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## A two-dimensional gel database of human plasma proteins

An updated two-dimensional electrophoretic map of human plasma proteins is presented, together with a complete listing of the individual protein spots, their locations, size and isoelectric points relative to internal charge standards. Forty-nine polypeptide species are identified, many consisting of multiple spots differing in glycosylation or sequence (e.g., immunoglobulins). A further series of 35 as yet uncharacterized proteins is indicated.

### Contents

1 Introduction.....	883
2 Materials and methods.....	883
3 Results.....	884
3.1 Plasma protein 2-D map.....	884
3.2 Plasma protein tables.....	884
4 Conclusions.....	884
5 References.....	884
6 Addendum 1: Figures 2-7.....	885
7 Addendum 2: Tables 1-4.....	891
Table 1. Master table of proteins in the human plasma protein database, showing spot master number, gel position ( <i>x</i> and <i>y</i> ), isoelectric point relative to CPK standards, predicted molecular mass (from the standard curve of Fig. 1), and identification information.....	891
Table 2. Sets of spots identified in the plasma protein pattern, showing the abbreviated population name (POP name) and the corresponding identifying label.....	898
Table 3. Master spot numbers of spots comprising identified proteins (IDS: series populations) and named but unidentified proteins (PLS: series).....	899
Table 4. Membership of individual spots in the populations shown in Table 3.....	901

### 1 Introduction

Following the introduction of high-resolution two-dimensional (2-D) electrophoresis [1-4], the human plasma pattern was one of the first on which a significant number of proteins was identified [5]. This paper provides an updated 2-D map of human plasma, extending the previous published versions [5-10]. A complete table of spot positions, fitted sodium dodecyl sulfate (SDS) molecular masses and isoelectric points (specified relative to the creatine phosphokinase, CPK, charge standard system [11]) is provided, together with tables of identified protein spots sorted by spot number and by identification. Several additional proteins have been identified, primarily as a result of the efforts of Hochstrasser's group [12-14] on lipoproteins and associated polypeptides.

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Abbreviations: 2-D, two-dimensional; CPK, creatine phosphokinase; MSN, master spot number; SDS, sodium dodecyl sulfate

### 2 Materials and methods

The pattern used here is identical to that presented in [8], and the reader is referred to that publication for a complete description of the methods used in its creation. Briefly, the pattern is a composite of several silver-stained 20 × 25 cm ISO-DALT<sup>®</sup> [15-19] 2-D gels run at various protein loadings, using Pharmacia wide-range carrier ampholytes (still the best choice for plasma) and SDS-gradient polyacrylamide slab gels. Carbamylated rabbit muscle CPK standards (now available from Pharmacia and BDH) were made according to [11]. The positions of plasma proteins within the range covered by the CPK charge train were interpolated linearly with respect to the two adjacent CPK spots. SDS molecular mass calibration was undertaken using a curve fitted to the known proteins (Fig. 1). This is an improved calibration scale as compared to the earlier published values. The numbers of residues present in the proteins used for internal standardization were taken from the Protein Identification Resource (PIR) sequence database [20]. We selected the best-fitting simple equation using the program "Tablecurve" on a PC, and multiplied the resulting predicted values by 112 (the weighted average mass of amino acids in sequenced proteins) to give the predicted molecular masses. The best-fitting equation was given by  $y = \exp(a+bx)$ , where *y* is the number of residues, *x* is the gel *Y* coordinate, *a* is 7.624669 and *b* is -0.001887. The gel images were originally processed using the TYCHO system [21-26], and the database converted to relational form and expanded using the commercially-available Kepler<sup>®</sup> software system (Large Scale Biology Corp.). Graphical results were prepared as Postscript output from the Kepler<sup>®</sup> system and printed on an Apple laserwriter or an ultra-high-resolution Postscript-compatible Linotronic output device.

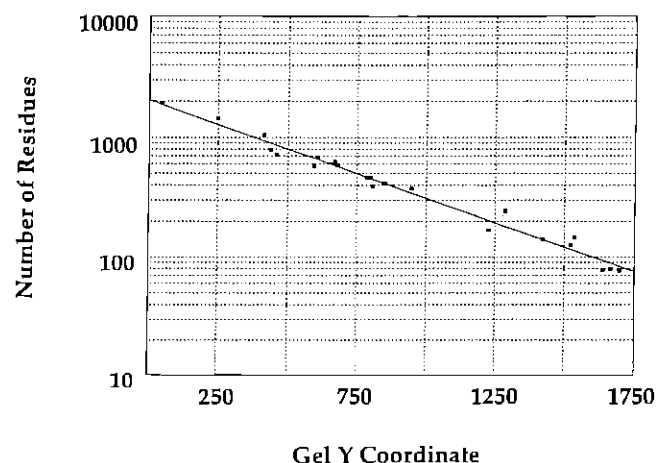


Figure 1. Plot of gel *Y* coordinate vs. number of amino acid residues in known plasma proteins.

Greyscale maps were reproduced from the workstation screen using a Seikosha video-printer. Patterns are shown in the standard orientation, with high molecular weight at the top and acidic proteins to the left.

### 3 Results

#### 3.1 Plasma protein 2-D map

The plasma protein pattern (Fig. 2) contains many easily remembered landmarks. Master spot numbers (MSN's) associated with all spots are shown in Fig. 3 (the acidic portion of the pattern) and Fig. 4 (the basic portion). The presence of numerous glycosylation trains in the plasma pattern leads to high numerical spot density in the higher molecular weight region; to identify spots in this region we have included enlarged plots of the acidic (Fig. 5) and basic (Fig. 6) portions of this area. Finally we have included a schematic plot of the entire pattern with the densest spots filled, as an aid to cross-locating protein spots between Fig. 2 and the numbered maps.

#### 3.2 Plasma protein tables

Table 1 lists all spots in the plasma protein database, with X and Y positions, isoelectric point relative to the CPK standards and SDS molecular weight computed according to the curve of Fig. 1. Table 2 lists the identified proteins in the pattern as spot populations, each having an abbreviated name (the POP name) and a label identifying the population more fully. Currently, 49 groups of spots are identified. Table 3 lists the spots (by master spot number) comprising each population. This table includes a series of as yet unidentified proteins (the PLS: series), some of which have been converted (through identification) to IDS: populations since the original nomenclature was devised [8]. PLS:33 is now listed as Apo-D lipoprotein, PLS:31 as Apo A-IV, PLS:29 as NA1 and PLS:30 as NA2 (D. Hochstrasser, personal communication and [12]). Table 4 presents the same data sorted by spot to enable lookup in either direction (population or spot). For details on the methods used to identify other proteins, the reader is referred to [8].

### 4 Conclusions

The human plasma protein map has turned out to be useful in a number of clinical and other investigations. Because of the remarkably constant appearance of the pattern in a range of different O'Farrell-type 2-D systems, it remains perhaps the best system for validating the gels themselves. Many hundreds of large-format reference plasma maps have been distributed (by ourselves and by Hoefer Scientific Instruments), and, given the existence of periodic updates such as the present paper, the plasma pattern seems destined to grow in usefulness for some time to come.

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6 Addendum 1: Figures 2-7

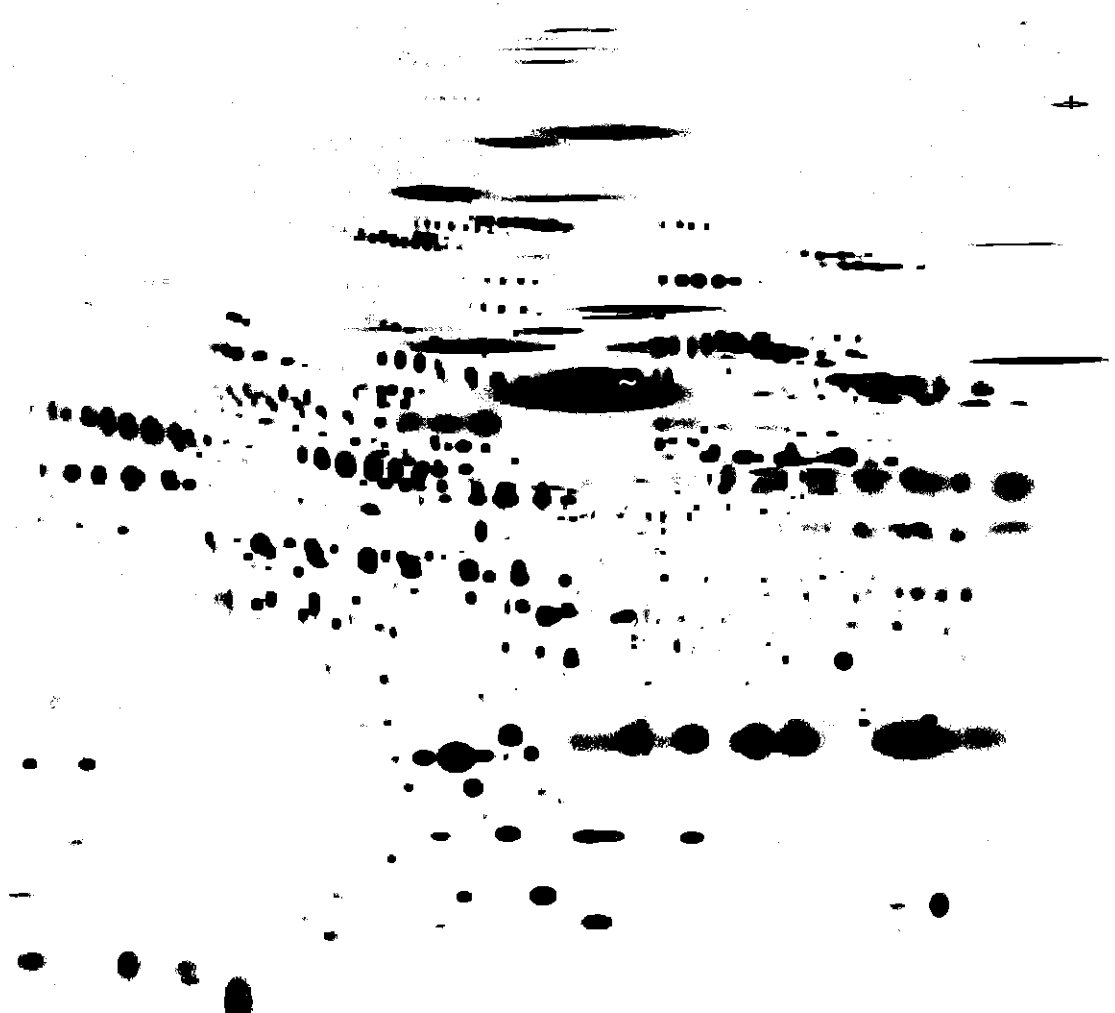


Figure 2. Greyscale image of plasma protein master pattern.

