued*)

Protein, source	ϵ_M^a $\times 10^{-4}$	$A_{1cm}^{1\%\,b}$	nm[c]	Ref.	Comments[d]
Clostridium botulinum					
Type E toxin	21.6	13.5	278	*149*	mw = 160,000 (*149*)
Type C toxin					
Heavy chain		12.02	278	*150*	AA
Light chain		9.03	278	*150*	AA

[a]ϵ_M is the molar absorptivity with units of $M^{-1}cm^{-1}$ and is either the value reported in the reference cited or calculated from the $A_{1cm}^{1\%}$ value and the molecular weight.

[b]$A_{1cm}^{1\%}$ is the absorption for a 1% solution in a 1 cm cuvet and is either the value reported in the reference cited or calculated from the ϵ_M and the molecular weight. The relationship between ϵ_M, $A_{1cm}^{1\%}$, and molecular weight, mw, is $10\epsilon_M = (A_{1cm}^{1\%})$ (mw).

[c]Refers to the wavelength cited and may not be the peak of the absorption band.

[d]*Abbreviations used:* Ac, acetate; AmBi, ammonium bicarbonate; DTT, dithiothreitol; EDTA, ethylenediaminetetraacetic acid; GCl, guanidinium chloride; HOAc, acetic acid; ME, mercaptoethanol; Ph, phosphate; TEAHCl, triethanolamine hydrochloride; Tris, tris[hydroxymethyl]-aminomethane. *Methods of protein determination:* Dry wt, dry weight; AA, amino acid analysis; Lowry/Biuret, colorimetric methods; Refr., refractometry; Interf., interferometry; LS, corrected for light scattering; N/KN, nitrogen determination.

[e]12.3% *N*, air dried.

[f]Absorbance close to 1.00 cm^{-1} when concentration is 1 mg/mL (*10*).

[g]PPB is *p*-phenacylbromide.

[h]nc is not cited.

[i]This is the value for the oxidized form minus reduced form.

[j]mw = 66,000 (*66*).

[k]From *E. coli* MRE 600.

[l]These are reported in cm^2/g.

[m]These are $A_{1cm}^{1\%}$ values calculated from Fig. 3 of (*78*).

[n]This is the correct value. The value cited in ref. (*81*) is in error [personal communication from Dr. Krebs].

[o]In ref. (*80a*) this value is given as 1.30 citing (*80*) as the source. Data from Fig. 2 of ref. (*80a*) gives a value of $A_{1cm}^{1\%} = 12.0$.

[p]Pyridoxal phosphate loaded.

[q]All extinction data has been normalized to the value at 498 nm.

[r]Determined by titration with riboflavin.

[s]When the Lowry method is used for protein determination the value for $A_{1cm}^{1\%}$ is 17.5.

[t]Using the data given in Fig. 2 of ref. (*128*) I have calculated the following values: Protein 1, $\epsilon_M = 1.16 \times 10^4$, $A_{1cm}^{1\%} = 2.02$ (275 nm); Protein 2, $\epsilon_M = 3.73 \times 10^4$, $A_{1cm}^{1\%} = 13.59$ (275 nm); $\epsilon_M = 0.462$, $A_{1cm}^{1\%} = 1.68$ (380 nm).

[u]The data reported in Fig. 8 (*132*) are incorrect. The values given in Table 1 are based on correct data supplied by Drs. Scandalios and Baum.

[v]This is a correction of data reported in paper VI of this series [Kirschenbaum, D. M. (1972), *Int. J. Pep. Prot. Res.* **4**, 125].

[w]Concentration determined by refractometry. In neutral salt solution, at 280 nm, the $A_{1cm}^{1\%}$ = 17.9–23.3 (uncorrected for light scattering) and 16.9–23.3 (corrected for light scattering).

[x]Absorption at 280 and 315 nm varies with extent of iodination and morphological state of thyroid gland.

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