

**Supplemental Table 4. Summary of data generated by liquid chromatography-tandem mass sp**

number	filename	parent_cha	score	percent_sc	totalIntens	previous_a
755	X2L_Roman.10910.11159.:	2	10.18	72.3	1.62E+06	(R)
782	L5_Roman.10727.10936.2	2	10.1	74.2	9.80E+05	(R)
9	S1_Roman.10721.11100.2	2	20.43	95.1	1.29E+08	(K)
15	X4L_Roman.10686.11009.:	2	20.06	94.2	3.37E+07	(K)
17	S3_Roman.10808.11067.2	2	19.93	95.2	6.69E+07	(K)
19	S2_Roman.10217.10598.2	2	19.92	95.3	6.36E+07	(K)
24	S4_Roman.10311.10711.2	2	19.67	94.6	9.30E+07	(K)
31	L3_Roman.10284.10676.2	2	19.15	94.8	1.14E+08	(K)
33	S5_Roman.10724.11126.2	2	18.9	92	7.14E+07	(K)
34	X4R_Roman.10850.11234.	2	18.71	95.9	2.26E+07	(K)
36	X3L_Roman.10933.11061.:	2	18.4	91.3	1.58E+07	(K)
40	S3_Roman.10551.10679.2	2	18.31	87.8	3.65E+07	(K)
46	L1_Roman.10620.10620.2	2	17.73	88.3	2.90E+06	(K)
50	S2_Roman.10090.10090.2	2	17.48	79.4	3.03E+07	(K)
59	X4L_Roman.10554.10554.:	2	17.05	83.7	1.59E+07	(K)
62	X3R_Roman.10639.10893.	2	16.92	92.5	1.10E+07	(K)
66	S1_Roman.10496.10496.2	2	16.82	96.9	6.25E+07	(K)
67	S1_Roman.10629.10629.2	2	16.62	81.4	6.25E+07	(K)
70	L5_Roman.10335.10335.2	2	16.45	78.9	2.24E+05	(K)
91	X2R_Roman.10452.10452.	2	15.95	92.5	6.68E+05	(K)
123	L4_Roman.10610.10755.2	2	15.11	82.2	9.25E+05	(K)
133	L3_Roman.10014.10155.2	2	14.83	84.4	5.81E+07	(K)
138	L1_Roman.10490.10490.2	2	14.73	81.7	2.90E+06	(K)
150	L1_Roman.10751.10751.2	2	14.46	81.8	2.90E+06	(K)
198	S5_Roman.10458.10597.2	2	13.63	73.6	3.70E+07	(K)
203	S4_Roman.10206.10206.2	2	13.56	72.2	4.81E+07	(K)
236	S4_Roman.10069.10069.2	2	13.26	74.3	4.81E+07	(K)
277	X1R_Roman.11156.11156.	2	12.79	73.8	1.99E+05	(K)
282	X1L_Roman.10898.10898.:	2	12.7	87.2	4.35E+05	(K)
410	X5R_Roman.10634.10634.	2	11.73	70.5	6.07E+05	(K)
485	L2_Roman.11591.11591.2	2	11.3	70.8	3.88E+04	(K)
214	X2L_Roman.10569.10569.:	2	13.46	73.3	1.15E+06	(K)
512	L4_Roman.30150.30150.2	2	11.21	78	1.27E+06	(R)
694	S5_Roman.30698.30825.2	2	10.37	73.3	2.03E+06	(R)
748	X2L_Roman.29747.29747.:	2	10.19	76.5	1.63E+06	(R)
525	X3R_Roman.13191.13482.	2	11.13	82.4	3.66E+06	(R)
653	X4R_Roman.14197.14473.	2	10.51	78.8	9.44E+05	(R)
753	S5_Roman.13920.14228.2	2	10.18	84.5	1.40E+06	(R)
289	S3_Roman.6375.7204.2	2	12.63	86.8	2.01E+06	(K)
555	X1R_Roman.6421.7281.2	2	10.99	77.9	1.04E+06	(K)
566	S1_Roman.6289.7191.2	2	10.93	87.3	3.35E+06	(K)
647	X1L_Roman.5856.6612.2	2	10.56	80.8	1.69E+06	(K)
685	S5_Roman.6190.6936.2	2	10.39	80.2	1.04E+06	(K)
776	L3_Roman.5961.6426.2	2	10.12	84.1	1.13E+06	(K)
385	X1R_Roman.20568.21360.	2	11.9	78.4	7.89E+07	(K)

690	S1_Roman.14842.14981.2	2	10.38	73.5	3.17E+06 (K)
502	X1L_Roman.7831.7981.2	2	11.27	75	3.40E+06 (R)
394	L3_Roman.14483.14483.2	2	11.84	80.5	4.02E+05 (K)
523	X1L_Roman.14730.14890.2	2	11.14	80.2	4.99E+05 (K)
612	X5R_Roman.14778.14917.2	2	10.73	87.1	6.65E+05 (K)
706	X1R_Roman.15287.15442.2	2	10.3	82.6	7.83E+05 (K)
703	S4_Roman.18604.18843.2	2	10.31	77.1	4.33E+07 (K)
741	L3_Roman.18133.18509.2	2	10.2	76.2	3.86E+07 (K)
489	X5R_Roman.17017.17017.2	2	11.3	76.4	1.56E+05 (R)
519	X2L_Roman.16543.16543.2	2	11.16	86.3	2.26E+05 (R)
800	X1L_Roman.17063.17063.2	2	10.03	78.7	1.39E+05 (R)
595	S5_Roman.20618.21812.2	2	10.79	88.2	9.86E+07 (K)
775	X3R_Roman.19350.20683.2	2	10.13	84.4	2.93E+07 (K)
661	S4_Roman.4595.4724.2	2	10.48	73.7	6.61E+07 (R)
427	S3_Roman.6990.6990.2	2	11.59	82	2.25E+07 (R)
643	S1_Roman.6980.6980.2	2	10.59	89.8	1.03E+07 (R)
659	S5_Roman.6872.7966.2	2	10.49	86.6	7.73E+06 (R)
747	S3_Roman.7906.7906.2	2	10.19	81.7	1.15E+06 (R)
89	L3_Roman.4070.4929.2	2	15.97	89.1	3.22E+07 (R)
126	S4_Roman.4083.4212.2	2	15.04	81.5	8.44E+06 (R)
140	S1_Roman.4333.4449.3	3	14.67	85.6	4.38E+07 (R)
145	X4L_Roman.4045.4045.2	2	14.6	82.4	3.14E+06 (R)
151	S1_Roman.4460.4460.2	2	14.46	81	2.05E+07 (R)
154	S5_Roman.4380.4511.2	2	14.36	85.2	3.65E+06 (R)
156	S3_Roman.4389.4518.3	3	14.35	85.3	2.40E+07 (R)
163	S3_Roman.4519.4519.2	2	14.19	84.5	1.16E+07 (R)
168	X4L_Roman.4035.4035.3	3	14.15	82.7	5.70E+06 (R)
171	S2_Roman.4198.4198.3	3	14.12	83	2.44E+07 (R)
192	X2L_Roman.4244.4244.3	3	13.74	77.3	1.77E+05 (R)
199	S2_Roman.4200.4200.2	2	13.62	82.2	1.59E+07 (R)
200	X5R_Roman.4052.4052.3	3	13.62	90.4	9.28E+04 (R)
206	X2L_Roman.4253.4253.2	2	13.54	84.4	1.17E+05 (R)
212	S5_Roman.4372.4372.3	3	13.48	89.7	7.40E+06 (R)
218	S5_Roman.4513.4513.3	3	13.42	74	7.40E+06 (R)
237	X3R_Roman.4310.4310.2	2	13.25	100	7.74E+05 (R)
264	X4R_Roman.4538.4654.3	3	12.87	75.8	9.27E+06 (R)
292	X2R_Roman.4065.4065.3	3	12.57	77.1	8.72E+04 (R)
306	L1_Roman.4172.4172.3	3	12.45	75.8	9.51E+05 (R)
323	S1_Roman.4340.4340.2	2	12.32	75.5	2.05E+07 (R)
351	L5_Roman.4076.4076.3	3	12.16	72.2	6.54E+04 (R)
354	X3R_Roman.4293.4293.3	3	12.15	76.4	1.66E+06 (R)
422	X3L_Roman.4463.4463.2	2	11.66	75.8	4.63E+05 (R)
432	X1L_Roman.4302.4302.2	2	11.57	79.2	4.34E+04 (R)
436	X2R_Roman.4074.4074.2	2	11.54	75.1	6.06E+04 (R)
453	X3L_Roman.4560.4560.3	3	11.45	92.2	9.31E+05 (R)
455	L5_Roman.4087.4087.2	2	11.44	87.7	3.95E+04 (R)
534	X4R_Roman.4556.4678.2	2	11.1	74.2	3.62E+06 (R)

692	X1R_Roman.4618.4618.3	3	10.38	70.4	1.74E+05 (R)
738	X1L_Roman.4277.4277.3	3	10.21	76.9	9.56E+04 (R)
225	S2_Roman.6168.6288.2	2	13.36	88.3	1.38E+07 (R)
228	X4L_Roman.6522.6638.2	2	13.34	87.3	9.16E+06 (R)
254	S4_Roman.6187.6330.2	2	12.99	87.4	1.29E+07 (R)
268	S3_Roman.6614.6734.2	2	12.83	89.3	4.65E+07 (R)
269	L3_Roman.6163.6297.2	2	12.82	88	8.97E+06 (R)
357	S5_Roman.6549.6683.2	2	12.13	88.6	2.03E+07 (R)
358	X4R_Roman.6775.6775.2	2	12.13	87.1	5.25E+06 (R)
430	X3R_Roman.6402.6521.2	2	11.58	89.1	7.30E+06 (R)
440	S1_Roman.6638.6761.2	2	11.5	86.8	2.12E+07 (R)
581	S1_Roman.6515.6515.2	2	10.84	83.4	2.12E+07 (R)
652	X3L_Roman.6579.6697.2	2	10.52	73	6.40E+06 (R)
321	L3_Roman.5309.5454.2	2	12.34	75	8.09E+06 (R)
688	X4R_Roman.5888.6152.2	2	10.39	74.6	1.99E+07 (R)
726	S5_Roman.5651.5798.2	2	10.23	73.8	9.96E+06 (R)
790	X4L_Roman.5448.5571.2	2	10.07	72.6	1.94E+07 (R)
474	X2R_Roman.45363.45569.	3	11.34	82.1	1.51E+07 (R)
514	L1_Roman.45627.45879.3	3	11.19	78.1	3.15E+07 (R)
586	X5R_Roman.46221.46472.	3	10.84	75.1	1.42E+07 (R)
620	S1_Roman.44668.44872.3	3	10.7	78	4.33E+07 (R)
626	X4R_Roman.45176.45280.	3	10.67	76.4	3.72E+07 (R)
729	S5_Roman.45638.45746.3	3	10.22	78.8	2.40E+07 (R)
759	X1R_Roman.45854.46068.	3	10.16	78.9	2.90E+07 (R)
773	S2_Roman.44503.44702.3	3	10.13	77.4	4.70E+07 (R)
452	X2R_Roman.12798.13362.	2	11.45	84	8.05E+06 (K)
616	S1_Roman.13371.13878.2	2	10.71	83.6	4.65E+07 (K)
720	X4R_Roman.13577.13980.	2	10.26	85.7	1.20E+07 (K)
754	X1L_Roman.13167.13492.	2	10.18	85	5.86E+06 (K)
607	S5_Roman.12742.12880.2	2	10.75	85.1	3.49E+05 (K)
654	L3_Roman.12122.12431.2	2	10.5	84.6	6.93E+05 (K)
801	L3_Roman.16734.16734.3	3	10.02	84.3	1.28E+07 (K)
61	L3_Roman.4588.4718.2	2	16.98	88.1	8.27E+06 (K)
153	S3_Roman.5073.5073.2	2	14.39	86.9	3.91E+06 (K)
162	S5_Roman.5059.5059.2	2	14.22	90.6	3.26E+06 (K)
424	S2_Roman.4634.4775.2	2	11.63	79.3	3.87E+06 (K)
610	S5_Roman.4933.4933.2	2	10.73	72.2	3.20E+06 (K)
166	X4R_Roman.20894.20894.	3	14.17	84.1	2.19E+06 (K)
213	S2_Roman.20108.20108.3	3	13.46	72.6	6.42E+06 (K)
556	X4L_Roman.20875.20875.	3	10.99	72.3	3.58E+06 (K)
247	L3_Roman.20301.20301.3	3	13.03	79	1.86E+07 (K)
350	S3_Roman.20978.20978.3	3	12.17	70.8	1.13E+07 (K)
359	L3_Roman.20116.20381.4	4	12.12	75	5.34E+06 (K)
378	X4R_Roman.20810.20936.	4	11.96	81.2	9.92E+05 (K)
411	S1_Roman.20761.20761.3	3	11.72	81.3	8.14E+06 (K)
493	S4_Roman.20505.20648.4	4	11.29	72.6	1.07E+06 (K)
494	S4_Roman.20645.20645.3	3	11.29	79.1	7.81E+06 (K)