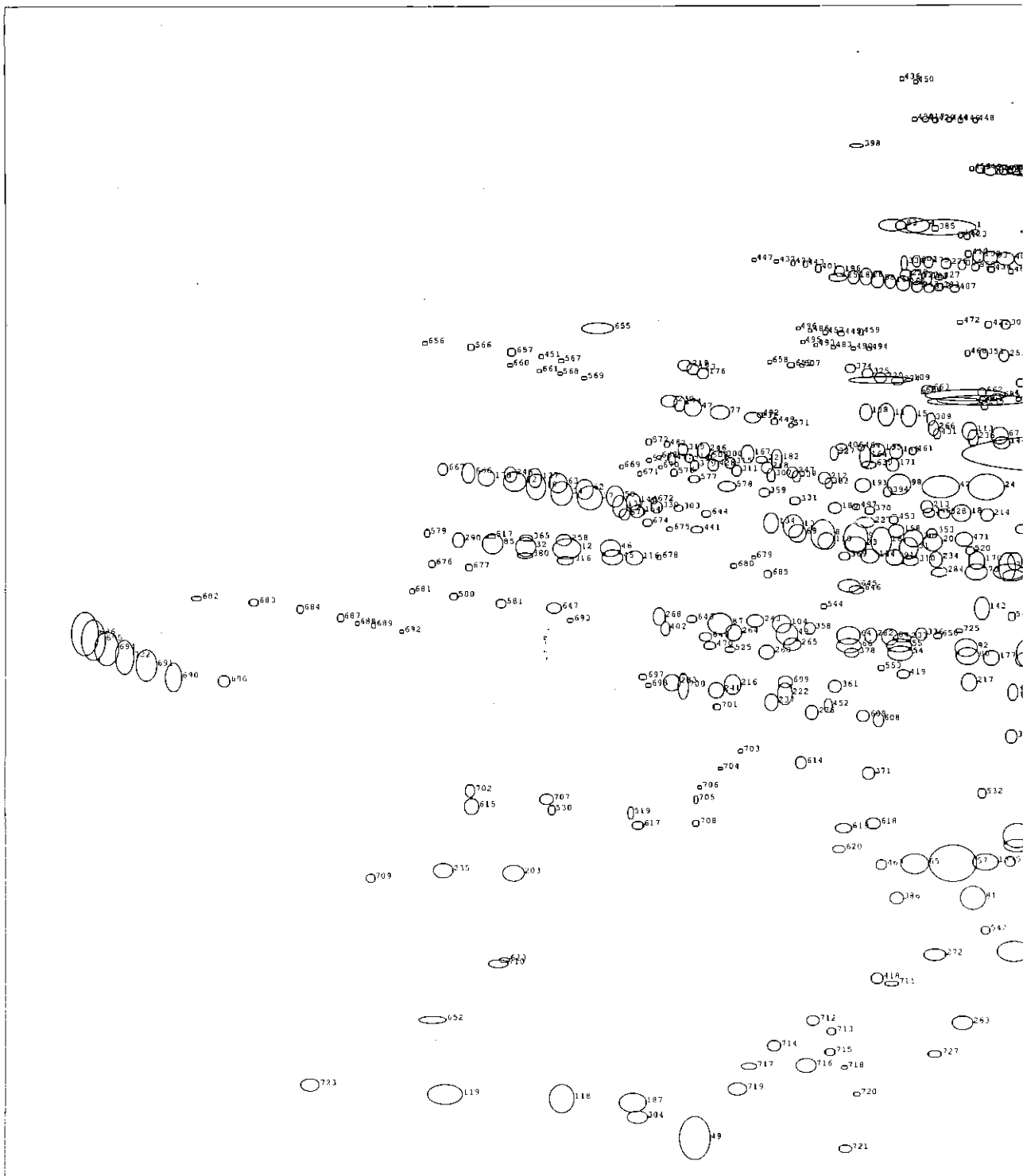


Figure 3. Acidic (left) portion of plasma protein map with spots numbered.

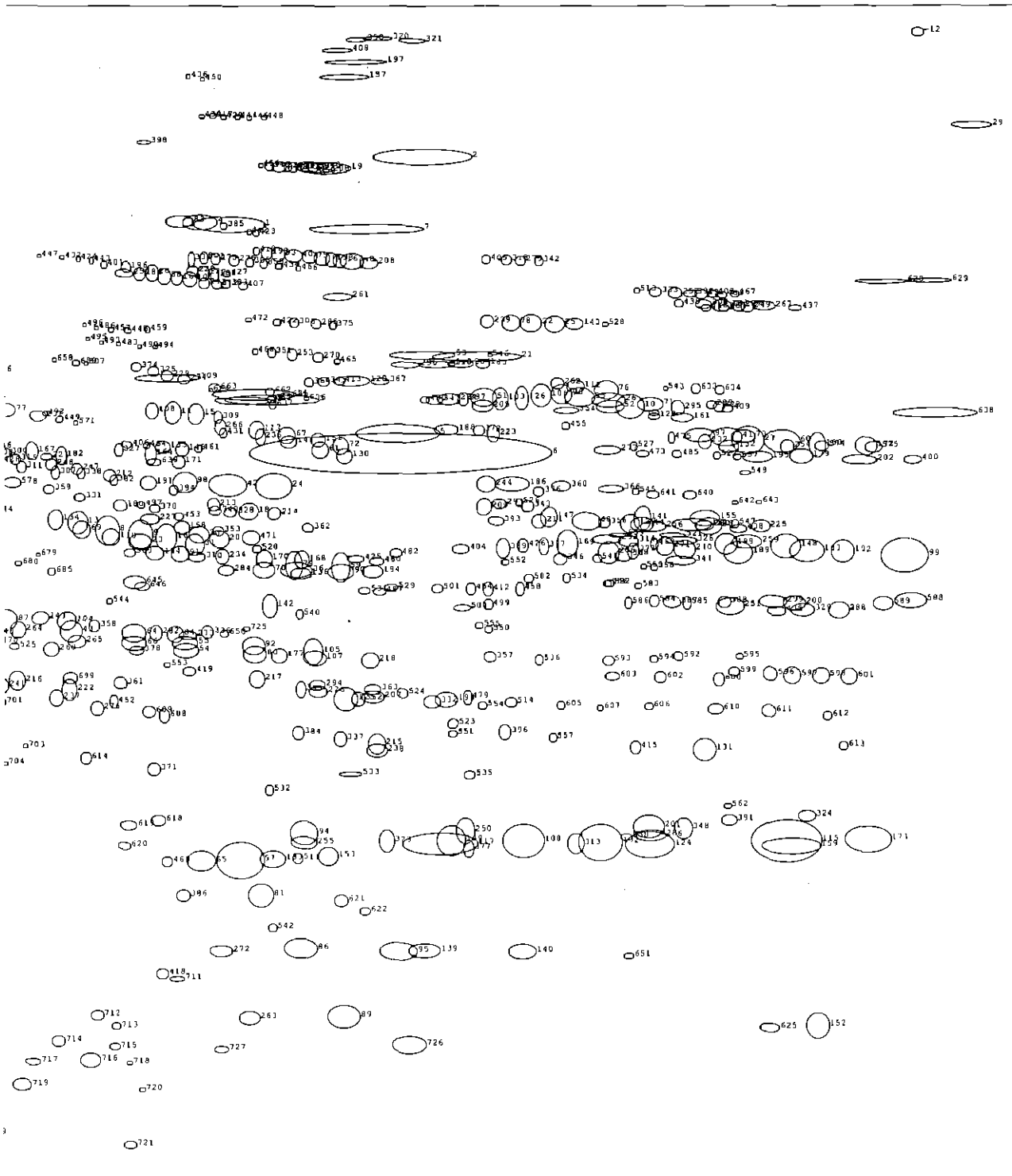


Figure 4. Basic (right) portion of plasma protein map with spots numbered.



