TABLE I

HYDRODYNAMIC PROPERTIES OF PROTEINS OF KNOWN STRUCTURE

Protein (source)(subunits)	Hydrodynamic data[a] $10^{13}s^0_{20,w}$	$10^7D^0_{20,w}$	$\bar{v}$[b]	Molecular weight composition S and D (% error)	f/f_0	Shape dimensions (a/b)[c]	f_e/f_0	f/f_e	Hydration g H_2O/g protein
(1) ACTH	0.736	13.19	0.717	4,690 (12)					
(bovine)	(12)	(12)		4,790 (+2.0)	1.447				
(2) Basic trypsin inhibitor	1.0	12.9[d]	0.718[e]	6,520[e]		29 × 19 × 19			
(bovine pancreas)	(13)			6,670 (+2.3)	1.321	(1.53)(15)	1.016	1.300	0.86
(3) Cytochrome C	1.83	13.0	0.715	12,310		25 × 25 × 37			
(equine)	(16)	(16)	(16)	11,990 (−2.6)	1.116	(1.48)(17)	1.014	1.101	0.24
(4) Ribonuclease-A	1.78	10.7	0.703	13,690		38 × 28 × 22			
(bovine)	(18)	(19)	(20)	13,600 (−0.7)	1.290	(1.52)(21)	1.016	1.269	0.73
(5) Lysozyme	1.91	11.3	0.703	14,320		45 × 30 × 30			
(hen)	(22)	(23)	(22)	13,800 (−3.6)	1.240	(1.50)(24)	1.015	1.221	0.57
(6) Myoglobin	1.97	11.3	0.745	17,800		44 × 44 × 25			
(sperm whale)	(25)	(26)	(26)	16,600 (−6.8)	1.170	(1.76)(27)	1.028	1.139	0.35
(7) Adenylate kinase	2.30	10.2	0.74	21,640		40 × 40 × 30			
(porcine)	(28)	(28)	(28)	21,030 (−2.8)	1.167	(1.33)(29)	1.007	1.159	0.41
(8) Trypsin	2.50	9.3	0.727	23,200		50 × 40 × 40[f]			
(bovine)	(30)	(30)		23,890 (+2.9)	1.187	(1.25)	1.004	1.183	0.47
(9) Bence Jones protein REI	2.6	10.0	0.726[g]	23,500[g]		40 × 43 × 28			
(human)(2)	(32)	(32)		23,020 (−2.1)	1.156	(1.48)(34)	1.013	1.142	0.35
(10) Chymotrypsinogen A	2.58	9.480	0.721	25,670		50 × 40 × 40			
(bovine)	(35)	(35)	(36)	23,660 (−7.8)	1.262	(1.25)(37)	1.004	1.257	0.71
(11) Elastase	2.6	9.5	0.73	25,900		55 × 40 × 38			
(porcine)	(38)	(38)	(38)	24,600 (−5.0)	1.214	(1.41)(39)	1.010	1.202	0.53
(12) Subtilysin (novo)	2.77	9.04	0.731	27,530		48 × 44 × 40			
(B. amyloliq.)	(40)	(40)		27,630 (+0.4)	1.181	(1.14)(41)	1.002	1.179	0.47
(13) Carbonic anhydrase B	3.23	10.7	0.729	28,800		47 × 41 × 41[h]			
(human)	(42)	(42)		27,020 (−6.0)	1.053	(1.15)	1.002	1.051	0.12
(14) Superoxide dismutase	3.35	8.92[i]	0.729	33,900[i]		72 × 40 × 38			
(bovine)(2)	(44)			33,600 (−0.9)	1.132	(1.85)(46)	1.034	1.095	0.23
(15) Carboxypeptidase A	3.55	9.2	0.733	34,500		50 × 42 × 38			
(bovine)	(47)	(47)		35,040 (+1.6)	1.063	(1.25)(48)	1.004	1.058	0.14
(16) Phosphoglycerate kinase	3.09	6.38[j]	0.749	45,800 (50)		70 × 45 × 35			
(yeast)	(49)			46,800 (+2.2)	1.377	(1.75)(51)	1.028	1.339	1.04
(17) Concanavalin A	3.8	6.34[k]	0.732	51,260		80 × 45 × 30			
(jack bean)(2)	(52)			54,240 (+5.8)	1.299	(2.13)(53)	1.053	1.233	0.64
(18) Hemoglobin, oxy	4.22	6.02	0.750	64,610		70 × 55 × 55			
(equine)(4)	(54)	(54)	(55)	67,980 (+5.2)	1.263	(1.22)(56)	1.005	1.257	0.74
(19) Serum albumin	4.44	6.09	0.734	66,300		140 × 40 × 40			
(bovine)	(57)	(58)	(59)	66,470 (+2.6)	1.308	(3.5) (60)	1.147	1.140	0.35
(20) Malate dehydrogenase	4.53	5.76[l]	0.742	74,900[l]		64 × 64 × 45			
(porcine cytosol)(2)	(61)		(61)	73,900 (−1.4)	1.344	(1.42)(62)	1.011	1.329	1.00
(21) Alcohol dehydrogenase	5.08	6.23	0.750	79,870		45 × 55 × 110			
(equine)(2)	(63)	(63)	(63)	79,070 (−1.0)	1.208	(2.2) (64)	1.058	1.141	0.37
(22) Lactate dehydrogenase	7.54	4.99[m]	0.74	146,200		74 × 74 × 84[n]			
(dogfish)(4)	(65)		(66)	141,000 (−3.5)	1.273	(1.20)	1.003	1.269	0.77

[a] Numbers found in parentheses below data values refer to reference numbers.

[b] The priority for determining the "best" $\bar{v}$ is: "best" values from reviews: experimental values:calculations by these authors from current amino acid compositions found in Dayhoff (11) (where no reference is shown). In cases where D was calculated from sedimentation equilibrium data, a corrected value for the molecular weight was used when the "best" value for $\bar{v}$ differed from that used by the original authors.

[c] In calculating axial ratios, the mean value of the two nearest dimensions was taken as twice the radius of gyration, thus some of the ellipsoids of revolution are oblate and others prolate.

[d] Calculated from values of molecular weight obtained from sedimentation equilibrium data in Cerwinsky *et al.* (14).

[e] Calculated from the amino acid composition found in Kassell *et al.* (13).

[f] Assume like chymotrypsinogen A, as indicated in Bode and Schwager (31).

[g] Calculated from amino acid composition in Palm and Hilschmann (33).

[h] Dimensions used are for form C, from Kannan *et al.* (43).

[i] Calculated from sedimentation equilibrium data and amino acid composition found in Keele, Jr. *et al.* (45).

[j] Calculated from sedimentation equilibrium data found in Krietsch and Bucher (50).

[k] Calculated from sedimentation equilibrium data found in McKenzie *et al.* (52).

[l] Calculated from data found in Gerding and Wolfe (61).

[m] Calculated from values of molecular weight obtained by the method of Ehrenberg in Pesce *et al.* (65).

[n] Dimensions were estimated from molecular photographs in Adams *et al.* (67).

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