571	S3_Roman.20805.21066.4	4	10.88	78.2	1.54E+05 (K)
617	S3_Roman.20854.20854.3	3	10.71	70.5	1.13E+07 (K)
680	X4R_Roman.20685.20685.	4	10.41	72.8	9.92E+05 (K)
691	S2_Roman.20245.20245.3	3	10.38	71.8	6.42E+06 (K)
699	S1_Roman.20792.20792.4	4	10.34	72.6	5.06E+06 (K)
781	L3_Roman.21423.21423.2	2	10.1	80.2	3.25E+04 (K)
65	S2_Roman.5366.5366.2	2	16.83	86.6	1.88E+06 (K)
110	S5_Roman.5592.5592.2	2	15.42	85.4	3.15E+06 (K)
128	S1_Roman.5677.5677.3	3	14.98	79.4	2.71E+07 (K)
137	S3_Roman.5709.5709.2	2	14.76	77.4	2.92E+06 (K)
202	S1_Roman.5727.5727.2	2	13.59	77.3	2.86E+06 (K)
232	L3_Roman.5158.5158.2	2	13.3	74.7	1.14E+06 (K)
314	L3_Roman.5289.5289.2	2	12.39	76.1	1.14E+06 (K)
319	S4_Roman.5269.5269.3	3	12.35	71.2	5.84E+06 (K)
339	S3_Roman.5667.5667.3	3	12.24	76.4	2.45E+07 (K)
529	S5_Roman.5468.5468.2	2	11.12	87.3	3.15E+06 (K)
667	S1_Roman.5604.5604.2	2	10.45	80.4	2.86E+06 (K)
75	S5_Roman.11830.11830.4	4	16.27	75.6	2.85E+06 (K)
193	L3_Roman.11311.11311.4	4	13.72	72.9	2.09E+06 (K)
258	S5_Roman.11854.11854.3	3	12.94	73.8	8.69E+05 (K)
462	S5_Roman.11716.11716.3	3	11.39	86.9	8.69E+05 (K)
541	S2_Roman.11466.11466.3	3	11.06	71.1	1.34E+06 (K)
60	L3_Roman.17387.17669.3	3	17.04	81.2	1.70E+06 (K)
81	S4_Roman.16210.16865.4	4	16.17	85.7	4.71E+07 (K)
90	S4_Roman.17871.18021.3	3	15.95	84.9	1.46E+06 (K)
106	S5_Roman.17047.17179.4	4	15.52	80.4	4.94E+07 (K)
116	S2_Roman.16303.16303.3	3	15.24	80.7	2.40E+07 (K)
129	S1_Roman.16969.17329.4	4	14.94	86.1	1.31E+08 (K)
152	S2_Roman.16548.16548.3	3	14.41	77.9	2.40E+07 (K)
157	S5_Roman.18262.18393.4	4	14.34	74.4	4.72E+06 (K)
169	S1_Roman.18237.18361.3	3	14.14	81.4	3.35E+06 (K)
179	S1_Roman.17105.17105.3	3	13.96	81.2	3.54E+07 (K)
183	L3_Roman.16381.16648.4	4	13.84	83	3.48E+07 (K)
188	S3_Roman.16732.17378.4	4	13.8	80.8	7.38E+07 (K)
222	S2_Roman.16346.16703.4	4	13.4	84.9	6.45E+07 (K)
227	S4_Roman.16454.16581.3	3	13.34	90.9	1.75E+07 (K)
239	S3_Roman.18282.18282.3	3	13.21	80.3	2.34E+06 (K)
245	S3_Roman.17080.17080.3	3	13.07	80.2	2.09E+07 (K)
256	S5_Roman.17049.17460.3	3	12.96	86.7	1.53E+07 (K)
257	S3_Roman.17120.17120.4	4	12.95	86.5	7.38E+07 (K)
265	S3_Roman.16962.16962.3	3	12.86	70.4	2.09E+07 (K)
272	X3R_Roman.15491.15491.	4	12.8	82.5	4.27E+06 (K)
322	X3R_Roman.15469.15469.	3	12.34	70.7	1.44E+06 (K)
340	S3_Roman.18417.18417.3	3	12.22	78.7	2.34E+06 (K)
346	S1_Roman.16867.17349.3	3	12.2	74.1	3.54E+07 (K)
352	S1_Roman.17236.17236.2	2	12.15	71.7	4.67E+06 (K)
362	X3L_Roman.17075.17191.4	4	12.11	80.1	1.26E+07 (K)

363	L3_Roman.17529.17529.3	3	12.09	79.7	1.70E+06 (K)
376	S4_Roman.16926.16926.2	2	11.97	74	2.95E+06 (K)
387	X3L_Roman.17228.17228.3	3	11.9	82	3.96E+06 (K)
397	S2_Roman.16497.16497.2	2	11.83	70.3	3.30E+06 (K)
398	L3_Roman.16252.16252.4	4	11.82	70.7	3.48E+07 (K)
416	L3_Roman.16340.16340.3	3	11.7	78	1.28E+07 (K)
442	X4R_Roman.17096.17096.2	2	11.5	77.8	3.07E+05 (K)
478	S1_Roman.16842.16842.4	4	11.33	79.3	1.31E+08 (K)
504	S5_Roman.17112.17112.2	2	11.25	74.5	2.49E+06 (K)
507	S1_Roman.17222.17222.3	3	11.24	73.2	3.54E+07 (K)
526	X4R_Roman.17255.17255.4	4	11.13	76.8	7.34E+06 (K)
545	S4_Roman.16330.16330.3	3	11.04	80	1.75E+07 (K)
548	S3_Roman.17322.17322.3	3	11.02	72.1	2.09E+07 (K)
567	S3_Roman.16841.16841.3	3	10.93	70.4	2.09E+07 (K)
569	S2_Roman.16615.16615.2	2	10.91	72.7	3.30E+06 (K)
589	L3_Roman.16468.16468.3	3	10.81	88.3	1.28E+07 (K)
592	S2_Roman.16422.16672.3	3	10.8	73.6	2.40E+07 (K)
642	L3_Roman.17651.17651.4	4	10.59	73.1	3.96E+06 (K)
649	X4R_Roman.17298.17298.3	3	10.56	76.3	2.27E+06 (K)
657	S3_Roman.18351.18351.4	4	10.49	80.5	5.99E+06 (K)
702	X4R_Roman.17152.17152.3	3	10.33	70.7	2.27E+06 (K)
750	X4L_Roman.16741.16741.4	4	10.19	73.3	7.82E+06 (K)
784	S5_Roman.17241.17241.2	2	10.1	74.7	2.49E+06 (K)
802	S1_Roman.16988.16988.3	3	10.02	71.9	3.54E+07 (R)
250	S4_Roman.20504.20504.3	3	13.01	74	7.81E+06 (K)
513	L3_Roman.14596.14596.3	3	11.2	75.2	4.19E+05 (K)
273	L3_Roman.20436.20436.3	3	12.79	80.4	1.86E+07 (K)
375	X4L_Roman.20812.21085.4	4	11.98	77.7	5.40E+05 (K)
211	L5_Roman.11737.12020.2	2	13.48	76.8	5.22E+06 (K)
807	X5R_Roman.26060.26205.3	3	10.02	80.5	4.64E+05 (K)
68	S3_Roman.10016.10016.2	2	16.57	81	6.08E+07 (R)
74	L3_Roman.9668.10390.2	2	16.34	78.7	6.68E+07 (R)
135	S5_Roman.10088.10808.2	2	14.8	75	5.58E+07 (R)
178	S1_Roman.9917.10785.2	2	13.98	78	6.57E+07 (R)
309	X1R_Roman.8834.9652.2	2	12.41	80.1	9.58E+06 (K)
799	S1_Roman.8990.9117.2	2	10.03	75.5	6.54E+06 (K)
809	L3_Roman.8380.8662.2	2	10.01	79	3.16E+07 (K)
577	X4R_Roman.18192.18487.4	4	10.86	78.8	1.77E+06 (R)
669	S5_Roman.18370.18370.3	3	10.45	78.5	3.86E+06 (R)
77	X4R_Roman.9696.10095.2	2	16.24	82.7	5.72E+07 (R)
88	X4L_Roman.9535.9799.2	2	15.99	85.1	3.76E+07 (R)
92	X3R_Roman.9538.9796.2	2	15.92	80	2.30E+07 (R)
101	S2_Roman.9173.9429.2	2	15.64	85.4	8.17E+07 (R)
113	S4_Roman.9062.9471.2	2	15.34	82.5	8.89E+07 (R)
125	S5_Roman.9472.9858.2	2	15.06	81.4	1.15E+08 (R)
148	S1_Roman.9465.9858.2	2	14.49	80	1.44E+08 (R)
204	L3_Roman.9027.9423.2	2	13.55	80.9	1.39E+08 (R)

276	S3_Roman.8635.9970.2	2	12.79	81.7	1.38E+08 (R)
475	X3L_Roman.9652.9917.2	2	11.34	77.8	2.37E+07 (R)
234	S4_Roman.20328.20605.4	4	13.28	70.2	1.38E+06 (R)
384	S4_Roman.20393.20393.3	3	11.92	70.2	4.91E+04 (R)
497	S1_Roman.20784.20784.4	4	11.28	76.5	7.90E+05 (R)
120	X4L_Roman.20778.20910.4	4	15.14	74.3	2.45E+06 (R)
287	S4_Roman.20269.20526.4	4	12.64	71.8	6.35E+06 (R)
425	S2_Roman.5743.5743.2	2	11.63	74.3	4.13E+07 (R)
447	X3L_Roman.18440.18581.4	4	11.46	75.4	1.27E+06 (R)
538	X4L_Roman.18714.18852.4	4	11.08	71.5	1.23E+06 (R)
716	X4R_Roman.18564.18702.4	4	10.27	75.9	1.04E+06 (R)
724	L2_Roman.18984.19125.4	4	10.23	77	7.80E+05 (R)
547	X3L_Roman.12639.12786.2	2	11.03	76.1	1.24E+07 (K)
562	S5_Roman.12456.12752.2	2	10.95	74.3	2.20E+07 (K)
635	X4L_Roman.12379.12526.2	2	10.64	78.4	1.46E+07 (K)
742	X2L_Roman.12170.12318.2	2	10.2	76.9	1.05E+07 (K)
763	X3L_Roman.12148.12294.3	3	10.15	75.2	1.65E+05 (R)
320	L3_Roman.20055.20435.2	2	12.34	85	2.22E+07 (R)
542	S4_Roman.20366.20773.2	2	11.06	82.3	1.63E+07 (R)
677	L1_Roman.20212.20502.2	2	10.41	81.1	1.02E+07 (R)
683	X5R_Roman.20339.20921.2	2	10.4	80.3	1.47E+07 (R)
732	X1R_Roman.20547.21208.2	2	10.22	82.9	1.84E+07 (R)
787	X2L_Roman.20281.20543.2	2	10.08	85	9.54E+06 (R)
666	L3_Roman.5069.5069.2	2	10.45	74.3	1.21E+08 (R)
761	S2_Roman.5106.5234.2	2	10.15	72.2	1.07E+08 (R)
54	S4_Roman.4801.4801.2	2	17.25	80.7	1.91E+05 (K)
73	X3R_Roman.4896.4896.2	2	16.38	80.3	1.27E+05 (K)
114	X3R_Roman.4894.4894.3	3	15.28	80.5	3.59E+05 (K)
146	S3_Roman.5246.5246.2	2	14.55	85.7	6.93E+04 (K)
160	X1L_Roman.4967.4967.3	3	14.3	72.8	6.01E+04 (K)
164	X2L_Roman.4926.4926.3	3	14.19	83.1	1.05E+05 (K)
170	X4R_Roman.5382.5382.2	2	14.14	73.6	2.60E+05 (K)
181	S1_Roman.5184.5184.2	2	13.9	75.7	1.31E+05 (K)
210	X4L_Roman.4893.4893.3	3	13.49	78.2	8.96E+05 (K)
220	S5_Roman.5136.5136.3	3	13.41	77.3	5.20E+05 (K)
266	X4R_Roman.5449.5449.3	3	12.85	73.5	1.34E+06 (K)
501	S5_Roman.5122.5122.2	2	11.27	74.4	1.56E+05 (K)
596	X2R_Roman.4785.4785.2	2	10.79	73.6	4.54E+04 (K)
1	S4_Roman.4985.5123.2	2	24.48	92.2	6.53E+06 (K)
2	S2_Roman.5117.5117.2	2	23	91	5.81E+06 (K)
3	S1_Roman.5443.5574.2	2	22.33	94.8	9.78E+06 (K)
7	L3_Roman.5128.5128.2	2	20.84	93.3	8.48E+06 (K)
23	X4L_Roman.5199.5327.2	2	19.81	86.6	1.06E+07 (K)
28	X4R_Roman.5629.5629.2	2	19.24	86.2	3.05E+06 (K)
41	S5_Roman.5416.5416.2	2	18.27	84.6	1.85E+06 (K)
45	S3_Roman.5327.5464.3	3	17.83	88.2	1.84E+07 (K)
51	X4L_Roman.5073.5073.2	2	17.45	78.7	1.06E+07 (K)