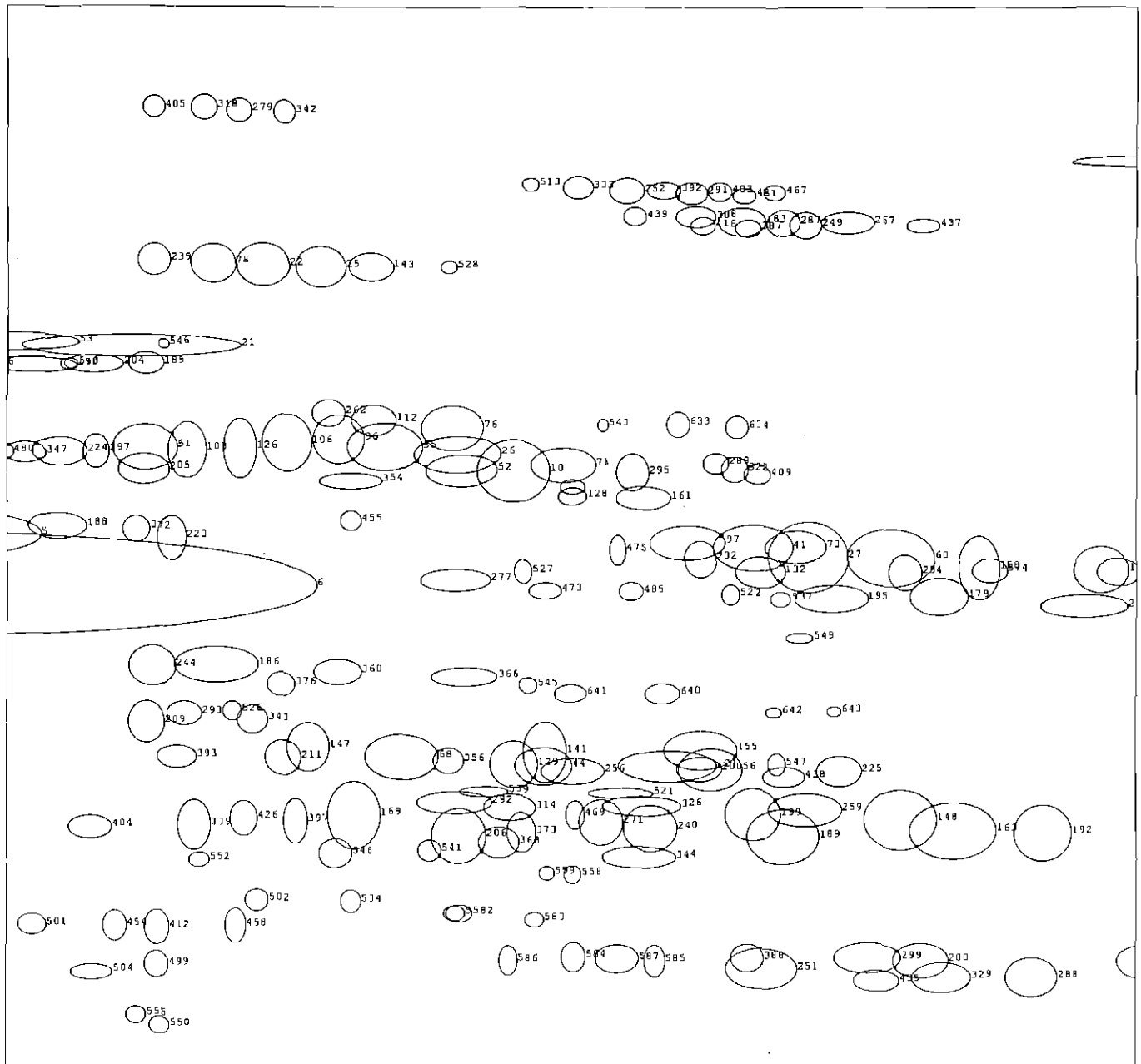


Figure 6. Basic (right) portion of the crowded region of the plasma protein map.

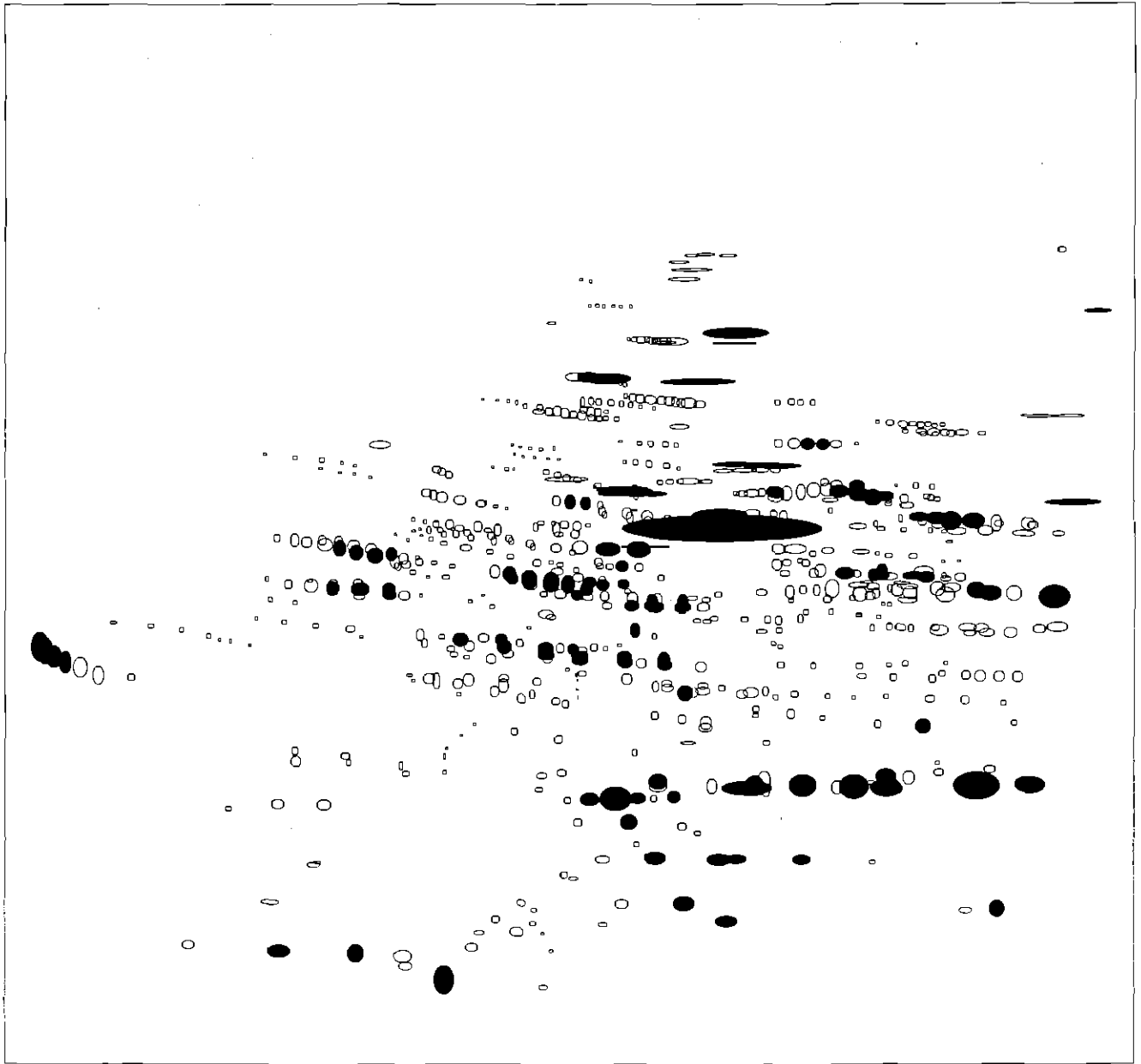


Figure 7. Schematic diagram of the plasma protein map showing most abundant proteins as filled ellipses for reference.



## 7 Addendum 2: Tables 1-4

**Table 1.** Master table of proteins in the human plasma protein database, showing spot master number, gel position (x and y), isoelectric point relative to CPK standards, predicted molecular mass (from the standard curve of Fig. 1), and identification information

MSN	X	Y	CPK pI	SDS MW	MSN	X	Y	CPK pI	SDS MW
1	837	334	-17.6	122,100	52	1371	605	-4.8	73,200
2	1108	232	-11.3	148,000	53	1108	528	-11.3	84,700
3	898	594	-16.0	74,700	54	779	972	-19.2	36,600
4	797	331	-18.7	122,800	55	778	960	-19.2	37,500
5	1075	644	-11.9	68,000	56	1512	786	-1.6	52,000
6	1079	674	-11.9	64,200	57	855	1286	-17.2	20,200
7	1030	341	-12.8	120,600	59	996	845	-13.6	46,500
8	670	791	-22.2	51,500	60	1615	659	>0.0	66,200
9	717	797	-21.0	51,000	61	967	669	-14.4	64,900
10	1400	605	-4.0	73,200	62	335	725	-32.7	58,400
11	759	614	-19.8	71,900	63	298	716	-33.7	59,400
12	311	814	-33.3	49,400	64	706	945	-21.3	38,500
13	628	779	-23.5	52,700	65	800	1287	-18.5	20,200
14	874	586	-16.7	75,800	66	707	960	-21.2	37,400
15	792	617	-18.8	71,600	67	921	647	-15.5	67,600
16	752	801	-20.0	50,600	68	1338	779	-5.5	52,700
18	867	762	-17.0	54,400	69	634	790	-23.3	51,600
19	969	250	-14.3	143,200	70	888	850	-16.3	46,100
20	826	803	-17.8	50,400	71	1428	602	-3.4	73,600
21	1185	530	-9.3	84,300	72	996	663	-13.6	65,600
22	1260	481	-7.3	92,500	73	1560	652	-0.6	67,000
23	716	807	-21.0	50,000	74	969	383	-14.3	111,300
24	902	724	-15.9	58,500	75	952	382	-14.8	111,600
25	1292	482	-6.5	92,300	76	1366	579	-5.0	76,800
26	1369	595	-4.9	74,600	77	525	610	-26.2	72,500
27	1567	658	-0.4	66,300	78	1231	481	-7.9	92,600
28	731	406	-20.6	106,600	79	931	843	-15.3	46,700
29	1881	184	>0.0	162,200	80	875	977	-16.7	36,300
30	798	798	-18.6	50,900	81	883	1339	-16.5	18,300
31	792	812	-18.8	49,500	82	237	714	<-35.0	59,600
32	253	811	<-35.0	49,700	83	768	330	-19.5	123,100
33	858	596	-17.2	74,500	84	764	947	-19.6	38,400
34	303	731	-33.5	57,700	85	207	806	<-35.0	50,100
35	1328	591	-5.7	75,200	86	940	1419	-15.0	15,800
36	934	850	-15.2	46,100	87	525	926	-26.1	39,900
37	343	738	-32.6	57,000	88	747	411	-20.1	105,600
38	268	721	-34.6	58,800	89	1001	1521	-13.5	13,000
40	929	381	-15.3	111,700	90	996	852	-13.6	45,900
41	1536	652	-1.1	67,000	91	772	826	-19.4	48,300
42	837	723	-17.6	58,600	92	873	965	-16.8	37,200
43	618	943	-23.8	38,700	93	907	379	-15.8	112,100
44	1417	784	-3.7	52,200	94	945	1245	-14.9	21,900
45	374	827	-31.7	48,200	95	1076	1423	-11.9	15,600
46	372	813	-31.8	49,400	96	1302	586	-6.2	75,800
47	487	604	-26.9	73,300	97	1499	649	-1.8	67,400
48	1010	388	-13.3	110,300	98	778	719	-19.2	59,000
49	491	1696	-26.8	9,300	99	1788	831	>0.0	47,800
50	378	736	-31.5	57,200	100	1250	1257	-7.5	21,400
51	1193	591	-9.1	75,200	101	783	416	-19.1	104,500