72	S2_Roman.4996.4996.2	2	16.43	88.6	5.81E+06 (K)
80	X3R_Roman.5047.5047.2	2	16.21	79.3	2.13E+06 (K)
82	X3R_Roman.5169.5169.2	2	16.17	76.8	2.13E+06 (K)
83	S4_Roman.4786.5100.3	3	16.15	89.9	1.33E+07 (K)
85	X2L_Roman.5114.5114.2	2	16.12	79.4	1.32E+05 (K)
93	L3_Roman.4798.5109.3	3	15.82	85.8	1.70E+07 (K)
95	S5_Roman.5283.5283.2	2	15.77	79	1.85E+06 (K)
100	X3L_Roman.5583.5583.2	2	15.7	92.5	9.23E+05 (K)
136	X4R_Roman.5505.5505.2	2	14.8	84.1	3.05E+06 (K)
141	S1_Roman.5319.5319.2	2	14.66	75.8	9.78E+06 (K)
191	X3L_Roman.5451.5451.2	2	13.78	79.9	9.23E+05 (K)
248	S3_Roman.5466.5466.2	2	13.02	79.7	6.72E+06 (K)
338	L1_Roman.5016.5016.2	2	12.25	75.7	7.26E+05 (K)
521	L3_Roman.4988.4988.2	2	11.14	82.3	8.48E+06 (K)
38	S5_Roman.5267.5433.3	3	18.38	87.8	4.37E+06 (K)
52	S3_Roman.5344.5344.2	2	17.44	71.9	6.72E+06 (K)
71	X4R_Roman.5475.5725.3	3	16.45	83	1.21E+07 (K)
78	X3L_Roman.5425.5549.3	3	16.23	84.4	3.19E+06 (K)
104	X4L_Roman.5014.5316.3	3	15.56	86.3	2.39E+07 (K)
112	S2_Roman.4972.5221.3	3	15.35	81.5	1.44E+07 (K)
121	S1_Roman.5297.5500.3	3	15.12	88.3	3.09E+07 (K)
298	X3R_Roman.5060.5225.3	3	12.51	74.4	4.36E+06 (K)
662	S3_Roman.14987.15261.2	2	10.47	84.6	1.01E+07 (R)
344	L5_Roman.15422.15695.2	2	12.21	82.8	3.11E+05 (R)
467	X4R_Roman.16184.16448.	2	11.37	78.1	6.85E+05 (R)
96	S5_Roman.15527.16057.2	2	15.76	89.1	1.30E+08 (R)
117	X4R_Roman.15364.15751.	2	15.23	88.9	8.31E+07 (R)
187	S3_Roman.15603.15960.2	2	13.82	87.2	1.22E+08 (R)
197	S1_Roman.15480.15853.2	2	13.65	87.3	2.88E+08 (R)
208	X4L_Roman.15000.15524.:	2	13.51	90.7	6.28E+07 (R)
224	X3L_Roman.15725.15725.:	2	13.37	81.7	3.26E+07 (R)
305	L1_Roman.14742.14874.2	2	12.46	83.5	4.14E+06 (R)
409	S5_Roman.11855.11855.2	2	11.73	74.6	4.65E+05 (R)
459	X3R_Roman.14084.14327.	2	11.41	75.8	6.56E+07 (R)
572	X4R_Roman.15235.15235.	2	10.88	72.1	8.31E+07 (R)
709	L3_Roman.11314.11314.2	2	10.29	85	4.39E+05 (R)
756	X3L_Roman.12109.12109.:	2	10.18	72.2	2.32E+04 (R)
760	X4L_Roman.11893.11893.:	2	10.16	71.5	1.34E+05 (R)
602	X5R_Roman.29943.30276.	3	10.77	80.2	9.63E+06 (R)
476	X4R_Roman.16555.16690.	2	11.34	75	4.05E+06 (R)
550	X5R_Roman.16402.16541.	2	11.02	72.4	7.11E+06 (R)
582	S3_Roman.14745.15136.2	2	10.84	79.3	4.35E+06 (R)
725	S4_Roman.35229.35229.3	3	10.23	73.9	2.57E+04 (R)
806	X1R_Roman.5731.6134.2	2	10.02	79.5	7.43E+06 (K)
53	S3_Roman.6893.7029.2	2	17.25	77.8	3.89E+06 (R)
142	S4_Roman.38855.39199.3	3	14.64	72.8	2.30E+06 (R)
144	X2L_Roman.37650.38087.:	3	14.6	72.9	7.50E+06 (R)

155	X2R_Roman.38257.38801.	3	14.36	73.6	7.17E+06 (R)
167	X4R_Roman.38675.39022.	3	14.16	70.2	6.19E+06 (R)
174	X5R_Roman.39144.39243.	3	14.08	73.3	3.28E+06 (R)
295	X3L_Roman.38376.38714.	3	12.56	76.4	6.73E+06 (R)
483	L4_Roman.38253.38676.3	3	11.31	70.2	4.19E+06 (R)
389	X4L_Roman.12571.12716.	2	11.88	91.6	2.51E+06 (R)
471	S1_Roman.12707.12968.2	2	11.34	89.4	1.09E+07 (R)
481	X3L_Roman.12725.12870.	2	11.32	88.6	1.06E+06 (R)
486	S2_Roman.12179.12325.2	2	11.3	87.9	9.43E+06 (R)
487	S4_Roman.12086.12378.2	2	11.3	89	9.76E+06 (R)
488	S5_Roman.12624.12919.2	2	11.3	88.3	1.55E+07 (R)
496	L3_Roman.11887.12324.2	2	11.28	86.8	1.12E+07 (R)
532	X3R_Roman.12127.12273.	2	11.11	83.5	1.65E+06 (R)
559	S3_Roman.12690.12832.2	2	10.97	94.1	1.54E+07 (R)
628	X4L_Roman.12428.12428.	2	10.66	73.2	2.51E+06 (R)
743	X4R_Roman.12765.12908.	2	10.2	85	1.84E+06 (K)
768	S3_Roman.12543.12543.2	2	10.14	70.4	1.54E+07 (R)
390	X4L_Roman.3689.3689.2	2	11.87	74	1.79E+06 (R)
399	S5_Roman.3848.3848.3	3	11.82	77.2	1.58E+07 (R)
509	S3_Roman.3886.3886.2	2	11.23	77.3	7.14E+05 (R)
173	L3_Roman.4846.4846.2	2	14.11	80.9	2.32E+07 (R)
235	S1_Roman.5133.5133.2	2	13.26	79	2.92E+07 (R)
279	X4L_Roman.4907.4907.2	2	12.75	79.3	1.42E+07 (R)
311	S3_Roman.5194.5194.2	2	12.4	74.5	2.67E+07 (R)
332	S5_Roman.5155.5155.2	2	12.28	76.7	8.60E+06 (R)
428	S4_Roman.4876.4876.2	2	11.59	76	9.82E+06 (R)
791	S2_Roman.4752.4880.2	2	10.06	70.6	1.22E+07 (R)
568	L3_Roman.4229.4496.2	2	10.92	73.3	6.86E+06 (R)
698	S1_Roman.4527.4789.2	2	10.35	82	5.88E+06 (R)
4	S5_Roman.9768.10173.2	2	21.32	97.9	6.94E+07 (R)
5	S1_Roman.9857.10121.2	2	21.09	98.3	8.97E+07 (R)
6	S2_Roman.9462.9724.2	2	20.86	98.9	6.35E+07 (R)
11	X4L_Roman.9912.10206.2	2	20.22	95.8	1.77E+07 (R)
14	X4R_Roman.10173.10447.	2	20.09	98.5	1.96E+07 (R)
37	X3R_Roman.9964.10089.2	2	18.39	93.1	5.05E+06 (R)
47	L1_Roman.9710.9861.2	2	17.68	84.5	1.99E+06 (R)
79	X2L_Roman.9846.9846.2	2	16.21	88.4	2.00E+06 (R)
194	L4_Roman.9957.9957.2	2	13.71	70.4	1.74E+06 (R)
209	X3L_Roman.10082.10225.	2	13.49	79	3.21E+06 (R)
437	X1L_Roman.9839.9839.2	2	11.53	71.4	8.61E+05 (R)
480	X1R_Roman.10170.10170.	2	11.32	77.6	1.04E+06 (R)
613	X2R_Roman.9579.9579.2	2	10.72	72.8	1.45E+06 (R)
103	X4L_Roman.26352.26352.	3	15.57	76.6	7.29E+05 (R)
434	S4_Roman.26024.26024.3	3	11.56	74	6.54E+05 (R)
196	S5_Roman.26536.26536.3	3	13.67	85.4	5.72E+05 (R)
243	L3_Roman.25599.25740.3	3	13.1	70.9	1.54E+06 (R)
573	S2_Roman.25393.25393.3	3	10.87	75.1	1.02E+06 (R)



35	S2_Roman.22717.22851.3	3	18.41	83.9	4.44E+06 (R)
57	S5_Roman.23623.23881.3	3	17.08	84	1.97E+06 (R)
58	S1_Roman.23199.23449.3	3	17.05	85.3	6.42E+06 (R)
84	X4L_Roman.23832.23832.3	3	16.15	73.6	1.01E+06 (R)
97	S4_Roman.23191.23468.3	3	15.74	88.1	5.33E+06 (R)
98	S3_Roman.23607.23861.3	3	15.71	81.9	1.62E+06 (R)
115	L3_Roman.22981.23238.3	3	15.24	76.6	1.72E+06 (R)
172	S4_Roman.23338.23338.3	3	14.12	80.5	5.33E+06 (R)
392	X4R_Roman.23743.23743.3	3	11.86	70.4	1.27E+06 (R)
161	S4_Roman.9309.9736.2	2	14.29	91.3	8.60E+07 (R)
241	L3_Roman.9217.9774.2	2	13.12	92.8	1.61E+08 (R)
713	X3R_Roman.22948.22948.3	3	10.28	87.5	2.56E+04 (R)
808	L3_Roman.45857.45857.3	3	10.01	72.2	3.66E+03 (R)
159	L1_Roman.23363.23490.2	2	14.32	80.5	3.12E+06 (R)
165	X4R_Roman.23898.24299.2	2	14.18	81.3	7.62E+06 (R)
184	S3_Roman.25589.26346.2	2	13.84	79.1	1.07E+08 (R)
233	X4L_Roman.24192.24320.2	2	13.3	83.6	9.76E+06 (R)
249	S3_Roman.23984.24238.2	2	13.01	77	1.76E+07 (R)
262	X3R_Roman.24967.25114.2	2	12.89	86.4	9.92E+06 (R)
263	S1_Roman.23509.23873.2	2	12.87	79.4	2.63E+07 (R)
280	S5_Roman.25996.26508.2	2	12.71	78.8	1.32E+08 (R)
290	X3L_Roman.23755.24002.2	2	12.62	80.1	5.97E+06 (R)
302	S2_Roman.23022.23269.2	2	12.48	80.1	1.84E+07 (R)
304	X4R_Roman.25707.26085.2	2	12.48	81.9	2.27E+07 (R)
310	X4L_Roman.26051.26305.2	2	12.41	82.4	2.34E+07 (R)
318	S2_Roman.24603.25218.2	2	12.36	78.9	1.50E+08 (R)
328	S4_Roman.23650.23926.2	2	12.29	82.2	2.76E+07 (R)
329	S5_Roman.24272.25868.2	2	12.29	85	1.32E+08 (R)
334	L3_Roman.23318.23701.2	2	12.27	77.9	4.22E+07 (R)
347	S1_Roman.25212.25975.2	2	12.2	80.1	2.24E+08 (R)
560	X3R_Roman.22813.22937.2	2	10.97	74.8	7.14E+06 (R)
583	S5_Roman.22591.24125.2	2	10.84	76	1.00E+07 (R)
598	S3_Roman.18959.18959.2	2	10.78	75.3	1.92E+06 (R)
625	X3L_Roman.25700.25951.2	2	10.67	72.7	9.98E+06 (R)
715	X3L_Roman.24125.25578.2	2	10.27	94.8	9.98E+06 (R)
794	X4L_Roman.24447.25925.2	2	10.05	90.3	2.34E+07 (R)
765	L2_Roman.8992.9166.3	3	10.14	84.7	6.16E+06 (K)
674	X1L_Roman.13062.13203.2	2	10.42	70.7	1.21E+06 (R)
190	X2L_Roman.8086.8478.2	2	13.78	78.9	1.48E+07 (K)
297	S3_Roman.8483.8738.2	2	12.52	79.2	1.78E+07 (K)
426	S1_Roman.8517.8783.2	2	11.61	75.8	2.00E+07 (K)
429	X1R_Roman.8503.8905.2	2	11.59	79.9	1.78E+07 (K)
604	S4_Roman.7996.8286.2	2	10.76	79.5	1.60E+07 (K)
687	X4L_Roman.8333.8761.2	2	10.39	75.7	2.11E+07 (K)
533	S3_Roman.6989.7117.2	2	11.1	94.5	3.34E+07 (K)
751	S1_Roman.6976.7101.2	2	10.18	91.4	2.54E+07 (K)
593	X5R_Roman.11377.11377.3	3	10.8	83.2	8.57E+05 (K)

665	X5R_Roman.11068.11068.	3	10.47	83.3	8.57E+05 (K)
584	X2L_Roman.10138.10264.:	2	10.84	87.3	2.82E+06 (R)
597	L5_Roman.9554.9698.2	2	10.78	86.8	1.28E+06 (R)
270	S1_Roman.16414.16545.2	2	12.8	76	8.52E+06 (R)
379	X3L_Roman.16424.16680.:	2	11.95	80.7	8.75E+06 (R)
580	X4L_Roman.16372.16501.:	2	10.85	72.4	6.85E+06 (R)
780	X4R_Roman.16466.16728.	2	10.11	76.9	7.74E+06 (R)
798	S1_Roman.16679.16679.2	2	10.03	84.8	8.51E+06 (R)
757	X5R_Roman.47183.48384.	3	10.18	78.6	3.45E+06 (K)
767	S1_Roman.46004.46004.3	3	10.14	86.2	3.99E+07 (K)
805	S5_Roman.5268.5268.2	2	10.02	75.3	9.84E+05 (R)
445	X5R_Roman.4098.4098.2	2	11.47	74.5	1.07E+07 (K)
400	X2L_Roman.15414.16325.:	2	11.82	92.6	5.32E+05 (-)
406	X3R_Roman.14638.14879.	2	11.79	81.5	6.43E+05 (-)
438	L5_Roman.15196.15459.2	2	11.51	89.7	9.10E+05 (-)
468	L1_Roman.15270.15412.2	2	11.36	84.9	3.36E+05 (-)
786	X2L_Roman.16183.16183.:	2	10.08	76.2	5.32E+05 (-)
618	S4_Roman.13067.13345.2	2	10.71	81.1	3.56E+06 (K)
365	S4_Roman.24585.25891.2	2	12.08	89.7	6.56E+07 (K)
608	S1_Roman.24542.25510.2	2	10.74	93.9	3.11E+07 (K)
500	L5_Roman.18337.19831.2	2	11.27	72.2	1.14E+06 (K)
704	L5_Roman.19063.19063.2	2	10.3	76	9.31E+05 (K)
803	S1_Roman.3632.3751.2	2	10.02	91.1	4.69E+06 (K)
707	X4L_Roman.23658.23658.:	3	10.3	88.1	3.11E+05 (R)
637	X1L_Roman.13576.13858.:	2	10.63	76.4	1.26E+07 (R)
737	L4_Roman.13629.13774.2	2	10.21	78.7	5.44E+06 (R)
108	L5_Roman.26053.26251.2	2	15.47	88.3	4.00E+06 (R)
134	X3L_Roman.26254.26553.:	2	14.83	84.9	1.02E+07 (R)
201	S3_Roman.26647.26775.2	2	13.61	76.8	2.18E+06 (R)
221	L3_Roman.26013.26205.2	2	13.4	83.3	5.62E+06 (R)
283	L4_Roman.26185.26517.2	2	12.68	79.1	3.42E+06 (R)
403	S5_Roman.26744.27003.2	2	11.8	84	3.61E+06 (R)
418	S2_Roman.25669.25920.2	2	11.68	79.8	9.81E+06 (R)
558	X2R_Roman.26158.26285.	2	10.98	82	7.04E+06 (R)
641	X3R_Roman.25347.25417.	2	10.6	74.9	2.59E+06 (R)
238	X2R_Roman.13640.13914.	2	13.23	71.2	1.04E+06 (K)
307	X5R_Roman.13821.14098.	2	12.43	72.8	2.96E+06 (K)
461	X4R_Roman.14212.14615.	2	11.41	71.5	6.02E+06 (K)
531	L3_Roman.13664.13935.2	2	11.11	73.3	9.41E+06 (K)
629	X3R_Roman.13304.13600.	2	10.65	72.5	4.74E+06 (K)
788	X1R_Roman.14291.14565.	2	10.07	74.9	4.23E+06 (K)
804	S4_Roman.13779.14061.2	2	10.02	72.4	8.99E+06 (K)
451	S2_Roman.18343.18481.2	2	11.45	75.5	3.54E+07 (R)
745	S2_Roman.19262.20511.2	2	10.19	70.4	2.18E+06 (R)
371	X4L_Roman.18912.18912.:	2	12.01	71.6	3.69E+07 (K)
695	X1R_Roman.19045.19315.	2	10.37	78.7	4.88E+07 (K)
672	X4L_Roman.20588.20588.:	2	10.43	88.7	1.88E+06 (K)

634	X2L_Roman.35065.35403.:	3	10.64	86.5	4.85E+06 (R)
670	L4_Roman.35546.35584.3	3	10.44	89.7	4.81E+06 (R)
316	S5_Roman.33413.33658.2	2	12.38	90.6	3.96E+06 (R)
330	X2L_Roman.32307.32545.:	2	12.29	87.7	1.07E+06 (R)
342	X2R_Roman.32952.33069.	2	12.22	86.9	6.76E+05 (R)
433	X5R_Roman.33026.33839.	2	11.57	94.5	1.55E+08 (R)
473	X1R_Roman.32956.33637.	2	11.34	83.7	1.73E+08 (R)
498	X1L_Roman.33511.34558.:	2	11.28	84.6	1.61E+08 (R)
530	X4L_Roman.33185.33427.:	2	11.12	84	2.11E+07 (R)
599	X3L_Roman.32696.32924.:	2	10.78	83.6	2.11E+07 (R)
600	X1R_Roman.32824.33761.	2	10.77	85.1	2.77E+08 (R)
656	S2_Roman.31909.32138.2	2	10.49	87.5	1.61E+05 (R)
423	S1_Roman.32593.32820.2	2	11.64	87	2.77E+06 (R)
458	L3_Roman.32992.33248.2	2	11.41	86.7	7.74E+06 (R)
689	L5_Roman.32592.32834.2	2	10.38	83.7	1.13E+06 (R)
528	S3_Roman.32774.33012.2	2	11.12	83.6	2.19E+06 (R)
448	X4R_Roman.7154.7280.2	2	11.46	90.3	1.42E+07 (K)
723	X4L_Roman.10019.10019.:	2	10.24	72.5	6.54E+05 (K)
557	L1_Roman.9816.9816.2	2	10.98	76.7	1.07E+06 (K)
693	S4_Roman.9282.9423.2	2	10.37	70.8	2.18E+06 (K)
771	L5_Roman.9473.9473.2	2	10.13	72.8	1.76E+05 (K)
353	S1_Roman.9944.10070.2	2	12.15	73.1	3.58E+06 (R)
671	X2R_Roman.9513.9513.2	2	10.44	76	7.86E+05 (R)
739	X1R_Roman.10231.10231.	2	10.21	90.2	1.09E+06 (R)
749	X2L_Roman.9790.9790.2	2	10.19	72.7	6.05E+05 (R)
752	S2_Roman.9649.9649.2	2	10.18	71.5	1.22E+06 (R)
678	S2_Roman.14056.14305.2	2	10.41	88	7.50E+06 (K)
463	X3L_Roman.22103.22103.:	2	11.39	77.5	2.88E+05 (K)
564	S4_Roman.22043.22043.2	2	10.94	82.1	2.25E+05 (K)
506	L5_Roman.36213.37591.2	2	11.24	73.5	4.88E+06 (K)
482	L3_Roman.33574.33574.3	3	11.31	71.8	8.81E+05 (R)
714	L1_Roman.44575.44575.3	3	10.27	73.9	1.00E+06 (R)
386	X2R_Roman.15398.16286.	2	11.9	87.2	6.99E+05 (-)
255	S2_Roman.26005.26432.2	2	12.96	89.2	2.69E+07 (R)
337	X2L_Roman.26069.26459.:	2	12.26	89.5	6.88E+07 (R)
296	S1_Roman.16463.16593.3	3	12.54	79.4	1.87E+06 (R)
675	X3L_Roman.15306.15553.:	2	10.42	87.9	4.64E+06 (K)
553	X3L_Roman.12308.12558.:	2	11.01	91.5	1.82E+07 (R)
682	X1R_Roman.15225.15515.	2	10.4	86.4	5.62E+06 (K)
684	S5_Roman.15191.15621.2	2	10.39	87.3	3.64E+07 (K)
515	S2_Roman.26002.26068.3	3	11.17	85.9	1.32E+06 (R)
407	L3_Roman.44626.44626.3	3	11.77	70.2	1.82E+05 (R)
585	X2R_Roman.16358.16358.	2	10.84	78.6	1.50E+06 (R)
408	X2L_Roman.11811.12087.:	2	11.77	92.6	1.46E+07 (K)
540	X1R_Roman.12245.12385.	2	11.07	94.1	4.03E+07 (K)
570	L3_Roman.9730.11384.2	2	10.9	86.7	2.74E+07 (K)
633	S5_Roman.12144.12437.2	2	10.64	97.3	4.06E+07 (K)

648	X4L_Roman.12158.12295.2	2	10.56	94	2.17E+07 (K)
679	X3R_Roman.11977.11977.2	2	10.41	88.8	6.43E+06 (K)
722	X1R_Roman.10506.12099.2	2	10.25	82.8	4.03E+07 (K)
8	X4L_Roman.30655.32012.2	2	20.64	97.7	4.00E+08 (-)
10	S2_Roman.29341.30708.2	2	20.4	98	6.08E+08 (-)
12	X3R_Roman.29747.30336.2	2	20.12	97.5	9.74E+07 (-)
13	X3L_Roman.30141.31251.2	2	20.09	97.2	1.48E+08 (-)
16	L3_Roman.30019.31499.2	2	19.94	99	8.86E+08 (-)
18	S1_Roman.30076.31216.2	2	19.92	98.3	9.48E+08 (-)
20	S3_Roman.30465.31751.2	2	19.89	97.9	6.94E+08 (-)
21	S4_Roman.30211.31637.2	2	19.86	97.2	8.19E+08 (-)
22	X4R_Roman.30489.31638.2	2	19.85	97.2	3.33E+08 (-)
25	L1_Roman.30489.30863.2	2	19.57	96.7	3.83E+07 (-)
26	S5_Roman.30826.32056.2	2	19.38	97.7	7.26E+08 (-)
32	L5_Roman.30803.30934.2	2	19.11	93.4	2.93E+06 (-)
43	X2R_Roman.30939.31305.2	2	18.12	93.1	1.10E+07 (-)
48	L4_Roman.30905.31279.2	2	17.64	93.8	2.28E+07 (-)
49	X2L_Roman.30371.30735.2	2	17.62	92.8	1.88E+07 (-)
64	X1L_Roman.31838.32122.2	2	16.85	91.2	2.52E+06 (-)
87	L3_Roman.31617.32687.2	2	16.04	96.8	3.68E+08 (-)
99	X5R_Roman.31353.31599.2	2	15.71	90.2	3.83E+06 (-)
107	X1R_Roman.31304.31543.2	2	15.5	89.5	6.31E+06 (-)
109	S4_Roman.31756.32599.2	2	15.42	88.9	4.40E+08 (-)
118	S1_Roman.31337.32024.2	2	15.2	90.1	6.63E+08 (-)
122	S5_Roman.32176.32820.2	2	15.12	87.3	4.44E+08 (-)
176	S3_Roman.31864.32262.2	2	14.02	88.2	2.39E+08 (-)
195	L2_Roman.31636.31753.2	2	13.68	89.5	3.18E+06 (-)
205	S1_Roman.29945.29945.2	2	13.54	83	5.65E+08 (-)
274	S1_Roman.32193.32193.2	2	12.79	70.6	1.98E+06 (-)
327	L3_Roman.30229.30229.2	2	12.29	86.4	6.84E+08 (-)
345	X3R_Roman.29628.29628.2	2	12.21	77.9	9.74E+07 (-)
431	X5R_Roman.31739.31739.2	2	11.58	80.6	3.83E+06 (-)
522	S3_Roman.30328.30328.2	2	11.14	76.6	3.89E+08 (-)
524	X4R_Roman.30637.30637.2	2	11.14	76.9	2.43E+08 (-)
622	S4_Roman.32726.32726.2	2	10.68	76.5	2.99E+06 (-)
638	S5_Roman.30708.30708.2	2	10.62	80.9	3.96E+08 (-)
676	X3R_Roman.30449.30449.2	2	10.42	77.7	9.74E+07 (-)
740	X1R_Roman.31672.31672.2	2	10.21	73	6.31E+06 (-)
421	S5_Roman.45074.45074.3	3	11.66	79.9	7.15E+03 (-)
94	S2_Roman.29711.29711.2	2	15.77	88.4	6.06E+05 (-)
102	L3_Roman.30266.30395.2	2	15.62	91.2	7.79E+05 (-)
177	S5_Roman.31080.31080.2	2	14.02	88.5	9.26E+05 (-)
189	S3_Roman.30776.30776.2	2	13.78	88.4	4.81E+05 (-)
614	X3R_Roman.12083.12230.2	2	10.72	83.6	1.26E+06 (R)
705	S5_Roman.12605.12751.2	2	10.3	86.4	3.04E+06 (R)
696	L3_Roman.10963.11353.2	2	10.36	83.2	1.34E+07 (K)
601	X4R_Roman.16455.16583.2	2	10.77	79.2	2.85E+05 (R)