MSN	X	Y	CPK pI	SDS MW	MSN	X	Y	CPK pI	SDS MW
102	1359	1259	-5.1	21,300	153	979	1280	-14.1	20,500
103	1217	593	-8.4	74,900	154	409	758	-31.0	54,900
104	612	927	-24.0	39,900	155	1507	774	-1.7	53,200
105	957	973	-14.6	36,600	157	1000	111	-13.5	186,200
106	1274	588	-7.0	75,600	158	774	787	-19.3	52,000
107	959	983	-14.6	35,900	159	1629	1265	>0.0	21,100
108	730	611	-20.6	72,400	160	765	414	-19.6	105,000
109	752	562	-20.0	79,400	161	1474	622	-2.4	70,900
110	675	801	-22.1	50,600	162	994	388	-13.7	110,300
112	1322	575	-5.8	77,500	163	1650	823	>0.0	48,500
113	878	640	-16.6	68,500	164	730	676	-20.6	64,100
114	736	824	-20.4	48,400	167	563	672	-25.3	64,600
115	1622	1257	>0.0	21,400	168	942	834	-15.0	47,500
116	405	827	-31.0	48,100	169	1311	813	-6.0	49,400
117	1133	1261	-10.7	21,200	170	889	833	-16.3	47,600
118	304	1637	-33.5	10,400	171	769	688	-19.5	62,600
119	141	1631	<-35.0	10,600	172	1734	666	>0.0	65,300
120	1010	566	-13.3	78,800	173	1737	1255	>0.0	21,500
121	1488	784	-2.1	52,200	174	469	598	-27.7	74,200
122	802	408	-18.5	106,200	176	502	552	-26.6	80,900
123	487	545	-26.9	82,000	177	909	979	-15.8	36,100
124	1429	1263	-3.4	21,200	178	198	707	<-35.0	60,400
125	1002	1046	-13.5	31,900	179	1642	682	>0.0	63,300
126	1247	592	-7.6	75,000	180	687	754	-21.8	55,300
127	266	708	-34.7	60,300	181	817	409	-18.0	106,000
128	1434	621	-3.3	71,100	182	605	679	-24.2	63,700
129	1401	783	-4.0	52,300	183	1529	456	-1.2	97,100
130	1001	679	-13.5	63,700	184	713	407	-21.1	106,300
131	1506	1122	-1.7	27,600	185	1193	541	-9.1	82,700
132	1540	667	-1.0	65,200	186	1233	722	-7.9	58,700
133	901	1285	-16.0	20,300	187	404	1643	-31.0	10,300
134	597	774	-24.4	53,200	188	1143	639	-10.4	68,700
135	747	666	-20.1	65,300	189	1553	827	-0.7	48,200
136	940	856	-15.0	45,600	190	1128	542	-10.8	82,500
137	385	751	-31.3	55,600	191	727	720	-20.7	59,000
138	982	386	-14.0	110,700	192	1701	825	>0.0	48,300
139	1112	1422	-11.2	15,700	193	1141	1046	-10.5	31,800
140	1249	1423	-7.5	15,600	194	1040	852	-12.6	45,900
141	1418	775	-3.6	53,100	195	1580	683	-0.1	63,200
142	896	905	-16.1	41,600	196	694	398	-21.6	108,300
143	1320	483	-5.8	92,200	197	1016	89	-13.1	194,100
144	924	658	-15.4	66,300	198	891	377	-16.2	112,600
145	774	669	-19.3	64,900	199	1536	814	-1.1	49,400
146	404	744	-31.0	56,400	200	1632	901	>0.0	41,900
147	1286	772	-6.7	53,400	201	1428	1236	-3.4	22,200
148	1620	817	>0.0	49,100	202	1724	688	>0.0	62,600
149	1149	1256	-10.3	21,400	203	236	1300	<-35.0	19,700
150	1665	665	>0.0	65,400	204	1163	541	-9.9	82,600
151	964	654	-14.4	66,800	205	1192	604	-9.1	73,300
152	1667	1535	>0.0	12,700	206	1370	826	-4.9	48,300

MSN	X	Y	CPK pI	SDS MW	MSN	X	Y	CPK pI	SDS MW
207	1040	1042	-12.6	32,100	258	307	801	-33.4	50,600
208	1034	391	-12.7	109,600	259	1566	811	-0.4	49,700
209	1194	758	-9.0	54,900	260	590	970	-24.6	36,800
210	907	248	-15.8	143,700	261	990	441	-13.8	99,900
211	1272	779	-7.0	52,800	262	1297	570	-6.4	78,200
212	672	709	-22.2	60,200	263	869	1524	-16.9	12,900
213	817	752	-18.0	55,500	264	544	941	-25.7	38,900
214	903	765	-15.9	54,100	265	626	958	-23.6	37,600
215	1046	1113	-12.5	28,100	266	827	636	-17.8	69,100
216	542	1018	-25.8	33,600	267	1589	456	>0.0	96,900
217	878	1015	-16.6	33,800	268	440	916	-29.1	40,700
218	1036	987	-12.7	35,600	270	964	530	-14.4	84,300
219	476	540	-27.3	82,800	271	1450	818	-3.0	49,000
220	787	404	-19.0	107,000	272	829	1423	-17.8	15,600
221	584	680	-24.8	63,600	273	819	386	-18.0	110,800
222	616	1031	-23.9	32,800	274	775	564	-19.3	79,100
223	1208	646	-8.6	67,800	275	845	388	-17.4	110,400
224	1144	594	-10.4	74,800	276	654	1060	-22.7	31,000
225	1585	788	0.0	51,900	277	1368	671	-4.9	64,600
226	964	1034	-14.4	32,600	278	927	248	-15.4	143,600
227	730	773	-20.6	53,300	279	1245	389	-7.6	110,200
229	752	559	-20.0	79,900	280	1506	786	-1.7	52,000
230	454	594	-28.4	74,800	282	737	945	-20.4	38,500
231	570	619	-25.1	71,300	283	458	1015	-28.2	33,800
232	1506	659	-1.7	66,100	284	835	850	-17.6	46,100
233	782	949	-19.1	38,300	285	960	481	-14.5	92,600
234	830	829	-17.7	47,900	286	1430	1249	-3.4	21,700
235	138	1297	<-35.0	19,800	287	1553	456	-0.7	96,900
236	884	650	-16.5	67,300	288	1695	912	>0.0	41,000
237	597	1044	-24.4	32,000	289	1515	603	-1.5	73,600
238	1045	1123	-12.5	27,500	290	159	800	<-35.0	50,600
239	1198	478	-8.9	93,000	291	1501	439	-1.8	100,300
240	1478	821	-2.3	48,700	292	1367	806	-4.9	50,100
241	519	1026	-26.3	33,100	293	1215	752	-8.4	55,500
242	803	422	-18.5	103,400	294	963	1024	-14.5	33,200
243	574	923	-25.0	40,200	295	1468	607	-2.6	72,900
244	1197	723	-9.0	58,600	296	1085	542	-11.7	82,400
245	231	703	<-35.0	60,900	297	1165	594	-9.9	74,800
246	503	666	-26.6	65,300	298	960	253	-14.5	142,400
247	627	699	-23.6	61,300	299	1602	900	>0.0	42,000
248	591	692	-24.6	62,100	300	524	675	-26.2	64,200
249	1566	458	-0.4	96,600	301	955	247	-14.7	143,800
250	1169	1242	-9.8	22,000	302	803	384	-18.5	111,100
251	1541	906	-1.0	41,500	303	468	753	-27.7	55,400
252	1464	437	-2.6	100,500	304	410	1665	-30.9	9,900
253	927	527	-15.4	84,800	305	867	390	-17.0	109,800
254	1623	667	>0.0	65,100	306	929	480	-15.3	92,700
255	945	1260	-14.9	21,300	307	597	704	-24.4	60,800
256	1434	787	-3.3	51,900	308	1503	453	-1.7	97,500
257	691	407	-21.7	106,400	309	823	622	-17.9	71,000