360	S1_Roman.26487.26651.2	2	12.12	71.3	2.06E+06 (R)
139	S2_Roman.16088.16220.2	2	14.71	90.1	3.44E+06 (K)
454	L3_Roman.14475.14612.2	2	11.44	90.4	9.30E+05 (R)
621	S2_Roman.14650.14775.2	2	10.7	91.4	6.98E+05 (R)
785	X4L_Roman.15001.15142.1	2	10.09	96.4	3.70E+05 (R)
734	X4R_Roman.29965.29980.	4	10.22	72.6	5.97E+05 (K)
579	S5_Roman.43112.43322.3	3	10.85	77.3	2.69E+07 (K)
252	S5_Roman.4494.4625.2	2	13	80.4	8.59E+05 (K)
554	S1_Roman.4505.4626.2	2	10.99	75.2	8.29E+05 (K)
576	S3_Roman.4549.4549.2	2	10.86	82.4	8.96E+05 (K)
769	S4_Roman.4229.4229.2	2	10.14	90.2	1.25E+06 (K)
779	X4L_Roman.4190.4317.2	2	10.11	70.3	1.21E+06 (K)
27	L3_Roman.6933.7326.3	3	19.26	88.5	2.70E+07 (R)
29	S3_Roman.7568.7957.3	3	19.23	89.2	4.60E+07 (R)
30	S1_Roman.7641.8033.3	3	19.17	91.7	5.67E+07 (R)
39	X3L_Roman.7754.8010.3	3	18.32	86.7	1.63E+07 (R)
44	S5_Roman.7435.7708.3	3	17.99	88	3.26E+07 (R)
56	S4_Roman.6971.7391.3	3	17.16	87.1	2.36E+07 (R)
63	X4R_Roman.7857.8122.3	3	16.9	86.5	6.82E+06 (R)
76	X4L_Roman.7478.7867.3	3	16.25	84.6	1.93E+06 (R)
175	X4L_Roman.7544.7950.2	2	14.03	93.4	1.90E+06 (R)
215	X3R_Roman.7174.7583.3	3	13.46	75.3	2.79E+06 (R)
240	S5_Roman.7517.7791.2	2	13.21	90.3	2.92E+07 (R)
244	S2_Roman.7205.7517.3	3	13.09	74	2.01E+07 (R)
275	S1_Roman.7623.8003.2	2	12.79	85.9	5.16E+07 (R)
333	X3L_Roman.7825.7959.2	2	12.28	86.8	1.55E+07 (R)
355	S3_Roman.7582.7956.2	2	12.13	90.9	3.98E+07 (R)
368	S2_Roman.7150.7539.2	2	12.02	92.8	4.47E+07 (R)
401	X3R_Roman.7269.7395.2	2	11.82	82.4	2.13E+06 (R)
499	X3L_Roman.8082.8082.2	2	11.28	78.7	1.10E+07 (R)
527	L3_Roman.6916.7313.2	2	11.12	86.2	3.00E+07 (R)
551	S4_Roman.6935.7352.2	2	11.01	88.3	3.00E+07 (R)
609	X4R_Roman.7941.8193.2	2	10.74	94	2.18E+07 (R)
708	L1_Roman.7107.7107.2	2	10.29	93.6	2.01E+07 (R)
587	S4_Roman.18888.18888.4	4	10.83	76	1.29E+05 (R)
356	S5_Roman.21916.21916.3	3	12.13	72.9	5.02E+05 (K)
182	X4R_Roman.46699.46699.	2	13.85	84.7	1.53E+05 (-)
539	S4_Roman.47525.47525.2	2	11.07	85	1.30E+05 (-)
456	X2L_Roman.24878.24878.1	2	11.44	75.9	9.14E+04 (K)
284	S4_Roman.4140.4140.3	3	12.68	76.5	8.35E+05 (R)
449	L3_Roman.4119.4119.3	3	11.45	79.9	2.10E+06 (R)
464	S2_Roman.4177.4177.3	3	11.38	72.1	1.99E+06 (R)
86	S4_Roman.3880.3885.2	2	16.05	84.4	7.06E+06 (R)
158	S1_Roman.4163.4163.3	3	14.33	72.2	3.22E+06 (R)
216	S3_Roman.4177.4177.2	2	13.45	81.9	3.39E+07 (R)
395	S5_Roman.4147.4147.4	4	11.84	78.3	5.62E+05 (R)
460	X4L_Roman.3778.3778.4	4	11.41	82.3	3.27E+05 (R)

469	S4_Roman.3855.3855.4	4	11.36	85.1	5.20E+05 (R)
472	S2_Roman.3835.3835.3	3	11.34	70.5	4.19E+06 (R)
42	S4_Roman.17057.17179.4	4	18.24	97.1	2.21E+07 (R)
105	L3_Roman.17652.17800.4	4	15.54	85.1	1.72E+06 (R)
130	S3_Roman.17574.17574.4	4	14.92	90.5	6.28E+06 (R)
131	L3_Roman.16814.16937.4	4	14.87	88.4	1.78E+07 (R)
185	X4L_Roman.17265.17265.4	4	13.84	87.7	8.86E+06 (R)
186	S1_Roman.17604.17604.3	3	13.83	82.8	2.09E+06 (R)
278	X4R_Roman.17542.17542.4	4	12.79	89	3.90E+06 (R)
372	L3_Roman.16959.16959.2	2	12	74.2	8.56E+05 (R)
712	S3_Roman.17697.17697.4	4	10.28	80	6.28E+06 (R)
127	S2_Roman.16936.17054.4	4	15.01	86.9	8.97E+06 (R)
55	S3_Roman.4824.4824.3	3	17.17	92.1	2.38E+06 (R)
312	S5_Roman.4739.4739.3	3	12.4	76.3	3.88E+06 (R)
313	L3_Roman.4448.4448.3	3	12.39	75.9	3.82E+06 (R)
143	S5_Roman.9882.9882.4	4	14.64	85.9	3.07E+06 (R)
746	S2_Roman.9468.9468.4	4	10.19	78.9	7.22E+05 (R)
69	S5_Roman.14164.14598.4	4	16.46	83.5	2.78E+07 (R)
111	S4_Roman.13997.14144.4	4	15.37	85.3	3.28E+07 (R)
251	S2_Roman.13960.13960.4	4	13	81.1	1.50E+07 (R)
286	S2_Roman.13829.13829.4	4	12.67	82.5	1.50E+07 (R)
315	S2_Roman.14089.14089.4	4	12.39	81.7	1.50E+07 (R)
364	S4_Roman.13904.13904.3	3	12.08	78.5	6.23E+06 (R)
369	S5_Roman.15401.15401.4	4	12.02	76.8	2.96E+06 (R)
380	S4_Roman.14835.14835.4	4	11.94	89.5	3.04E+06 (R)
381	L3_Roman.13989.13989.4	4	11.93	74.7	1.85E+07 (R)
413	L3_Roman.13580.13580.4	4	11.71	81.6	1.85E+07 (R)
414	S5_Roman.14447.14447.4	4	11.71	78.9	2.78E+07 (R)
466	X4R_Roman.14426.14426.4	4	11.37	77.3	1.05E+06 (R)
492	S4_Roman.13862.13862.4	4	11.29	76.8	3.28E+07 (R)
518	X4L_Roman.14177.14177.4	4	11.17	78.2	5.56E+06 (R)
535	X3L_Roman.14617.14617.4	4	11.09	72.8	4.03E+06 (R)
561	L3_Roman.13855.13855.4	4	10.95	81.6	1.85E+07 (R)
575	L3_Roman.13857.13857.5	5	10.86	70.7	1.04E+07 (R)
578	S3_Roman.14663.14663.3	3	10.85	74.7	3.97E+05 (R)
594	S1_Roman.14481.14481.4	4	10.79	79.3	2.95E+07 (R)
627	S3_Roman.15390.15390.4	4	10.66	80.9	1.05E+06 (R)
632	S4_Roman.14047.14047.3	3	10.64	72.5	6.23E+06 (R)
660	S3_Roman.14575.14706.4	4	10.48	81.6	1.61E+07 (R)
697	S4_Roman.14125.14125.5	5	10.36	75.3	1.73E+07 (R)
766	L3_Roman.13717.13717.4	4	10.14	70.5	1.85E+07 (R)
778	X4L_Roman.14181.14181.4	5	10.11	73	3.98E+06 (R)
590	S3_Roman.18416.18416.4	4	10.81	74.4	6.60E+05 (R)
646	S4_Roman.17882.18020.4	4	10.56	75	1.51E+06 (R)
226	S4_Roman.14182.14182.5	5	13.34	82	1.18E+06 (R)
230	S3_Roman.14812.14812.5	5	13.31	86	7.98E+05 (R)
288	X4L_Roman.14448.14448.4	5	12.64	83.2	1.84E+06 (R)

417	S1_Roman.14799.14799.5	5	11.69	86	4.57E+06 (R)
636	S5_Roman.14811.14811.5	5	10.63	78.6	9.33E+05 (R)
149	S2_Roman.36441.36659.3	3	14.49	85.5	2.65E+06 (K)
223	L1_Roman.36974.37317.3	3	13.37	86.9	1.51E+06 (K)
261	X5R_Roman.37948.38292.3	3	12.9	87.5	1.72E+06 (K)
271	X1R_Roman.37845.38177.3	3	12.8	86.5	2.57E+06 (K)
382	S3_Roman.37073.37286.3	3	11.93	84	2.11E+06 (K)
457	X2R_Roman.37245.37464.3	3	11.42	88.4	1.46E+06 (K)
477	L3_Roman.37246.37625.3	3	11.33	83	2.15E+06 (K)
479	X1L_Roman.38508.38904.3	3	11.32	79.5	3.36E+05 (K)
505	X4R_Roman.37519.37734.3	3	11.25	84.2	3.46E+06 (K)
591	L5_Roman.37300.37532.3	3	10.8	79.2	1.02E+06 (K)
605	X4L_Roman.37679.37906.3	3	10.76	80.7	1.99E+06 (K)
783	S1_Roman.36980.37096.3	3	10.1	78.3	7.35E+05 (K)
606	S3_Roman.5430.6521.3	3	10.75	76.4	4.40E+07 (R)
793	S5_Roman.5341.6468.3	3	10.05	75.2	2.50E+07 (R)
718	X2L_Roman.37825.37825.3	3	10.26	75.2	1.75E+06 (R)
619	X2R_Roman.11672.11819.2	2	10.71	74.9	1.12E+07 (R)
650	S2_Roman.11785.11912.2	2	10.55	73.3	1.56E+07 (R)
731	X1R_Roman.12246.12384.2	2	10.22	74.9	3.40E+07 (R)
744	L5_Roman.11704.11853.2	2	10.19	72.1	1.17E+07 (R)
789	X3L_Roman.12142.12416.2	2	10.07	76.4	1.52E+07 (R)
658	S4_Roman.4070.4070.2	2	10.49	83.1	2.04E+05 (R)
701	X4L_Roman.4029.4029.2	2	10.33	70.8	8.39E+04 (R)
281	X2L_Roman.26745.26874.2	2	12.71	74.5	2.26E+06 (K)
644	X3R_Roman.26489.26489.2	2	10.59	72.8	1.05E+06 (K)
402	L4_Roman.15531.15927.2	2	11.8	84	2.66E+07 (R)
450	L5_Roman.15195.15691.2	2	11.45	81.6	2.25E+07 (R)
495	X2R_Roman.15113.15616.2	2	11.29	83.4	2.84E+07 (R)
508	X2L_Roman.15088.15710.2	2	11.24	82.9	5.49E+07 (R)
640	S4_Roman.15410.15806.2	2	10.61	84.4	2.55E+07 (R)
664	X4R_Roman.16050.16301.2	2	10.47	84	1.92E+07 (R)
717	X5R_Roman.15540.15937.2	2	10.27	82.9	3.24E+07 (R)
735	L3_Roman.15334.15623.2	2	10.21	82.5	1.18E+07 (R)
810	S2_Roman.15291.15681.2	2	10.01	83.8	2.26E+07 (R)
537	X3R_Roman.8703.8703.2	2	11.08	84.1	1.47E+06 (R)
772	S2_Roman.19406.19406.2	2	10.13	72.5	1.82E+04 (R)
180	X2L_Roman.12381.12509.2	2	13.92	85.4	1.58E+06 (-)
259	L5_Roman.12054.12211.2	2	12.92	85.2	2.19E+06 (-)
267	S1_Roman.12881.13009.2	2	12.84	83.7	2.52E+06 (-)
294	L3_Roman.12237.12237.2	2	12.56	82.4	1.01E+06 (-)
349	X5R_Roman.12097.12256.2	2	12.18	86.1	6.55E+05 (-)
377	X2R_Roman.12036.12196.2	2	11.96	88.6	1.81E+06 (-)
415	X4L_Roman.12718.12864.2	2	11.71	73.4	6.72E+05 (-)
443	L2_Roman.13580.13830.2	2	11.48	72.8	6.83E+06 (-)
444	L1_Roman.12253.12398.2	2	11.47	81.3	1.39E+06 (-)
446	S2_Roman.12259.12517.2	2	11.46	77.6	1.23E+06 (-)