MSN	X	Y	CPK pI	SDS MW	MSN	X	Y	CPK pI	SDS MW
310	795	831	-18.7	47,800	361	687	1021	-21.8	33,400
311	548	696	-25.6	61,600	362	950	787	-14.8	52,000
312	820	424	-17.9	103,000	363	1040	1030	-12.6	32,800
313	1323	1261	-5.8	21,200	364	950	568	-14.8	78,500
314	1398	809	-4.1	49,800	365	254	798	<-35.0	50,900
315	540	685	-25.8	63,000	366	1373	730	-4.8	57,800
316	309	832	-33.4	47,700	367	1050	567	-12.5	78,700
317	943	248	-15.0	143,600	368	1392	830	-4.2	47,900
318	1226	387	-8.1	110,600	369	701	824	-21.4	48,500
319	474	665	-27.4	65,400	370	736	757	-20.4	54,900
320	1045	54	-12.5	207,000	371	734	1151	-20.5	26,100
321	1093	58	-11.6	205,700	372	1188	641	-9.2	68,500
322	1525	606	-1.3	73,100	373	1405	824	-3.9	48,500
323	1060	1257	-12.3	21,400	374	709	545	-21.2	82,000
324	1651	1221	>0.0	22,900	375	983	483	-13.9	92,200
325	733	552	-20.5	80,900	376	1270	734	-7.0	57,400
326	1473	808	-2.4	49,900	377	1173	1269	-9.6	20,900
327	686	671	-21.8	64,700	378	710	971	-21.1	36,700
328	841	763	-17.5	54,300	379	491	689	-26.8	62,500
329	1644	912	>0.0	41,000	380	252	824	<-35.0	48,400
330	437	752	-29.2	55,500	381	937	247	-15.1	143,800
331	630	741	-23.4	56,600	382	678	716	-22.0	59,400
332	1122	1049	-11.0	31,700	383	834	423	-17.7	103,300
333	1436	435	-3.3	100,900	384	937	1097	-15.1	29,000
334	785	386	-19.0	110,600	385	829	335	-17.8	121,800
336	809	944	-18.3	38,600	386	775	1339	-19.3	18,300
337	995	1105	-13.7	28,500	387	1533	460	-1.1	96,300
338	632	705	-23.4	60,600	388	1533	900	-1.1	42,000
339	1221	819	-8.2	48,900	391	1541	1227	-1.0	22,600
340	820	761	-17.9	54,500	392	1485	437	-2.1	100,600
341	920	247	-15.5	143,800	393	1211	779	-8.5	52,800
342	1271	389	-7.0	110,000	394	762	730	-19.7	57,800
343	1255	756	-7.4	55,100	395	939	1031	-15.1	32,800
344	1472	839	-2.5	47,100	396	1224	1095	-8.1	29,100
345	971	567	-14.3	78,700	397	1278	817	-6.8	49,100
346	1301	836	-6.3	47,300	398	718	209	-20.9	154,600
347	1124	595	-10.9	74,600	400	1799	688	>0.0	62,700
348	1477	1238	-2.3	22,200	401	663	394	-22.5	109,000
349	893	247	-16.2	144,000	402	449	934	-28.6	39,400
350	1016	57	-13.1	206,200	403	1517	438	-1.5	100,400
351	898	524	-16.0	85,300	404	1162	820	-10.0	48,800
352	1020	1045	-13.0	31,900	405	1197	387	-9.0	110,600
353	825	791	-17.8	51,600	406	697	662	-21.5	65,800
354	1309	611	-6.1	72,300	407	857	425	-17.2	102,800
355	886	393	-16.4	109,200	408	989	71	-13.8	200,600
356	1364	781	-5.0	52,500	409	1538	609	-1.0	72,700
357	1203	981	-8.8	36,000	410	876	373	-16.7	113,400
358	651	935	-22.8	39,300	411	459	678	-28.2	63,800
359	587	729	-24.7	58,000	412	1199	881	-8.9	43,500
360	1302	727	-6.3	58,200	413	994	566	-13.7	78,900

MSN	X	Y	CPK pI	SDS MW	MSN	X	Y	CPK pI	SDS MW
414	483	678	-27.0	63,800	467	1548	438	-0.8	100,300
415	1409	1119	-3.8	27,800	468	875	523	-16.7	85,500
416	1507	458	-1.7	96,600	469	1435	813	-3.3	49,400
417	815	170	-18.1	166,400	470	511	959	-26.4	37,500
418	747	1458	-20.1	14,600	471	870	802	-16.9	50,500
419	783	1003	-19.1	34,500	472	865	476	-17.0	93,400
422	905	479	-15.9	92,800	473	1418	678	-3.6	63,900
423	875	348	-16.7	119,000	475	1460	654	-2.7	66,800
424	627	385	-23.5	110,900	479	1171	1043	-9.7	32,100
425	1017	833	-13.1	47,600	480	1111	595	-11.2	74,700
426	1249	815	-7.5	49,200	481	1531	440	-1.2	100,000
427	835	408	-17.6	106,200	482	1072	825	-12.0	48,400
428	516	688	-26.3	62,600	483	684	512	-21.8	87,300
429	829	171	-17.8	166,000	485	1467	678	-2.6	63,800
430	799	170	-18.6	166,300	486	652	488	-22.8	91,400
431	832	644	-17.7	68,000	487	1049	884	-12.5	43,300
432	604	383	-24.2	111,300	490	713	515	-21.1	86,800
434	908	397	-15.8	108,400	492	580	615	-24.8	71,900
435	1607	913	>0.0	40,900	493	660	509	-22.5	87,700
436	781	111	-19.1	186,100	494	735	515	-20.4	86,700
437	1633	458	>0.0	96,600	495	641	504	-23.1	88,500
438	1554	791	-0.7	51,500	496	635	484	-23.3	92,100
439	1469	453	-2.5	97,600	497	717	752	-21.0	55,500
440	967	247	-14.4	143,900	499	1200	904	-8.9	41,700
441	493	786	-26.8	52,100	501	1128	879	-10.8	43,600
442	865	345	-17.0	119,500	502	1257	864	-7.3	44,900
443	645	388	-23.0	110,300	503	968	255	-14.3	141,600
444	849	171	-17.3	166,000	504	1163	908	-9.9	41,400
445	696	492	-21.5	90,700	507	640	540	-23.2	82,800
446	865	173	-17.0	165,600	508	509	677	-26.5	63,900
447	572	381	-25.1	111,800	510	1149	542	-10.3	82,500
448	886	172	-16.4	165,700	511	936	1284	-15.1	20,300
449	601	625	-24.3	70,600	513	1409	433	-3.8	101,200
450	801	115	-18.5	184,600	514	1232	1050	-7.9	31,600
451	275	526	-34.4	85,000	517	205	796	<-35.0	51,100
452	677	1050	-22.0	31,600	519	400	1211	-31.0	23,300
453	770	770	-19.5	53,700	520	879	819	-16.6	48,900
454	1176	880	-9.6	43,600	521	1461	800	-2.7	50,600
455	1309	636	-6.1	69,100	522	1523	681	-1.3	63,500
456	881	246	-16.5	144,200	523	1151	1082	-10.2	29,700
457	673	491	-22.2	90,900	524	1080	1036	-11.8	32,500
458	1245	880	-7.6	43,600	525	538	966	-25.9	37,000
459	724	490	-20.8	90,900	526	1243	750	-7.7	55,700
460	1046	837	-12.5	47,300	527	1406	666	-3.9	65,200
461	797	668	-18.6	65,000	528	1364	483	-5.0	92,300
462	451	659	-28.5	66,200	529	1065	877	-12.1	43,800
463	753	1289	-20.0	20,200	530	289	1206	-33.9	23,600
464	724	663	-20.8	65,700	531	1028	882	-12.9	43,400
465	990	536	-13.8	83,400	532	896	1182	-16.1	24,600
466	936	400	-15.1	107,900	533	1009	1158	-13.3	25,800

MSN	X	Y	CPK pI	SDS MW	MSN	X	Y	CPK pI	SDS MW
534	1310	865	-6.1	44,800	593	1370	986	-4.9	35,600
535	1174	1159	-9.6	25,700	594	1434	985	-3.3	35,700
536	1272	986	-7.0	35,700	595	1555	981	-0.7	36,000
537	1552	683	-0.7	63,200	596	1598	1008	>0.0	34,200
538	1396	1252	-4.1	21,600	597	1629	1010	>0.0	34,100
539	1384	799	-4.5	50,700	598	1670	1011	>0.0	34,100
540	937	917	-15.1	40,600	599	1547	1004	-0.8	34,500
541	1354	835	-5.2	47,500	600	1526	1016	-1.3	33,700
542	901	1388	-15.9	16,700	601	1710	1012	>0.0	34,000
543	1451	579	-3.0	77,000	602	1443	1013	-3.1	33,900
544	671	898	-22.2	42,100	603	1375	1010	-4.7	34,100
545	1408	735	-3.8	57,300	605	1302	1055	-6.3	31,300
546	1203	529	-8.8	84,500	606	1427	1057	-3.5	31,200
547	1550	784	-0.8	52,300	607	1358	1058	-5.1	31,100
549	1562	707	-0.5	60,400	608	748	1071	-20.1	30,400
550	1202	940	-8.8	38,900	609	727	1065	-20.7	30,700
551	1150	1097	-10.3	28,900	610	1521	1061	-1.4	31,000
552	1224	840	-8.1	47,000	611	1596	1064	>0.0	30,800
553	752	994	-20.0	35,200	612	1679	1071	>0.0	30,400
554	1192	1055	-9.1	31,300	613	1702	1117	>0.0	27,900
555	1188	934	-9.2	39,300	614	639	1135	-23.2	26,900
556	1368	873	-4.9	44,200	615	177	1201	<-35.0	23,800
557	1291	1104	-6.5	28,600	617	410	1229	-30.9	22,500
558	1434	849	-3.3	46,200	618	741	1227	-20.3	22,600
559	1420	848	-3.6	46,300	619	699	1234	-21.4	22,400
562	1538	1206	-1.0	23,600	620	693	1265	-21.6	21,100
566	176	511	<-35.0	87,400	621	996	1347	-13.6	18,100
567	303	532	-33.6	84,100	622	1029	1362	-12.9	17,500
568	301	551	-33.6	81,100	623	223	1430	<-35.0	15,400
569	335	559	-32.7	79,900	625	1599	1538	>0.0	12,600
571	624	630	-23.6	69,900	628	1754	420	>0.0	103,900
572	426	655	-29.9	66,700	629	1823	420	>0.0	103,900
573	427	681	-29.8	63,500	633	1493	578	-2.0	77,100
574	1671	666	>0.0	65,200	634	1527	580	-1.3	76,700
575	1744	668	>0.0	65,100	635	917	588	-15.6	75,500
576	462	700	-28.0	61,300	636	947	593	-14.9	74,900
577	489	709	-26.8	60,200	637	899	603	-16.0	73,600
578	535	719	-25.9	59,000	638	1830	616	>0.0	71,700
579	114	790	<-35.0	51,600	639	735	688	-20.5	62,600
580	152	885	<-35.0	43,200	640	1485	740	-2.2	56,800
581	218	896	<-35.0	42,300	641	1432	740	-3.3	56,800
582	1370	873	-4.9	44,200	642	1548	752	-0.8	55,500
583	1412	876	-3.8	43,900	643	1582	751	-0.1	55,600
584	1435	899	-3.3	42,000	644	506	762	-26.5	54,400
585	1481	901	-2.2	41,900	645	707	868	-21.2	44,600
586	1398	901	-4.1	41,900	646	718	874	-20.9	44,100
587	1459	900	-2.8	42,000	647	292	902	-33.8	41,800
588	1796	899	>0.0	42,000	648	486	920	-26.9	40,400
589	1757	903	>0.0	41,700	649	505	947	-26.5	38,400
592	1469	981	-2.5	36,000	650	833	946	-17.7	38,500