511	X3R_Roman.12281.12281.	2	11.23	73	1.47E+06 (-)
517	X1R_Roman.12970.12970.	2	11.17	87.6	6.22E+05 (-)
543	L4_Roman.12529.12529.2	2	11.05	82.2	1.07E+06 (-)
563	X3L_Roman.12939.13068.:	2	10.95	77.8	2.82E+06 (-)
624	S4_Roman.12167.12167.2	2	10.67	86.3	8.91E+05 (-)
639	X1L_Roman.12353.12511.:	2	10.62	85	1.10E+06 (-)
668	S4_Roman.12317.12317.2	2	10.45	86.1	8.91E+05 (-)
623	L3_Roman.9115.9381.2	2	10.67	82	2.49E+07 (K)
681	L1_Roman.9312.9735.2	2	10.4	82.7	3.30E+07 (K)
762	X2L_Roman.9407.9657.2	2	10.15	82.6	1.86E+07 (K)
293	L2_Roman.18826.18826.3	3	12.56	76	1.90E+06 (R)
490	L2_Roman.18960.18960.3	3	11.29	83	1.90E+06 (R)
719	X2R_Roman.9023.9456.2	2	10.26	83.9	1.22E+07 (R)
736	L3_Roman.4658.4804.2	2	10.21	74.1	4.12E+06 (K)
317	S2_Roman.4286.4415.2	2	12.37	90.4	3.60E+07 (K)
331	S3_Roman.4674.4807.2	2	12.28	92.2	4.23E+07 (K)
370	S1_Roman.4524.4655.2	2	12.01	87.7	2.48E+07 (K)
388	L3_Roman.4201.4602.2	2	11.88	91.7	1.12E+08 (K)
405	S4_Roman.4216.4470.2	2	11.79	88.9	4.54E+07 (K)
544	X4R_Roman.4792.5038.2	2	11.05	89.6	3.44E+07 (K)
611	X3L_Roman.4690.4817.2	2	10.73	84.4	1.00E+07 (K)
366	X4R_Roman.11256.11256.	3	12.08	83.6	6.82E+05 (K)
615	X3R_Roman.7272.7524.2	2	10.72	77.8	8.01E+06 (K)
631	S1_Roman.8422.8550.3	3	10.64	73.8	1.84E+06 (K)
710	X4R_Roman.8235.8577.3	3	10.29	73.5	2.04E+06 (K)
324	S3_Roman.4307.4581.2	2	12.32	92.1	4.78E+07 (K)
439	S5_Roman.4312.4570.2	2	11.51	93.4	2.48E+07 (K)
470	S4_Roman.4027.4169.2	2	11.36	89.8	5.72E+07 (K)
536	S1_Roman.4258.4500.2	2	11.08	89.4	7.43E+07 (K)
774	X2R_Roman.45134.45134.	3	10.13	83.9	1.85E+05 (K)
404	L4_Roman.7154.7419.2	2	11.79	74.5	1.23E+07 (R)
391	X4R_Roman.14111.14251.	2	11.86	79.8	4.74E+04 (K)
546	S3_Roman.14192.14493.2	2	11.03	75.2	4.69E+05 (K)
603	S4_Roman.14030.14030.2	2	10.76	82	1.83E+06 (K)
758	X3L_Roman.14084.14211.:	2	10.17	85.5	1.77E+05 (K)
777	X3R_Roman.13253.13394.	2	10.11	89.9	3.06E+05 (K)
792	X4L_Roman.14186.14186.:	2	10.06	72.8	3.94E+05 (K)
673	L1_Roman.13781.13781.2	2	10.42	80.7	1.24E+05 (K)
795	S2_Roman.13844.13844.2	2	10.04	72.1	4.24E+05 (K)
588	X3R_Roman.15742.15742.	4	10.82	71.4	1.51E+06 (R)
308	L5_Roman.18855.18979.4	4	12.41	71.2	8.55E+06 (R)
341	X2R_Roman.30585.30822.	2	12.22	86.6	5.65E+05 (K)
733	X4L_Roman.31021.31252.:	2	10.22	75.9	1.20E+06 (K)
651	X1L_Roman.32587.32950.:	2	10.52	76.9	3.94E+06 (K)
291	X3R_Roman.25290.25439.	2	12.59	88.5	3.67E+05 (R)
441	S4_Roman.5823.5979.2	2	11.5	78.9	7.49E+05 (R)
217	S5_Roman.17184.17584.2	2	13.44	87.1	2.97E+06 (R)



231	X4L_Roman.16997.17268.2	2	13.31	77.3	1.25E+06 (R)
301	X2R_Roman.16392.16518.2	2	12.49	83.2	5.14E+05 (R)
336	X4R_Roman.17292.17545.2	2	12.27	76.6	3.82E+06 (R)
361	X2L_Roman.16412.16539.2	2	12.12	78.7	6.27E+05 (R)
383	X3L_Roman.17240.17490.2	2	11.93	81.4	3.73E+06 (R)
412	S4_Roman.16622.16887.2	2	11.72	94.3	2.98E+06 (R)
491	S1_Roman.17186.17426.2	2	11.29	73.5	4.08E+06 (R)
552	X1R_Roman.17277.17420.2	2	11.01	71.4	5.33E+05 (R)
663	X3R_Roman.15913.15913.2	2	10.47	82.6	9.98E+05 (R)
700	S3_Roman.17081.17448.2	2	10.33	85.8	3.74E+06 (R)
246	X2R_Roman.10151.10300.2	2	13.06	82.4	3.47E+06 (K)
253	X1R_Roman.10852.10997.2	2	13	86.8	9.29E+06 (K)
260	L1_Roman.10387.10535.2	2	12.9	84.2	1.00E+07 (K)
300	X3R_Roman.10668.10813.2	2	12.5	85.3	4.35E+06 (K)
335	S2_Roman.10249.10500.2	2	12.27	86.7	2.07E+07 (K)
348	L4_Roman.10502.10628.2	2	12.19	84.8	4.25E+06 (K)
367	L2_Roman.11581.11581.2	2	12.02	82.7	2.82E+06 (K)
373	X3L_Roman.10777.11025.2	2	11.99	81.4	1.08E+07 (K)
393	L3_Roman.10200.10347.2	2	11.85	86.5	7.73E+06 (K)
420	X4R_Roman.10920.11059.2	2	11.67	77.2	6.80E+06 (K)
435	S3_Roman.10765.11027.2	2	11.54	80.3	1.76E+07 (K)
516	S5_Roman.10721.11005.2	2	11.17	82.7	2.85E+07 (K)
549	S4_Roman.10170.10442.2	2	11.02	82	2.02E+07 (K)
565	X2L_Roman.10401.10672.2	2	10.94	82.9	9.79E+06 (K)
574	S2_Roman.9634.9634.2	2	10.87	85.5	1.92E+07 (K)
711	S1_Roman.10693.10942.2	2	10.28	82.1	7.02E+07 (K)
721	L2_Roman.11711.11711.2	2	10.25	79.3	2.82E+06 (K)
797	X4L_Roman.10742.10742.2	2	10.04	76.4	4.00E+06 (K)
655	X1L_Roman.13107.13107.2	2	10.5	72.7	4.86E+05 (R)
419	X2R_Roman.26829.26960.3	3	11.68	76.9	7.45E+05 (K)
484	X4R_Roman.27163.27288.3	3	11.31	79	9.61E+05 (K)
503	L5_Roman.26677.26800.3	3	11.26	73.4	1.10E+06 (K)
510	X3L_Roman.26954.26954.3	3	11.23	75.9	1.59E+05 (K)
645	L1_Roman.26373.26523.3	3	10.57	77.2	1.61E+05 (K)
730	X1L_Roman.27424.27661.3	3	10.22	75.1	5.07E+04 (K)
764	L2_Roman.27386.27644.3	3	10.14	74.5	1.89E+06 (K)
727	L3_Roman.7130.7395.2	2	10.22	80.3	7.17E+06 (R)
796	S3_Roman.10371.10371.2	2	10.04	84.2	8.68E+05 (R)
630	L1_Roman.29771.29771.3	3	10.64	70.9	9.74E+05 (R)
229	S1_Roman.43754.43858.3	3	13.32	81.7	1.23E+06 (K)
299	L3_Roman.44516.44621.3	3	12.5	79.2	2.82E+06 (K)
325	X4R_Roman.44089.44089.3	3	12.31	81.5	1.82E+06 (K)
520	X3L_Roman.43754.43754.3	3	11.16	75.4	1.17E+06 (K)
686	X3R_Roman.42291.42418.3	3	10.39	74.3	1.10E+06 (K)
728	S2_Roman.43272.43380.3	3	10.22	86.6	3.12E+06 (K)
326	X4R_Roman.43976.43976.3	3	12.3	78	1.82E+06 (K)
465	L3_Roman.44420.44420.3	3	11.37	84.6	2.82E+06 (K)

770 X2R_Roman.30902.30902.	3	10.14	83.4	4.40E+07 (K)
374 X3L_Roman.19527.19783.:	3	11.98	81.9	3.92E+06 (-)
119 S5_Roman.5199.5329.2	2	15.16	90.4	6.03E+07 (K)
124 X4L_Roman.5086.5086.2	2	15.07	89.3	5.70E+07 (K)
132 X4R_Roman.5469.5594.2	2	14.86	90.7	4.54E+07 (K)
147 S3_Roman.5274.5408.2	2	14.53	78	9.17E+07 (K)
207 X2L_Roman.5001.5001.2	2	13.51	87.1	1.42E+06 (K)
219 S1_Roman.5351.5415.2	2	13.41	80.7	1.68E+08 (K)
242 X3L_Roman.5499.5499.2	2	13.11	73.8	1.68E+07 (K)
285 L1_Roman.4928.4928.2	2	12.67	88.7	3.82E+06 (K)
303 X1L_Roman.5032.5032.2	2	12.48	85.3	5.87E+05 (K)
343 L4_Roman.5042.5042.2	2	12.21	92.7	1.78E+06 (K)
396 X5R_Roman.4865.4865.2	2	11.84	83	6.88E+05 (K)





AYHDMR	(E)	792.346	F7BBH8	F7BBH8 F6	Serum amyloid A prote
AYHDMR	(E)	792.346	F7BBH8	F7BBH8 F6	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
AYNDMR	(E)	769.33	P19857	P19857 AC	Serum amyloid A prote
CASFR	(L)	606.303	A0A224Z8C	A0A224Z8C	Serum amyloid A prote
CASFR	(L)	606.303	A0A224Z8C	A0A224Z8C	Serum amyloid A prote
CASFR	(L)	606.303	A0A224Z8C	A0A224Z8C	Serum amyloid A prote
CASFR	(L)	606.303	A0A224Z8C	A0A224Z8C	Serum amyloid A prote
CPGGVWAAKVISDAREDLQR	(L)	2125.115	P53614	P53614	Serum amyloid A-1 pro
CPGGVWAAKVISDAREDLQR	(L)	2125.115	P53614	P53614	Serum amyloid A-1 pro
CPGGVWAAKVISDAREDLQR	(L)	2125.115	P53614	P53614	Serum amyloid A-1 pro
CPGGVWAAKVISDAREDLQR	(L)	2125.115	P53614	P53614	Serum amyloid A-1 pro
CPGGVWAAKVISDAREDLQR	(L)	2125.115	P53614	P53614	Serum amyloid A-1 pro
CPGGVWAAKVISDAREDLQR	(L)	2125.115	P53614	P53614	Serum amyloid A-1 pro
CPGGVWAAKVISDAREDLQR	(L)	2125.115	P53614	P53614	Serum amyloid A-1 pro
CPGGVWAAKVISDAREDLQR	(L)	2125.115	P53614	P53614	Serum amyloid A-1 pro
DIPSLK	(A)	706.377	A0A4X2KG	A0A4X2KG	Serum amyloid A like 1
DIPSLK	(A)	706.377	A0A4X2KG	A0A4X2KG	Serum amyloid A like 1
DLPSLK	(A)	706.377	G3WV59	G3WV59	Serum amyloid A like 1
DLPSLK	(A)	706.377	A0A4X2KG	A0A4X2KG	Serum amyloid A like 1
DLSLR	(E)	630.357	A0A147BE	A0A147BE	Putative serum amyloi
DLSLR	(E)	630.357	A0A147BE	A0A147BE	Putative serum amyloi
DPNFFRPPDLPSKY	(-)	1634.833	A0A5F8HF	A0A5F8HF	Serum amyloid A prote
DPNHFR	(S)	786.353	A0A2K5QF	A0A2K5QF	Serum amyloid A prote
DPNHFR	(S)	786.353	A0A2K5QF	A0A2K5QF	Serum amyloid A prote
DPNHFR	(S)	786.353	A0A2K5QF	A0A2K5QF	Serum amyloid A prote
DPNHFR	(S)	786.353	A0A2K5QF	A0A2K5QF	Serum amyloid A prote
DPNHFR	(S)	786.353	A0A2K5QF	A0A2K5QF	Serum amyloid A prote
DPNHFRPAGLDPKY	(-)	1626.802	A0A4X2KB	A0A4X2KB	Serum amyloid A prote
DPNHFRPAGLDPKY	(-)	1626.802	A0A4X2KB	A0A4X2KB	Serum amyloid A prote
DPNHFRPAGLDPKY	(-)	1626.802	A0A4X2KB	A0A4X2KB	Serum amyloid A prote
DPNHFRPAGLDPKY	(-)	1626.802	A0A023VM	A0A023VM	Serum amyloid A prote
DPNHFRPAGLDPKY	(-)	1626.802	A0A023VM	A0A023VM	Serum amyloid A prote
DPNHFRPAGLDPKY	(-)	1626.802	A0A023VM	A0A023VM	Serum amyloid A prote
DPNHFRPAGLDPKY	(-)	1626.802	P19708	P19708 P3	Serum amyloid A prote
DPNHFRPAGLDPKY	(-)	1626.802	A0A023VM	A0A023VM	Serum amyloid A prote
DPNHFRPAGLDPKY	(-)	1626.802	P19708	P19708 P3	Serum amyloid A prote
DPNHFRPAGLDPKY	(-)	1626.802	A0A023VM	A0A023VM	Serum amyloid A prote





EANYIGADK	(Y)	980.468	P19707	P19707 P1	Serum amyloid A prote
EANYIGADK	(Y)	980.468	P19707	P19707 P1	Serum amyloid A prote
EANYIGADKYFHAR	(G)	1654.797	P19707	P19707 P1	Serum amyloid A prote
EANYIGADKYFHAR	(G)	1654.797	P19707	P19707 P1	Serum amyloid A prote
EANYIGADKYFHAR	(G)	1654.797	P19707	P19707 P1	Serum amyloid A prote
EANYINADKYFHAR	(G)	1711.819	P53614	P53614 F7	Serum amyloid A-1 pro
EANYINADKYFHAR	(G)	1711.819	P53614	P53614 F7	Serum amyloid A-1 pro
EDFQR	(F)	660.331	A0A1A6G0	A0A1A6G0	Serum amyloid A prote
EDIQkFLGHAEDtLADQAANEWGRS (D)	(D)	3043.45	A0A2K5HM	A0A2K5HM	Serum amyloid A prote
EDIQkFLGHAEDtLADQAANEWGRS (D)	(D)	3043.45	A0A2K5HM	A0A2K5HM	Serum amyloid A prote
EDIQkFLGHAEDtLADQAANEWGRS (D)	(D)	3043.45	A0A2K5HM	A0A2K5HM	Serum amyloid A prote
EDIQkFLGHAEDTLADQAANEWGRS (D)	(D)	3043.45	A0A2K5HM	A0A2K5HM	Serum amyloid A prote
EGASLIR	(V)	731.405	A0A671FZ7	A0A671FZ7	Serum amyloid A prote
EGASLIR	(V)	731.405	A0A671FZ7	A0A671FZ7	Serum amyloid A prote
EGASLIR	(V)	731.405	A0A671FZ7	A0A671FZ7	Serum amyloid A prote
EGASLIR	(V)	731.405	A0A671FZ7	A0A671FZ7	Serum amyloid A prote
EGNDPNLFRPAGLPEK	(Y)	1777.862	A0A4W6DC	A0A4W6DC	Serum amyloid A prote
EITDPYIK	(G)	1009.52	A0A315BD	A0A315BD	Serum amyloid a prote
EITDPYIK	(G)	1009.52	A0A315BD	A0A315BD	Serum amyloid a prote
EITDPYIK	(G)	1009.52	A0A315BD	A0A315BD	Serum amyloid a prote
EITDPYIK	(G)	1009.52	A0A315BD	A0A315BD	Serum amyloid a prote
EITDPYIK	(G)	1009.52	A0A315BD	A0A315BD	Serum amyloid a prote
EITDPYIK	(G)	1009.52	A0A315BD	A0A315BD	Serum amyloid a prote
ENFQR	(L)	693.332	A0A1S3GU	A0A1S3GU	Serum amyloid A prote
ENFQR	(L)	693.332	A0A1S3GU	A0A1S3GU	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAADSR	(A)	1176.503	F6ZL17	F6ZL17 A0	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6 AC	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6 AC	Serum amyloid A prote



FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6 AC	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6 AC	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6 AC	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6 AC	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6 AC	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6 AC	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6 AC	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGAEDSR	(A)	1234.508	F6ZPQ6	F6ZPQ6	Serum amyloid A prote
FGDSGHGEADSR	(A)	1234.508	A0A5F5PVI	A0A5F5PVI	Serum amyloid A prote
FGDSGHGEADSR	(A)	1234.508	A0A5F5PVI	A0A5F5PVI	Serum amyloid A prote
FGDSGHGEADSR	(A)	1234.508	A0A5F5PVI	A0A5F5PVI	Serum amyloid A prote
FGDSGHGEADSR	(A)	1234.508	A0A5F5PVI	A0A5F5PVI	Serum amyloid A prote
FGDSGHGEADSR	(A)	1234.508	A0A5F5PVI	A0A5F5PVI	Serum amyloid A prote
FGDSGHGEADSR	(A)	1234.508	A0A3Q2HV	A0A3Q2HV	Serum amyloid A prote
FGDSGHGEADSR	(A)	1234.508	A0A3Q2HV	A0A3Q2HV	Serum amyloid A prote
FGDSGHGVEDSK	(A)	1234.534	J9NVE9	J9NVE9 A0	Serum amyloid A prote
FNFGGSGR	(G)	814.384	A0A5F5PJJ	A0A5F5PJJ	Serum amyloid A prote
FPALR	(L)	619.356	A0A452GU	A0A452GU	Serum amyloid A like 1
FPALR	(L)	619.356	A0A452GU	A0A452GU	Serum amyloid A like 1
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FSFGGSGR	(G)	814.384	P19857	P19857 AC	Serum amyloid A prote
FTGFFRPGSSGHGAEDSK	(A)	1941.873	A0A667IN1	A0A667IN1	Serum amyloid A prote
FTGRGIEDSR	(A)	1103.58	P20726	P20726 Q5	Serum amyloid A-1 pro
FTGRGIEDSR	(A)	1103.58	P20726	P20726 Q5	Serum amyloid A-1 pro
FVYCIWR	(R)	944.466	A0A131YNi	A0A131YNi	Serum amyloid A prote
GAGGRVAAAVISnTWEGIQRAR	(G)	2240.201	A0A5C6NP	A0A5C6NP	Serum amyloid A prote
GFPSK	(Y)	501.303	A0A091GCI	A0A091GCI	Serum amyloid A prote
GGAWAAK	(V)	660.346	Q7M3A4	Q7M3A4	Serum amyloid A prote
GLLWGRNPEGGTTAFR	(V)	1755.867	Q64423	Q64423	Serum amyloid A prote
GLLWGRNPEGGTTAFR	(V)	1755.867	Q64423	Q64423	Serum amyloid A prote



GPGGKWAAKVISDGR	(E)	1498.813	A0A553RF\	A0A553RF\	Serum amyloid A prote
GPGGKWAAKVISDGR	(E)	1498.813	A0A553RF\	A0A553RF\	Serum amyloid A prote
GPGGKWAAKVISDGR	(E)	1498.813	A0A553RF\	A0A553RF\	Serum amyloid A prote
GPGGKWAAKVISDGR	(E)	1498.813	A0A553RF\	A0A553RF\	Serum amyloid A prote
GPGGKWAAKVISDGR	(E)	1498.813	A0A553QR	A0A553QR	Serum amyloid A prote
GPGGKWAAKVISDGR	(E)	1498.813	A0A553RF\	A0A553RF\	Serum amyloid A prote
GPGGKWAAKVISDGR	(E)	1498.813	A0A553QR	A0A553QR	Serum amyloid A prote
GPGGKWAAKVISDGR	(E)	1498.813	A0A553RF\	A0A553RF\	Serum amyloid A prote
GPGGKWAAKVISDGR	(E)	1498.813	A0A553RF\	A0A553RF\	Serum amyloid A prote
GPGGTRAAK	(V)	826.489	F7ANU9	F7ANU9	Serum amyloid A prote
GPGGTRAAK	(V)	826.489	F7ANU9	F7ANU9	Serum amyloid A prote
GPGGVWAAEVLSDARENFQRVTDFK	(F)	2836.401	L5L5Z0	L5L5Z0	Serum amyloid A prote
GPGWAWAAKVISDAREDIQR	(F)	2097.084	A0A1A6G0	A0A1A6G0	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
GTWDMIR	(A)	878.419	P19857	P19857 F6	Serum amyloid A prote
IAKTGKFEGSK	(K)	1166.616	A0A0F2IUK	A0A0F2IUK	Serum amyloid A prote
IDEKIVNAGK	(F)	1070.657	A0A6I9HRC	A0A6I9HRC	Serum amyloid A prote
IEAIEK	(F)	690.367	A0A1T4VW	A0A1T4VW	Serum amyloid A prote
IEAIEK	(F)	690.367	A0A1T4VW	A0A1T4VW	Serum amyloid A prote
IEAIEK	(F)	690.367	A0A1T4VW	A0A1T4VW	Serum amyloid A prote
IEAIEK	(F)	690.367	A0A1T4VW	A0A1T4VW	Serum amyloid A prote
IEAIEK	(F)	690.367	A0A1T4VW	A0A1T4VW	Serum amyloid A prote
IEAIEK	(F)	690.367	A0A1T4VW	A0A1T4VW	Serum amyloid A prote
IEAIEK	(F)	690.367	A0A1T4VW	A0A1T4VW	Serum amyloid A prote
IEKEK	(Y)	574.356	A0A2I3SXC	A0A2I3SXC	Serum amyloid A like 1
IEKEK	(Y)	574.356	A0A2I3SXC	A0A2I3SXC	Serum amyloid A like 1
IEKLLR	(L)	745.457	A0A6I8NN\	A0A6I8NN\	Serum amyloid A like 1

IEKLLR	(L)	745.457	A0A6I8NN\	A0A6I8NN\	Serum amyloid A like 1
IELER	(Q)	658.425	A0A120D7.	A0A120D7.	Putative serum amyloi
IELTR	(Q)	658.425	A0A120D7.	A0A120D7.	Putative serum amyloi
IEQDVHHR	(C)	991.47	W5PJR0	W5PJR0	Serum amyloid A prote
IEQDVHHR	(C)	991.47	W5PJR0	W5PJR0	Serum amyloid A prote
IEQDVHHR	(C)	991.47	W5PJR0	W5PJR0	Serum amyloid A prote
IEQDVHHR	(C)	991.47	W5PJR0	W5PJR0	Serum amyloid A prote
IEQDVHHR	(C)	991.47	W5PJR0	W5PJR0	Serum amyloid A prote
IGNARENLRVTDFFK	(Y)	1938.019	A0A2U3X1\	A0A2U3X1\	Serum amyloid A prote
IGPGGAWAAEVISDARENIQR	(F)	2253.148	D3DQX7	D3DQX7	Serum amyloid A prote
IGQGGHHR	(C)	933.465	A0A6P7D9.	A0A6P7D9.	Serum amyloid A prote
IGQVVDK	(L)	759.425	A0A667HZI	A0A667HZI	Serum amyloid A like 1
IGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
IGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
IGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
IGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
IGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
IISRVK	(L)	747.455	L9LAH9	L9LAH9	Serum amyloid A-3 pro
ILLPMYR	(S)	906.487	A0A4X2KG.	A0A4X2KG.	Serum amyloid A like 1
ILLPMYR	(S)	906.487	A0A4X2KG.	A0A4X2KG.	Serum amyloid A like 1
ILYEVGK	(T)	879.482	G1PAL8	G1PAL8	Serum amyloid A like 1
ILYEVGK	(T)	879.482	G1PAL8	G1PAL8	Serum amyloid A like 1
ITCTSR	(K)	664.362	A0A1A6G0	A0A1A6G0	Serum amyloid A prote
ITDLIKYGDSGHGVEDsK	(A)	1933.95	P18575	P18575	Serum amyloid A-1 pro
ITDSLLK	(G)	799.492	A0A6P3EFE	A0A6P3EFE	Serum amyloid A prote
ITDSLLK	(G)	799.492	A0A6P3EFE	A0A6P3EFE	Serum amyloid A prote
IVFCVLEAAK	(Q)	1089.597	A0A5F9DK\	A0A5F9DK\	Serum amyloid A like 1
IVFCVLEAAK	(Q)	1089.597	G1SHI3	G1SHI3	Serum amyloid A like 1
IVFCVLEAAK	(Q)	1089.597	A0A5F9DK\	A0A5F9DK\	Serum amyloid A like 1
IVFCVLEAAK	(Q)	1089.597	A0A5F9DK\	A0A5F9DK\	Serum amyloid A like 1
IVFCVLEAAK	(Q)	1089.597	A0A5F9DK\	A0A5F9DK\	Serum amyloid A like 1
IVFCVLEAAK	(Q)	1089.597	A0A5F9DK\	A0A5F9DK\	Serum amyloid A like 1
IVFCVLEAAK	(Q)	1089.597	A0A5F9DK\	A0A5F9DK\	Serum amyloid A like 1
IVFCVLEAAK	(Q)	1089.597	A0A5F9DK\	A0A5F9DK\	Serum amyloid A like 1
IVFCVLEAAK	(Q)	1089.597	A0A5F9DK\	A0A5F9DK\	Serum amyloid A like 1
IVFCVLEAAK	(Q)	1089.597	A0A5F9DK\	A0A5F9DK\	Serum amyloid A like 1
IVFCVLEAAK	(Q)	1089.597	A0A5F9DK\	A0A5F9DK\	Serum amyloid A like 1
KGGALEAVK	(T)	896.495	A0A120D7.	A0A120D7.	Putative serum amyloi
KGGALEAVK	(T)	896.495	A0A120D7.	A0A120D7.	Putative serum amyloi
KGGALEAVK	(T)	896.495	A0A120D7.	A0A120D7.	Putative serum amyloi
KGGALEAVK	(T)	896.495	A0A120D7.	A0A120D7.	Putative serum amyloi
KGGALEAVK	(T)	896.495	A0A120D7.	A0A120D7.	Putative serum amyloi
KGGALEAVK	(T)	896.495	A0A120D7.	A0A120D7.	Putative serum amyloi
KGGALEAVK	(T)	896.495	A0A120D7.	A0A120D7.	Putative serum amyloi
KGGALEAVK	(T)	896.495	A0A120D7.	A0A120D7.	Putative serum amyloi
LAAEVISNAI	(E)	1043.584	A0A6G1P8\	A0A6G1P8\	Serum amyloid A prote
LAAEVISNAI	(E)	1043.584	A0A6G1P8\	A0A6G1P8\	Serum amyloid A prote
LAAGVISDVR	(E)	1073.574	A0A087T1\	A0A087T1\	Serum amyloid A prote
LAAGVISDVR	(E)	1073.574	A0A087T1\	A0A087T1\	Serum amyloid A prote
LAKDWGRR	(G)	987.512	A0A2K6EY\	A0A2K6EY\	Serum amyloid A prote