MSN	X	Y	CPK pI	SDS MW	MSN	X	Y	CPK pI	SDS MW
651	1400	1430	-4.0	15,400	703	554	1117	-25.5	27,900
652	123	1519	<-35.0	13,100	704	526	1143	-26.1	26,500
655	354	483	-32.3	92,100	705	492	1190	-26.8	24,300
656	112	505	<-35.0	88,400	706	497	1172	-26.7	25,100
657	233	519	<-35.0	86,200	707	282	1190	-34.2	24,300
658	595	534	-24.5	83,700	708	492	1226	-26.8	22,700
659	625	539	-23.6	82,900	709	35	1308	<-35.0	19,400
660	230	539	<-35.0	83,000	710	215	1435	<-35.0	15,300
661	271	548	-34.5	81,600	711	767	1465	-19.5	14,400
662	896	582	-16.1	76,500	712	656	1520	-22.7	13,000
663	818	577	-18.0	77,200	713	683	1537	-21.9	12,600
664	812	580	-18.2	76,700	714	601	1558	-24.3	12,100
665	897	594	-16.0	74,800	715	680	1567	-21.9	11,900
666	173	700	<-35.0	61,200	716	646	1587	-23.0	11,500
667	137	695	<-35.0	61,800	717	566	1589	-25.2	11,400
668	440	677	-29.0	63,900	718	701	1590	-21.4	11,400
669	388	690	-31.2	62,300	719	550	1623	-25.6	10,700
670	443	691	-28.9	62,200	720	719	1631	-20.9	10,600
671	413	701	-30.9	61,100	721	702	1713	-21.4	9,000
672	433	742	-29.4	56,600	722	-311	977	<-35.0	36,300
673	391	763	-31.0	54,400	723	-49	1616	<-35.0	10,900
674	423	775	-30.0	53,100	725	863	939	-17.1	39,000
675	455	786	-28.3	52,100	726	1091	1563	-11.6	12,000
676	121	836	<-35.0	47,400	727	829	1570	-17.8	11,800
677	173	841	<-35.0	46,900					
678	440	827	-29.0	48,100					
679	572	827	-25.1	48,200					
680	544	840	-25.7	47,000					
681	93	877	<-35.0	43,800					
682	-209	888	<-35.0	42,900					
683	-129	894	<-35.0	42,400					
684	-64	904	<-35.0	41,700					
685	591	852	-24.6	45,900					
686	-365	942	<-35.0	38,800					
687	-7	917	<-35.0	40,600					
688	16	926	<-35.0	40,000					
689	39	929	<-35.0	39,800					
690	-241	1006	<-35.0	34,300					
691	-279	989	<-35.0	35,500					
692	79	938	<-35.0	39,000					
693	315	921	-33.2	40,300					
694	-335	964	<-35.0	37,200					
695	-354	951	<-35.0	38,100					
696	-171	1013	<-35.0	33,900					
697	417	1006	-30.9	34,300					
698	425	1019	-29.9	33,500					
699	617	1013	-23.9	33,900					
700	474	1020	-27.4	33,500					
701	521	1051	-26.2	31,600					
702	175	1177	<-35.0	24,900					

Table 2. Sets of spots identified in the plasma protein pattern, showing the abbreviated population name (POP name) and the corresponding identifying label

POP name	Label
IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
IDS:A1_AT	Alpha1 Antitrypsin, MM form.
IDS:ACTIN_BETA	Platelet-derived beta actin.
IDS:ACTIN_GAMMA	Platelet-derived gamma actin.
IDS:ALBUMIN	Serum albumin, the most abundant plasma protein.
IDS:ALPHA1-B	Alpha1-B glycoprotein
IDS:ALPHA1_AP	Alpha1 AP-glycoprotein.
IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
IDS:ALPHA2-M	Alpha2 macroglobulin.
IDS:APO_A-I	Apo A-I lipoprotein, mature circulating form.
IDS:APO_A-II	Apo A-II lipoprotein.
IDS:APO_A-IV	Apo A-IV lipoprotein, present as two polymorphic forms. Formerly PLS:31.
IDS:APO_C-II	Apo C-II lipoprotein.
IDS:APO_C-III	Apo C-III lipoprotein, forms 1 (basic) and 2 (acidic).
IDS:APO_D	Apo D lipoprotein (previously known as PLS:33).
IDS:APO_E	Apo E lipoprotein; several charge-shift alleles exist, mainly acidic shifted.
IDS:AT-III	Antithrombin III.
IDS:C1S	Complement component C1s.
IDS:C1S_INACT	C1s inactivator.
IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
IDS:FIB_ALPHA	Fibrinogen alpha chain.
IDS:FIB_BETA	Fibrinogen beta chain.
IDS:FIB_GAMMA	Fibrinogen gamma chain.
IDS:FIB_GAMMA_EXT	An extended version of the fibrinogen gamma chain.
IDS:GC-GLOB	GC-globulin, a simple polymorphic system.
IDS:HB_BETA	Hemoglobin beta chain (probably due to RBC hemolysis).
IDS:HPX	Hemopexin.
IDS:HP_ALPHA_1F	Haptoglobin alpha 1F light chain.
IDS:HP_ALPHA_1S	Haptoglobin alpha 1S light chain.
IDS:HP_ALPHA_2	Haptoglobin alpha 2 chain (allelic with alpha 1S and 1F light chains).
IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
IDS:HP_BETA_CLEAVED	A cleaved haptoglobin beta chain, missing a peptide and a glycosylation site.
IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
IDS:IG_J_CHAIN	Immunoglobulin J-chain.
IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
IDS:IG_MU	Immunoglobulin mu chains (very heterogeneous).
IDS:NA1	HDL-associated protein, formerly PLS:29.
IDS:NA2	HDL-associated protein, formerly PLS:30.
IDS:OROSOMUCOID	Orosomuroid, also called alpha-1 acid glycoprotein.
IDS:PLASMINOGEN_GLU	Plasminogen glu-form (terminal peptide).
IDS:PLASMINOGEN_LYS	Plasminogen, lys-form (terminal peptide).
IDS:PROTHROMBIN	Prothrombin (streaks in IEF).
IDS:PRO_APO_A-I	Pro-form of Apo A-I lipoprotein.
IDS:SRBP	Serum retinol-binding protein (sRBP). Shifts to lower MW in renal insufficiency.
IDS:TF	Transferrin, main form (with glycosylation heterogeneity).
IDS:TF_CLEAVED	Two lower MW (presumably cleaved) forms of transferrin.
IDS:TF_PRO	Higher MW form of transferrin, presumably the pro-form.
IDS:TRANSTHYRETIN	Transthyretin (TTR), formerly called prealbumin (thyroxine-binding).
IDS:ZN_A2	Zinc alpha2 glycoprotein.





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POP name	Spot MSN's
PLS:21	185 190 204 296 510
PLS:22	543 633 634
PLS:23	289 322 409
PLS:24	27 60
PLS:25	223 372
PLS:26	180 331 359 370
PLS:27	580 581 681
PLS:28	682 683 684 687 688 689 692
PLS:32	371 614 703
PLS:34	200 388
PLS:35	640 641
PLS:36	645 646
PLS:37	596 597 598 601
PLS:38	94
PLS:39	449 492 571

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Table 4. Membership of individual spots in the populations shown in Table 3

MSN	POP name	Label
1	IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
2	PLS:4	Unidentified protein PLS:4.
3	IDS:PROTHROMBIN	Prothrombin (streaks in IEF).
4	IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
6	IDS:ALBUMIN	Serum albumin, the most abundant plasma protein.
8	IDS:A1_AT	Alpha1 Antitrypsin, MM form.
9	IDS:A1_AT	Alpha1 Antitrypsin, MM form.
10	IDS:TF	Transferrin, main form (with glycosylation heterogeneity).
11	IDS:ALPHA1-B	Alpha1-B glycoprotein
12	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
13	IDS:A1_AT	Alpha1 Antitrypsin, MM form.
14	IDS:PROTHROMBIN	Prothrombin (streaks in IEF).
15	IDS:ALPHA1-B	Alpha1-B glycoprotein
16	IDS:A1_AT	Alpha1 Antitrypsin, MM form.
18	IDS:AT-III	Antithrombin III.
19	IDS:ALPHA2-M	Alpha2 macroglobulin.
20	IDS:GC-GLOB	GC-globulin, a simple polymorphic system.
21	PLS:20	Unidentified protein PLS:20.
23	IDS:A1_AT	Alpha1 Antitrypsin, MM form.
24	IDS:ALPHA1_AP	Alpha1 AP-glycoprotein.
26	IDS:TF	Transferrin, main form (with glycosylation heterogeneity).
27	PLS:24	Unidentified protein PLS:24.
30	IDS:GC-GLOB	GC-globulin, a simple polymorphic system.
31	IDS:A1_AT	Alpha1 Antitrypsin, MM form.
32	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
34	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
36	IDS:FIB_GAMMA	Fibrinogen gamma chain.
37	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
38	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
40	PLS:5	Unidentified protein PLS:5.
42	IDS:ALPHA1_AP	Alpha1 AP-glycoprotein.
43	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
44	IDS:FIB_BETA	Fibrinogen beta chain.
45	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
46	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
47	PLS:14	Unidentified protein PLS:14.
48	PLS:5	Unidentified protein PLS:5.
49	IDS:APO_A-II	Apo A-II lipoprotein.
50	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
52	IDS:TF	Transferrin, main form (with glycosylation heterogeneity).
53	PLS:20	Unidentified protein PLS:20.
54	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
55	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
56	IDS:FIB_BETA	Fibrinogen beta chain.
57	IDS:APO_A-I	Apo A-I lipoprotein, mature circulating form.
59	IDS:FIB_GAMMA	Fibrinogen gamma chain.
60	PLS:24	Unidentified protein PLS:24.
61	IDS:HPX	Hemopexin.
62	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
63	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
64	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
65	IDS:APO_A-I	Apo A-I lipoprotein, mature circulating form.
66	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
67	IDS:HPX	Hemopexin.
69	IDS:A1_AT	Alpha1 Antitrypsin, MM form.
70	IDS:FIB_GAMMA	Fibrinogen gamma chain.
71	IDS:TF	Transferrin, main form (with glycosylation heterogeneity).
72	IDS:HPX	Hemopexin.
74	PLS:5	Unidentified protein PLS:5.
75	PLS:5	Unidentified protein PLS:5.
77	PLS:14	Unidentified protein PLS:14.
79	IDS:FIB_GAMMA	Fibrinogen gamma chain.
80	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
81	IDS:SRBP	Serum retinol-binding protein (sRBP). Shifts to lower MW in renal insufficiency.

MSN	POP name	Label
82	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
83	IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
84	IDS:APO A-IV	Apo A-IV lipoprotein, present as two polymorphic forms. Formerly PLS:31.
85	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
86	IDS:HP_ALPHA_2	Haptoglobin alpha 2 chain (allelic with alpha 1S and 1F light chains).
87	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
88	IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
89	IDS:TRANSTHYRETIN	Transthyretin (TTR), formerly called prealbumin (thyroxine-binding).
90	IDS:FIB_GAMMA	Fibrinogen gamma chain.
91	IDS:FIB_GAMMA_EXT	An extended version of the fibrinogen gamma chain.
92	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
93	PLS:5	Unidentified protein PLS:5.
94	PLS:38	Unidentified protein PLS:38.
95	IDS:HP_ALPHA_2	Haptoglobin alpha 2 chain (allelic with alpha 1S and 1F light chains).
98	IDS:ALPHA1_AP	Alpha1 AP-glycoprotein.
99	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
100	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
101	IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
102	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
104	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
105	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
107	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
108	IDS:ALPHA1-B	Alpha1-B glycoprotein
110	IDS:A1_AT	Alpha1 Antitrypsin, MM form.
112	IDS:TF_PRO	Higher MW form of transferrin, presumably the pro-form.
113	IDS:HPX	Hemopexin.
114	IDS:FIB_GAMMA_EXT	An extended version of the fibrinogen gamma chain.
115	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
116	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
117	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
118	IDS:APO_C-III	Apo C-III lipoprotein, forms 1 (basic) and 2 (acidic).
119	IDS:APO_C-III	Apo C-III lipoprotein, forms 1 (basic) and 2 (acidic).
123	IDS:C1S	Complement component C1s.
124	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
127	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
128	IDS:TF_CLEAVED	Two lower MW (presumably cleaved) forms of transferrin.
130	IDS:HPX	Hemopexin.
132	IDS:FIB_ALPHA	Fibrinogen alpha chain.
133	IDS:APO_A-I	Apo A-I lipoprotein, mature circulating form.
134	IDS:A1_AT	Alpha1 Antitrypsin, MM form.
135	PLS:19	Unidentified protein PLS:19.
136	IDS:FIB_GAMMA	Fibrinogen gamma chain.
137	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
138	PLS:5	Unidentified protein PLS:5.
139	IDS:HP_ALPHA_2	Haptoglobin alpha 2 chain (allelic with alpha 1S and 1F light chains).
140	IDS:HP_ALPHA_2	Haptoglobin alpha 2 chain (allelic with alpha 1S and 1F light chains).
144	IDS:HPX	Hemopexin.
145	PLS:19	Unidentified protein PLS:19.
146	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
148	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
149	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
151	IDS:HPX	Hemopexin.
152	IDS:HB_BETA	Hemoglobin beta chain (probably due to RBC hemolysis).
153	IDS:PRO_APO_A-I	Pro-form of Apo A-I lipoprotein.
154	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
160	IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
161	IDS:TF_CLEAVED	Two lower MW (presumably cleaved) forms of transferrin.
162	PLS:5	Unidentified protein PLS:5.
163	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
167	PLS:15	Unidentified protein PLS:15.
169	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
170	IDS:FIB_GAMMA	Fibrinogen gamma chain.
171	PLS:18	Unidentified protein PLS:18.
173	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
174	PLS:14	Unidentified protein PLS:14.

MSN	POP name	Label
176	IDS:C1S	Complement component C1s.
178	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
179	IDS:FIB_ALPHA	Fibrinogen alpha chain.
180	PLS:26	Unidentified protein PLS:26.
182	PLS:15	Unidentified protein PLS:15.
183	IDS:PLASMINOGEN_LYS	Plasminogen, lys-form (terminal peptide).
184	IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
185	PLS:21	Unidentified protein PLS:21.
189	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
190	PLS:21	Unidentified protein PLS:21.
191	IDS:ALPHA1_AP	Alpha1 AP-glycoprotein.
192	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
193	IDS:HP_BETA_CLEAVED	A cleaved haptoglobin beta chain, missing a peptide and a glycosylation site.
195	IDS:FIB_ALPHA	Fibrinogen alpha chain.
198	PLS:5	Unidentified protein PLS:5.
199	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
200	PLS:34	Unidentified protein PLS:34.
201	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
202	IDS:FIB_ALPHA	Fibrinogen alpha chain.
203	IDS:IG_J_CHAIN	Immunoglobulin J-chain.
204	PLS:21	Unidentified protein PLS:21.
206	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
207	IDS:HP_BETA_CLEAVED	A cleaved haptoglobin beta chain, missing a peptide and a glycosylation site.
208	PLS:5	Unidentified protein PLS:5.
210	IDS:ALPHA2-M	Alpha2 macroglobulin.
211	IDS:FIB_BETA	Fibrinogen beta chain.
212	PLS:16	Unidentified protein PLS:16.
214	IDS:AT-III	Antithrombin III.
215	IDS:APO_E	Apo E lipoprotein; several charge-shift alleles exist, mainly acidic shifted.
216	PLS:30	NA2 (HDL-associated protein).
217	IDS:HP_BETA_CLEAVED	A cleaved haptoglobin beta chain, missing a peptide and a glycosylation site.
218	IDS:HP_BETA	Haptoglobin beta chain, uncleaved form.
219	IDS:C1S	Complement component C1s.
222	PLS:30	NA2 (HDL-associated protein).
223	PLS:25	Unidentified protein PLS:25.
224	IDS:IG_MU	Immunoglobulin mu chains (very heterogeneous).
225	IDS:FIB_BETA	Fibrinogen beta chain.
226	IDS:HP_BETA_CLEAVED	A cleaved haptoglobin beta chain, missing a peptide and a glycosylation site.
230	PLS:14	Unidentified protein PLS:14.
231	PLS:14	Unidentified protein PLS:14.
232	IDS:FIB_ALPHA	Fibrinogen alpha chain.
235	IDS:IG_J_CHAIN	Immunoglobulin J-chain.
236	IDS:HPX	Hemopexin.
237	PLS:29	NA1 (HDL-associated protein).
238	IDS:APO_E	Apo E lipoprotein; several charge-shift alleles exist, mainly acidic shifted.
240	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
241	PLS:29	NA1 (HDL-associated protein).
242	IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
245	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
246	PLS:15	Unidentified protein PLS:15.
247	PLS:16	Unidentified protein PLS:16.
248	PLS:16	Unidentified protein PLS:16.
249	IDS:PLASMINOGEN_LYS	Plasminogen, lys-form (terminal peptide).
250	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
252	IDS:PLASMINOGEN_GLU	Plasminogen glu-form (terminal peptide).
253	PLS:9	Unidentified protein PLS:9.
254	IDS:FIB_ALPHA	Fibrinogen alpha chain.
257	IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
258	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
259	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
260	IDS:ZN_A2	Zinc alpha2 glycoprotein.
262	IDS:TF_PRO	Higher MW form of transferrin, presumable the pro-form.
263	IDS:TRANSTHYRETIN	Transthyretin (TTR), formerly called prealbumin (thyroxine-binding).
266	IDS:HPX	Hemopexin.
267	IDS:PLASMINOGEN_LYS	Plasminogen, lys-form (terminal peptide).

MSN	POP name	Label
270	PLS:9	Unidentified protein PLS:9.
271	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
272	IDS:HP_ALPHA_2	Haptoglobin alpha 2 chain (allelic with alpha 1S and 1F light chains).
273	PLS:6	Unidentified protein PLS:6.
275	PLS:6	Unidentified protein PLS:6.
276	PLS:29	NA1 (HDL-associated protein).
278	IDS:ALPHA2-M	Alpha2 macroglobulin.
279	PLS:7	Unidentified protein PLS:7.
284	IDS:FIB_GAMMA	Fibrinogen gamma chain.
285	PLS:8	Unidentified protein PLS:8.
286	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
287	IDS:PLASMINOGEN_LYS	Plasminogen, lys-form (terminal peptide).
289	PLS:23	Unidentified protein PLS:23.
290	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
291	IDS:PLASMINOGEN_GLU	Plasminogen glu-form (terminal peptide).
292	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
294	IDS:HP_BETA_CLEAVED	A cleaved haptoglobin beta chain, missing a peptide and a glycosylation site.
296	PLS:21	Unidentified protein PLS:21.
297	IDS:IG_MU	Immunoglobulin mu chains (very heterogeneous).
301	IDS:ALPHA2-M	Alpha2 macroglobulin.
302	PLS:6	Unidentified protein PLS:6.
304	IDS:APO_C-II	Apo C-II lipoprotein.
305	PLS:6	Unidentified protein PLS:6.
306	PLS:8	Unidentified protein PLS:8.
307	PLS:16	Unidentified protein PLS:16.
308	IDS:PLASMINOGEN_LYS	Plasminogen, lys-form (terminal peptide).
311	PLS:16	Unidentified protein PLS:16.
312	IDS:CERULOPLAS	Ceruloplasmin: the copper transport protein in plasma, present in two forms.
313	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
315	PLS:16	Unidentified protein PLS:16.
316	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
317	IDS:ALPHA2-M	Alpha2 macroglobulin.
318	PLS:7	Unidentified protein PLS:7.
322	PLS:23	Unidentified protein PLS:23.
323	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
326	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
331	PLS:26	Unidentified protein PLS:26.
333	IDS:PLASMINOGEN_GLU	Plasminogen glu-form (terminal peptide).
334	PLS:6	Unidentified protein PLS:6.
336	IDS:APO_A-IV	Apo A-IV lipoprotein, present as two polymorphic forms. Formerly PLS:31.
337	IDS:APO_E	Apo E lipoprotein; several charge-shift alleles exist, mainly acidic shifted.
338	PLS:16	Unidentified protein PLS:16.
339	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
341	IDS:ALPHA2-M	Alpha2 macroglobulin.
342	PLS:7	Unidentified protein PLS:7.
344	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
347	IDS:IG_MU	Immunoglobulin mu chains (very heterogeneous).
348	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
349	IDS:ALPHA2-M	Alpha2 macroglobulin.
351	PLS:9	Unidentified protein PLS:9.
355	PLS:6	Unidentified protein PLS:6.
359	PLS:26	Unidentified protein PLS:26.
365	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
368	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
369	IDS:FIB_GAMMA_EXT	An extended version of the fibrinogen gamma chain.
370	PLS:26	Unidentified protein PLS:26.
371	PLS:32	Unidentified protein PLS:32.
372	PLS:25	Unidentified protein PLS:25.
373	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
375	PLS:8	Unidentified protein PLS:8.
377	IDS:IG_LIGHT_CHAINS	Immunoglobulin light chains: lambda above and kappa below, but overlapping.
379	PLS:16	Unidentified protein PLS:16.
380	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
381	IDS:ALPHA2-M	Alpha2 macroglobulin.
382	PLS:16	Unidentified protein PLS:16.