LDQEANRWGRR	(G)	1400.714	A0A6I9HRC	A0A6I9HRC	Serum amyloid A prote
LDQEANRWGRR	(G)	1400.714	A0A6I9HRC	A0A6I9HRC	Serum amyloid A prote
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BY	A0A2U9BY	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLLDAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLVEAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLVEAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LDVASCLVEAAK	(Q)	1289.677	A0A2U9BV	A0A2U9BV	Serum amyloid A-like p
LEKEK	(Y)	588.371	A0A315BD	A0A315BD	Serum amyloid a prote
LFALDEK	(L)	879.446	A0A0D9QY	A0A0D9QY	Serum amyloid A like 1
LFDLAEK	(L)	879.446	A0A0G2JUI	A0A0G2JUI	Similar to Serum amylc
LFDLAEK	(L)	879.446	A0A0D9QY	A0A0D9QY	Serum amyloid A like 1
LFDLAEK	(L)	879.446	A0A0G2JUI	A0A0G2JUI	Similar to Serum amylc
LFDNAKK	(S)	809.415	A0A452GU	A0A452GU	Serum amyloid A like 1
LFDNAKK	(S)	809.415	A0A452GU	A0A452GU	Serum amyloid A like 1
LFDNAKK	(S)	809.415	A0A452GU	A0A452GU	Serum amyloid A like 1
LFDNAKK	(S)	809.415	A0A452GU	A0A452GU	Serum amyloid A like 1
LFDNAKK	(S)	809.415	A0A452GU	A0A452GU	Serum amyloid A like 1
LFNLR	(E)	602.362	A0A671FZ7	A0A671FZ7	Serum amyloid A prote
LFVLDEK	(L)	879.446	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
LFVLDEK	(L)	879.446	A0A0D9QY	A0A0D9QY	Serum amyloid A like 1
LGETAWSPSYK	(T)	1180.6	A0A0C9SC1	A0A0C9SC1	Putative serum amyloi
LGKNPNHFRPQGLPEK	(F)	1805.94	A0A6I9M4I	A0A6I9M4I	Serum amyloid A prote
LGNDPEHFRPAGLPNKY	(-)	1898.914	F7ANU9	F7ANU9	Serum amyloid A prote
LGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
LIALISPEK	(S)	1041.619	A0A669R1/	A0A669R1/	Serum amyloid A like 1
LIALISPEK	(S)	1041.619	A0A669R1/	A0A669R1/	Serum amyloid A like 1
LIELISHEK	(S)	1041.619	A0A669R1/	A0A669R1/	Serum amyloid A like 1
LIELK	(R)	658.425	A0A120D7.	A0A120D7.	Putative serum amyloi
LIINK	(Y)	634.392	A0A315BD	A0A315BD	Serum amyloid a prote
LLELK	(A)	614.46	R5HKY8	R5HKY8	A( Serum amyloid A prote
LLELK	(A)	614.46	R5HKY8	R5HKY8	Serum amyloid A prote
LLLTCLSQPQMADIWVQR	(I)	2140.158	A0A4X2KG.	A0A4X2KG.	Serum amyloid A like 1
LLLTCMSQTEVASVWVRR	(I)	2131.169	A0A0G2JUI	A0A0G2JUI	Similar to Serum amylc
LLLTCSQSK	(D)	1075.618	A0A1A7WC	A0A1A7WC	Serum amyloid A-like 1
LLNLK	(A)	614.46	R5HKY8	R5HKY8	Serum amyloid A prote
LLNLK	(A)	614.46	R5HKY8	R5HKY8	Serum amyloid A prote
LLNLK	(A)	614.46	R5HKY8	R5HKY8	Serum amyloid A prote
LLNLK	(A)	614.46	R5HKY8	R5HKY8	Serum amyloid A prote











VGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
VGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
VGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
VGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
VGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
VGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
VGWVR	(S)	648.329	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
VIADVR	(E)	688.399	P22000	P22000 Q2	Serum amyloid A-2 pro
VIADVR	(E)	688.399	P22000	P22000 Q2	Serum amyloid A-2 pro
VIADVR	(E)	688.399	P22000	P22000 Q2	Serum amyloid A-2 pro
VICDAREHSQR	(V)	1297.661	A0A2Y9JNC	A0A2Y9JNC	Serum amyloid A prote
VICDAREHSQR	(V)	1297.661	A0A2Y9JNC	A0A2Y9JNC	Serum amyloid A prote
VIIDGR	(E)	646.352	A0A0S1YD:	A0A0S1YD:	Serum amyloid A prote
VISAFR	(E)	705.371	A0A131YN:	A0A131YN:	Serum amyloid A prote
VISDAR	(E)	660.367	P04918	P04918 P1	Serum amyloid A-3 pro
VISDAR	(E)	660.367	P04918	P04918 P1	Serum amyloid A-3 pro
VISDAR	(E)	660.367	P04918	P04918 P1	Serum amyloid A-3 pro
VISDAR	(E)	660.367	P04918	P04918 P1	Serum amyloid A-3 pro
VISDAR	(E)	660.367	P04918	P04918 P1	Serum amyloid A-3 pro
VISDAR	(E)	660.367	P04918	P04918 P1	Serum amyloid A-3 pro
VISDAR	(E)	660.367	P04918	P04918 P1	Serum amyloid A-3 pro
VISDAREGFkr	(I)	1277.696	P20726	P20726 P2	Serum amyloid A-1 pro
VISDARESXR	(V)	1145.627	A0A384BRI	A0A384BRI	Serum amyloid A prote
VISDAREYIQK	(L)	1273.675	A0A2K5CB:	A0A2K5CB:	Serum amyloid A prote
VISDAREYIQK	(L)	1273.675	A0A2K5CB:	A0A2K5CB:	Serum amyloid A prote
VISDGR	(E)	646.352	A0A671KLF	A0A671KLF	Serum amyloid A prote
VISDGR	(E)	646.352	A0A671KLF	A0A671KLF	Serum amyloid A prote
VISDGR	(E)	646.352	A0A671KLF	A0A671KLF	Serum amyloid A prote
VISDGR	(E)	646.352	A0A671KLF	A0A671KLF	Serum amyloid A prote
VISDGREFVQGITQR	(G)	1689.928	A0A498M3	A0A498M3	Serum amyloid A-5-like
VISFPEIGKR	(G)	1161.699	A0A384BSF	A0A384BSF	Serum amyloid A prote
VISLSKLVSCR	(V)	1233.698	A0A452V4I	A0A452V4I	Serum amyloid A prote
VISLSKLVSCR	(V)	1233.698	A0A452V4I	A0A452V4I	Serum amyloid A prote
VISLSKLVSCR	(V)	1233.698	A0A452V4I	A0A452V4I	Serum amyloid A prote
VISLSKLVSCR	(V)	1233.698	A0A452V4I	A0A452V4I	Serum amyloid A prote
VISLSKLVSCR	(V)	1233.698	A0A452V4I	A0A452V4I	Serum amyloid A prote
VISLSKLVSCR	(V)	1233.698	A0A452V4I	A0A452V4I	Serum amyloid A prote
VISLSKLVSCR	(V)	1233.698	A0A452V4I	A0A452V4I	Serum amyloid A prote
VISLSRLASCR	(V)	1233.698	A0A452V4I	A0A452V4I	Serum amyloid A prote
VISLSRLASCR	(V)	1233.698	A0A452V4I	A0A452V4I	Serum amyloid A prote
VISNAREGWQSRVSGR	(G)	1732.872	A0A6J2I0K:	A0A6J2I0K:	Serum amyloid A prote
VISNARENWQSRVSGR	(G)	1859.947	U3K998	U3K998	Serum amyloid A prote
VLADDLAK	(S)	902.483	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
VLAGDLEK	(S)	902.483	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
VLKEGQLSK	(K)	959.552	A0A061I10	A0A061I10	Serum amyloid A prote
VLSFPGPK	(D)	818.477	A0A287AKI	A0A287AKI	Serum amyloid A prote
VSGRGAEATR	(A)	1047.518	A0A091KJC	A0A091KJC	Serum amyloid A prote
VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P1	Serum amyloid A prote

VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P	Serum amyloid A prote
VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P	Serum amyloid A prote
VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P	Serum amyloid A prote
VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P	Serum amyloid A prote
VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P	Serum amyloid A prote
VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P	Serum amyloid A prote
VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P	Serum amyloid A prote
VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P	Serum amyloid A prote
VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P	Serum amyloid A prote
VTDLFK	(H)	722.408	Q2HXZ9	Q2HXZ9 P	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(G)	648.331	A0A6P5CU	A0A6P5CU	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(G)	648.331	A0A6P5CU	A0A6P5CU	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTFDAR	(G)	648.331	A0A6P5CU	A0A6P5CU	Serum amyloid A prote
VTFDAR	(G)	648.331	A0A6P5CU	A0A6P5CU	Serum amyloid A prote
VTFDAR	(E)	648.331	Q5XXU7	Q5XXU7	Serum amyloid A prote
VTHLLK	(F)	688.424	A0A2U3X5, A0A2U3X5,		Serum amyloid A prote
VVDLLLVRDQKCQ	(-)	1583.911	A0A6G1RV, A0A6G1RV,		Serum amyloid A like 1
VVDLLLVRDQKCQ	(-)	1583.911	A0A6G1RV, A0A6G1RV,		Serum amyloid A like 1
VVDLLLVRDQKCQ	(-)	1583.911	A0A6G1RV, A0A6G1RV,		Serum amyloid A like 1
VVDLLLVRDQKCQ	(-)	1583.911	A0A6G1RV, A0A6G1RV,		Serum amyloid A like 1
VVDLLLVRDQKCQ	(-)	1583.911	A0A6G1RV, A0A6G1RV,		Serum amyloid A like 1
VVDLLLVRDQKCQ	(-)	1583.911	A0A6G1RV, A0A6G1RV,		Serum amyloid A like 1
VVDLLLVRDQKCQ	(-)	1583.911	A0A6G1RV, A0A6G1RV,		Serum amyloid A like 1
VVDLLLVRDQKCQ	(-)	1583.911	A0A6G1RV, A0A6G1RV,		Serum amyloid A like 1
VVVANK	(S)	643.45	A0A293M7, A0A293M7,		Serum amyloid A prote
VYRDAAGR	(G)	929.491	A0A151MC, A0A151MC,		Serum amyloid A prote
WAAEISDGGREALQGLTR	(H)	1971.077	A0A2I6QR2, A0A2I6QR2,		Serum amyloid A prote
WIAEVISNAREWIQGMSVR	(G)	2203.108	A0A3Q3NIF, A0A3Q3NIF,		Serum amyloid A prote
WIAEVISNAREWIQGMSVR	(G)	2203.108	A0A3Q3NIF, A0A3Q3NIF,		Serum amyloid A prote
WIAEVISNAREWIQGMSVR	(G)	2203.108	A0A3Q3NIF, A0A3Q3NIF,		Serum amyloid A prote
WIAEVISNAREWIQGMSVR	(G)	2203.108	A0A3Q3NIF, A0A3Q3NIF,		Serum amyloid A prote
WIAEVISNAREWIQGMSVR	(G)	2203.108	A0A3Q3NIF, A0A3Q3NIF,		Serum amyloid A prote
WIAEVISNAREWIQGMSVR	(G)	2203.108	A0A3Q3NIF, A0A3Q3NIF,		Serum amyloid A prote
WIAEVISNAREWIQVMSGR	(G)	2203.108	A0A3Q3NIF, A0A3Q3NIF,		Serum amyloid A prote
WIAEVISNAREWIQVMSGR	(G)	2203.108	A0A3Q3NIF, A0A3Q3NIF,		Serum amyloid A prote





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