MSN	POP name	Label
384	IDS:APO_E	Apo E lipoprotein; several charge-shift alleles exist, mainly acidic shifted.
386	IDS:SRBP	Serum retinol-binding protein (sRBP). Shifts to lower MW in renal insufficiency.
387	IDS:PLASMINOGEN_LYS	Plasminogen, lys-form (terminal peptide).
388	PLS:34	Unidentified protein PLS:34.
392	IDS:PLASMINOGEN_GLU	Plasminogen glu-form (terminal peptide).
397	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
400	IDS:FIB_ALPHA	Fibrinogen alpha chain.
403	IDS:PLASMINOGEN_GLU	Plasminogen glu-form (terminal peptide).
405	PLS:7	Unidentified protein PLS:7.
409	PLS:23	Unidentified protein PLS:23.
410	PLS:5	Unidentified protein PLS:5.
411	PLS:16	Unidentified protein PLS:16.
414	PLS:16	Unidentified protein PLS:16.
416	IDS:PLASMINOGEN_LYS	Plasminogen, lys-form (terminal peptide).
417	PLS:2	Unidentified protein PLS:2.
422	PLS:8	Unidentified protein PLS:8.
426	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
428	PLS:16	Unidentified protein PLS:16.
429	PLS:2	Unidentified protein PLS:2.
430	PLS:2	Unidentified protein PLS:2.
431	IDS:HPX	Hemopexin.
434	PLS:6	Unidentified protein PLS:6.
436	PLS:1	Unidentified protein PLS:1.
437	IDS:PLASMINOGEN_LYS	Plasminogen, lys-form (terminal peptide).
439	IDS:PLASMINOGEN_LYS	Plasminogen, lys-form (terminal peptide).
444	PLS:2	Unidentified protein PLS:2.
445	PLS:10	Unidentified protein PLS:10.
446	PLS:2	Unidentified protein PLS:2.
448	PLS:2	Unidentified protein PLS:2.
449	PLS:39	Unidentified protein PLS:39.
450	PLS:1	Unidentified protein PLS:1.
451	PLS:13	Unidentified protein PLS:13.
452	PLS:30	NA2 (HDL-associated protein).
455	IDS:TF_CLEAVED	Two lower MW (presumably cleaved) forms of transferrin.
456	IDS:ALPHA2-M	Alpha2 macroglobulin.
457	PLS:10	Unidentified protein PLS:10.
459	PLS:10	Unidentified protein PLS:10.
463	IDS:APO_A-I	Apo A-I lipoprotein, mature circulating form.
465	PLS:9	Unidentified protein PLS:9.
466	PLS:6	Unidentified protein PLS:6.
467	IDS:PLASMINOGEN_GLU	Plasminogen glu-form (terminal peptide).
468	PLS:9	Unidentified protein PLS:9.
470	IDS:ZN_A2	Zinc alpha2 glycoprotein.
471	IDS:GC-GLOB	GC-globulin, a simple polymorphic system.
472	PLS:8	Unidentified protein PLS:8.
480	IDS:IG_MU	Immunoglobulin mu chains (very heterogeneous).
481	IDS:PLASMINOGEN_GLU	Plasminogen glu-form (terminal peptide).
483	PLS:11	Unidentified protein PLS:11.
486	PLS:10	Unidentified protein PLS:10.
490	PLS:11	Unidentified protein PLS:11.
492	PLS:39	Unidentified protein PLS:39.
493	PLS:11	Unidentified protein PLS:11.
494	PLS:11	Unidentified protein PLS:11.
495	PLS:11	Unidentified protein PLS:11.
496	PLS:10	Unidentified protein PLS:10.
507	PLS:12	Unidentified protein PLS:12.
508	PLS:16	Unidentified protein PLS:16.
510	PLS:21	Unidentified protein PLS:21.
511	IDS:PRO_APO_A-I	Pro-form of Apo A-I lipoprotein.
513	IDS:PLASMINOGEN_GLU	Plasminogen glu-form (terminal peptide).
519	IDS:APO_D	Apo D lipoprotein (previously known as PLS:33).
521	IDS:IG_GAMMA	Immunoglobulin gamma chains (very heterogeneous).
522	IDS:FIB_ALPHA	Fibrinogen alpha chain.
530	IDS:APO_D	Apo D lipoprotein (previously known as PLS:33).
537	IDS:FIB_ALPHA	Fibrinogen alpha chain.
543	PLS:22	Unidentified protein PLS:22.

MSN	POP name	Label
566	PLS:13	Unidentified protein PLS:13.
567	PLS:13	Unidentified protein PLS:13.
568	PLS:13	Unidentified protein PLS:13.
569	PLS:13	Unidentified protein PLS:13.
571	PLS:39	Unidentified protein PLS:39.
574	IDS:FIB_ALPHA	Fibrinogen alpha chain.
575	IDS:FIB_ALPHA	Fibrinogen alpha chain.
576	PLS:17	Unidentified protein PLS:17.
577	PLS:17	Unidentified protein PLS:17.
578	PLS:17	Unidentified protein PLS:17.
579	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
580	PLS:27	Unidentified protein PLS:27
581	PLS:27	Unidentified protein PLS:27
596	PLS:37	Unidentified protein PLS:37.
597	PLS:37	Unidentified protein PLS:37.
598	PLS:37	Unidentified protein PLS:37.
601	PLS:37	Unidentified protein PLS:37.
608	PLS:30	NA2 (HDL-associated protein).
609	PLS:30	NA2 (HDL-associated protein).
614	PLS:32	Unidentified protein PLS:32.
615	IDS:APO_D	Apo D lipoprotein (previously known as PLS:33).
617	IDS:APO_D	Apo D lipoprotein (previously known as PLS:33).
625	IDS:HB_BETA	Hemoglobin beta chain (probably due to RBC hemolysis).
633	PLS:22	Unidentified protein PLS:22.
634	PLS:22	Unidentified protein PLS:22.
639	PLS:18	Unidentified protein PLS:18.
640	PLS:35	Unidentified protein PLS:35.
641	PLS:35	Unidentified protein PLS:35.
645	PLS:36	Unidentified protein PLS:36.
646	PLS:36	Unidentified protein PLS:36.
650	IDS:ACTIN_BETA	Platelet-derived beta actin.
655	IDS:C1S_INACT	C1s inactivator.
656	PLS:13	Unidentified protein PLS:13.
657	PLS:13	Unidentified protein PLS:13.
658	PLS:12	Unidentified protein PLS:12.
659	PLS:12	Unidentified protein PLS:12.
660	PLS:13	Unidentified protein PLS:13.
661	PLS:13	Unidentified protein PLS:13.
666	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
667	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
673	IDS:A1-ANTICHY	Alpha1-Antichymotrypsin
678	IDS:ALPHA2-HS	Alpha2 HS glycoprotein, a plasma protein abundant in bone, with two genetic form
681	PLS:27	Unidentified protein PLS:27
682	PLS:28	Unidentified protein PLS:28
683	PLS:28	Unidentified protein PLS:28
684	PLS:28	Unidentified protein PLS:28
686	IDS:OROSOMUCOID	Orosomuroid, also called alpha-1 acid glycoprotein.
687	PLS:28	Unidentified protein PLS:28
688	PLS:28	Unidentified protein PLS:28
689	PLS:28	Unidentified protein PLS:28
690	IDS:OROSOMUCOID	Orosomuroid, also called alpha-1 acid glycoprotein.
691	IDS:OROSOMUCOID	Orosomuroid, also called alpha-1 acid glycoprotein.
692	PLS:28	Unidentified protein PLS:28
694	IDS:OROSOMUCOID	Orosomuroid, also called alpha-1 acid glycoprotein.
695	IDS:OROSOMUCOID	Orosomuroid, also called alpha-1 acid glycoprotein.
696	IDS:OROSOMUCOID	Orosomuroid, also called alpha-1 acid glycoprotein.
702	IDS:APO_D	Apo D lipoprotein (previously known as PLS:33).
703	PLS:32	Unidentified protein PLS:32.
707	IDS:APO_D	Apo D lipoprotein (previously known as PLS:33).
708	IDS:APO_D	Apo D lipoprotein (previously known as PLS:33).
722	IDS:OROSOMUCOID	Orosomuroid, also called alpha-1 acid glycoprotein.
725	IDS:ACTIN_GAMMA	Platelet-derived gamma actin.
726	IDS:HP_ALPHA_1F	Haptoglobin alpha 1F light chain.
727	IDS:HP_ALPHA_1S	Haptoglobin alpha 1S light chain.
766	PLS:3	Unidentified protein PLS:3.